# वार्षिक प्रतिवेदन
# ANNUAL REPORT

2019-2020


वै.औ.अ.प.–राष्ट्रीय वनस्पति अनुसंधान संस्थान, लखनऊ

CSIR-NATIONAL BOTANICAL RESEARCH INSTITUTE, LUCKNOW

# वार्षिक प्रतिवेदन
# Annual Report

## 2019-2020

With best compliments from

**Director**

**CSIR-NBRI, Lucknow**


**वै.औ.अ.प.-राष्ट्रीय वनस्पति अनुसंधान संस्थान**

(वैज्ञानिक तथा औद्योगिक अनुसंधान परिषद, नई दिल्ली)

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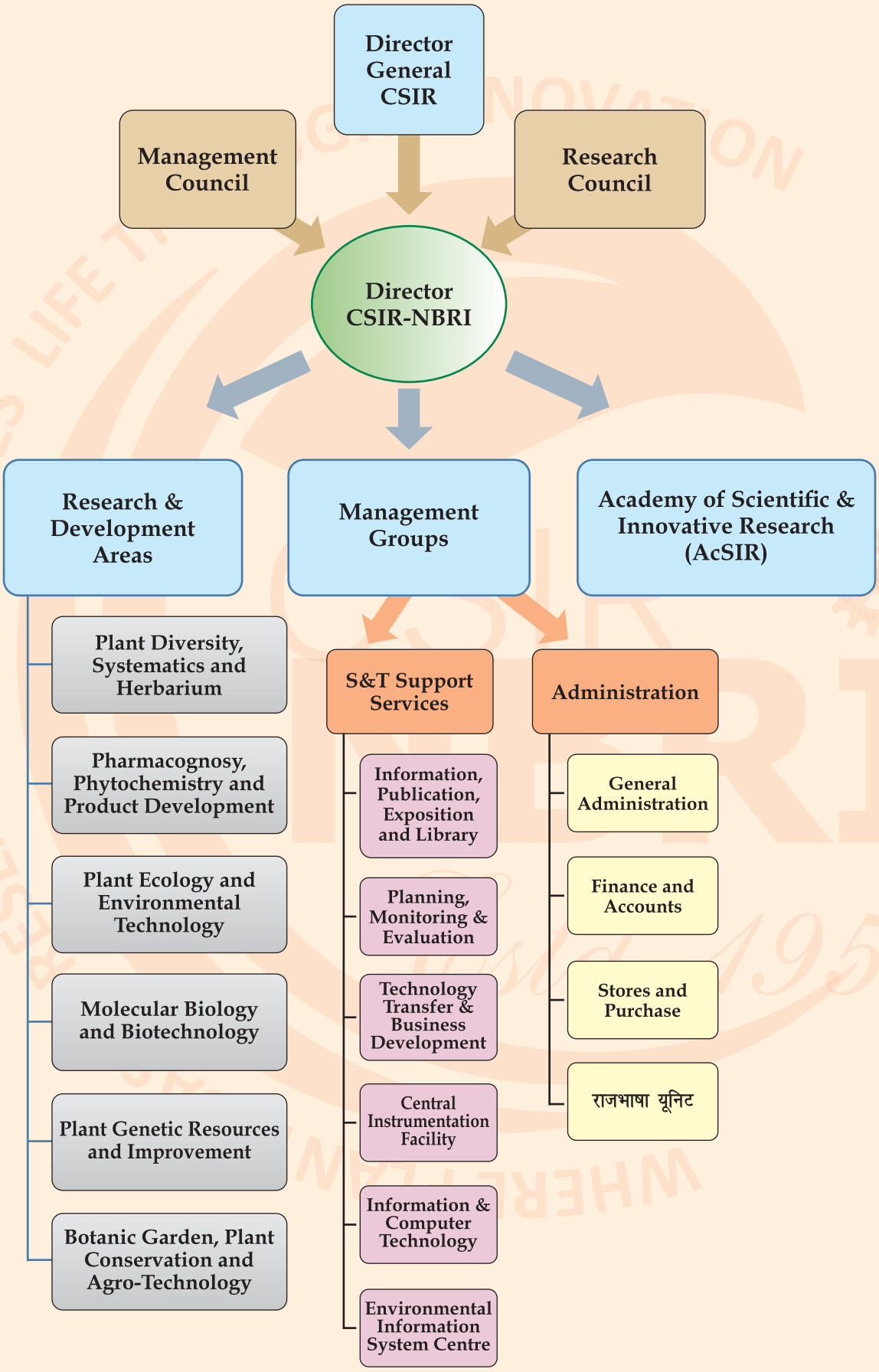
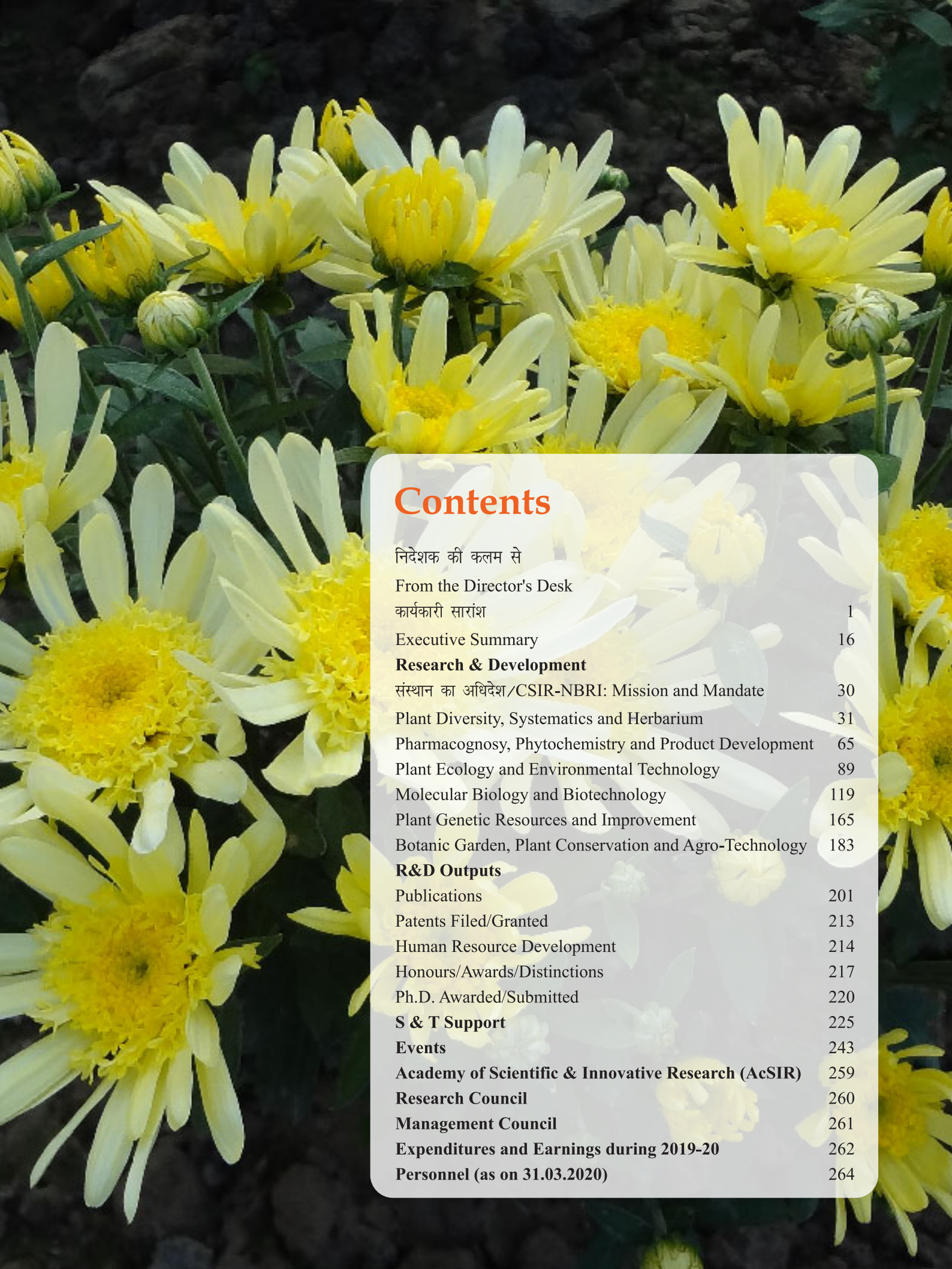
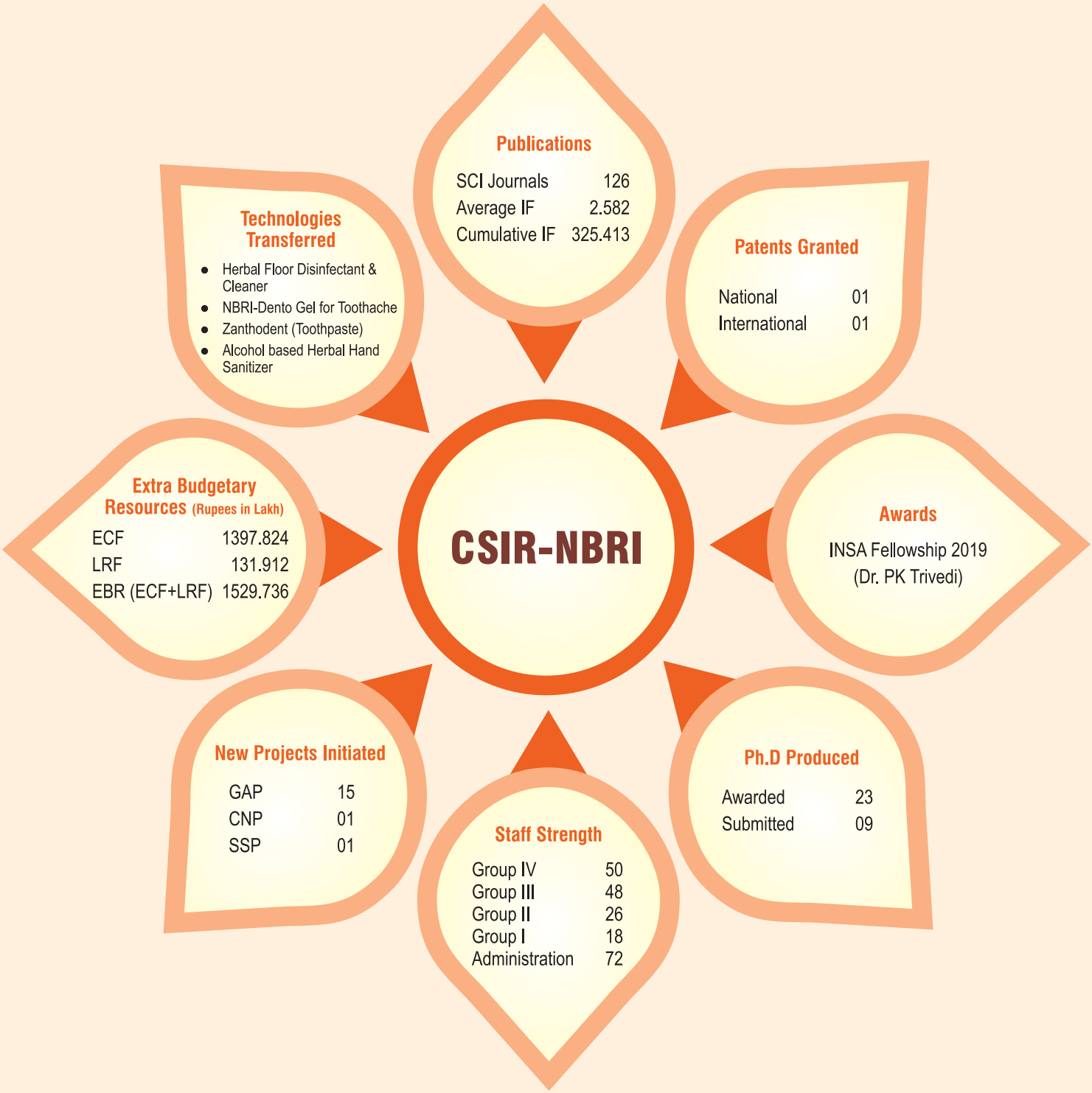
# Organizational Set-Up





# Contents

# Annual Progress At A Glance



# Visit of DG, CSIR, New Delhi

## Maiden visit of Dr. Shekhar C. Mande, DG, CSIR to CSIR-NBRI, Lucknow during May 02-03, 2019
















(A & B) Prof. SK Barik, Director, CSIR-NBRI welcoming Dr. Shekhar C Mande, DG, CSIR, New Delhi; (C & D) Dr. Mande during his visit to Exposition and Herbarium of the institute; (E & F) Dr. Mande addressing scientists and other staff of the institute; (G & H) Launching of the two new herbal products by Dr. Mande, viz. NBRI-URO-Five and NBRI-Dento Gel, a Triple Herbal Hydrogel for Toothache; (I & J) Dr. Mande releasing the three new High thebaine rich Opium Poppy varieties (Developed by CSIR-NBRI) (viz. Ayush, Abha and Madakini) and a natural colour producer *Bixa* variety 'Arunima'; (K & L) Dr. Mande during morning walk at Botanic Garden, CSIR-NBRI with Dr. Rakesh Mishra, Director, CSIR-CCMB, Hyderabad; (M & N) Dr. Mande and Dr. Mishra visiting the 'Touch, Smell and Feel'- a special garden at Botanic Garden, CSIR-NBRI; (O) Dr. Mande and Dr. Mishra visiting dehydrated artifacts developed by the institute

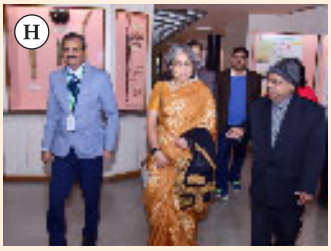
# Visit of DG, CSIR, New Delhi

**Dr. Shekhar C Mande, DG, CSIR on his second visit to CSIR-NBRI, Lucknow along with his wife Dr. (Mrs.) Sharmila Mande during Rose and Gladiolus Show, January 18-19, 2020**















(A & B) Dr. Shekhar C. Mande inaugurating the newly developed Threatened Plant Conservation Centre at DRC, Gehru; (C & D) Dr. Mande planting a Bamboo plant in newly established 'Bambusetum' at DRC, Banthra; (E & F) Dr. Mande inaugurating Cannabis Research & Development Centre and Cannabis Field Farm at DRC, Banthra; (G & H) Dr. (Mrs.) Sharmila Mande, during her visit to Herbarium and Exposition of the institute; (I & J) Dr. Mande at Rose and Gladiolus Flower Show-2020; (K) Dr. (Mrs.) Mande releasing the new variety *Chrysanthemum* 'NBRI-Shekhar'; (L & M) Dr. Mande visiting newly developed Ficus House and Advanced Propagation Unit at Botanic Garden; (N & O) Dr. Mande and Dr. (Mrs.) Mande distributing the prizes to winners of the Flower Show.

# निदेशक की कलम से.....

हम इस वर्ष वै.औ.अ.प.-राष्ट्रीय वनस्पति अनुसंधान संस्थान की 67 वीं वर्षगांठ मना रहे हैं। यह हमारी प्रगति को प्रतिबिंबित करने और पादप विज्ञान में हमारे अधिदेशित अनुसंधान और विकास कार्यक्रमों को निष्पादित करने के लिए ठोस कार्य योजना के साथ आगे बढ़ने का एक उपयुक्त समय है। हमें इस बात पर गर्व है कि संस्थान ने पिछले छह दशकों में भारत के अल्प-प्रयुक्त, गैर-पारंपरिक और वन्य पौधों के आनुवंशिक संसाधनों के प्रलेखन, संरक्षण और सतत उपयोग में महत्वपूर्ण योगदान दिया है। 2019 -2020 के दौरान, वै.औ.अ.प.-रा.व.अ.सं. ने मौलिक अनुसंधान, प्रौद्योगिकी विकास, आउटरीच और मानव संसाधन विकास में उल्लेखनीय प्रगति की।

संस्थान द्वारा पारंपरिक एवं उत्परिवर्तन प्रजनन विधियों (रासायनिक एवं गामा रेडिएशन), आणुविक प्रजनन, जीनोम सुधार एवं पारजीनी तरीकों से विभिन्न पुष्पीय, औषधीय एवं कृषि फसलों की नई किस्मों को तैयार किया जा रहा है। इसके साथ-साथ पादप एवं जैव उपचार तरीकों पर आधारित पर्यावरणीय प्रौद्योगिकियों को भी विकसित किया गया है।

भारत में कई गैर-अन्वेषित वानस्पतिक क्षेत्रों में पादप और शैक विविधता को सूचीबद्ध करने के हमारे प्रयास बहुत प्रगति के साथ जारी रहे। गहन अन्वेषण और आलोचनात्मक वर्गीकरण अध्ययनों ने विज्ञान के लिए छह नई प्रजातियों और भारत के नए भौगोलिक रिकॉर्ड के रूप में 21 प्रजातियों को खोजा। वै.औ.अ.प.-रा.व.अ.सं. के पादपालय (LWG) ने 2200 से अधिक नमूनों के नए परिवर्धन के साथ अपने संग्रह को समृद्ध किया और हजारों आगंतुकों को अनुसंधान, पादप पहचान और प्रमाणीकरण की सुविधा प्रदान की।

पादप-सूक्ष्म जीव संबंध शोध ने हमें कई महत्वपूर्ण सुराग दिए। इनमें से सबसे प्रमुख टमाटर के विल्ट रोग प्रबंधन के लिए *फ्यूसेरियम ऑक्सिस्पोरम* के खिलाफ छह प्रतिरोधी अन्तः-पादपीय जीवाणुओं, *बेसिलस टेकीलेंसिस* (PBE1) (MTCC25188), क्लोरपायरीफॉस के क्षरण के लिए एक शक्तिशाली जीवाणु प्रभेद के रूप में *अल्कालीजीन्स फेसिएलिस* (NBRI OSS2-5), और धान में आर्सेनिक तनाव के संशोधन के लिए एक यीस्ट प्रभेद *डिबेरियोमाइसिस हंसनाई* की पहचान है।

जैव प्रौद्योगिकी और आणुविक जीव-विज्ञान में मौलिक और अनुप्रयुक्त अनुसंधान ने बेहतर उत्पादन, तनाव सहिष्णुता और वर्धित पोषण गुणवत्ता हेतु पादप जींस का उपयोग कर फसल अभियांत्रिकी हेतु नवीन रणनीतियों को विकसित करने में महत्वपूर्ण अंतर्दृष्टि प्रदान किया। CaMV35Es के डबल एनहान्स प्रमोटर के डाउन स्ट्रीम Dhi31 को अभिव्यक्त करने वाली 18 एफीड प्रतिरोधी ट्रांसजेनिक कपास लाइनों का विकास किया गया।

*विथानिया सोम्नीफेरा* से पृथक एक PME जीन, WsPME-26 को व्यक्त करने वाली ट्रांसजेनिक *निकोटियाना टैबैकम* लाइनों ने चबाने वाले (*स्पोडोप्टेरा लिटुरा* और *हेलिकोवर्पा आर्मिजेरा*) और रस चूसने वाले (एफिड और व्हाइटफ्लाइ) दोनों ही कीट/कीटों के खिलाफ 75-85% मृत्यु दर प्रदर्शित की। काबुली चने से कई मजबूत शीघ्र-क्रियाशील वुण्ड-इण्ड्यूसेबल जीन की पहचान की गई।

एक लघु-शृंखला डिहाइड्रोजिनेस/रिड्क्टेज, PsDeHase का कार्यात्मक चित्रण किया गया एवं इसका पैपावरीन जैव-संश्लेषण में शामिल होना प्रदर्शित किया गया। आम में फल पकने से संबंधित दो MAPK जीन की पहचान की गई है और इनका सुगंध के नियमन में शामिल होना प्रदर्शित किया गया। धान में Me-JA प्रेरित आणुविक संकेतन तंत्र और आर्सेनिक विषाक्तता के प्रति सहिष्णुता के महत्व का अध्ययन किया गया। OsMYB-R1 की अधिक-अभिव्यक्ति वाले धान के पारजीनी पौधों ने Cr(VI) और शुष्कता के तहत बढ़ी हुई सहिष्णुता प्रदर्शित की। काबुली चने के एक ग्लूटेराडोक्सिन (CaGrx) जीन (LOC101493651) ने भारी धातु तनाव – AsIII, AsV एवं Cr(VI) के प्रति सहिष्णुता प्रदर्शित की। उपज और तनाव सहिष्णुता में सुधार के लिए टमाटर और कपास में जीनोम-संपादन अध्ययन शुरू किया गया। जड़ की वृद्धि को बदल देने वाले दो जींस *SlWRKY75* और *SlWRKY23* के लिए लगभग 10-15 CRISPR लाइनें विकसित की गईं और मान्यता प्रदान की गई। *गॉसिपियम हर्बेसियम* 'वगड' के पूरे जीनोम अनुक्रम को संकलित और एनोटेट किया गया। *गॉसिपियम हिर्सुटम* के A एवं D दोनों ही उप-जीनोम में कपास के रेशों के विकास की शुरुआत में शामिल पंद्रह HDACs होम्योलोग्स की पहचान की गई। *मूसा एक्युमिनाटा* और *मूसा बल्बिसियाना* में MADS बॉक्स जीन परिवार के विकास और विचलन का भी अध्ययन किया गया।

पादप आनुवांशिक और जीनोमिक संसाधन वृद्धि शोध ने अलसी में प्रमुख वसीय अम्लों जैसे लिनोलेइक अम्ल (एलए) लिनोलेनिक अम्ल (एलएनए), पामिटिक अम्ल (पीए), ओलिक अम्ल (ओए) और स्टेरिक अम्ल (ओ) और ओपियम पॉपी में थीबेन के लिए जिम्मेदार प्रमुख सिंगल न्यूक्लियोटाइड पॉलीमोर्फिस्म (एसएनपी) की पहचान करने में सक्षम बनाया है। 16 लिंकेज समूहों में विभिन्न फाइबर लक्षणों से संबंधित कुल 34 क्यूटीएल की पहचान की गई। संस्थान ने

निम्न टेट्राहाइड्रोकैनाबिनोल (THC) और उच्च कैनाबिडियोल (CBD) कैनाबिस लाइनों को औषधीय उपयोग के लिए और औद्योगिक उपयोग के लिए कम THC एवं उच्च फाइबर कैनाबिस लाइनों के विकास के लिए एक पहल की है। दूरस्थ अनुसंधान केंद्र, बंथरा में एक कैनाबिस केंद्र स्थापित किया गया।

वनस्पति उद्यान और दूरस्थ अनुसंधान केंद्रों ने पुष्पकृषि की लोकप्रिय फसलों की नई किस्मों के विकास, पौधों की विविधता के संवर्धनय पौधों के विविध समूहों के संरक्षणय जननद्रव्य के DUS परीक्षण; प्रशिक्षण, कौशल विकास, आउट रीच कार्यक्रमों और वार्षिक पुष्प प्रदर्शनी आदि के आयोजन से क्षमता निर्माण के क्षेत्र में अपने प्रयासों को बनाए रखा।

वर्ष 2019-2020 के दौरान *क्राइसेंथेमम मोरिफोलियम* (गुलदाउदी) की दो गामा किरण प्रेरित उत्परिवर्ती किस्में 'एनबीआरआई-पुखराज' एवं 'एनबीआरआई-शेखर' विकसित एवं जारी की गईं, साथ ही अन्नाटो (*बिक्सा ओरेलाना*) के एक बेहतर चयन 'अरुणिमा' की पहचान की गई और जारी किया गया। कुछ नई सुविधाएं जैसे 'फाईकस गृह', 'उन्नत प्रसार केंद्र', नवग्रह वाटिका', 'बम्बूसेटम' एवं 'संकट ग्रस्त पौधों के संरक्षण के लिए सुविधा' को वनस्पति उद्यान एवं दूरस्थ शोध केन्द्रों पर स्थापित किया गया। *फाइलेन्थस अमारस, साइपेरस रोटंडस, वायोला पाइलोसा* जैसे औषधीय पौधों और हल्दी की किस्म 'केसरी' के खेती के लिए कृषि प्रौद्योगिकियाँ एवं अच्छी कृषि पद्धतियों के पैकेज विकसित एवं प्रचारित किए गए। छात्रों, किसानों, उद्यमियों आदि सहित 500 से अधिक व्यक्तियों को बागवानी और कृषि-तकनीकों के विभिन्न पहलुओं पर प्रशिक्षण दिया गया। संस्थान ने आठ 'जिज्ञासा' कार्यक्रम आयोजित किए जिसमें 1682 छात्रों और 121 शिक्षकों ने भाग लिया।

वर्ष 2019-2020 के दौरान हमने चार पादप आधारित उत्पादों क्रमशः 'हर्बल फ्लोर कीटाणुनाशक और क्लीनर', दांतदर्द के लिए 'एनबीआरआई-डेंटोजेल', 'जैंथोडेंट (टूथपेस्ट)' और अल्कोहल आधारित हर्बल हैंड सैनिटाइजर जेल' के लिए चार प्रौद्योगिकियों / जानकारी का उद्योगों को हस्तांतरण किया। घाव भरने में तेजी लाने और घाव में संक्रमण को कम करने के लिए एक सरल और सुगम बायोजेनिक सिल्वर नैनोपार्टिकल्स (BSNP) विकसित किया गया। भांग (*कैनाबिस सैटाईवा*) से आयुष फोर्मूलेशन पर आधारित एक शोधन प्रोटोकॉल और मानकीकृत भांग का अर्क बनाने की विधि विकसित की गई।

भारत के विभिन्न विश्वविद्यालयों के स्नातकोत्तर छात्रों को अल्पावधि (3-6 महीने) के प्रशिक्षण/परियोजना कार्य/शोध प्रबंध में 83 छात्रों को पादप विज्ञान और संबंधित विषयों के विभिन्न विषयों में प्रशिक्षण दिया गया। वर्ष 2019-2020 के दौरान छात्रों, विभिन्न विश्वविद्यालयों, स्कूलों और कॉलेजों के छात्रों, किसानों, सामान्य जनता सहित 5000 से अधिक व्यक्तियों ने संस्थान की सुविधाओं जैसे वनस्पति उद्यान, अभिदर्शन और विभिन्न प्रयोगशालाओं का दौरा किया।

2019-2020 के दौरान, वै.औ.अ.प.-रा.व.अ.सं. ने 125 प्रायोजित परियोजनायें संचालित की गयी, 325.413 (IF 2.582 प्रति पेपर) के संचयी प्रभाव कारक के साथ SCI पत्रिकाओं में 126 शोध पत्र/समीक्षा प्रकाशित किए और 23 छात्रों को वैज्ञानिक और औद्योगिक अनुसंधान अकादमी (AcSIR) और भारत के अन्य विश्वविद्यालयों से पीएचडी की डिग्री से सम्मानित किया गया। हमारे वैज्ञानिक डॉ. प्रबोध कुमार त्रिवेदी को भारतीय राष्ट्रीय विज्ञान अकादमी (INSA) फैलोशिप (FNA) 2019 के लिए चुना गया।

मैं 2019-2020 के लिए वै.औ.अ.प.-रा.व.अ.सं. की वार्षिक रिपोर्ट पेश करना अपना सौभाग्य मानता हूँ। इस अवसर पर मैं अपने वैज्ञानिकों, तकनीकी और प्रशासनिक कर्मचारियों और छात्रों में से प्रत्येक को रिपोर्ट में प्रस्तुत उत्कृष्ट उपलब्धियों के लिए बधाई देता हूँ। यह उपलब्धियां वास्तव में प्रशंसनीय हैं और आप में से प्रत्येक के अथक प्रयासों के परिणाम हैं। मुझे विश्वास है कि अधिक तालमेल और उत्साही प्रयासों के साथ हम खुद को विश्व स्तर के पादप विज्ञान केंद्र के रूप में स्थापित करने में सक्षम होंगे। हमें नवाचार के प्रति अधिक समर्पण और उच्च भावना लाने की आवश्यकता है, ताकि हम वांछित लक्ष्यों को प्राप्त करें और वैज्ञानिक और सामाजिक प्रगति की राष्ट्रीय आकांक्षाओं को पूरा करें।

मैं इस संस्थान में विज्ञान एवं तकनीक के प्रबंधन में निरंतर समर्थन, प्रोत्साहन और मार्गदर्शन के लिए वैज्ञानिक और औद्योगिक अनुसंधान परिषद के महानिदेशक डॉ. शेखर सी. मांडे के प्रति अपनी कृतज्ञता व्यक्त करना चाहता हूँ। हम वर्ष 2019-2020 के दौरान दो बार हमारे संस्थान का दौरा करने और हमारे वैज्ञानिकों, छात्रों और कर्मचारियों के साथ वैज्ञानिक बातचीत में सक्रिय रूप से भाग लेने तथा हमें अपनी बहुमूल्य सलाह और ज्ञान के माध्यम से प्रेरित करने के लिए डॉ. मांडे को विशेष रूप से धन्यवाद देते हैं। मैं शोध परिषद के अध्यक्ष प्रोफेसर दीपक पेन्टल एवं शोध एवं प्रबंधन परिषद के सदस्यों का आभार व्यक्त करता हूँ, जिन्होंने हमें अनुसंधान और विकास कार्यक्रमों और संस्थान के प्रबंधन में मार्गदर्शन दिया। हमारे अनुसंधान एवं विकास और आउटरीच गतिविधियों को निष्पादित करने में हमारे शुभचिंतक और सहकर्मी हमेशा उपयोगी सलाह के साथ समर्थन और मार्गदर्शन प्रदान करते रहे हैं। मैं आप सभी को फिर से धन्यवाद देता हूँ और हमारे भविष्य के प्रयासों में आपके निरंतर समर्थन और मार्गदर्शन की आशा करता हूँ।

सरोज बारिक

**(सरोज के बारिक)**
निदेशक

# From the Director's Desk

We are celebrating the 67th anniversary of CSIR-National Botanical Research Institute (CSIR-NBRI) this year. It is an opportune time to reflect on our progress, and move forward with concrete action plan to execute our mandated research and development programmes. We are proud of the significant contributions, which our institute has made over the past six decades in different disciplines of plant science. The institute has contributed significantly towards country's effort to document, conserve and sustainably use the under-exploited and non-traditional wild plant resources. Several new varieties of floricultural, medicinal and agricultural crops have been/are being developed following conventional breeding, mutation breeding (both gamma radiation and chemical), molecular breeding, genome editing, and transgenic approaches. A wide range of need-based environmental technologies following phyto- and microbial remediation approaches have been developed and deployed. CSIR-NBRI made remarkable progress in basic science research, technology and product development, outreach, and human resource development in the year 2019-20.

Our efforts to inventorying plant and lichen diversity in several unexplored areas of the country led to discovery of six new species to science and 21 species as new geographic records to India. The herbarium of CSIR-NBRI (LWG) was enriched with addition of more than 2200 specimens. Thousands of visitors used the herbarium resources for research, plant identification and authentication during the year under report.

Important antagonistic bacterial endophytes viz., *Bacillus tequilensis* (PBE1) (MTCC25188) (against *Fusarium oxysporum* for tomato wilt disease management), *Alcaligenes faecalis* (NBRI OSS2-5) (as a potent bacterial strain for Chlorpyrifos (Chlp) degradation), and a yeast strain *Debaryomyces hansenii* (for amelioration of arsenic stress in rice) were discovered and their effectiveness was established.

Research in biotechnology and molecular biology not only provided mechanistic explanation to several challenging areas of science but also led to develop new strategies for engineering crops for better yield, stress tolerance and enhanced nutritional quality using genes of plant origin. Eighteen aphid resistant cotton transgenic lines, expressing Dhi31 constitutively downstream of the CaMV35Es double enhance promoter were developed. Transgenic *Nicotiana tabacum* lines expressing *WsPME-26*, a PME gene isolated from *Withania somnifera*, showed 75-85% mortality against both the chewing (*Spodoptera litura* & *Helicoverpa armigera*) and sap sucking (Aphid and Whitefly) insect/pests. Several strong early-acting wound-inducible genes were identified from chickpea.

A short-chain dehydrogenase/reductase, PsDeHase has been functionally characterized and shown to be involved in the synthesis of papaverine. Two ripening related MAPK genes have been identified in mango and these were shown to have been involved in regulation of aroma. The mechanisms of Me-JA induced molecular signalling and tolerance towards arsenic toxicity in rice was elucidated. Transgenic rice plants over-expressing OsMYB-R1 were shown to have increased tolerance under Cr (VI) and drought exposure. A chickpea glutaredoxin (CaGrx) gene (LOC101493651) exhibited tolerance during heavy metal stress due to AsIII, AsV, and Cr (VI). Genome-editing studies were initiated in tomato and cotton to improve yield and stress tolerance. About 10-15 CRISPR lines for two genes SlWRKY75 and SlWRKY23 that alter root growth were developed and validated. The whole genome sequence of *Gossypium herbaceum* 'Vagad' was assembled and annotated. Fifteen HDACs homoeologs involved in cotton fibre initiation were identified in each of the A and D sub-genomes of *Gossypium hirsutum*. The evolution and divergence of MADS box gene family in *Musa acuminata* and *Musa balbisiana* were also studied.

Plant genetic and genomic resource augmentation research group identified key Single Nucleotide Polymorphisms (SNPs) responsible for major fatty acids such as linoleic acid (LA) linolenic acid (LNA), palmitic acid (PA), oleic acid (OA) and steric acid (SA) in Linseed and thebaine in opium poppy. A total of 34 QTLs related

to different fibre traits were identified in 16 linkage groups in *Gossypium hirsutum*. The institute has taken an initaitive for development of low Tetrahydrocannabinol (THC) and high Cannabidiol CBD Cannabis lines for medicinal use, and low THC and high fiber Cannabis lines for industrial use. A Cannabis Research Centre was set up at Distant Research Centre, Banthra.

The Botanic Garden and Distant Research Centres sustained their efforts in development of new varieties of floricultural crops, enrichment of plant diversity, conservation of diverse groups of threatened plants, DUS testing of germplasm in respect of three floriculture crops, capacity building by organizing training and skill development programmes, undertaking out-reach programmes and organizing Annual Flower Shows. During the year 2019-2020, two gamma-ray induced mutant varieties of *Chrysanthemum morifolium* viz. 'NBRI- Pukhraj' and 'NBRI-Shekhar' were developed and released, and an improved selection of Annato (*Bixa orellana* L.) viz. 'Arunima' was identified and released. A few new facilities such as 'Ficus House', 'Advanced Propagation Centre', 'Navgrah Vatika', 'Bambusetum', and 'Facility for conservation of threatened plants' were established at the Botanic Garden and Distant Research Centres. Agrotechniques and packages of good agricultural practices were developed and popularized for cultivation of medicinal plants such as *Phyllanthus amarus*, *Cyperus rotundus, Viola pilosa* and Turmeric variety 'Kesari'. More than 500 persons including students, farmers, entrepreneurs and researchers were imparted training on different aspects of gardening and agro-techniques.

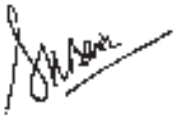
During the year under report, we transferred four technologies/know-how in respect of four plant-based products viz., 'Herbal floor disinfectant and cleaner', 'NBRI-DentoGel for Toothache', 'ZanthoDent (Toothpaste)' and 'Alcohol based herbal hand sanitizer (gel and liquid)' to industry. A simple and facile biogenic silver nanoparticles (BSNP) was developed for wound healing acceleration and suppression of wound infections. A Shodhan protocol and preparation of standardized Cannabis extract, based on AYUSH formulation, was developed from *Cannabis sativa*.

The Institute conducted eight 'Jigyasa' programms in which 1682 students and 121 teachers participated. Short term (3-6 months) training/project work/dissertation for Post Graduate students of various universities of India was imparted to 83 students in different disciplines of plant science. More than 5000 individuals including research scholars, students from various universities, schools and colleges, farmers, and general public visited the institute's facilities such as botanic garden, exposition and various laboratories during 2019- 2020.

During 2019-2020, CSIR-NBRI implemented 125 sponsored projects, published 126 research papers in SCI journals with a cumulative impact factor of 325.413 (IF 2.582 per paper), and 23 students were awarded PhD degree by the Academy of Scientific and Industrial Research (AcSIR) and other Universities of India. Our scientist, Dr. Prabodh Kumar Trivedi was elected as Fellow of Indian National Science Academy (INSA) in the year 2019.

It is my privilege to present before you the Annual Report of CSIR-NBRI for the year 2019-2020. I take this opportunity to congratulate each one of my scientific, technical and administrative staff, and students for their excellent accomplishments as reflected in the report. I am confident, that with more synergestic and enthusiastic efforts by each one of us, we shall be able to position ourselves as a world class plant science research centre. We need to dedicate more quality time towards our research and bring in greater innovation to our science, so that we achieve the desired goals and fulfil the national aspiration.

I would like to express my sincere gratitude to Dr. Shekhar C. Mande, the Director General of Council of Scientific and Industrial Research for his continued support, encouragement and guidance in maintaining the highest possible standard of S&T in CSIR-NBRI. I specially thank him for taking keen interest in our works, and visiting our Institute twice during 2019-2020. During his visits, he actively interacted with our scientists, students and staff, and motivated us through his valuable advice and words of wisdom. I wish to thank Prof. Deepak Pental, the Chairman, Research Council and all the members of our Research and Management Councils for guiding and shaping our R&D programmes and management of the Institute. I thank our industry partners, funding agencies and well-wishers for their continued support and guidance. We look forward to receive greater cooperation than ever from all our stakeholders in our future endeavours.



**Saroj K Barik**
Director

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पौधों की दुनिया की बहुआयामी विविधता की खोज और पादप जीवन के संरचनात्मक और कार्यात्मक पहलुओं को समझना आज पादप विज्ञान की प्रमुख चुनौतियां हैं। एक पादप जीवविज्ञानी के लिए इस विविधता को समझने की चुनौती केवल पौधों, कवक और रोगाणुओं में विविधता की खोज, उनके वर्णन, दस्तावेजीकरण और संरक्षण तक ही सीमित नहीं है, बल्कि उनमें उपयोगी गुणों की पहचान करना भी है, ताकि देश और उसके नागरिकों की बढ़ती जरूरतों और आकांक्षाओं को पूरा किया जा सके। लखनऊ स्थित वै.औ.अ.व.–राष्ट्रीय वनस्पति अनुसंधान संस्थान (वै.औ.अ.व.–रा.व.अ.सं.) 1953 में अपनी स्थापना के बाद से ही पादप विज्ञान के बुनियादी एवं व्यावहारिक वानस्पतिकी और संबद्ध विषयों, दोनों ही में नवीन अनुसंधान और विकास कार्य में लगा हुआ है। संस्थान के अनुसंधान, विकास और आउटरीच कार्यक्रमों का प्रमुख मिशन भारत की पौधों की विविधता और इसके व्यवस्थित प्रलेखन, संरक्षण, जैव–पूर्वेक्षण और मानव कल्याण एवं सतत विकास के लिए ज्ञान आधार को समृद्ध करना रहा है। वै.औ.अ.व.–रा.व.अ.सं. 67 से अधिक वर्षों के अपने समर्पित प्रयासों के माध्यम से वर्गिकी, पारिस्थितिकी, पर्यावरण जीव–विज्ञान, पादप रासायनिकी, भेषज विज्ञान, शरीर विज्ञान, जैव प्रौद्योगिकी, आणुविक जीव विज्ञान, बागवानी और संरक्षण जीव विज्ञान जैसे विविध विषयों में पारंपरिक और अत्याधुनिक अनुसंधान का कार्य करते हुए भारत में एक प्रमुख पादप अनुसंधान केंद्र के रूप में उभरा है। संस्थान पादप संसाधनों की पहचान, दस्तावेजीकरण और संरक्षण से लेकर जैव–पूर्वेक्षण के माध्यम से नए हर्बल, जैव–प्रौद्योगिक, सूक्ष्मजैविक एवं कृषि–बागबानी प्रौद्योगिकियों के विकास और औद्योगिक उपयोग और सामाजिक लाभ के लिए उत्पाद जैसे विभिन्न क्षेत्रों में वैज्ञानिक एवं तकनीकी सेवाएं प्रदान करता है।

वर्ष 2019–2020 वै.औ.अ.व.–रा.व.अ.सं. के लिए एक और उत्पादक वर्ष था। वर्ष के दौरान संस्थान ने अनुसंधान, विकास और आउटरीच गतिविधियों में कई महत्वपूर्ण योगदान दिए हैं। इन उपलब्धियों का संक्षिप्त विवरण निमन्वत है:

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संस्थान में पादप विविधता और वर्गिकी शोधों के अंतर्गत भारत के अन्वेषित/गैर–अन्वेषित क्षेत्रों के पौधों और शैकों के विविध समूहों के साथ–साथ इनसे जुड़े पारंपरिक ज्ञान के प्रलेखन, वर्गिकी पुर्नअध्ययनों, आर्थिक एवं वर्गिकी के रूप से महत्वपूर्ण पौधों के आणुविक अध्ययनों तथा भारत के विभिन्न पादप–भौगोलिक क्षेत्रों से संग्रहों को जोड़कर संस्थान के पादपालय को भी समृद्ध करने की दिशा में कार्य किए जा रहे हैं। उत्तर प्रदेश के सुहेलवा वन्यजीव अभयारण्य में पौधों और शैकों की खोज के कार्य को जारी रखा गया और शैवाल के चार वर्गों की 22 जातियों के अंतर्गत 35 प्रजातियों, ब्रायोफाइट्स की 10 कुलों की 13 जातियों के अंतर्गत 20 प्रजातियों, टेरिडोफाइट्स की पाँच कुलों की पाँच जातियों के अंतर्गत छह प्रजातियों तथा शैकों की 14 कुलों की 20 जातियों के अंतर्गत 30 प्रजातियों को इस वर्ष के दौरान प्रलेखित किया गया। सुहेलवा वन्यजीव अभ्यारण्य से एकत्र किए गए पौधों और शैक प्रजातियों के विस्तृत वर्गीकरण और वितरण संबंधी विश्लेषण में शैवाल की एक प्रजाति, शैक की 12 प्रजातियों और ब्रायोफाइट्स की पांच प्रजातियों के उत्तर प्रदेश में नवीन वितरण की जानकारी प्राप्त हुई। पूर्वोत्तर भारत के असम और मेघालय में ग्रिड– आधारित मात्रात्मक सर्वेक्षण में असम के पांच जिलों में 16 कुलों की 34 जातियों के अंतर्गत शैक की 138 प्रजातियों को देखा गया, जिसमें 37 प्रजातियाँ असम और 131 प्रजातियाँ खासी एवं जयंतिया में प्रथम बार दर्ज की गईं, जिनमें मेघालय में प्रथम बार देखी गईं 98 प्रजातियां शामिल हैं। मेघालय में इसी तरह के ग्रिड–आधारित सर्वेक्षणों में ब्रायोफाइट्स की 173 प्रजातियों की पहचान की गई जिसमें से नौ प्रजातियां उत्तर–पूर्व भारत में और 20 प्रजातियां मेघालय के लिए नई पाई गईं। मेघालय में 26 ग्रिडों में टेरिडोफाइट्स सर्वेक्षण में 28 कुलों के तहत 52 जातियों से संबंधित 67 प्रजातियों के वितरण का पता चला। पचमढ़ी बायोस्फीयर रिजर्व, मध्य प्रदेश में टेरिडोफाइट्स के सर्वेक्षण के परिणामस्वरूप 41 जातियों के अंतर्गत 52 प्रजातियों को प्रलेखित किया गया।

जिम कॉर्बेट नेशनल पार्क, उत्तराखंड में ऋतु–आधारित सर्वेक्षणों में 128 प्रजातियों की पहचान की गयी जिनमें से एक दुर्लभ प्रजाति *ऊकार्डियम स्ट्रेटम* को भारतीय उप–महाद्वीप में नौ दशकों के बाद देखा गया।

लखनऊ और आसपास के पांच जिलों (बाराबंकी, सीतापुर, हरदोई, उन्नाव और रायबरेली) की वनस्पतियों का सर्वेक्षण जारी रखा गया और शाकीय पौधों की सूची तैयार की गई जिसमें 71 कुलों की 340 जातियों के तहत 457 प्रजातियां शामिल हैं। विभिन्न वन क्षेत्रों के साथ–साथ महाराष्ट्र के विदर्भ क्षेत्र में नागपुर, भंडारा और गोंदिया जिलों में खेती और परती भूमि के अंतर्गत आने वाले क्षेत्रों का सर्वेक्षण किया गया और पुष्पीय पौधों के 79 कुलों की 242 जातियों के अंतर्गत 324 प्रजातियों की पहचान की गई। इसी तरह, हिमाचल प्रदेश, जम्मू एवं कश्मीर और उत्तराखंड के पश्चिम हिमालयी क्षेत्र में सर्वेक्षण के दौरान घास की 55 जातियों से संबंधित 170 प्रजातियों का संग्रह किया गया।

उत्तर प्रदेश के एस्टेरेसी व यूफोरबिएसी कुलों व खेती वाले दलहनी पौधों का वर्गिकी अध्ययन और विविधता आंकलन का कार्य आरंभ किया गया। पहली बार, सिक्किम हिमालय के 102 विदेशी पौधों की प्रजातियों की एक सूची तैयार की गई है, जिसमें द्विबीजपत्री पौधों के 30 कुलों की 75 जातियों के अंतर्गत 93 प्रजातियाँ एवं एकबीजपत्री पौधों की तीन कुलों की सात जातियों के अंतर्गत नौ प्रजातियां सम्मिलित हैं।

महाराष्ट्र के यवतमाल जिले में नृवंशविज्ञान संबंधी सर्वेक्षणों और अध्ययनों के दौरान आठ नए पवित्र वन–स्थलों की खोज की गई। इन पवित्र वन–स्थलों से औषधीय पौधों की लगभग 126 प्रजातियों, 22 सजावटी प्रजातियों, 17 जंगली खाद्य प्रजातियों, छह तेल उत्पादक एव चारे की 15 प्रजातियों को प्रलेखित किया गया। इसी तरह, मध्य प्रदेश के झाबुआ जिले में भील और भिलाला जनजातियों से त्वचा रोगों के उपचार में औषधीय पौधों के उपयोग पर जानकारी एकत्र करने के लिए सर्वेक्षण किया गया। पौधों के 58 कुलों से संबंधित 103 जातियों की कुल 116 प्रजातियों की पहचान की गई, जिनका उपयोग 21 विभिन्न त्वचा संबंधी विकारों के उपचार में किया जाता है। उत्तर प्रदेश के विभिन्न तराई जंगलों में सर्वेक्षण के परिणामस्वरूप 50 उपयोगी पौधों की प्रजातियों का संग्रह और उनसे संबंधित पारंपरिक ज्ञान का व्यवस्थित प्रलेखन किया गया।

आर्थोनिएल्स, *बुएलिया, पाइरेनोकार्पस, रिनोडिना* (शैक); निएसी, मार्केन्शिएल्स (ब्रायोफाइट्स); आर्टिकेसी की जनजाति *बोहमेरी, डेस्मोडियम, जेरेनियम, रिंकोसिया* और *सैक्सीफरेगा* (पुष्पीय पौधे) एवं *जूनीपेरस* (जिमनोस्पर्म) की वर्गिकी के संशोधन अध्ययन किए गए। शैक जाति *शिस्माटोमा* के भारत में विवरणों की जांच की गई और अंततः देश की वानस्पतिक सूची से बाहर किया गया।

*प्लैटीग्राफा एटोमेल्ला* स्टर्ट. पर आधारित एक नए नामकरण संयोजन *फ्लिक्टिस एटोमेल्ला* (स्टर्ट.) एस. जोसेफ व अन्य का प्रस्ताव किया गया और चार प्रजातियों को इसमे समाहित किया गया। पाइरोनोकार्पस शैक के संशोधन अध्ययनों ने 12 कुलों की 49 जातियो से संबंधित 396 प्रजातियों को मान्यता दी। अध्ययन ने भारत में नए वितरण रिकॉर्ड के रूप में नौ प्रजातियों की सूचना दी। शैक जातियों *बुएलिया* और *रिनोडिना* पर वर्गिकी अध्ययन ने दोनों जातियों के अंतर्गत प्रत्येक में पाँच प्रजातियों के साथ भारत में 10 नए वितरण रिकॉर्ड की जानकारी दी।

भारतीय हिमालयी क्षेत्र के एक महत्वपूर्ण औषधीय पौधे *बर्जेनिया सिलियाटा* में दो एसपीएआर मार्करों क्रमशः डाइरेक्ट एंप्लीफिकेशन ऑफ मिनीसैटेलाइट रीजन डीएनए (डीएएमडी–9 प्राइमर) एवं इंटर सिंपल सीक्वेंस रिपीट्स (आईएसएसआर–15 प्राइमर) का उपयोग कर आनुवंशिक परिवर्तनशीलता और जनसंख्या संरचना का अनुमान लगाया गया। जम्मू और कश्मीर, हिमाचल प्रदेश, उत्तराखंड, पश्चिम बंगाल और सिक्किम से पौधों की 11 आबादियों से जुड़े 111 नमूनों के अध्ययन में *बर्जेनिया सिलियाटा* में दो आनुवंशिक समूहों के साथ प्रजातियों और जनसंख्या के स्तर पर मध्यम स्तर की आनुवंशिक विविधता और एक कमजोर आनुवंशिक संरचना का पता चला। एक अन्य अध्ययन में, 'सोप नट पौधे' (*सैपिंडस इमर्जिनैटस*) की भविष्य की संभावित वितरण सीमा और इसके वितरण को सीमित करने वाले जैव–रासायनिक चरों की जांच की गई और विभिन्न पारिस्थितिक निश मॉडल (ईएनएम,बायोक्लाइम एवं मैक्सएंट) का प्रयोग करते हुए

रियल अकरेंस डेटा (n = 88 स्थान) पर इन चरों के लिए अनुकूली फिटनेस और जीनोमिक लचीलेपन का मूल्यांकन किया गया। एएफएलपी मार्करों और मार्कर–पर्यावरणीय संघों के साथ, एएफएलपी–संबंधित बायेसियन आंकड़ों का उपयोग करते हुए आनुवंशिक परिवर्तनशीलता के आंकलन के द्वारा प्रजातियों के अनुकूली फिटनेस का मूल्यांकन किया गया। दक्षिण प्रायद्वीप जैव–भौगोलिक क्षेत्र की निशों को *सैपिंडस इमर्जिनैटस* के अस्तित्व के लिए सबसे उपयुक्त होने की भविष्यवाणी की गई। उच्च विषमता (0.40–0.43) और उच्च–जनसंख्या परिवर्तनशीलता (91.63±0.31%) के संयोजन ने प्रजनन सफलता बनाए रखने के लिए *सैपिंडस इमर्जिनैटस* में उच्च अनुकूली फिटनेस की पुष्टि की।

*बेटुला, सिट्रस, कॉमिफोरा, डिडिमोकार्पस, हेंकेलिया, एनसेटे, जिमनेमा, जूनिपेरस* और *यूरेरिया* के आणुविक वर्गिकी, वंशावली एवं वंश–भौगोलिकी अध्ययन प्रगति पर हैं।

वर्गिकी अनुसंधान प्रयासों से सबसे महत्वपूर्ण परिणाम छह नई प्रजातियों की खोज और भारत में 21 प्रजातियों के नए वितरण रिकॉर्ड सम्मिलित हैं। इस वर्ष खोजी गयी नवीन प्रजातियों में सम्मिलित हैं: भारत के मणिपुर, म्यांमार के चिन राज्य एवं उत्तर एवं पश्चिम थाईलैंड से पुष्पीय पौधे की प्रजाति *हेटेरोस्टेम्मा बारिकियाना* पी. अग्निहोत्री एवं अन्य (एपोसाइनेसी), तीन शैक प्रजातियाँ क्रमशः *आयोप्लाका रिनोडीनोयडिस* एस. वाई. कोंद्र व अन्य, *लेट्रोयटिया असमाना* एस. वाई. कोंद्र व अन्य, *रूसावस्किया इंडोचाइनेन्सिस* एस. वाई. कोंद्र व अन्य, एवं उत्तराखंड के गोविंद वन्य जीव अभयारण्य से दो ब्रायोफाइट्सः *कोलोलेज्यूनिया लोबूलोपैपिलाटा* ए. के. अस्थाना, वी. साहू एवं डी. गुप्ता (लेज्यूनिएसी) एवं *पैराल्यूकोब्रायम एनेर्वे* किस्म सिकंडम ए. के. अस्थाना एवं वी. साहू (डाइक्रेनेसी)। भारत के लिए 21 नवीन भौगोलिक वितरण रिकार्डों में 20 शैक प्रजातियाँ क्रमशः *अमंडिनिया एफ्लोरेसेन्स, अमंडिनिया इंकृष्टेंस, एनाइसोमेरीडियम अल्बिडोएट्राम, बैकुलिफेरा ओरोसा, हफेल्लिया डिस्सा, हफ्फेलिया रेगेन्स, रिनोडीना आर्किया, रिनोडीना एस्कोसिकाना, रिनोडीना केपेंसिस, रिनोडीना इसिडिओयडिस, रिनोडीना लेविगेटा, पोरिना एटलांटिका, पोरिना एक्सर्टा, पोरिना सियामेंसिस, पाइरेनूला कोंकास्ट्रोमा, पाइरेनूला क्रूएण्टा, पाइरेनूला डिस्सिमुलांस, पाइरेनूला पाइरेनास्ट्रोस्पोरा, पाइरेनूला रिनोडीनोस्पोरा, पिक्सीन डैक्टाइलोशिमिदार्इय* एवं एक ब्रायोफाइट प्रजाति *ओर्थोनियोन जावेन्से* शामिल हैं।

संस्थान के पादपालय को भारत के राष्ट्रीय जैव विविधता प्राधिकरण द्वारा 'राष्ट्रीय कोष' के रूप में मान्यता प्राप्त है। पौधों के नमूनों के अनेकों संग्रह किए गए हैं और पादपालय नमूना तैयार करने के लिए उनका प्रसंस्करण और पहचान जारी है। इस बीच 2200 से अधिक नमूनों को उनकी उचित पहचान के बाद पादपालय में सम्मिलित किया गया है। पहचान और प्रमाणीकरण प्रमाण पत्र के लिए अन्य संगठनों के शोधकर्ताओं से भी लगभग 25 पौधे प्राप्त किए गए।

दुर्लभ और संकट ग्रस्त पौधों की संरक्षण रणनीतियों का समर्थन करने और बड़े पैमाने पर प्रसार के लिए एक भारतीय स्थानिक ब्रायोफाइट *एंथोसेरोस भारद्वाजाई,* और एक वृक्ष फर्न *साइथिया स्पाइनुलोसा* पर इन विट्रो अध्ययन किए गए। टेरिडोफाइट्स की 13 सजावटी प्रजातियों के 2500 पौधों का बड़े पैमाने पर बिक्री के लिए उत्पादन किया गया। वै.औ.अ.व.–रा.व.अ.सं. के फर्न हाउस में कुछ संकट ग्रस्त प्रजातियों सहित लगभग 67 प्रजातियों के फर्न का रखरखाव और संरक्षण किया गया है। इसके अलावा, संभावित अणुओं हेतु स्क्रीनिंग के लिए *माइक्रोसोरम स्कोलोपेंड्रिया* का बड़े पैमाने पर प्रसार किया गया है। *एस्पलेनियम निडस फर्न* को इन–विट्रो बीजाणु संवर्धन के माध्यम से गुणित किया गया है और इसे फर्न हाउस में सम्मिलित किया गया है।

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कई दवाओं, विशेष रूप से छाल से प्राप्त औषधियों के औषधीय मूल्यांकन में रासायनिक मार्कर के साथ–साथ ऑर्गेनोलेप्टिक लक्षणों, दीर्ध–सूक्ष्मदर्शिक विवरणों, भौतिक–रसायनिक मापदंडों और एचपीटीएलसी/फिंगरप्रिंट प्रोफाइल का उपयोग किया जा रहा है।

*कमीफोरा वाईटाई* और *कमीफोरा अगालोचा* के विभिन्न नमूनों में आरपी–एचपीएलसी के उपयोग द्वारा क्विनिक

अम्ल की मात्रा में भिन्नता की जाँच की गई। *कमीफोरा वाईटाई* और *कमीफोरा अगालोचा* की पत्तियों के जलीय अर्क में एक प्रमुख मेटाबोलाइट के रूप में क्विनिक अम्ल का पता चला था।

*स्पैरैन्थस इंडिकस* एक महत्वपूर्ण आयुर्वेदिक औषधीय पौधा है जो पूरे भारत में चावल के खेतों में खरपतवार के रूप में उगता है। *स्पैरैन्थस इंडिकस* के दो जैव–क्रियाशील यौगिकों यूजेनॉल और बीटा–साइटोस्टारोल के एक साथ एचपीटीएलसी परिमाणीकरण के लिए एक सरल, तीव्र, संवेदनशील और पुनुर्त्पादनीय विधि विकसित की गई थी। एक व्यापक रूप से इस्तेमाल किए जाने वाले पारंपरिक औषधीय पौधे *एलिफेनटॉपस स्केबर* में चार महत्वपूर्ण फेनोलिक यौगिकों, अर्थात् क्लोरोजेनिक एसिड, फेरुलिक एसिड, गैलिक एसिड और प्रोटोकैटेचिन की पहचान की गई और आरपी–एचपीएलसी तकनीक के माध्यम से इसकी मात्रा निर्धारित की गई।

शैक प्रजाति, *अस्निया लोंगिसीमा* के औषधीय अध्ययन ने पेप्टिक अल्सर के उपचार के लिए संभावित चार यौगिकों: 18आर–हाइड्रोक्सी–डाइहाइड्रोएलोप्रोटोलाइकेस्टेरिनिक अम्ल, न्यूरोपोगोलिक अम्ल, बारबैटिक अम्ल, और अस्निक अम्ल की पहचान की। इन यौगिकों की पहचान मास स्पेक्ट्रोमेट्री और एनएमआर स्पेक्ट्रोस्कोपी के माध्यम से की गई। सभी चार यौगिकों ने कोशिकीय विषाक्तता गतिविधि प्रदर्शित की। *अस्निया लोंगिसीमा* से प्राप्त संभावित सुरागों को चूहों में जांचा गया।

प्रमुख रासायनिक मार्कर यौगिकों, जैसे कि जिम्नेमाजेनिन, डिएसील जिम्नेमिक अम्ल, लूप्योल और स्टिग्मास्टेरोल का अनुमान लगाने के लिए भारत के विभिन्न राज्यों से एकत्र किए गए *जिम्नेमा सिल्वेस्ट्रे* के नमूनों की पादप–रासायनिक स्क्रीनिंग की गई। *मैंगीफेरा इंडिका* की पत्तियों से रासायनिक संदर्भ मार्कर, मैंगीफेरिन को अलग किया गया। मैंगीफेरिन में एंटीऑक्सिडेंट, रोगाणुरोधी, एंटीएजिंग, कैंसररोधी और यकृतरक्षण जैसे कई स्वास्थ्य संबंधी गुण होते हैं।

*आर्टेमिसिया अब्सिंथियम* पत्तियों, तने और बीजों से प्राप्त आवश्यक तेल का दीमक प्रतिकर्षण और मृत्यु दर के लिए मूल्यांकन किया गया। पत्तियों से प्राप्त तेल ने तने और बीज की तुलना में सबसे महत्वपूर्ण दीमक प्रतिकर्षण क्रिया प्रदर्शित की और इसे दीमक भगाने के लिए इस्तेमाल किया जा सकता है।

लखनऊ और वाराणसी के मंदिरों से गेंदे (*टैगेटस*) के फूलों (पीले और लाल) को एकत्र किया गया एवं रंग निष्कर्षण प्रक्रिया के मानकीकरण और रंग अणुओं की रासायनिक रूपरेखा के लिए उपयोग किए गए। निकाले गए रंगों को प्राकृतिक अवयवों के साथ मिलाया गया। रंगीन सूखे पाउडर के तैयार मिश्रण में त्वचा से चिपकने की अच्छी क्षमता होती है और इसे नरम पोंछे द्वारा आसानी से हटाया जा सकता है। यह त्वचा के लिए विषैले नहीं हैं।

गुणवत्ता मूल्यांकन हेतु विभिन्न किसानों से एकत्रित हल्दी की पत्ती के तेल के विभिन्न नमूनों का जीसीएमएस के उपयोग द्वारा विश्लेषण किया गया। मौजूद प्रमुख रासायनिक यौगिकों में एल्फा–फेलेण्ड्रींस (32%), टेरपिनोलीन (26%), पी–साइमीन (5.9%) और 1,8 साइनोल (6.5%) शामिल हैं।

भांग (*कैनाबिस सैटाईवा*) से आयुष फॉर्मूलेशन पर आधारित एक शोधन प्रोटोकॉल और मानकीकृत भांग के अर्क बनाने की विधि विकसित की गई।

बायोमार्कर प्रभेद *क्रोमोबैक्टीरियम वायोलेसियम* का उपयोग करके एंटी–कोरम सेंसिंग गतिविधि के लिए एंडोलाइकेनिक कवक (ईएलएफ) (एमईएलई) से निष्कर्षित मेटाबोलाइट्स की जांच की गई। एमईएलई के प्रभाव का मूल्यांकन *स्यूडोमोनास एरुजिनोसा* के उग्र कारकों के उत्पादन और बायोफिल्म के गठन पर भी किया गया। अध्ययन से पता चला कि ईएलएफ, *एस्परगिलस क्वैंड्रिसिंक्टस* में कोरम सेंसिंग को रोकने एवं *स्यूडोमोनास एरुजिनोसा* की बायोफिल्म गठन को रोकने की क्षमता होती है और इसका उपयोग अस्पताल और स्वास्थ्य सुविधाओं के लिए किया जा सकता है।

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पादप पारिस्थितिकी एवं पर्यावरण प्रौद्योगिकी समूह द्वारा किए गए विभिन्न शोध वायु प्रदूषण और जलवायु परिवर्तन की प्रतिक्रिया में पादप पर्यावरण–शारीरिक और

जैवरासायनिक प्रक्रियाओं, वन पारिस्थितिकी तंत्र के संरचनात्मक और कार्यात्मक विश्लेषण, वन जैव–भार एवं वन कार्बन जब्तीकरण, पर्यावरणीय मैट्रिक्स में फ्लोराइड और आर्सेनिक की मॉनिटरिंग एवं सिडेरोफोर स्रावक सूक्ष्म जीवों का उपयोग करते हुए चावल के आयरन एव जिंक बायो–फोर्टिफिकेशन पर केंद्रित रहे। रिपोर्टिंग वर्ष के दौरान समूह की अनुसंधान उपलब्धियों के मुख्य आकर्षण इस प्रकार हैं:

हाई एम्बिएंट ओजोन के तहत एपोप्लास्ट और क्लोरोप्लास्ट प्रोटिओम पर एथिलीनडाईयूरिया (ईडीयू) के प्रभाव के लिए गेहूं की दो किस्मों का मूल्यांकन किया गया। प्रकाश संश्लेषण, कार्बन चयापचय, प्रोटीन उपापचय तंत्र क्षरण, रक्षा और ऊर्जा चयापचय से संबंधित प्रोटीन में शामिल कई क्लोरोप्लास्ट प्रोटीन की पहचान की गई।

उन्नत कार्बन डाईआक्साइड, ओजोन और तापमान की प्रतिक्रिया में भारतीय गांगेय मैदानों की 23 चावल की किस्मों की अनुकूलन रणनीतियों का अध्ययन किया गया। एनडीआर–359 ने सभी परीक्षणों में बेहतर उपज प्रदर्शित की। आजाद बासमती ने उन्नत कार्बन डाईआक्साइड स्थिति में, एनडीआर–3112 ने उच्च आक्सीजन में, जबकि सरजू–52, शांभा सब–1 एवं पंत 12 ने उच्च तापमान में बेहतर प्रदर्शन किया।

कपास में कार्यिकी प्रयोगों से पता चला कि एब्सिसिक अम्ल का अंतर्जात स्तर मुख्य रूप से कपास की पत्तियों में रंध्रों के व्यवहार को बनाए रखता है और पानी की कमी के संकेतों के साथ समन्वय करने के लिए 6–बेंजाइलअमीनोप्यूरिन को रोककर कार्यिकी को नियंत्रित करता है।

यह प्रदर्शित किया गया कि *साइमोप्सिस टेट्रैगोनोलोबा* (ग्वार) पौधों में कार्बन मेटाबोलाइजिंग एंजाइमों की जीन अभिव्यक्ति में परिवर्तनशीलता, सीमित पानी की आपूर्ति के तहत कार्बोहाइड्रेट के संचय को नियंत्रित करती है।

गर्मी के मौसम में मृदा कार्बन डाई आक्साइड एफ्लक्स के लिए उत्तर प्रदेश के तराई क्षेत्र में स्थित कतर्नियाघाट वन्यजीव अभयारण्य में तीन वन समुदायों, शुष्क मिश्रित, साल मिश्रित और सागौन वृक्षारोपण का अध्ययन किया गया। शुष्क मिश्रित और साल मिश्रित वन में हवा और मिट्टी के तापमान में बढ़ोत्तरी के साथ–साथ मृदा कार्बन डाई आक्साइड एफ्लक्स में महत्वपूर्ण वृद्धि देखी गई। एक अन्य अध्ययन में अपुष्पीय पादप विविधता पर ग्लोबल ऑब्जर्वेशन रिसर्च इनिशिएटिव इन अल्पाइन एनवायरमेंट (GLORIA) से अपनाए गए मानक प्रोटोकॉल के आधार पर एक आधार डेटा उत्पन्न किया गया। इस डेटा का उपयोग भारतीय हिमालय में अल्पाइन एकोटोन क्षेत्रों में सामुदायिक संरचना और क्रिया पर सूक्ष्म–जलवायु की कार्यात्मक भूमिका को समझने के लिए किया जाएगा।

उन्नाव जिले के कृषि क्षेत्रों में तीन अलग–अलग मौसमों (मानसून पूर्व, मानसून और मानसून पश्चात) के दौरान *जिया मेस* (मक्का), *कैप्सिकम एनम* (शिमला मिर्च), *गोसिपियम अर्बोरेटम* (कपास), *ओराईजा सैटाइवा* (चावल), और *विग्ना मुंगो* (मूंग) में फ्लोराइड आयन के स्तर का अनुमान लगाया गया।

चावल की चार किस्मों (स्वर्ण सब –1, जयंती, शरबती और BPT–5204) में चार सिडेरोफोर स्रावक सूक्ष्मजैविक प्रभेदों क्रमशः NBRI-D1.2, NBRI-D1.16, NBRI-D1.20, NBRI-D2.16 (क्रमशः *स्यूडोमोनास पुटिडा, स्यूडोमोनास मोहनाई, स्यूडोमोनास* प्रजाति और *स्यूडोमोनास फ्लोरेसेंस*) का उपयोग करके जिंक उर्वरीकरण की दो स्थितियों के तहत जिंक और आयरन अपटेक का तुलनात्मक मूल्यांकन किया गया था। जिंक संशोधित मृदा में प्रयोग किए गए गए सभी चार सूक्ष्मजैविक इनोकुलम की स्थिति में जड़ की लंबाई (आरएल), तने की लंबाई (एसएल) और शुष्क भार (डीडब्ल्यू) में काफी स्पष्ट वृद्धि हुई, जबकि बगीचे की मिट्टी में डाले गए किसी भी सूक्ष्मजैविक इनोकुलम की स्थिति में कोई वृद्धि प्रदर्शित नहीं हुई। जिंक संशोधित मृदा में उगाये जाने पर स्वर्ण सब–1, जयंती, सरबती और BPT–5204 किस्मों में जड़ की लंबाई औसतन 29.19%, 21.87%, 18.92% और 52.33% बढ़ी। स्वर्ण सब–1, जयंती, और BPT–5204 किस्मों में तने की लंबाई में क्रमशः 10.04%, 0.625% एवं 8.65% की वृद्धि देखी गई। इसी प्रकार, स्वर्ण सब–1, सरबती और BPT–5204 किस्मों में शुष्क भार में औसत 25.6%, 54.3% एवं 88.8% की वृद्धि देखी गयी। सामान्य मिट्टी पर उगाए जाने वाले पौधों के मामले में, स्वर्ण सब–1 में *स्यूडोमोनास*

*फ्लोरेसेंस* की स्थिति में उच्चतम आरएल, एसएल और डीडब्ल्यू को देखा गया। दूसरी ओर जिंक संशोधित मृदा में खेती वाले पौधों में, *स्यूडोमोनास मोहनाई* की स्थिति में जयंती किस्म में उच्चतम आरएल और डीडबल्यू को देखा गया। सरबती और जयंती किस्मों में विभिन्न इनोकुलम की स्थितियों में दानों में आयरन के स्तर में क्रमशः 52.2% से 111.6% के बीच वृद्धि हुई है, अनाजों में प्रतिशत में वृद्धि हुई है। अन्य दो किस्मों में, आयरन का उच्च स्तर जयंती किस्म में *स्यूडोमोनास मोहनाई* की स्थिति में (22.3±2.4) तथा सरबती किस्म में *स्यूडोमोनास पुटिडा* की स्थिति में (18.7±2) देखा गया। इसके अतिरिक्त वैकल्पिक रूप से जिंक संशोधित मृदा में उगाये जाने पर जयंती एवं सरबती किस्म में दानों में आयरन मात्रा क्रमशः 59.31% से 28.3% के बीच पाई गई।

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यह समूह व्यावसायिक रूप से मूल्यवान फसलों के रोग प्रबंधन और पर्यावरण के अनुकूल स्थायी उपचार विकसित; जैविक नियंत्रण, पादप सूक्ष्म जीव संबंध और सोडिक मृदा उपचारय कृषि भूमि और तनाव ग्रसित मृदा दोनों के लिए किफायती और कुशल जैव–इनोकुलेशन फॉर्मूले के विकास के माध्यम से खाद्य सुरक्षा और पर्यावरण संरक्षणय विभिन्न फसली पौधों में सूक्ष्मजीव मध्यस्थता के द्वारा अजैविक और जैविक तनाव सहिष्णुता के आणविक तंत्र (तंत्रों) के प्रसार करने पर केंद्रित है। प्रमुख शोध एवं विकास विशेषताएँ निम्नलिखित हैं:

टमाटर विल्ट रोग प्रबंधन के लिए *फ्यूसेरियम ऑक्सीस्पोरम* के खिलाफ रासायनिक फफूंदनाशकों के सबसे प्रभावी और पर्यावरण हितैषी विकल्प के रूप में छह प्रतिरोधी अंतः–पादपीय जीवाणुओं, *बेसिलस टेकीलेंसिस* (पीबीई1) (एमटीसीसी25188) की पहचान की गई है। चावल की विभिन्न किस्मों में शारीरिक, जैव–रासायनिक और आणविक स्तरों पर पोषक तत्वों के तनाव को कम करने के लिए *ट्राइकोडर्मा रीसीआई* के पूरक की जांच की गयी और जैव उर्वरक के रूप में पहचान की गई है। घाव भरने में तेजी लाने और घाव में संक्रमण को कम करने के लिए एक सरल और सुगम बायोजेनिक सिल्वर नैनोपार्टिकल्स (BSNP) विकसित किया गया। यह बीएसएनपी एक मरहम बेस में तैयार किया गया है, और घाव भरने की प्रक्रिया को तेज करने के लिए चूहे के मॉडल में अध्ययन किया गया।

*अराबिडोप्सिस थैलियाना* में नेक्रोट्रॉफिक कवक *अल्टर्नेरिया ब्रैसीकोला* के कारण होने वाले ब्लैक स्पॉट रोग का मुकाबला करने में जैव–अभियांत्रिक सिल्वर नैनोपार्टिकल्स के उपयोग को प्रदर्शित करने के लिए फोलियर स्प्रे के माध्यम से एक अध्ययन किया गया था। क्लोरपाइरीफोस क्षरण करने वाले मृदा सूक्ष्मजीवों की पहचान करने के लिए किए गए एक अन्य अध्ययन से पता चला कि *अल्कलीजींस फीकेलिस* (एनबीआरआई ओएसएस2–5) क्लोरपाइरीफोस के क्षरण के लिए एक शक्तिशाली जीवाणु प्रभेद है। इस प्रभेद को कीटनाशक दूषित स्थलों में पौधे के विकास को बढ़ावा देने और जैव उपचार के लिए उपयोग किया जा सकता है।

*ट्राइकोडर्मा कोनिंजियोप्सीस* एनबीआरआई–पीआर 5 और *ट्राइकोडर्मा एस्परेलम* एनबीआरआई–के 14 के एक ट्राइकोडर्मा संघ के अनुप्रयोग ने लवण तनाव के अंतर्गत धान की जड़ों की शारीरिक और रूपात्मक विशेषताओं में सुधार किया और उपज, बीज आकार और वजन में भी सुधार किया। पोषण तनाव की स्थिति के तहत उगाए गए काबुली चने के पौधों पर प्रयोग किए गए एक पादप वृद्धि प्रेरक *राइजोबैक्टीरिया* (पीजीपीआर), *पैनीबैसिलस लेंटिमोरबस* एनआरआरएल बी–30488 ने उपापचय मार्गों को संशोधित करके पौधो में बेहतर विकास और विकास प्रदर्शित किया। लवण तनाव में उगाए गए धान (*ओराईजा सैटाईवा*) में *बेसिलस एमाइलोलिक्विफैसिएन्स*–एसएन 13 ने रूट ट्रांस्क्रिप्टोम में जीन अभिव्यक्ति में व्यापक परिवर्तन दिखाय तथा जैवभार और कुल घुलनशील शर्करा में उल्लेखनीय वृद्धि देखी गई।

शुष्कता तनाव के तहत उगाए गए काबुली चने के अंकुरों की जड़ों का तुलनात्मक विश्लेषण किया गया। उत्पन्न डेटा का उपयोग शुष्कता सहिष्णु काबुली चने को विकसित करने के लिए आनुवंशिक सुधार कार्यक्रमों के लिए किया जा सकता है। एक सिलिकॉन सॉल्युबिलाईजिंग राइजोस्फेरिक सूक्ष्मजीव (एनबीआरआईएसएसएम) और जड़ संबंधित सूक्ष्म जीव *स्यूडोमोनास पुटिडा* (एमटीसीसी 5279) के आणविक तंत्र को स्पष्ट किया गया। बैसिलस

*एमाइलोलिक्विफैसिएन्स* (एनबीआरआईएसएन13) का अध्ययन किया गया कि यह कैसे *राइजोक्टोनिया सोलेनी* की जैविक तनाव स्थितियों के तहत पादप मेटाबोलाइट प्रणाली को संशोधित करता है। रोगाणुरोधी गतिविधि और रक्षा संकेतन से संबंधित इक्कीस यौगिकों की पहचान की गई।

धान में आर्सेनिक तनाव के संशोधन के लिए एक यीस्ट प्रभेद *डिबेरियोमाइसीज हंसनाई* की पहचान की गई। *डिबेरियोमाइसीज हंसनाई* ने दानों में आर्सेनिक की मात्रा को कम किया और पादप वृद्धि प्रेरक लक्षणों को भी दर्शाया। चावल के भूसे के स्वस्थानिक अपघटन और मृदा स्वास्थ्य में सुधार और साथ ही अगली गेहूं की फसल की उत्पादकता में वृद्धि के लिए एक सूक्ष्मजैविक फोर्मूलेशन विकसित किया गया।

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विभिन्न दृष्टिकोणों से मौजूदा जर्मप्लाज्म/किस्मों में आनुवांशिक स्तर पर होने वाले बदलावों को समझना तथा उत्पन्न जानकारी को बेहतर किस्मों को विकसित करने से बढ़ती जनसंख्या की मांग को पूरा करने के लिए उपज में वृद्धि की जा सकती है। प्रमुख रूप से पादप जीन का उपयोग करके बेहतर उपज, तनाव सहिष्णुता और बेहतर पोषण गुणवत्ता में वृद्धि के लिए इंजीनियरिंग फसलों के लिए नई रणनीति विकसित करने की आवश्यकता है। इन उद्देश्यों के अनुरूप आणुविक जैविकी एवं जैव प्रौद्योगिकी समूह ने उपज और गुणवत्ता के लिए विभिन्न आनुवंशिक निर्धारकों को समझने और किसानों और उपभोक्ताओं के लाभों के लिए पादप जीनों का उपयोग करके बेहतर उपज और गुणवत्ता के लिए बेहतर पौधों की किस्मों को विकसित करने के उद्देश्य से कई अनुसंधान और विकास कार्यक्रमों को आगे बढ़ाया है। इन उद्देश्यों की पूर्ति के लिए विभिन्न फसलों पर जीन–माइनिंग, पारजीनी पादप विकास और जीनोम–संपादन तकनीकों को लागू किया गया। रिपोर्टिंग वर्ष के दौरान समूह द्वारा अनुसंधान और विकास की प्रमुख उपलब्धियों में शामिल हैं:

एक एमओयू के तहत हैदराबाद के टिएरा एग्रोटेक से कपास के 1000 जीनोटाइप का एक बड़ा संग्रह प्राप्त किया गया। यह जीनोटाइप संग्रह समूह में कपास जीनोमिक्स गतिविधि को बढ़ावा देगा और कपास में महत्वपूर्ण कृषि संबंधी लक्षणों को विनियमित करने वाले प्रमुख जीन की पहचान करने में हमारी सहायता करेगा।

कपास जीनोमिक्स के क्षेत्र में, *गोसीपियम हिर्सुटम* के ए और डी उप–जीनोम में से प्रत्येक में कुल 15 एचडीएसी होमियोलोग्स की पहचान की गई। उनमें से, GhHDA5 रेशों की शुरुआत के समय महत्वपूर्ण रूप से अभिव्यक्त हुआ। हिस्टोन डिएसीटेलेज गतिविधि के लिए इन–विट्रो जांच ने संकेत दिया कि GhHDA5 मुख्य रूप से H3K9 एसिटिलेशन मार्क्स को डीएसिलिटेट करता है। RNAi लाइनों में GhHDA5 के डाउन–रेगुलेशन में ChIP–जांच द्वारा मूल्यांकन किए गए कुछ DEG के प्रमोटर क्षेत्र पर H3K9 हाइपर–एसिटिलेशन हुआ। परिणामों ने एचडीए 5 की हिस्टोन मिथाइल ट्रांसफरैस (एचएमटी), एचएसपी और अन्य एचडीएसी के साथ संबंधता प्रदर्शित की। परिणाम बड़े दमनकारी संघ की भागीदारी का संकेत देते हैं जो कपास में रेशों के विकास की शुरुआत को नियमित करते हैं। कपास फाइबर विकास में GhHSP70 और GhHSP90 की भागीदारी की जांच की गई। इन चयनित जीनों के कार्यात्मक जीनोमिक्स का अध्ययन किया जा रहा है। इसके अलावा, GhHMT जो संभवतः जटिल गठन में शामिल है, को क्लोन किया गया और इसके अभिलक्षणन पर कार्य चल रहा है।

एफिड प्रतिरोधी कपास ट्रांसजेनिक लाइनों को विकसित करने के लिए, CaMV35Es के डबल एन्हांस प्रमोटर के डाउनस्ट्रीम Dhi31 को अभिव्यक्त करने वाली 18 ट्रांसजेनिक लाइनों को विकसित किया गया। Dhi31 को निम्न से उच्च स्तर तक व्यक्त करने वाले चौदह ट्रांसजेनिक पौधों का विकास और विश्लेषण किया गया। मध्यम से उच्च व्यक्त ट्रांसजेनिक पौधों के लिए लीफ–डिस्क और टीएसपी के साथ कीट बायोएसे किया गया और 30–80% मृत्यु दर दर्ज की गई। हालांकि, ये पौधे प्रजनन संरचना में असामान्यताओं के कारण अगली पीढ़ी में आगे नहीं

बढ़ सके। इसलिए, ऊतक विशिष्ट तरीके से Dhi31 को व्यक्त करना आवश्यक हो गया। ऊतक (फ्लोएम) विशिष्ट अभिव्यक्ति के लिए जीन को *अराबिडोप्सिस थैलियाना* सुक्रोज सिंथेज 1 (AtSuS11) प्रमोटर के डाउनस्ट्रीम पर क्लोन किया गया। ट्रांसफोर्म्ड कॉटन एक्सप्लेंट्स ने हार्मोन सेलेक्शन मीडिया पर ~ 50–60% कैलस इंडक्शन दिखाया। ये कैली बाद में दैहिक भ्रूण बनाएंगे जो अगले 6–7 महीनों में ट्रांसजेनिक पौधों में विकसित होंगे।

पाथवे संवर्धन और द्वितीयक पादप उत्पादों की अभियांत्रिकी के क्षेत्र में, *पैपावर सोम्नीफेरम* और *विथानिया सोम्नीफेरम* का विस्तार से अध्ययन किया गया। हाल ही में एक लघु–श्रृंखला डिहाइड्रोजनेज / रिडक्टेस, PsDeHase, जो कि पैपावरिन जैवसंश्लेषण में निर्जलीकरण में भाग ले सकता है, को कार्यात्मक रूप से चित्रित किया गया है और इसका पेपावरिन के संश्लेषण में शामिल होना दिखाया गया। फ्लैवोनोयड जैवसंश्लेषण मार्ग में शामिल miRNA और miPEPs का *अराबिडोप्सिस थैलियाना* में CRISPR/Cas दृष्टिकोण का उपयोग करके कार्यात्मक विश्लेषण किया गया। आर्सेनिक तनाव में शामिल होने वाले विभिन्न जीनों की भूमिका को स्पष्ट करने के लिए, *अराबिडोप्सिस थैलियाना* के दो नमूनोंः सल्फर सीमा और As (III) तनाव के प्रति सहिष्णु (Koz2–2) और संवेदनशील (Ri–0), की पहचान की गई और विस्तार से विश्लेषण किया गया।

उपलब्ध ट्रांसक्रिप्टोमिक डेटा की मदद से *विथानिया सोम्नीफेरा* में कुल 46 पीएमई जीन की पहचान की गई। डब्ल्यूएसपीएमई –26 को जैविक तनाव के दौरान सबसे संभावित सक्रिय पीएमई जीन पाया गया। इस जीन का उपयोग करते हुए रचनात्मक और प्रेरक प्रमोटर सिस्टम का उपयोग करके ट्रांसजेनिक *निकोटियाना टैबैकम* को विकसित किया गया। संवेदी अभिव्यक्ति प्रणाली ने प्रयोग के चौथे दिन चबाने वाले (*स्पोडोप्टेरा लिटुरा* और *हेलिकोवर्पा आर्मिजेरा*) और रस चूसने वाले (एफिड और व्हाइटफ्लाइ) दोनों ही तरह के कीटों के खिलाफ 75–85% मृत्यु दर दिखाया, जबकि स्वैच्छिक प्रणाली ने प्रयोग के 6वें दिन मृत्यु दर प्रदर्शित की।

टमाटर की जड़ के अप–रेगुलेटेड *SlWRKY23* जीन को तनाव की स्थिति के तहत जड़ की वृद्धि को नियंत्रित करता पाया गया। यह 300 mM मैनीटोल द्वारा जड़ों में असरदार रूप से प्रेरित होता है और इसकी अभिव्यक्ति ट्रांसजेनिक *अराबिडोप्सिस* में मैनीटोल द्वारा पार्श्व जड़ के और NaCl द्वारा प्राथमिक और पार्श्व दोनों जड़ों के विकास को रोकती है। यह जीन विशेष रूप से टमाटर की रोमिल जड़ों में पार्श्व रूट प्राइमोर्डिया में प्रेरित होता है और मैनिटोल द्वारा दृढ़ता से प्रेरित होता है जो पार्श्व जड़ विकास के नियमन में इसकी भूमिका का संकेत देता है। जड़ के विकास और रचना में सुधार करने के लिए दो जीन, *SlWRKY75* और *SlWRKY23* जो जड़ की वृद्धि को बदलते हैं, को चुना गया। प्रत्येक के लिए लगभग 10–15 CRISPR लाइनों को विकसित और मान्य किया गया है।

कपास और काबुली चने जैसी महत्वपूर्ण फसलों में विभिन्न वुण्ड–इंड्यूसेबल प्रमोटरों के तहत कई कीटनाशक प्रोटीन जीनों की अभिव्यक्ति के लिए, कई मजबूत शीघ्र क्रियाशील वुण्ड–इंड्यूसेबल जीनों को काबुली चने में पहचाना गया। उनकी अभिव्यक्ति की *हेलिकोवर्पा आर्मेजेरा* द्वारा क्रत्रिम शाकाहार की प्रतिक्रिया में में एवं जेए, एथिलीन, एसए, हाइड्रोजन पराक्साइड जैसे अन्य रक्षा संकेतों के जवाब में पुष्टि की गयी। 1.7 से 2 kb लंबाई वाले प्रमोटरों को अलग किया गया है और उनका अध्ययन किया जा रहा है।

ABA प्रतिक्रियाओं द्वारा फल पकने की शुरुआत में परिवर्तन से संबन्धित टमाटर के SlERF6 जीन को, एबीए स्तरों को कम करने एवं इस प्रकार एबीए प्रतिक्रियाओं में सम्मिलित रहने वाले जीनों *SlCYP707A3* और *SlUGT75C1*, दोनों की अभिव्यक्ति को नियमित करने के लिए जिम्मेदार पाया गया। आम में फल पकने से संबंधित दो MAPK जीन की पहचान की गई है और इनका सुगंध के नियमन में शामिल होना प्रदर्शित किया गया। यह समझने के लिए आगे के अध्ययन चल रहे हैं कि ये एमएपी काइनेज, आम और अन्य फलों में सुगंध उत्पादन को कैसे नियंत्रित करते हैं।

धान में Me-JA प्रेरित आणुविक संकेतन और आर्सेनिक विषाक्तता के प्रति सहिष्णुता के महत्व का अध्ययन किया गया। आर्सेनाइट (AsIII; 25-M) तनाव ने धान के अंकुर के समग्र विकास और विकास में बाधा उत्पन्न की। हालाँकि, सह–अनुप्रयोग (25–M AsIII + 0.25 MeM

Me-JA) के परिणामस्वरूप AsIII उपचारित पौधों की तुलना में जैव भार, क्लोरोफिल मात्रा, एंटीऑक्सिडेंट एंजाइम गतिविधियों में बढ़ोत्तरी देखी गयी। सह–अनुप्रयोग ने मैलोंडाईएल्डिहाइड मात्रा, इलेक्ट्रोलाइट रिसाव और कुल AsIII मात्रा (जड़ + तना) के संचय में भी AsIII उपचारित पौधों की तुलना में उल्लेखनीय कमी का प्रदर्शन किया। सह–अनुप्रयोग को डाउनस्ट्रीम जेए सिग्नलिंग पाथवे (*OsCOI*, *OsJAZ3*, *OsMYC2*), AsIII अपटेक (*OsLsi1*, *OsLsi2*, *OsNIP1;1*, *OsNIP3;1*), ट्रांसलोकेशन (*OsLsi6*, and *OsINT5*) एवं विषहरण (OsNRAMP1, OsPCS2 और OsABCC2) में शामिल जीनों की अभिव्यक्ति को भी संशोधित करता पाया गया जिससे आर्सेनिक तनाव का सामना करने के लिए चावल के पौधे की संभावित अनुकूली प्रतिक्रिया का पता लगा। Me-JA को धान में आर्सेनिक अपटेक, स्थानांतरण, विषहरन एवं JA सिग्नलिंग से जुड़े सिग्नलिंग घटकों को संशोधित करके AsIII विषाक्तता को कम करता पाया गया।

अजैविक तनाव चयापचय में शामिल जीनों के कार्यात्मक अभिलक्षणन के क्षेत्र में विभिन्न दृष्टिकोणों का उपयोग किया गया। विभिन्न दृष्टिकोणों का उपयोग करते हुए कई जीनों को कार्यात्मक रूप से अभिलक्षणित किया गया। यह विश्लेषण दृढ़ता से सुझाव देता है कि वुण्ड–इंडयूसिबल और तनाव–प्रतिक्रियाशील OsMYB-R1 ट्रांसक्रिप्शन फैक्टर के हार्मोनल सहसंबंध से एबोटिक [Cr (VI) और सूखा/पीईजी, के साथ–साथ जैविक (राइजोक्टोनिया सोलेनी) तनाव का मुकाबला किया जाता है। OsMYB-R1 की अधिक–अभिव्यक्ति वाले धान के पारजीनी पौधे पार्श्व जड़ों में एक महत्वपूर्ण वृद्धि दर्शाते हैं, जो Cr (VI) और शुष्कता के तहत बढ़ी हुई सहिष्णुता से जुड़ा हो सकता है। इसके विपरीत, इसके कार्य में कमी तनाव सहिष्णुता को कम करता है। OsMYB-R1 अधिक अभिव्यक्त लाइनों में उच्च ऑक्सिन संचय तनाव की स्थिति के तहत पार्श्व जड़ों की सुरक्षात्मक भूमिका को और मजबूत करता है। आरएनए सीक्वेंसिंग डेटा, सैलिसिलिक एसिड सिग्नलिंग अणु कैल्शियम–आश्रित प्रोटीन काईनेसेस के अति–अभिव्यक्ति को प्रकट करता है, जो संभवतः तनाव–प्रतिक्रियाशील डाउनस्ट्रीम जीन (पेरॉक्सिडेसेस, ग्लूटाथियोन एस–ट्रांसफरैसेस, ओस्मोटिंस, हीट शॉक प्रोटीन, रोगजनन संबंधित प्रोटीन) को सक्रिय करता है। परिणाम बताते हैं कि OsMYB-R1 आणविक संकेतन, आंतरिक कोशकीय होम्योस्टैसीस और जड़ संरचना को संशोधित करके कई तनावों की प्रतिक्रिया में ऑक्सिन और सैलिसिलिक एसिड सिग्नलिंग और अन्य जीन के क्रॉस–टॉक को नियंत्रित करने वाले ट्रांसक्रिप्शन फैक्टरों के एक जटिल नेटवर्क का हिस्सा है।

धान के दो ग्लूटेराडोक्सिन (*OsGrx*) जीन (*LOC_Os02g40500* और *LOC_Os01g27140*) को *अराबिडोप्सिस थैलियाना* में सूखे के तनाव में उनकी भूमिका को प्रकट करने के लिए अति–व्यक्त किया गया था। दोनों *OsGrx* जीन की सापेक्ष अभिव्यक्ति ट्रांसजेनिक लाइनों में अधिक थी, जो सूखे के तनाव के दौरान लंबी जड़ें, उच्च बीज अंकुरण और जीवित रहने की दक्षता को दर्शाती थी। शुष्कता सहिष्णुता प्रदान करने के लिए दोनों *OsGrxs* की ट्रांसजेनिक लाइनों के शारीरिक पैरामीटर ($P_N$, $g_s$, E, WUE, qP, NPQ एवं ETR), एंटीऑक्सिडेंट एंजाइम (GRX, GR, GPX, GST, APX, POD, SOD, CAT, DHAR, एवं MDHAR), एंटीऑक्सिडेंट अणु (एस्कॉर्बेट और जीएसएच) और तनाव–प्रतिक्रियाशील अमीनो अम्ल (सिस्टीन और प्रोलिन) के स्तरों में अतिरिक्त रूप से वृद्धि देखी गयी।

भारी धातु के तनाव (AsIII-25-M] AsV-250-M] Cr (VI) -300-M, और Cd-500-M) में भूमिका को प्रकट करने के लिए *एराबीड़ोप्सिस थैलियाना* में काबुली चने के एक ग्लूटेराडोक्सिन (CaGrx) जीन (LOC101493651) को व्यक्त किया गया। CaGrx जीन की सापेक्ष अभिव्यक्ति ट्रांसजेनिक लाइनों में अधिक देखी गयी। ट्रांसजेनिक पौधों ने धातु के तनाव के दौरान लंबी जड़ें, उच्च बीज अंकुरण और जीवित रहने की दक्षता को दिखाया। तनाव मार्करों TBARS, $H_2O_2$ के स्तर, और इलेक्ट्रोलाइट रिसाव को WT की तुलना में ट्रांसजेनिक लाइनों में कम पाया गया जिससे ट्रांसजेनिक लाइनों में कम विषाक्तता का पता चला। सभी भारी धातु उपचारों में, सभी ट्रांसजेनिक लाइनों में Cd को छोड़कर (जो कि बहुत थोड़ा कम हो पाया) AsIII, AsV और Cr (VI) का संचय स्पष्ट रूप से कम हो गया था। ट्रांसजेनिक पौधों में शारीरिक पैरामीटर ($P_N$, $g_s$, E, WUE, *q*P, NPQ एवं ETR), एंटीऑक्सिडेंट

एंजाइम (GRX, GR, GPX, GST, APX, POD, SOD, CAT, DHAR, एवं MDHAR), एंटीऑक्सिडेंट अणु (एस्कॉर्बेट और जीएसएच) और तनाव–प्रतिक्रियाशील अमीनो अम्ल (सिस्टीन और प्रोलिन) के स्तरों में अतिरिक्त रूप से वृद्धि देखी गयी। इस अध्ययन के परिणाम दृढ़ता से इंगित करते हैं कि CaGrx जीन एराबीड़ोप्सिस में धातु तनाव के मॉडरेशन में भाग लेता है।

उपज और तनाव सहिष्णुता में सुधार के लिए जीनोम–संपादन के क्षेत्र में समूह ने विभिन्न फसलों पर अध्ययन शुरू किया। फसल कटाई के बाद लंबे जीवनकाल के लिए, टमाटर में जीनोम संपादन के लिए दो जीन [एल्फा–मैनोसिडेस (α-Man) और बीटा–डी–एन एसीटिलहेक्सोसामिनिडेस (β-Hex), चुने गए। टमाटर में कंस्ट्रक्ट्स को बदला गया और आगे के विश्लेषण के लिए पुष्टिकारक लाइनों का चयन किया गया। पौधे के विकास में संभावित कार्य और पोषण महत्व के अणुओं के संश्लेषण के लिए miR858 को कार्यात्मक रूप से चिह्नित करने के लिए, इस miRNA के परिपक्व और फोल्ड बैक क्षेत्र को संपादित किया गया है और विकसित उत्परिवर्तित पौधों का विस्तार से विश्लेषण किया गया है। संकल्पित/अर्ध संकल्पित सिंपोडियल कपास की किस्मों को विकसित करने के लिए कपास में तीन जीन, MYB1, SELF PRUNING (SP) और SINGLE FLOWER TRUSS (SFT), को जीनोम एडिटिंग के लिए चुना गया है। इस उद्देश्य को पूरा करने के लिए, GhSP और GhSFT दोनों ही जीन के प्रमोटर और जीन अनुक्रमों का इन–सिलिको विश्लेषण किया गया और संभावित क्षेत्रों से gRNA को डिजाइन किया गया है। दानों में कम आर्सेनिक संचय वाली चावल की किस्मों को विकसित करने के लिए, आर्सेनिक परिवहन और संचय में शामिल जीनों (Lsi1, Lsi2, Inositol फॉस्फेट ट्रांसपोर्टर, NIP3 और NRAMP) के sgRNAs का कंस्ट्रक्ट्स विकसित करने हेतु प्रयोग किया गया, धान के पौधों को रूपांतरित किया गया एवं संपादित लाइनें बनाई गईं। आगे का विश्लेषण जारी है। जीनोम एडिटिंग टूल्स का उपयोग करके छोटी अवधि की सरसों की किस्म के विकास के प्रयास भी जारी हैं। भारतीय *एराबिडोप्सिस थैलियाना* में पहचाने गए प्राकृतिक उत्परिवर्ती से पहले से प्राप्त सबूतों के आधार पर, शीघ्र परिपक्वता के लिए जिम्मेदार स्थलों को लक्षित करने के लिए gRNA निर्देशित कंस्ट्रक्ट्स को विकसित किया गया एवं एक पादप रूपान्तरण वेक्टर में क्लोन किया गया तथा सरसों में रूपांतरित किया गया। इस अवधि के दौरान तीन स्थानिक ट्रांसजेनिक लाइनें उत्पन्न की गईं।

कम्प्यूटेशनल जीव–विज्ञान के क्षेत्र में *गॉसेपियम हर्बेसियम* 'वगड' के पूरे जीनोम अनुक्रम को संकलित कर एनोटेट किया गया। इसकी तुलना *गॉसेपियम आरबोरेटम* के जीनोम और *गॉसेपियम हिर्सुटम* के ए–उप–जीनोम के साथ की गई। *सेस्ट्रम नोक्टर्नम* (CS1) और *सेस्ट्रम डाईर्नम* (CS2) में पुष्पन और तनाव के लिए जिम्मेदार miRNAs को इन–सिलिको विश्लेषण द्वारा पहचाना गया। होमोलोगी–खोज आधारित कम्प्यूटेशनल विश्लेषण को जिम्मेदार miRNAs की पहचान और उनके लक्ष्यों के लिए नियोजित किया गया। *मूसा एक्युमिनाटा* और *मूसा बाल्बिसियाना* में MADs बॉक्स जीन परिवार के विकास और विचलन का भी अध्ययन किया गया। इस संदर्भ में पौधों में एचपीटी जीन परिवार के विकास के लिए विशेष संदर्भ के साथ 'दो घटक प्रणाली मॉड्यूल' का विकास भी दो प्रजातियों में किया गया।

## ikni l/kkj d fy, fodkl vkuoa f'kdh vkj thukfed l lk/ku

पादप आनुवांशिक संसाधन एवं सुधार समूह द्वारा किए गए अनुसंधान एवं विकास में प्रमुख तौर पर वन्य और अल्पविकसित फसलों के आनुवांशिक सुधार एवं चयन, आनुवांशिक मानचित्रण, क्यूटीएल, जीडब्ल्यूएएस और फसल सुधार हेतु जीनोमिक्स–सहायक प्रजनन शामिल थे। रिपोर्टिंग वर्ष के दौरान की प्रमुख शोध एवं विकास विशेषताएँ निम्नलिखित हैं:

खेती की ऋतु में विपरीत लक्षणों वाले माता–पिता पौधों में क्रासिंग के द्वारा अलसी की नई मैपिंग आबादीयों के विभिन्न सेटों को विकसित किया गया। ये आबादी F2 पीढ़ी हैं जो अलसी के आर्थिक रूप से महत्वपूर्ण लक्षणों वाले जीन युक्त रीकाम्बीनेंट इनब्रेड लाइनों के विकास के लिए आगे SSD (सिंगल सीड डेसेंड) के माध्यम से F7 / F8 पीढ़ियों तक आगे बढ़ेगी। विभिन्न RIL जैसे.

तेल की मात्रा के लिए RIL Pop- 1: आरकेवाई–14 (उच्च) × केएल–213 (निम्न); आल्टर्नेरिया ब्लाइट हेतु RIL Pop- 2: जेआरएफ–4 (सहिष्णु) × चंबल (संवेदनशील); उपज एवं इससे संबन्धित गुणों हेतु RIL Pop- 3: हीरा (उच्च) × जवाहर–17 (निम्न) एवं पुष्पन/परिपक्वता हेतु RIL Pop- 4: पदमिनी (शीघ्र) × केएल–213 (विलंबित), जो पहले से F8 पीढ़ी में हैं, को एक और पीढ़ी तक बढ़ाया गया ताकि एकसार एवं स्थिर आबादी प्राप्त हो सके।

प्रमुख वसीय अम्लों के लिए अलसी के 86 नमूनों की एसोसिएशन मैपिंग की गई। जीएलएम दृष्टिकोण ने लिनोलिक एसिड (एलए) और पामिटिक एसिड (पीए), लिनोलेनिक एसिड (एलएनए), स्टेरिक एसिड (एसए) और ओलिक एसिड (ओए) के साथ प्रत्येक एसएनपी से जुड़े 2 एसएनपी की पहचान की। एमएलएम दृष्टिकोण में, एलए के साथ 2 एसएनपी और एलएनए, एसए और ओए प्रत्येक के साथ एक एसएनपी जुड़े हुए पाए गए। उपरोक्त 86 नमूने आनुवंशिक विविधता के मूल्यांकन के लिए भारत के 16 अलग–अलग राज्यों से एकत्र किए गए थे।

अलसी के अलावा *लिमोनिया एसिडिसिमा* के 96 नमूनों को भारत के 16 विभिन्न राज्यों से एकत्र किया गया और एसएसआर का उपयोग करके आनुवंशिक विविधता के आंकलन के लिए मूल्यांकन किया गया। इन नमूनों को 3 प्रमुख समूहों यानी क्लस्टर I, क्लस्टर II और क्लस्टर III में वर्गीकृत किया गया। इन 96 नमूनों में से अधिकतम नमूनों (46) को क्लस्टर II में वर्गीकृत किया गया था, जबकि न्यूनतम नमूनों की संख्या (7) क्लस्टर III में मौजूद थी। क्लस्टर II में बड़ी संख्या में नमूनों का वितरण उनकी समान उत्पत्ति और आनुवंशिक समानता को इंगित करता है।

अल्पप्रयुक्त उष्णकटिबंधीय फलीदार पौधे विंग्ड बीन (*सोफोकार्पस टेट्रागोनोलोबस*) के पचहत्तर नमूनों को आगे के उपयोग के लिए संस्थान के वनस्पति उद्यान में उगाया और बनाए रखा गया। इन लाइनों का परिष्कृत बीज–तेल उपयुक्त एवं सोयाबीन के बीज–तेल के साथ तुलनीय हैं। अल्बिनो चूहों पर इस रिफाइंड तेल के सुरक्षा मूल्यांकन में शरीर के वजन, अंग के वजन, हेमाटोलॉजिकल और सीरम जैव–रासायनिक परिवर्तनों के संदर्भ में गैर–महत्वपूर्ण परिवर्तन सामने आए। इसके अलावा *सोफोकार्पस टेट्रागोनोलोबस* के सीड–केक में प्रोटीन (34.7–35.6%), कार्बोहाइड्रेट (21.4–23.1%), पॉलीफेनोल्स (0.45–0.49%), L-DOPA (0.35–0.38%) और फाइटिक अम्ल (0.18–0.23%) की मात्रा देखी गई। ये मूल्य सोयाबीन के बीज–केक के साथ नजदीकी रूप से तुलनात्मक हैं।

अफ्रीकी और एशियाई मूल के सात देशों से संबंधित *सोफोकार्पस टेट्रागोनोलोबस* के 95 नमूनों के बीच आनुवंशिक विविधता को एम्प्लीफाइड फ्रैगमेंट लेंथ पॉलीमोर्फिस्म (AFLP) मार्करों और इंटर्नल ट्रांसकाइब्ड न्यूक्लियर राइबोसोमल डीएनए (nrDNA-ITS) के द्वारा जांच की गई। AFLP मार्करों और फूल, फली और बीज लक्षणों के बीच संबंध जैसे 50% पुष्पन की अवधि (DFW), फली की लंबाई (PDL), फली की चौड़ाई (PDW), हरी फली की लंबाई (GPL), प्रति पौधे फली की संख्या (PDSP), प्रति फली बीजों की संख्या (SDPD), वजन प्रति 100 बीज (SWT) और बीज–तेल मात्रा (SOC) का अनुमान लगाया गया। सात एएफएलपी मार्करों की एसओसी से संबद्ध ता पहचानी गई और न्यूनतम दो एएफएलपी मार्करों को पीडीडब्ल्यू के साथ संबद्ध पाया गया। इन नमूनों के बीच जनसंख्या संरचना विश्लेषण ने उनकी उत्पत्ति के देश के साथ भौगोलिक क्षेत्र के साथ किसी भी संबंध के बिना उप–आबादी को असतत पहचान दी।

'एनबीआरआई–पुखराज' नामक *क्राइसेंथेमम मोरिफोलियम* की एक नई बौनी किस्म विकसित की गई। नई किस्म एक नवीन बौनी, 'नो–पिंच नो–स्टेक', 'एनेमोन' प्रकार की, पुष्पमय गुलदाउदी है जिसमें नवंबर के अंत से जनवरी की शुरुआत में पीले फूल खिलते हैं। नई किस्म उसकी पैतृक किस्म 'हिमांशु' से गामा विकिरण द्वारा उत्परिवर्तन प्रेरण के माध्यम से विकसित किया गया है। किस्म का विमोचन उत्तर प्रदेश सरकार के विधि एवं न्याय मंत्री माननीय श्री ब्रजेश पाठक ने किया।

'एनबीआरआई–शेखर' नाम की *क्राइसेंथेमम मोरिफोलियम* की एक और नई बौनी किस्म को इसके मूल संस्करण 'सु–नील' के गामा विकिरण द्वारा विकसित किया गया। यह एक नवीन, देर से खिलने वाली, पुष्प–आकार में उत्परिवर्ती किस्म है। नई किस्म में माव रंग के फूल लगते

हैं जो दिसंबर के अंत से फरवरी के मध्य तक खिलते हैं। इस किस्म का विमोचन डॉ शेखर सी मांडे की पत्नी एवं गुलाब एवं ग्लैडिओलस पुष्प प्रदर्शनी 2020 के पुरस्कार वितरण समारोह की मुख्य अतिथि डॉ (श्रीमती) शर्मिला मांडे ने किया।

गुलदाउदी की विभिन्न पुष्पीय गामा किरण उत्परिवर्ती लाइनों को परिवर्तित लक्षणों जैसे पंखुड़ियों के रंग, आकार, रंग एवं आकार दोनों, रंग के अलग अलग शेड, विलंबित पुष्पन आदि के आधार पर कटिंग एवं सकर्स के माध्यम से अपनी अगली पीढ़ियों में बढ़ाया गया।

मौजूदा वै.औ.अ.व.–रा.व.अ.सं. जननद्रव्य के अनूठे पुष्प लक्षणों के आधार पर बीस नए अंतर–किस्मी *क्राइसेंथेमम मोरिफोलियम* चयन किए गए हैं। सजावटी लक्षणों के अद्वितीय संयोजनों के साथ जर्मप्लाज्म का विस्तार किया गया है। इन चयनों में विभिन्न मान्यता प्राप्त सजावटी श्रेणियां– 'कोरियन', डबल–कोरियन', 'एनेमोन', 'मिनी', 'डेकोरेटिव', सेमी–क्विल्ड', 'स्टेलेट' और 'सिनेरेरिया' प्रकार शामिल हैं। वै.औ.अ.व.–रा.व.अ.सं. का गुलदाउदी जननद्रव्य देश में उपलब्ध 'गार्डन गुलदाउदी' के सबसे अनोखे आनुवंशिक संसाधनों में से एक है।

*क्राइसेंथेमम मोरिफोलियम* के प्रेरित पुष्पीय म्यूटेंट में उनके सूक्ष्म–आकारिकी पर्ण विशेषताओं जैसे रंध्र आकार, घनत्व एवं रेशों के लक्षण आदि में मौजूद संभावित विभिन्नताओं को खोजने हेतु उनके दैहिक माता–पिता के सापेक्ष SEM अध्ययन शुरू किया गया जो कि विभिन्न पर्यावरणीय तनावों को समझने में भूमिका निभाते हैं।

कई पौधों की प्रजातियों के लिए एसएनपी जीनोटाइपिंग एसे विकसित किया गया है जिसे लिंकेज मैप बनाने के लिए, विभिन्न कृषि संबंधी लक्षणों हेतु क्यूटीएल की टैगिंग और इंट्रोग्रेशन तथा मार्कर असिस्टेड प्रजनन कार्यक्रमों में प्रयोग किया जाता है। कपास (*गॉसिपियम हिर्सुटम*) में इंटरवल मैपिंग और कंपोसिट मैपिंग का उपयोग करके स्पिन लंबाई, एकरूपता, फाइबर लंबाई, बंडल शक्ति, लोच और लघु फाइबर सूचकांक जैसे छह फाइबर लक्षणों के लिए क्यूटीएल विश्लेषण किया गया। 16 लिंकेज ग्रुप (एलजी) में विभिन्न फाइबर लक्षणों से संबंधित कुल 34 क्यूटीएल की पहचान की गई। LG–16 में फाइबर क्यूटीएल की अधिकतम छह संख्या पाई गयी।

जीनोम–वाइड एसोसिएशन (GWAS) का अध्ययन ओपियम पॉपी में किया गया था ताकि संबंधित एसएनपी मार्करों की पहचान की जा सके। GWAS के इस अध्ययन के परिणामस्वरूप प्लांट लेटेक्स और एक महीने के पौधे के पत्तों के नमूनों से थीबेन से जुड़े महत्वपूर्ण एसएनपी पहचाने गए। इन प्रमुख एसएनपी और उनके संबंधित जीनों को थीबेन विकास में इन जीनों की संबद्धता स्थापित करने के लिए एनोटेट किया जा रहा है।

वै.औ.अ.व.–रा.व.अ.सं. में 11 विदेशी जननद्रव्य सहित 221 जननद्रव्य का एक विस्तृत कैनबिस जीन बैंक संग्रह उपलब्ध है। वै.औ.अ.व.–रा.व.अ.सं. के बंथरा रिसर्च स्टेशन में एक कैनबिस सेंटर स्थापित किया गया। संस्थान ने औषधीय उपयोग हेतु कम टेट्राहाइड्रोकैनाबिनोल (THC) और उच्च कैनाबिडियोल CBD कैनबिस लाइनों और औद्योगिक उपयोग के लिए कम THC तथा उच्च फाइबर कैनबिस लाइनों के विकास के लिए पहल की है। विभिन्न कैनाबिडिओइड्स के निर्धारण के लिए एचपीएलसी प्रोटोकॉल स्थापित किया गया है।

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समूह द्वारा अपनाए गए अनुसंधान और आउटरीच कार्यक्रमों की मुख्य विशेषताएं उपलब्धियों की एक विस्तृत श्रृंखला हैं जिसमें रूपात्मक और आनुवंशिक लक्षण वर्णन, क्षेत्र विस्तार, मूल्य संवर्धन और उत्पाद विकास के साथ लोकप्रिय पुष्पकृषि फसलों की नई किस्मों का विकासय पौधों (विशेष रूप से संकटग्रस्त पौधों) की विविधता का संवर्धन, उनके गुणन, जलवायु अनुकूलन, मूल्यांकन और प्रलेखनय विशिष्ट गृहों और क्षेत्र संरक्षणशालाओं में विभिन्न समूह के पौधों का संरक्षण, उनका प्रसार और अभिलक्षणन, जननद्रव्य का डीयूएस परीक्षण, विभिन्न स्तरों पर सजावटी बागवानी में प्रशिक्षण और कौशल विकास कार्यक्रमों के आयोजन द्वारा क्षमता निर्माण, विभिन्न समूहों के लिए विस्तार और संवाद कार्यक्रम तथा वार्षिक पुष्प प्रदर्शनी शामिल हैं।

जननद्रव्य संवर्धन के रूप में कुछ दिलचस्प पौधों अर्थात *वुडफोर्डिया फ्रूटिकोसा, एहरेशिया कैनेरेन्सिस, अब्रस प्रीकेटोरियस* और *कैपरिस जेलेनिका* को महाराष्ट्र और तेलंगाना में क्षेत्र से एकत्र किया गया। आईएआरआई, नई दिल्ली से ग्लैडियोलस की तेरह किस्मों (पूसा श्रीयान, पूसा धनवंतरी, पूसा गुणयान, पूसा बिंदिया, पूसा उर्वशी, पूसा सूर्या किरण, क्रीमी ग्रीन, पूसा शांतिमान, पूसा मोहनी, सांकरी, ऑस्ट्रेलियन फेयर, स्वेता, पूसा किरण) की खरीद की गई एवं वानस्पतिक उद्यान में लगाई गईं।

बोगनविलिया की 11 किस्मों ('ब्लोंडी', 'ड्रीम', 'एलिजाबेथ', 'गार्डन ग्लोरी', 'गोपाल', 'फिलोमन', 'मिसेज ऐलिस', 'महाराज', 'मैरी पामर स्पेशल', 'ओडिसी एवं 'पार्थसारथी') कैना की पांच किस्मों ('पिंक सनराइज', 'किंग सिटी गोल्ड', 'येलो क्वीन', 'एंबेसडर' और 'कैटल्या') और ग्लेडियोलस की 10 किस्में ('अल्डेबरन', 'पेसिफिका', 'प्राहा', 'प्रिसिल्ला', 'रीजेंसी', 'रोज सुप्रीम', 'स्नो प्रिंसेस', 'टाइगर फ्लेम', 'वीडियो', 'येलो स्टोन') के आकारकीय अभिलक्षणन पीपीवी और एफआरए के वर्णनकर्ताओं के अनुसार पूरे हो चुके हैं।

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रिपोर्टिंग वर्ष के दौरान वनस्पति उद्यान और दूरस्थ अनुसंधान केंद्रों में निम्नलिखित नए पादप गृह और सुविधाओं का निर्माण किया गया:

(i) वनस्पति उद्यान में 'फाइकस गृह

(ii) वनस्पति उद्यान में पौधों के उन्नत प्रसार के लिए एक नई सुविधा

(iii) वनस्पति उद्यान में नौ विभिन्न ग्रहों का प्रतिनिधित्व करने वाले पौधों वाली 'नवग्रह वाटिका'।

(iv) दूरस्थ अनुसंधान केंद्र, गेहरु में संकट ग्रस्त पौधों के संरक्षण के लिए एक नई सुविधा।

(v) दूरस्थ अनुसंधान केंद्र, बंथरा में बांस के विभिन्न जननद्रव्य संग्रह युक्त एक 'बम्बुसेटम'

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(i) *क्राइसेंथेमम मोरिफोलियम* की गामा–किरण उत्प्रेरित दो किस्में 'एनबीआरआई–पुखराज' और 'एनबीआरआई–शेखर' विकसित और जारी किए गए।

(ii) अन्नाटो (*बिक्सा ओरेलाना*) के एक बेहतर चयन 'अरुणिमा' की पहचान, DUS लक्षणों के लिए परीक्षण की गई और जारी की गई।

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व्यावसायिक खेती और किसानों के लिए आय सृजन के लिए आंशिक रूप से उपचारित सोडिक मिट्टी की स्थिति में मूल्यांकन के लिए देश के सभी कोनों से कंद किस्मों को एकत्र किया गया था।

बांस की 61 प्रजातियों को भारत के विभिन्न हिस्सों से एकत्र किया गया है और प्रदर्शन, शिक्षा, संरक्षण और संबंधित अध्ययनों के लिए डीआरसी, बंथरा में बम्बुसेटम में बनाए रखा गया है। सोडिक मिट्टी की स्थिति में सफल खेती के लिए सबसे उपयुक्त नमूने का मूल्यांकन करने के लिए अमरन्थ के कुल 94 नमूने एकत्र किए गए और संरक्षित किए गए।

निम्न औषधीय पौधों के खेती के लिए अच्छी कृषि पद्ध तियों के पैकेज विकसित किए गए: *फाइलेन्थस अमारस, साइपेरस रोटंडस, वायोला पाइलोसा* और हल्दी की किस्म 'केसरी'। कृषि–प्रौद्योगिकी और कृषि–अर्थव्यवस्था के लिए बेहतर करकुमा किस्म (किस्मों) का विकास किया गया। बागों की छांव वाली भूमि में खेती के लिए, साथ ही विभिन्न कृषि–जलवायु क्षेत्रों में कृषि–प्रौद्योगिकी हेतु बहु–स्थानीय मूल्यांकन, विभिन्न कृषि–जलवायु क्षेत्रों के लिए पोस्ट–हार्वेस्ट ऑप्टिमाइजेशन सहित कृषि–तकनीक, कृषि–तकनीक पर क्षमता निर्माण और प्रशिक्षण कार्यक्रम, आसवन और मूल्यवर्धन आदि हेतु फसल को लोकप्रिय बनाया गया। केसरी किस्म वै.औ.अ.व.–रा.व.अ.सं. द्वारा विकसित की गई है, जो उच्च प्रकंद पैदावार देने के अलावा, पत्तियों के आवश्यक तेल का स्रोत भी हो सकती है। पत्ती से उच्चतम मात्रा और सर्वोत्तम गुणवत्ता वाले आवश्यक को तेल निकालने के लिए, पत्तियों को तीन अवस्थाओं अर्थातः हरी, आंशिक रूप से जीर्ण और पूरी तरह से जीर्ण, में एकत्र किया गया। पत्तियों का जल–आसवन किया गया। तेल की न्यूनतम मात्रा (0.88%) हरी पत्तियों से प्राप्त हुई जबकि पूरी तरह से जीर्ण

किए गए पत्तों में 1.40% तेल होता है। आवश्यक तेल की अधिकतम मात्रा (1.70%) आंशिक रूप से जीर्ण पत्तियों से प्राप्त हुई। प्रमुख घटक एल्फा–फेलेण्ड्रींस (32%), टेरपिनोलीन (26%), पी–साईमीन (5.9%) और 1,8 सिनोल (6.5%) हैं। हमने जीर्ण पत्तियों से आवश्यक तेल निष्कर्षण के लिए हल्दी की खेती के लिए कृषि प्रौद्योगिकी भी विकसित की है।

दूरस्थ केंद्र, बंथरा में तीन पादप प्रजातियों *टीनोस्पोरा कॉर्डिफोलिया, जिमनेमा सिल्वेस्ट्रे* और *कॉमिफोरा वाइटाई* की गुणवत्ता युक्त रोपण सामग्री यानी के लिए बड़ी मात्रा में गुणन का प्रयास किया गया।

दूरस्थ केंद्र बंथरा में उच्च लिमोनोइड मात्रा के साथ चार बौनी किस्मों का संरक्षण किया गया। इन सभी किस्मों में पत्तियों, फूलों और छालों के आकार, आकार और रंग के आधार पर रूपात्मक अंतर देखे गए। इन किस्मों को मैक्रो (कटिंग के माध्यम से) और माइक्रो (टिशू कल्चर) उत्पादन के माध्यम से उगाने के प्रयास किए गए। नीम संरक्षण स्थल पर क्रमशः मृदा पीएच (8.80), विद्युत चालकता (0.67 dSm–1), मृदा N, P और K (110, 18.5 और 276 किग्रा प्रति हेक्टेयर) का विश्लेषण किया गया। क्लोनल प्रसार के लिए नीम कल्टीवर की कुल 889 कटिंग लगाई गई हैं। कटिंग में जड़ और उत्तरजीविता को बढ़ाने के लिए हमने नियंत्रित परीक्षण के साथ–साथ पौधों के दो हार्मोन (इंडोल एसिटिक अम्ल और जिबेरेलिक अम्ल) और एक जैव उर्वरक (फॉस्फेट सोलुबिलाइजिंग बैक्टीरिया) का उपयोग करके एक प्रयोग भी स्थापित किया। नीम का औसत बीज वजन 71 मिलीग्राम/बीज से लेकर 111.9 मिलीग्राम/बीज के साथ औसतन 92.9 मिलीग्राम/बीज होता है। बीज में तेल की मात्रा 40.2% के औसत के साथ 38% से 43.9% तक थी। इथेनॉल घुलनशील मात्रा 9.7% के औसत के साथ 9.2% से 10.4% तक थी। नीम के बीज के नमूनों में अजादिराक्तिन की मात्रा भिन्न–भिन्न पाई गई।

कार्बनिक पदार्थों के स्रोतों और स्तरों के मानकीकरण के लिए कालमेघ (*एन्ड्रोग्राफिस पैनिकुलाटा*) की खेती हेतु FYM, प्रेसमड और वर्मी–कम्पोस्ट की विभिन्न खुराकों के साथ तीन प्रयोग किए गए। परिणामों से संकेत मिलता है कि पौधे की ऊँचाई, शाखाओं की संख्या, तने का व्यास, पौधे का फैलाव, पौधे का ताजा और सूखा जैवभार, FYM, प्रेसमॉड और वर्मी–कम्पोस्ट की बढ़ती खुराक के साथ बढ़ गया। हालाँकि, यह केवल FYM की 15 टन प्रति हेक्टेयर, प्रेसमड की 7.5 टन प्रति हेक्टेयर और वर्मी कम्पोस्ट की 7.5 टन प्रति हेक्टेयर खुराक तक ही महत्वपूर्ण देखा गया। कालमेघ की जैविक खेती के लिए उपरोक्त खुराक पर्याप्त हैं।

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संस्थान ने औषधीय और सुगंधित प्रकृति के कुछ व्यावसायिक रूप से महत्वपूर्ण प्रमाणित संदर्भ सामग्री (सीआरएम)/संदर्भ सामग्री (आरएम) तैयार करने की पहल की है।

वै.औ.अ.व.–रा.व.अ.सं. को एनएबीएल (नेशनल एक्रीडिएशन बोर्ड फॉर कैलिब्रेशन एंड टेस्टिंग लैब्रोटेरीज) क्वालिटी काउंसिल ऑफ इंडिया (QCI), भारत सरकार से ISO/IEC–17025/2005 की आवश्यकताओं के अनुसार 2008 से मान्यता प्राप्त है। मार्च 2020 में निगरानी ऑडिट के बाद एनएबीएल–गुड़गांव ने ISO/IEC–17025–2017 की आवश्यकताओं के अनुसार 17.10.2020 तक संस्थान के एनएबीएल–एक्रीडिएशन को जारी रखने की सिफारिश की है।

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रिपोर्टिंग के दौरान विभिन्न कार्यक्रमों, प्रशिक्षण सत्रों, आउटरीच गतिविधियों का आयोजन किया गया। छात्रों, किसानों, उद्यमियों आदि सहित 500 से अधिक व्यक्तियों को बागवानी और कृषि–तकनीकों के विभिन्न पहलुओं पर प्रशिक्षण दिया गया। युवाओं, महिलाओं आदि के सशक्तिकरण के लिए घरेलू बागबानी, बोन्साई तैयारी, निर्जलित फूलों की तकनीक पर लघु अवधि प्रशिक्षण सत्र का आयोजन संस्थान के साथ–साथ विभिन्न गांवों में भी किया गया। कुल 83 छात्रों को पादप विज्ञान और संबन्धित विषयों के विभिन्न विषयों में अनुसंधान प्रशिक्षण प्रदान किया गया था। वै.औ.अ.व. और केंद्रीय विद्यालय संगठन की पहल के अंतर्गत संस्थान ने छात्रों और वैज्ञानिकों को जोड़ने के लिए आठ "जिज्ञासा' कार्यक्रम

आयोजित किए जिसमें 1682 छात्रों और 121 शिक्षकों ने भाग लिया। टिशू कल्चर, डीएनए आइसोलेशन और माइक्रोस्कोपी जैसे विभिन्न बुनियादी प्रयोगशाला प्रयोगों को भी कार्यक्रम में शामिल किया गया। विज्ञान शिक्षण क्षमताओं को बढ़ाने के लिए संस्थान द्वारा केंद्रीय विद्यालय के शिक्षकों के लिए एक रिफ्रेशर कोर्स भी आयोजित किया गया। संस्थान के प्रसिद्ध वनस्पति उद्यान की यात्रा ने अनोखे और नवीन पौधों के बारे में जानने का एक शानदार अवसर प्रदान किया। देश के तीसरे सबसे बड़े पादपालय की विशेष यात्रा विज्ञान के छात्रों के बीच जागरूकता पैदा करने का एक बड़ा साधन है। भारत के विभिन्न विश्वविद्यालयों के स्नातकोत्तर छात्रों के अल्पावधि (3–6 महीने) के प्रशिक्षण/परियोजना कार्य/शोध प्रबंध में 83 छात्रों को पादप विज्ञान और संबंधित विषयों के विभिन्न विषयों में प्रशिक्षण दिया गया। वर्ष 2019–2020 के दौरान शोध छात्रों, विभिन्न विश्वविद्यालयों, स्कूलों और कॉलेजों के छात्रों, किसानों, सामान्य जनता सहित 5000 से अधिक व्यक्तियों ने संस्थान की सुविधाओं जैसे वनस्पति उद्यान, अभिदर्शन और विभिन्न प्रयोगशालाओं का दौरा किया।

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2019–2020 के दौरान, वै.औ.अ.व.–रा.व.अ.सं. द्वारा 125 प्रायोजित परियोजनाओं को संचालित किया गया, 325.413 (IF 2.582 प्रति पेपर) के संचयी प्रभाव कारक के साथ SCI शोध पत्रिकाओं में 126 शोध पत्र/समीक्षा प्रकाशित किए और 23 छात्रों को वैज्ञानिक और औद्योगिक अनुसंधान अकादमी (AcSIR) और भारत के अन्य विश्वविद्यालयों से पीएचडी की डिग्री से सम्मानित किया गया। डॉ. प्रबोध कुमार त्रिवेदी को भारतीय राष्ट्रीय विज्ञान अकादमी (INSA) फैलोशिप (FNA) 2019 के लिए चुना गया।

# EXECUTIVE SUMMARY

Discovering the myriad diversity of plant world and understanding the structural and functional complexities of plant life are the major challenges in plant science research. The challenges in plant diversity research are not limited only to discovering, describing, documenting and conserving the diversity of plants, fungi and microbes, but also to identify useful traits in them from human use perspective. The novel genes and biomolecules are to be identified and put to use following genetic engineering and other biotechnological approaches to meet the ever-growing needs and aspirations of our nation. Since its inception in 1953, the CSIR- National Botanical Research Institute (CSIR-NBRI) has been engaged in cutting-edge innovative research both in basic and applied plant sciences. One of the thrust areas of the Institute's research is enriching the knowledge base on plant diversity of India and its systematic documentation, conservation, bioprospection and utilization for human welfare. Through its dedicated efforts of 67 years, CSIR-NBRI has excelled into a premier plant research center in India. It undertakes research in such diverse disciplines as systematic botany, ecology, environmental biology, phytochemistry, pharmacognosy, pharmacology, physiology, biotechnology, molecular biology, horticulture, microbiology and conservation biology. The Institute provides S&T services to various sectors that span from plant identification, documentation and conservation to bioprospection and crop improvement. Plant and microbe-based technologies are developed for environmental amelioration, herbal products are developed for nutraceutical, pharmaceutical and cosmaceutical industries, and plant varieties are developed for improved yield, enhanced secondary metabolite production, and biotic and abiotic stress resistance in target crops. The Institute undertakes floricultural, medicinal and agricultural plant improvement programmes by deploying conventional breeding, mutation breeding (Gamma radiation and Chemical), genome editing, and transgenic approaches. Agro-technologies are standardized for each variety developed and also for putting problematic lands into productive use.

The year 2019-2020 was yet another productive period for CSIR-NBRI. During the year, the Institute made significant contributions in each of its R&D areas and outreach activities. The highlights of these achievements are summarized below:

## Plant diversity exploration and documentation

The plant diversity and taxonomic research at the institute was actively pursued by focusing on survey and documentation of diverse groups of plants and lichens from under-explored/un-explored areas of the country along with associated traditional knowledge. Undertaking taxonomic revisions, molecular systematic studies of economically and taxonomically important plants, and enrichment of herbarium of the institute by adding representative collections from different phyto-geographical regions of India were other activities carried out by the Group during the year 2019-20. Plant and lichen explorations in Suhelwa Wildlife Sanctuary in Uttar Pradesh were continued and 35 species belonging to 22 genera of algae under four classes, 20 species of bryophytes belonging to 13 genera and 10 families, six species of pteridophytes under five genera and five families, and 30 species of lichens belonging to 20 genera and 14 families were documented during the year. Grid-based quantitative surveys in Assam and Meghalaya revealed the occurrence of 138 species of lichens belonging to 34 genera and 16 families from five districts of Assam, with 37 species recorded new to Assam, and 131 lichen species from Khasi and Jaintia Hills of Meghalaya. Pteridophytes survey in Meghalaya revealed the occurrence of 67 species belonging to 52 genera under 28 families in the sample plots surveyed in 26 grids. Survey of pteridophytes from Pachmarhi Biosphere Reserve (PBR), Madhya Pradesh resulted in documentation of 52 species and 41 genera. Season-based explorations in Jim Corbett National Park, Uttarakhand identified 128 species of algae, including a rare species, *Oocardium stratum* Nägeli, which was recollected after nine decades from the Indian sub-continent.

Floristic survey of herbaceous flora of Lucknow and surrounding five districts (Barabanki, Sitapur, Hardoi, Unnao and Raebareli) was continued. The checklist contains 457 species under 340 genera and 71 families. Different forest areas as well as field under cultivation and fallow lands in Nagpur, Bhandara, and Gondia districts in Vidarbha region of Maharashtra were surveyed and 324 species

belonging to 242 genera and 79 families of flowering plants were identified. Similarly, surveys in the Western Himalayan region of Himachal Pradesh, Jammu & Kashmir and Uttarakhand resulted in collection of 170 species belonging to 55 genera of grasses.

Taxonomic study on Asteraceae, Euphorbiaceae, and introduced and cultivated legumes of Uttar Pradesh was taken up. For the first time, a list of 102 alien plant species has been prepared from Sikkim, of which 93 species are dicots belonging to 75 genera and 30 families while nine species of monocots fall under seven genera and three families.

Ethnobotanical studies in eight sacred groves were undertaken in Yavatmal district of Maharashtra. About 126 species of medicinal plants, 22 ornamental, 17 wild edible, six oil yielding and 15 species of fodder values were documented from these sacred groves. Forest areas in Jhabua district of Madhya Pradesh were surveyed for collecting information from the Bhil and Bhilala tribes on the use of medicinal plants in the treatment of dermatological diseases. A total of 116 plant species belonging to 103 genera and 58 families was identified. These species are used for the treatment of 21 different dermatological disorders. Field surveys in different Terai forests ranges of Uttar Pradesh resulted in collection and systematic documentation of 50 useful plant species along with associated indigenous knowledge.

Revisionary studies on Arthoniales, *Buellia*, *Pyrenocarpus*, *Rinodina* (Lichens); Mniaceae, Marchantiales (Bryophytes), tribe *Boehmeriae* of Urticaceae, *Desmodium, Geranium, Rhynchosia* and *Saxifraga,* (Angiosperms) and *Juniperus* (Gymnosperm) were actively pursued. The taxonomic status of the lichen genus, *Schismatomma* Flot. & Körb. ex A. Massal. in India was examined in detail and excluded from the country.

A new combination *Phlyctis atomella* (Stirt.) S. Joseph *et al*. was proposed, based on *Platygrapha atomella* Stirt. (*S. atomellum* (Stirt.) Zahlbr.) and four species names were synonymized under it. The taxonomic revision of pyrenocarpous lichens recognized 396 species belonging to 49 genera and 12 families. The study also reported nine species as new distributional records to India. Systematic study on the lichen genera, *Buellia s.l.* and *Rinodina* revealed the occurrence of 10 new distributional records for India, five each under the two genera.

Genetic variability and population structure in *Bergenia ciliata,* a high value medicinal plant of the Indian Himalayan region, were estimated using two SPAR markers namely, Directed Amplification of Minisatellite region DNA (DAMD-9 primers) and Inter Simple Sequence Repeats (ISSR-15 primers). The study comprising 111 accessions sampled from 11 populations from Jammu & Kashmir, Himachal Pradesh, Uttarakhand, West Bengal and Sikkim (12) detected two genetic clusters, with a moderate level of genetic diversity at species and population levels and a weak population genetic structure in *Bergenia ciliata*. Future distribution range of the soap nut tree (*Sapindus emarginatus)* and the bioclimatic variables limiting its distribution were examined and the adaptive fitness and genomic resilience towards these variables were evaluated using different ecological niche models (ENMs; BioClim and MaxEnt) on occurrence data (n=88 locations). The adaptive fitness of the species was evaluated by quantifying the genetic variability with AFLP markers and marker-environmental associations, using AFLP-associated Bayesian statistics. The niches from Deccan peninsula biogeographic region were predicted to be the most suitable for survival of *S. emarginatus*. A combination of high heterozygosity (0.40-0.43) and high within-population variability (91.63±0.31%) confirmed high adaptive fitness to maintain reproductive success of *S. emarginatus*.

Molecular systematics, phylogeny and phylogeography studies of *Betula, Citrus*, *Commiphora, Didymocarpus, Henckelia, Ensete, Gymnema, Juniperus,* and *Uraria* are in progress.

The most significant outcome from the systematics research efforts is the discovery of six new species to science and new distributional records of 21 species to India. The new species discovered and described during the year include a flowering plant, *Heterostemma barikiana* P.Agnihotri *et al*. (Apocyanaceae) from Manipur in India, Chin State in Myanmar and North and West Thailand; three Lichens: *Ioplaca rinodinoides* S. Y. Kondr. *et al*.; *Letrouitia assamana* S. Y. Kondr *et al*., *Rusavskia indochinensis* S. Y. Kondr. *et al*.; and two bryophytes: *Cololejeunea lobulopapillata* A.K. Asthana, V. Sahu & D. Gupta (Lejeuneaceae), and *Paraleucobryum enerve* var. *secundum* A.K. Asthana & V. Sahu (Dicranaceae), both from Govind Wild Life Sanctuary (GWLS), Uttarakhand. The 21 new geographical records to India include 20 lichen species, viz. *Amandinea efflorescens* (Müll.

Arg.) Marbach, *A. incrustans* (J. Steiner) Marbach, *Anisomeridium albidoatrum* (Nyl.) R.C. Harris, *Baculifera orosa* Marbach, *Hafellia dissa* (Stirt.) H. Mayrhofer & Sheard, *H. reagens* Pusswald, *Rinodina archaea* (Ach.) Arnold, *R. ascociscana* (Tuck.) Tuck., *R. capensis* Hampe, *R. isidioides* (Borrer) H. Olivier, *R. laevigata* (Ach.) Malme, *Porina atlantica* (Erichsen) P. M. Jorg., *P. exserta* Müll. Arg., *P. siamensis* P.M. McCarthy, *Pyrenula concastroma* R.C. Harris, *P. cruenta* (Mont.) Vain., *P. dissimulans* (Müll. Arg.) R.C. Harris, *P. pyrenastrospora* Aptroot, *P. rinodinospora* Aptroot, *Pyxine dactyloschmidtii* Kalb & Mongkols; and a bryophyte species, *Orthomnion javense* Koponen.

The Herbarium (LWG) of the institute is recognized as a 'National Repository' by the National Biodiversity Authority (NBA) of India. Thousands of collections have been made and their processing to prepare herbarium specimen and identification is in progress. Meanwhile more than 2200 specimens have been accessioned and incorporated in the herbarium after their proper identification. About 25 plants were received from researchers of other organizations for identification and authentication certificates.

In order to support conservation strategies and mass propagation of threatened plants, *in vitro* studies were carried out on *Anthoceros bharadwajii* Udar & Asthana, an Indian endemic hornwort, and *Cyathea spinulosa*, a threatened tree fern. Mass propagation of 2500 individuals (replicates) of 13 ornamental species of pteridophytes was also made for sale. About 67 species of ferns, including some threatened species, have been maintained and conserved in the Fern house of CSIR-NBRI. Besides, large scale propagation of *Microsorum scolopendria* has been made for screening for potential molecules. The bird's nest fern, *Asplenium nidus* has been multiplied through *in-vitro* spore culture and has been introduced in the Fern house.

## Bioprospecting for biomolecules and natural product development

Pharmacognostic evaluation of several drugs is being made using organoleptic characters, macro-microscopic details, physicochemical parameters and HPTLC/ fingerprint profiles along with the chemical markers.

Variations in quinic acid content in different accessions of *Commiphora wightii* and *Commiphora agallocha* were investigated using RP HPLC. Quinic acid was detected as a major metabolite in aqueous extracts of leaves of *Commiphora wightii* and *C. agallocha*.

*Sphaeranthus indicus* is an important medicinal plant in Ayurveda. It grows as a weed in rice fields throughout India. A simple, rapid, sensitive and reproducible method was developed for simultaneous HPTLC quantification of two bioactive compounds eugenol and b-sitosterol from *S. indicus*. Four important phenolic compounds, i.e chlorogenic acid, ferulic acid, gallic acid and protocateuchine were identified and quantified through RP-HPLC technique in *Elephantopus scaber*, a widely used traditional medicinal plant.

Pharmacological studies of lichen species, *Usnea longissima* identified four compounds with potential for treatment of peptic ulcer: 18R-hydroxy-dihydroalloprotolichesterinic acid, neuropogolic acid, barbatic acid and usnic acid. These compounds were identified through mass spectrometry and NMR spectroscopy. All the four compounds displayed cytotoxic activity. The potential leads from *Usnea longissima* were validated in rats.

Phytochemical screening of *Gymnema sylvestre* samples collected from different states of India was carried out to estimate the major chemical marker compounds, such as Gymnemagenin, Deacyl gymnemic acid, Lupeol and Stigmasterol. Chemical reference marker, Mangiferin was isolated from the leaves of *Mangifera indica*. Mangiferin possesses several health endorsing properties such as antioxidant, antimicrobial, antiaging, anticancer, and hepatoprotection.

Essential oil from *Artemisia absinthium* leaves, stem and seeds was evaluated for termite repellency and mortality. The essential oil from leaves showed significant termite repellency in comparison to stem and seed and can be used as a termite repellent.

*Tagetes* flowers (yellow and red) collected from temples of Lucknow and Varanasi were used for standardization of colour extraction process and chemical profiling of the colour molecules. The colours extracted were mixed with natural ingredients. The prepared synergistic mixture of colored dry powder has good sticking capacity to skin and can be easily removed by soft mop. It is non-toxic to skin.

Various samples of turmeric leaf oil collected from different farmers were analyzed using GCMS for

quality assessment. The major chemical compounds present were, phellandrenes (32%), terpinolene (26%), p-cymene (5.9%) and 1, 8 cineole (6.5%).

A *Shodhan* protocol and preparation of standardized *Cannabis* extracts, based on AYUSH formulation, was developed from *Cannabis sativa*.

The extracted metabolites of endolichenic fungi (ELF) (MELE) were investigated for anti-quorum sensing activity using the biomarker strain *Chromobacterium violaceum*. The effect of MELE was also evaluated on the production of virulence factors and biofilm formation of *Pseudomonas aeruginosa*. The study showed that the ELF, *Aspergillus quandricinctus* possesses potential to inhibit quorum sensing and biofilm formation of *P. aeruginosa* and can be further exploited for hospital and healthcare facilities.

## Biomonitoring, phytoremediation and climate change research

The research programme of Plant Ecology and Environmental Technology Group focused on eco-physiological and biochemical processes of plants in response to air pollution and climate change, forest biomass and carbon sequestration, and monitoring of Fluoride and Arsenic in environmental matrices, and Fe and Zn bio-fortification of rice using siderophore secreting microbes. The highlights of the research achievements by the Group are as follows:

Two varieties of wheat were assessed for effect of ethylenediurea (EDU) on apoplast and chloroplast proteome under high ambient ozone. Several chloroplast proteins involved in photosynthesis, carbon metabolism, protein synthesis assembly degradation, defense, and energy metabolism-related proteins were identified.

Adaptation strategies of twenty three rice varieties of Indo-Gangetic Plains were studied in response to elevated $CO_2$, Ozone and temperature. NDR-359 showed the best yield in all the treatments. Azad basmati performed very well in elevated $CO_2$, NDR-3112 was better under elevated $O_3$, while, Sarju-52, Shambha sub-1 and Pant 12 did well at elevated temperature. Physiological experiments in cotton revealed that endogenous levels of abscisic acid predominantly maintains the stomatal behavior in cotton leaves and regulates its physiology by antagonizing 6-Benzylaminopurine to coordinate with water deficit signals.

It was demonstrated that the variability in the gene expression of carbon metabolising enzymes modulates the accumulation of carbohydrate in *Cyamopsis tetragonaloba* (Guar) plants under restricted water supply.

Three forest communities, dry mixed, Sal mixed and teak plantation in Katerniaghat Wildlife Sanctuary located in Terai region of Uttar Pradesh were studied for the soil $CO_2$ efflux in summer season. Significant increase in soil $CO_2$ flux was observed with increasing air and soil temperature in dry mixed and Sal mixed forest. In another study a baseline data on cryptogamic plant diversity was generated with a standard protocol adopted from Global Observation Research Initiative in Alpine Environments (GLORIA). This data will be utilized to understand the functional role of microclimate on community structure and functioning at Alpine ecotones in Indian Himalayas.

The level of $F^-$ was estimated in *Zea mays* (maize), *Capsicum annum* (capsicum), *Gossypium arboreum* (cotton), *Oryza sativa* (rice), and *Vigna mungo* (moong) cultivated in the agricultural fields of Unnao district, which were collected during Pre-monsoon, Monsoon and Post monsoon seasons.

A comparative assessment of Zn and Fe uptake in four rice cultivars (*Swarn sub-1, Jayanti, Sharbati* and *BPT-5204*) was carried out using four siderophore secreting microbial strains viz, NBRI-D1.2, NBRI-D1.16, NBRI-D1.20, NBRI-D2.16 (*Pseudomonas putida, P. mohnii, Pseudomonas* spp. and *P. fluorescens*, respectively) under two regimes of Zn fertilization. The root length (RL), shoot length (SL) and dry weight (DW) increased significantly against all the four microbial inoculums, applied in the Zn amendment soil, whereas they did not show any increase against any microbial inoculums applied in garden soil. The SL increased by 10.04%, 0.625% and 8.65% in *Swarn sub-1, Jayanti* and *BPT5204*, respectively. Similarly, the DW increased by 25.6%, 54.3% and 88.8% in *Swarn sub-1, Sarbati* and *BPT 5204*, respectively when grown in Zn amended soil. In grains, the percentage increase in the Fe level, against the different inoculums ranged between 52.2% to 111.6% in *Sarbati* and *Jayanti*, respectively. In the rest two other cultivars, the highest level of Fe was observed against *P. mohnii* in cv. *Jayanti* (22.3±2.4) and against *P. putida* in *Sarbati* (18.7±2). Alternatively, the grain Fe content when cultivated with Zn amendment ranged between 59.31% to 28.3% in *Jayanti* and *Sarbati*, respectively.

## Microbial Technologies

The group focuses on disease management of valuable crops and developing sustainable eco-friendly remedies. Biological control, plant microbe interactions and sodic soil reclamation, food safety and environmental protection through development of cost-effective and efficient bio-inoculants formulations both for agricultural lands and stressed soils, and elucidation of molecular mechanism(s) of microbe mediated abiotic and biotic stress tolerance in different crop plants are the activities undertaken by the group during the year under report. The major R & D highlights are:

*Bacillus tequilensis* (PBE1) (MTCC25188) was identified to be effective against *Fusarium oxysporum* for tomato wilt disease management. *Trichoderma reesei* was identified as a biofertilizer (BF) to ameliorate nutrient stress in different rice cultivars based on physiological, biochemical and molecular evidences, both in the presence and absence of NPK chemical fertilizers.

A simple and facile biogenic silver nanoparticles (BSNP) was developed for wound healing acceleration and suppression of wound infections. The BSNP is formulated in an ointment base, and the study to accelerate the wound healing process was conducted in a rat model.

A study was conducted to demonstrate the use of bioengineered silver nanoparticles in combating black spot disease caused by necrotrophic fungus *Alternaria brassicicola* in *Arabidopsis thaliana* via foliar spray.

Another study conducted to identify and characterize Chlorpyrifos (Chlp) degrading soil microbes revealed *Alcaligenes faecalis* (NBRI OSS2-5) as a potent bacterial strain for Chlp degradation. This strain can be used for plant growth promotion and bioremediation in pesticide contaminated sites.

Application of a *Trichoderma* consortium comprising *T. koningiopsis* NBRI-PR5 and *T. asperellum* NBRI-K14 improved the anatomical and morphological features of the rice roots under salt stress and also improved the yield and seed size and weight. A plant growth promoting rhizobacteria (PGPR), *Paenibacillus lentimorbus* NRRL B-30488, on inoculating chickpea plants grown under nutrient stress condition, showed better growth and development by modulating its metabolic pathways. *Bacillus amyloliquefaciens*-SN13 in rice (*Oryza sativa*) grown under salt stress showed extensive alterations in gene expression in root transcriptome, and a significant increase in biomass, and total soluble sugar was observed.

Molecular mechanism of a silicon solubilising rhizospheric microbe (NBRISSM) and root associated microbe, *Pseudomonas putida* (MTCC 5279) was elucidated. *Bacillus amyloliquefaciens* (NBRISN13) was studied as to how it modulates plant metabolite system under biotic stress conditions of *Rhizoctonia solani*. Twenty one compounds related to antimicrobial activity and defense signalling was identified.

A yeast strain *Debaryomyces hansenii* was identified for amelioration of arsenic stress in rice. *D. hansenii* reduced grain arsenic content and also showed plant growth promoting traits. A microbial formulation was developed for faster *in situ* rice straw decomposition and soil health improvement and also enhancement of the subsequent wheat crop productivity.

## Gene-mining, transgenic plant development and genome-editing technologies for crop improvement

Understanding changes at genetic level in existing germplasm/ cultivars through various approaches and utilization of information generated to develop improved varieties can lead to enhancement in the yield to meet demand of increasing population. There is need to develop new strategies for engineering crops for better yield, stress tolerance and enhanced nutritional quality preferably using genes of plant origin. In line with these premises, the Molecular Biology and Biotechnology Group has pursued several R&D programs aimed at understanding various genetic determinants for yield and quality to develop superior plant varieties for enhanced yield and quality using plant genes for the benefits of farmers and consumers. To fulfill these objectives, gene-mining, transgenic plant development and genome-editing technologies were applied on various crops. The salient achievements of R& D pursued by the Group during the reporting year include:

A large collection of 1000 genotypes of cotton was obtained from Tierra Agrotech, Hyderabad under an MoU. This genotype collection will boost cotton genomics activity in the Group and help us in identification of key genes regulating important agronomical traits in cotton.

In the area of cotton genomics, a total 15 HDACs homoeologs were identified in each of the A and D sub-genomes of *Gossypium hirsutum*. Among them, GhHDA5 expressed significantly at the time of fiber initiation. The *in-vitro* assay for histone deacetylase activity indicated that GhHDA5 primarily deacetylate H3K9 acetylation marks. The down-regulation of GhHDA5 in the RNAi lines resulted in H3K9 hyper-acetylation on the promoter region of few DEGs assessed by ChIP-assay. The results showed HDA5 interact with Histone Methyl Transferases (HMTs), HSPs and other HDACs. The results also indicate involvement of large suppressive complex which regulates cotton fiber initiation. The involvement of GhHSP70 and GhHSP90 in cotton fiber development has been investigated. The functional genomics of these selected genes were studied. Besides, the role of GhHMT in the complex formation was investigated through its cloning and characterization.

To develop aphid resistant cotton transgenic lines, 18 transgenic lines expressing Dhi31 constitutively downstream of the CaMV35Es double enhance promoter were developed. Fourteen transgenic plants expressing Dhi31 from low to high levels were developed and analyzed. Insect bioassay was carried out with leaf-discs and TSP of moderate to high expressing transgenic plants and 30-80% mortality was recorded. However, these plants could not advance to next generation due to abnormalities in the reproductive structure. Therefore, it became necessary to express Dhi31 in tissue specific manner. The gene was cloned at the downstream of *Arabidopsis thaliana* sucrose synthase 1 (AtSuS1) promoter for tissue (phloem) specific expression. Transformed cotton explants showed callus induction to ~50-60% on hormone selection media. These calli will subsequently form somatic embryos which will develop into transgenic plants in next 6-7 months.

In the area of pathway elucidation and engineering of secondary plant products, *Papaver somniferum* and *Withania somnifera* have been studied and characterized in detail. Recently a Short-chain dehydrogenase/reductase, PsDeHase, which might participate in the dehydrogenation in the papaverine biosynthesis, has been functionally characterized and has been shown to be involved in the synthesis of papaverine. The miRNA and miPEPs involved in the flavonoid biosynthesis pathway have been functionally characterized in *Arabidopsis thaliana* using the CRISPR/Cas approach. Further to elucidate the role of various genes that are involved in Arsenic stress, two *Arabidopsis thaliana* accessions Koz2-2 (tolerant) and Ri-0 (sensitive) to sulphur limitation and As(III) stress have been identified and characterized in detail.

A total of 46 PME genes were identified in *Withania somnifera* with the help of available transcriptomic data. WsPME-26 was the most potential putative active PME gene during biotic stress. Transgenic lines of *Nicotiana tabacum* using this gene were developed using constitutive and inducible promoter systems. Constitutive expression system showed 75-85% mortality against both the chewing (*Spodoptera litura* and *Helicoverpa armigera*) and sap sucking (Aphid and Whitefly) insect pests at 4th day of experiment whereas inducible system showed mortality at 6th day of the experiment.

The root up-regulated tomato *SlWRKY23* gene was found to govern root growth under stress conditions. It is strongly induced in roots by 300 mM mannitol and its expression ameliorates the inhibition of lateral root growth in transgenic *Arabidopsis* by mannitol and both primary and lateral root growth by NaCl. The gene is specifically induced in lateral root primordia in tomato hairy root and is strongly enhanced by mannitol suggesting its role in regulation of lateral root growth. In order to improve root growth and architecture, two genes *SlWRKY75* and *SlWRKY23* that alter root growth were chosen. About 10-15 CRISPR lines for each have been developed and validated.

In order to facilitate expression of multiple insecticidal protein genes under different wound-inducible promoters in important crops like cotton and chickpea, several strong early-acting wound-inducible genes were identified from chickpea. Their expression was validated in response to simulated herbivory by *Helicoverpa armigera* and in response to other defense cues like JA, ethylene, SA, $H_2O_2$. Promoters ranging in length from 1.7 to 2 kb have been isolated and are being studied.

The *SlERF6* gene from tomato, associated with altering the onset of fruit ripening by ABA responses, was found to regulate the expression of *SlCYP707A3* and *SlUGT75C1* –both involved in reducing ABA levels and thereby ABA responses. Two ripening related MAPK genes have been identified in mango and these were shown to have been involved in

regulation of aroma. Further studies are underway to understand how these MAP kinases regulate aroma production in mango and in other fruits.

The significance of Me-JA induced molecular signaling and tolerance towards arsenic toxicity in rice was studied. The arsenite (AsIII; 25µM) stress hampered the overall growth and development of the rice seedling. However, the co-application (25µM AsIII+0.25µM Me-JA) resulted in increased biomass, chlorophyll content, enhanced antioxidant enzyme activities as compared to AsIII treated plants. The co-application also demonstrated marked decrease in malondialdehyde content, electrolyte leakage and accumulation of total AsIII content (root + shoot) as compared to AsIII treated plants. The co-application was also found to modulate the expression of genes involved in downstream JA signaling pathway (*OsCOI,OsJAZ3,OsMYC2*), AsIII uptake (*OsLsi1*, *OsLsi2*, *OsNIP1;1*, *OsNIP3;1*), translocation (*OsLsi6*, and *OsINT5*) and detoxification (*OsNRAMP1*, *OsPCS2* and *OsABCC2*) revealed the probable adaptive response of the rice plant to cope up arsenic stress. Me-JA was found to alleviate AsIII toxicity by modulating signaling components involved in As uptake, translocation and detoxification and JA signaling in rice.

In the area of functional characterization of genes involved in abiotic stress metabolism, various approaches were used. A number of genes were functionally characterized using different approaches. Analysis strongly suggest that the hormonal crosstalk of wound inducible and stress-responsive OsMYB-R1 transcription factor in combating abiotic [Cr(VI) and drought/PEG] as well as biotic (*Rhizoctonia solani*) stress. OsMYB-R1 over-expressing rice transgenic plants exhibit a significant increase in lateral roots, which may be associated with increased tolerance under Cr (VI) and drought exposure. In contrast, its loss-of-function reduces stress tolerance. Higher auxin accumulation in the OsMYB-R1 over-expressed lines further strengthens the protective role of lateral roots under stress conditions. RNA-seq. data reveals over-representation of salicylic acid signaling molecule calcium-dependent protein kinases, which probably activate the stress-responsive downstream genes (Peroxidases, Glutathione S-transferases, Osmotins, Heat Shock Proteins, Pathogenesis Related-Proteins). The results suggest that OsMYB-R1 is part of a complex network of transcription factors controlling the cross-talk of auxin and salicylic acid signaling and other genes in response to multiple stresses by modifying molecular signaling, internal cellular homeostasis and root morphology.

Two rice glutaredoxin (*OsGrx*) genes (*LOC_Os02g40500* and *LOC_Os01g27140*) were over-expressed in *Arabidopsis thaliana* to examine their role in drought stress. The relative expression of both *OsGrx* genes was higher in the transgenic lines, which showed longer roots, higher seed germination, and survival efficiency during drought stress. The physiological parameters ($P_N$, $g_s$, *E*, WUE, *q*P, NPQ and ETR), antioxidant enzymes (GRX, GR, GPX, GST, APX, POD, SOD, CAT, DHAR, and MDHAR), antioxidant molecules (ascorbate and GSH) and stress-responsive amino acids (cysteine and proline) levels were additionally increased in transgenic lines of both *OsGrxs* to provide drought tolerance.

A chickpea glutaredoxin (*CaGrx*) gene (*LOC101493651*) was over-expressed in *Arabidopsis thaliana* to reveal its role in heavy metal stress (AsIII-25µM, AsV-250µM, Cr(VI)-300µM, and Cd-500µM). The relative expression of *CaGrx* gene was higher in the transgenic lines. Transgenic plants showed longer roots, higher seed germination, and survival efficiency during metal stress. The levels of stress markers, TBARS, $H_2O_2$, and electrolyte leakage were found to be less in transgenic lines as compared to WT, revealed less toxicity in transgenic lines. In all the heavy metal treatments, accumulation of AsIII, AsV, and Cr(VI) was significantly reduced in all the transgenic lines except Cd, which was slightly reduced. The physiological parameters ($P_N$, $g_s$, *E*, WUE, *q*P, and ETR), antioxidant enzymes (GRX, GR, GPX, GST, APX, SOD, CAT, DHAR, and MDHAR), antioxidant molecules (ascorbate, GSH) and stress-responsive amino acids (proline and cysteine) levels were significantly increased in the transgenic lines. The outcome from this study strongly indicates that the *CaGrx* gene participates in the moderation of metal stress in Arabidopsis.

In the area of genome-editing to improve yield and stress tolerance, the Group initiated studies on different crops. To delay the post-harvest life, two genes [α-mannosidase (α-Man) and β-D-N-acetylhexosaminidase (β-Hex)] were selected for genome editing in tomato. Constructs were transformed in tomato and putative lines have been selected for further analysis. To functionally characterize miR858 for its function in plant

development and synthesis of molecules of nutritional importance, mature and fold back region of this miRNA have been edited and developed mutants plants have been analyzed in detail. In cotton, three genes, MYB1, SELF PRUNING (SP) and SINGLE FLOWER TRUSS (SFT), have been selected for genome editing with objective to develop determinate/semi-determinate sympodial cotton varieties. To meet this objective, *in silico* analysis of the promoter and gene sequences of both the GhSP and GhSFT genes has been carried out and gRNA from the potential regions has been designed. To develop rice varieties with low arsenic accumulation in grain, sgRNAs for genes involved in arsenic transport and accumulation (Lsi1, Lsi2, Inositol phosphate transporter, NIP3 and NRAMP) have been utilized to develop constructs, rice plants have been transformed and edited lines have been raised. Further analysis is in progress. Efforts to develop short duration mustard variety development using genome editing tools are also underway. Based on an earlier lead from natural mutant identified in Indian *Arabidopsis thaliana*, gRNA guided construction to target the locus responsible for early maturity was developed and cloned in a plant transformation vector and transformed into Mustard. Three putative transgenic lines were generated during this period.

In the area of computational biology the whole genome sequence of *Gossypium herbaceum* 'Wagad' was assembled and annotated and compared with the A genome of *G. arboreum* and the A sub-genome of *G. hirsutum*. The miRNAs responsible for flower-anthesis and stress in *Cestrum nocturnum* (CS1) and *Cestrum diurnum* (CS2) were identified by *in-silico* analyses. Homology-search based computational analysis was employed for the identification of responsible miRNAs and their targets. The evolution and divergence of MADS box gene family in *Musa acuminata* and *Musa balbisiana* was also studied. In this context the evolution of the 'two component system module' was also studied in the two species with special reference to the evolution of HPT gene family in plants.

## Development of genetic and genomic resources for plant improvement

The major thrust of R& D carried out by the Plant Genetic Resources and Improvement Group included genetic improvement of wild and underutilized crops and selection, genetic mapping, QTL, GWAS and Genomics-assisted breeding for crop improvement. Following are the major R&D highlights during the reporting year:

Various sets of new mapping populations of linseed were developed in cropping season by crossing different lines as parents having contrasting traits. These populations are in F2 generation which will be further progressed through SSD (single seed descend) up to F7/F8 generations for the development of recombinant inbred lines consisting genes for economically important traits of linseed. The RILs i.e. RIL Pop. 1 for oil content: RKY-14 (high) x KL-213 (Low); RIL Pop. 2 for *Alternaria* blight: JRF-4 (Tol.) x Chambal (Sus.); RIL Pop. 3 for yield and its attributes: Hira (High) x Jawahar-17 (Low) and RIL Pop. 4 for flowering/maturity: Padmini (Early) x KL-213 (Late) that are already in F8 generations, were advanced to one more generation to get a homogenous and stabilized population.

Association mapping for major fatty acids was done from 86 accessions of linseed. The GLM approach identified 2 SNPs associated each with linoleic acid (LA) and palmitic acid (PA), 3 SNPs each with linolenic acid (LNA), steric acid (SA) and oleic acid (OA). In MLM approach, 2 SNPs with LA and 1 SNP each with LNA, SA and OA were found to be associated. The above 86 accessions were collected from 16 different states of India for evaluation of genetic diversity.

Besides linseed, 96 accessions of *Limonia acidissima* were collected from 16 different states of India and evaluated for estimation of genetic diversity using SSRs. These accessions were grouped into 3 major clusters i.e. Cluster I, Cluster II and Cluster III. Out of 96, maximum number of accessions (46) was grouped into cluster II while minimum (7) number of accessions was present in cluster III. The distribution of large number of accessions in cluster II indicates their common origin and genetic similarity.

Ninety five accessions of the underutilized tropical legume, winged bean (*Psophocarpus tetragonolobus)* were grown and maintained in the botanic garden of

CSIR-NBRI for further utilization. The refined seed-oil of these lines is suitable and comparable with soybean seed-oil. Safety evaluation of this refined oil on *albino* mice revealed non-significant changes in terms of body weight, organ weight, haematological and serum biochemical changes. Furthermore, the seed-cake of *P. tetragonolobus* contained proteins in a range of (34.7-35.6%), carbohydrates (21.4-23.1%), polyphenols (0.45-0.49%), *L*-DOPA (0.35-0.38%) and phytic acid (0.18-0.2%). These values are closely comparable with the soybean seed-cake.

Genetic diversity among 95 accessions of *Psophocarpus tetragonolobus* belonging to seven countries of African and Asiatic origin was examined by amplified fragment length polymorphism (AFLP) markers and internal transcribed spacer of nuclear ribosomal DNA (nrDNA-ITS). Associations between AFLP markers and flower, pod and seed traits like, days to 50% flowering (DFW), pod length (PDL), pod width (PDW), green pod length (GPL), number of pods per plant (PDSP), number of seeds per pod (SDPD), 100 seed weight (SWT) and seed-oil content (SOC) were estimated. Seven AFLP markers were identified to be associated with SOC and minimum two AFLP markers were found to be associated with PDW. The population structure analysis among these accessions identified discrete sub-populations without any relationship with the geographical region with the country of their origin.

A new dwarf *Chrysanthemum morifolium* variety, named 'NBRI- PUKHRAJ', was developed. The new variety is a novel dwarf, 'no-pinch no-stake', 'Anemone' type, floriferous *Chrysanthemum* which bears yellow flowers that bloom during late-November to early January. The new variety has been developed through mutation induction by gamma irradiation of the parent variety 'Himanshu'.

Another new dwarf *Chrysanthemum morifolium* variety named 'NBRI- SHEKHAR' was developed by gamma irradiation of its parent variety 'Su-Neel. The variety is a novel late blooming, floral-shape mutant. The new variety bears mauve flowers that start to bloom late during end-December to mid-February.

The different floral gamma ray mutant lines of *Chrysanthemum* with altered trait(s) i.e. floret colour; shape; both colour as well as shape; different shades of floret colour; late-flowering were advanced to their respective next vegetative generations through rooted cuttings and suckers.

Twenty new inter-varietal *Chrysanthemum morifolium* selections have been made on the basis of floral characteristics unique to the existing CSIR-NBRI germplasm. Further expansion of the germplasm has been made with unique combinations of ornamental traits. These selections include different recognized ornamental categories- 'Korean', 'Double-Korean', 'Anemone', 'Mini', 'Decorative', 'Semi-Quilled', 'Stellate' and 'Cineraria' types. The chrysanthemum germplasm at CSIR-NBRI is one of the most unique genetic resources of 'Garden chrysanthemum' available in the country.

SEM studies were initiated in induced floral mutants of *Chrysanthemum morifolium* vis-à-vis their respective two somatic parents to find differences that may exist in their micro-morphological foliar characteristics i.e. stomatal size, density and trichome features which play role in withstanding various environmental stresses.

SNP genotyping arrays have been developed for a number of plant species which are being employed for construction of linkage maps, tagging and introgression of QTLs for important agronomical traits, and use in marker assisted breeding programs. QTL analysis was performed in cotton (*Gossypium hirsutum*) for six fibre traits such as spin length, uniformity, fiber length, bundle strength, elasticity and short fiber index by using approaches of interval mapping and composite interval mapping. A total of 34 QTLs related to different fibre traits were identified in 16 linkage group (LG). LG-16 has the maximum six number of fiber QTLs.

Genome-wide association (GWAS) study was conducted in Opium poppy to identify the potential SNP markers associated. This GWAS study resulted in key important SNPs associated with Thebaine from both plant latex and leaf samples of one month old plant. These key SNPs and their associated genes are being annotated to establish a linkage of these genes in thebaine development.

CSIR-NBRI has a wide Cannabis gene bank collection of 221 germplasm including 11 exotic germplasm. A Cannabis Centre was set up at distant research centre, Banthra. The institute has taken an initaitive for development of low Tetrahydrocannabinol (THC) and high Cannabidiol CBD *Cannabis* lines for medicinal use and low THC and high fiber *Cannabis* lines for industrial use. HPLC protocol for

determination of various cannabidiods has been established.

## Botanic Garden, and Plant Conservation & Agro-Technology

The highlights of research and outreach programs pursued by the Group covered a wide spectrum of achievements, including development of new varieties of popular floricultural crops with their morphological and genetic characterization, area expansion, value addition and product development, enrichment of plant diversity specially threatened plants, their multiplication, acclimatization, assessment and documentation, conservation of diverse groups of plants in specialized houses and field conservatories, their propagation and characterization, DUS testing of germplasm; capacity building by organizing trainings and skill development programs in ornamental horticulture at various levels, extension and outreach programs for various segments and Annual Flower Shows.

As part of the germplasm enrichment, some interesting plants viz., *Woodfordia fruiticosa, Ehretia canarensis, Abrus precatorius* and *Capparis zeylanica* were collected through field work in Maharashtra and Telengana. Thirteen varieties of Gladiolus (*viz.* Pusa Sriyan, Pusa Dhanwantri, Pusa Gunyan, Pusa Bindiya, Pusa Urvashi, Pusa Surya Kiran, Creamy Green, Pusa Shantiman, Pusa Mohni, Sancri, Australian Fair, Sweta, Pusa Kiran) were procured from IARI, New Delhi and introduced to the Botanic Garden.

Morphological Characterization of 11 varieties of Bougainvillea ('Blondie','Dream','Elizabeth','Garden Glory', 'Gopal', 'Filomon', 'Mrs Alice', 'Mahara', 'Mary Palmer Special', 'Odisee' and 'Parthasarthy'), five varieties of Canna ('Pink Sunrise', 'King City Gold', 'Yellow Queen', 'Ambassador' and 'Cattleya') and 10 varieties of Gladiolus ('Aldebaran', 'Pacifica', 'Praha', 'Priscilla', 'Regency', 'Rose Supreme', 'Snow Princes', 'Tiger Flame', 'Video', 'Yellow Stone') have been completed as per PPV&FRA descriptors.

During the year under report the following new plant houses and facilities were created at the Botanic Garden and Distant Research Centres:

(i) 'Ficus House' at the botanic garden.

(ii) A new facility for advanced propagation of plants at botanic garden.

(iii) 'Navgrah Vatika', comprising of nine different plants each representing the nine planets, at botanic garden.

(iv) A new facility for conservation of threatened plants at distant research centre, Gehru.

(v) A 'Bambusetum' containing various Bamboo germplasm collection at distant research centre, Banthra.

An improved selection of Annato (*Bixa orellana* L.) *viz.* 'Arunima' was identified, tested for DUS characters and released.

## Plant Conservation and Agro-Technology

Twenty nine tuberose varieties from different parts of the country were collected for evaluation in partially reclaimed sodic soil condition for their commercial cultivation and income generation for the farmers.

Sixty one species of bamboos have been collected from different parts of India and maintained in Bambusetum at DRC, Banthra for display, education, conservation and related studies.

A total of 94 accessions of Amaranths were collected and conserved to evaluate the best suited ones for successful cultivation on sodic soil conditions.

Packages of good agricultural practices were developed for cultivation following medicinal plants: *Phyllanthus amarus*, *Cyperus rotundus, Viola pilosa* and Turmeric variety 'Kesari'. Agro-technology and agro-economics for improved *Curcuma* variety (ies) were develped. The crop was popularized for cultivation under the shade of orchards, and for multi-locational assessment for their suitability in different agro-climatic regions, agro-technology including postharvest optimization for different agro-climate zones, capacity building and training programmes on agro-techniques, distillation and value addition. Kesari variety has been developed by CSIR-NBRI, which apart from giving high rhizome yields, can also be a source of leaf essential oil. To extract the highest quantity and best quality leaf essential oil, leaves were harvested at three stages; viz. green, partially senesced and fully senesced. The leaves were hydro-distilled. Minimum amount of oil (0.88%) was obtained from green leaves whereas fully senesced leaves yielded 1.40% oil. The highest amount of leaf essential oil (1.70%) was obtained from partially senesced leaves. The major constituents of the essential oil are α-Phellandrenes

(32%), terpinolene (26%), p-cymene 5.9%) and 1,8 cineole (6.5%). Agrotechnology for cultivation of turmeric for essential oil extraction from senescing leaf was also developed.

Mass multiplication for quality planting material of three plant species i.e. *Tinospora cordifolia, Gymnema sylvestre* and *Commiphora wightii* was attempted at DRC, Banthra.

The conservation of four dwarf cultivars of Neem with high Limonoid content was done at DRC, Banthra. The morphological differences in all these cultivars were observed on the basis of shape, size and colour of leaves, flowers and barks. Efforts were made to propagate these cultivars through macro (through cuttings) and micro (tissue culture) propagation. The soil pH 8.80, electrical conductivity 0.67 $dSm^{-1}$, soil N, P and K 110, 18.5 and 276 kg $ha^{-1}$, respectively of Neem conservation site have been analysed. A total of 889 cuttings of neem cultivars have been planted for clonal propagation during the year. To enhance the rooting and survival of the cuttings, an experiment was established using two plant hormones (indole acidic acid and gibberellic acid) and one bio fertilizer (phosphate solubilizing bacteria) along with control. Average seed weight of neem seeds varied from 71 mg/seed to 111.9 mg/seed with an average of 92.9 mg/seed. The seed oil content ranged from 38% to 43.9% in sample with an average of 40.2%. Ethanol soluble content ranged from 9.2% to 10.4% with an average of 9.7%. Azadirachtin content varied significantly among different neem seed samples.

For standardization of the sources and levels of organic matter for the cultivation of Kalmegh (*Andrographis paniculata*), three experiments have been conducted with different doses of FYM, Pressmud and vermi-compost. Results indicated that plant height, number of branches, stem diameter, plant spread, fresh and dry biomass of the plant increased with increasing doses of FYM, Pressmud and vermi-compost. However, it was significant only up to FYM @ 15 t $ha^{-1}$, Pressmud @ 7.5 t $ha^{-1}$ and vermi-compost @ 7.5 t $ha^{-1}$. The above doses are sufficient for organic cultivation of Kalmegh.

## Certified reference materials/refrence materials

The Institute has taken an initiative to prepare some of the commercially important Cerified Refrence Materials (CRMs)/Refrence Materials (RMs) of the following medicinal phytochemicals, Andrographolide, Wogonin, Bixin, Guggulsterone Z, Azadirachtin, Curcumin, Galactomannan, Sennoside B, Mangiferin, Embelin and aromatic, Geraniol, Citronellol, Methyl chevicol, Citronellal, Linalool, Limonene, Camphor, Menthol, Carvone, Eugenol phytochemicals. CSIR-NBRI has been accredited since 2008 as per the requirements of ISO/IEC-17025/2005 from NABL (National Accreditation Board for Calibration and Testing Laboratories) Quality Council of India (QCI), Govt. of India. NABL-Gurgaon after surveillance audit in March 2020 recommends for continuation of NABL-Accreditation of the institute up to 17.10.2020 as per the requirements of ISO/IEC-17025-2017.

## Out-reach/Training/Skill Development

During the reporting peroid, various programmes, training sessions, out-reach activities were organized. More than 500 persons including students, farmers and entrepreneurs were imparted training on different aspects of gardening and agro-techniques. Short term training sessions on home gardening, bonsai preparation, dehydrated flower technique were also organized at the institute and at different villages for empowerment of youth and women etc. A total of 83 students were imparted research trainings in different disciplines of the plant science and applied subjects. The Institute conducted eight "Jigyasa' programms, a CSIR and Kendriya Vidyalaya (KV) Sansthan national initiative to connect students and scientists, in which 1682 students and 121 teachers participated. Different basic lab experiments covering tissue culture, DNA isolation, and microscopy were also included in the programme. A refresher course for the KV teachers was also organized by the institute to enhance the science teaching capabilities. The guided tour to famous botanic garden of the institute provided a great opportunity to learn about the curious and novel plants. Special visit to the institute's herbarium was also a greate opportunity to create awareness among the science students. Short term (3-6 months) training/ project work/dissertation of Post Graduate students of various universities of India was imparted to 83 students in different disciplines of the plant science and applied subjects. More than 5000 individuals including research scholars, students from various universities, schools and colleges, farmers, general public students visited the institute's facilities such

as botanic garden, herbarium, exposition and various laboratories during 2019- 2020.

## Projects, Publications and Awards

During 2019-2020, CSIR-NBRI implemented 125 sponsored projects, published 126 research papers in SCI journals with a cumulative impact factor of 325.413 (IF 2.582 per paper), and 23 students were awarded PhD degree by the Academy of Scientific and Industrial Research (AcSIR) and other Universities of India. Dr. Prabodh Kumar Trivedi was elected as Fellow of Indian National Science Academy (INSA) in the year 2019.

# Research & Development

## lLFkku dk vf/kn'k

वै.औ.अ.प.–राष्ट्रीय वनस्पति अनुसंधान संस्थान, लखनऊ की स्थापना वर्ष 1953 में हुई थी। यह वैज्ञानिक एवं औद्योगिक अनुसंधान परिषद, वैज्ञानिक एवं औद्योगिक अनुसंधान विभाग, विज्ञान एवं प्रौद्योगिकी मंत्रालय, भारत सरकार के 38 संस्थानों में से एक है।

संस्थान पिछले छह दशकों से राष्ट्रीय महत्व के संस्थान के रूप में पादप अनुसंधान के क्षेत्र में पूरे देश में अग्रणी रहा है। विश्व स्तर पर वानस्पतिक अनुसंधान के एक आधुनिक केन्द्र के रूप में मान्यता प्राप्त यह संस्थान पादप विज्ञान के लगभग सभी क्षेत्रों में बहुआयामी अनुसंधान एवं विकास कार्यक्रम चला रहा है। संस्थान का मूल उद्देश्य सतत विकास एवं मानव कल्याण हेतु देश के गैर–पारंपरिक, अल्प–प्रयुक्त एवं वन्य पादप आनुवांशिक संसाधनों पर विशेष ध्यान देते हुए पादप विज्ञान के विभिन्न पहलुओं जैसे कि संरक्षण, वर्गिकी, प्रलेखन, पूर्वेक्षण एवं आनुवांशिक सुधार आदि पर बुनियादी एवं प्रायोगिक अनुसंधान करना है। संस्थान निम्न क्षेत्रों के प्रमुख सामर्थ्य रखता है।

- पादप विविधता, वर्गिकी एवं निम्न तथा उच्च पादप समूहों के लिए डेटाबेस
- जैव पूर्वेक्षण तथा पौष्टिक–औषधीय, प्रसाधन–औषधीय एवं स्वास्थ्य देखभाल हेतु उत्पादों का विकास
- जलवायु परिवर्तन अनुकूलन अध्ययन एवं कार्बन जब्तीकरण
- वर्धित पादप उत्पादकता हेतु सूक्ष्मजीवी
- पारंपरिक एवं आणुविक प्रजनन द्वारा पादप सुधार एवं आनुवांशिक अभियांत्रिकी
- वनस्पति उद्यान, पादप संरक्षण एवं पुष्प कृषि हेतु पौधों की नवीन किस्मों का विकास
- सोडिक एवं अन्य बंजर भूमि के सतत् विकास हेतु कृषि–प्रौद्योगिकियाँ
- आउटरीच कार्यक्रमों के द्वारा समाज कल्याण हेतु गतिविधियाँ

संस्थान नये ज्ञान का सृजन करने और मानव स्वास्थ्य, कृषि और पर्यावरण संरक्षण के लिए सस्ती प्रौद्योगिकियों के निर्माण हेतु देश की गैर–अन्वेषिक पादप विविधता की अप्रयुक्त क्षमता की खोज करने के लक्ष्य के साथ आगे बढ़ रहा है।

## CSIR-NBRI: Mission and Mandate

The Council of Scientific and Industrial Research-National Botanical Research Institute (CSIR-NBRI), Lucknow was established in the year 1953. It is one of the 38 constituent laboratories of CSIR, Department of Scientific and Industrial Research, Ministry of Science and Technology, Government of India.

The institute has been in the forefront of plant sciences research in the country for past six decades and is an institution of national importance. As globally recognized advance center of botanical research, CSIR-NBRI carries out multidisciplinary R&D Programmes in almost all fields of plant sciences.

The mandate of the institute is to undertake basic and applied research on various aspects of plant sciences, including conservation, systematics, documentation, prospection and genetic improvement with particular emphasis on under-exploited, non-traditional and wild plant genetic resources of the country for the sustainable development and human welfare.

The institute has core strength in the following areas:

- Plant diversity, systematics and database for lower and higher plant groups.
- Bio-prospection and development of nutraceutical, cosmaceutical and health care products.
- Climate change adaptation studies and carbon sequestration.
- Microbes for enhanced plant productivity.
- Plant improvement through conventional and molecular breeding and genetic engineering.
- Botanic garden, plant conservation and development of new varieties of floriculture plants.
- Agro-technologies for sustainable development of sodic land and other wastelands.
- Societal development activities through outreach programmes.

The institute is surging ahead with its envisioned goals of exploring the untapped potential of the underexplored and unexplored plant diversity of the country for generating new knowledge, and affordable technologies for human health care, agriculture and environmental protection.

# Plant Diversity, Systematics and Herbarium

# PLANT DIVERSITY, SYSTEMATICS & HERBARIUM (PDSH)

## Area Co-ordinator

Dr. TS Rana, Senior Principal Scientist

## Scientific Staff

- Dr. KN Nair, Senior Principal Scientist
- Mr. Anand Prakash, Senior Principal Scientist
- Dr. LB Chaudhary, Senior Principal Scientist
- Dr. Sanjeeva Nayaka, Senior Principal Scientist
- Dr. AK Asthana, Senior Principal Scientist
- Dr. AP Singh, Principal Scientist
- Dr. Baleshwar, Principal Scientist
- Dr. Priyanka Agnihotri, Senior Scientist
- Dr. VV Wagh, Senior Scientist

## Technical and Support Staff

- Mr. Alok Kumar, Senior Technical Officer
- Dr. Kiran Toppo, Senior Technical Officer
- Dr. Sushma Verma, Senior Technical Officer
- Dr. Vinay Sahu, Senior Technical Officer
- Dr. KK Rawat, Senior Technical Officer
- Mr. Rameshwar Prasad, Technical Assistant
- Dr. KK Ingle, Technical Assistant
- Dr. Vandana Tiwari, Technical Assistant
- Mr. Jyoti Tandon, Senior Technician
- Mr. MK Srivastava, Senior Technician
- Smt. Gomta Devi, Lab Assistant
- Mr. Mohan Lal, MTS
- Mr. Mauje Lal, Lab Assistant

## Research Scholars Statistics

| Sr. No. | Position Name | Numbers |
|---|---|---|
| 1. | CSIR Pool Scientist | 01 |
| 2. | NPDF | 01 |
| 3. | Inspire Faculty | 01 |
| 4. | Research Associate | 02 |
| 5. | Young Scientist | 01 |
| 6. | JRF/SRF Fellow | 28 |
| 7. | Project Staff | 16 |
| 8. | CSIR-TWAS Fellow | 02 |

## Broad Areas of R&D

Taxonomy of Algae, Fungi (Lichens), Bryophytes, Pteridophytes, Gymnosperms and Angiosperms, Molecular Systematics, Conservation of threatened plants and Herbarium

## Aims and Objectives

- Plant and Lichen diversity of under-explored/ un-explored areas of India.
- Revisionary and monographic studies of Algae, Lichens, Bryophytes, Pteridophytes, Gymnosperms and Angiosperms.
- Molecular systematics of plants.
- Conservation of threatened plants of India.
- Enrichment of the herbarium (LWG).
- Digital databases of plant resources.

## R&D Highlights

- Plant Diversity, Systematics and Herbarium (PDSH) Division is focusing on the documentation of plants and Lichens from under explored/ un-explored areas of India; revisionary, monographic and molecular systematic studies of economically and taxonomically interesting group of plants; conservation of threatened and endemic plants; and enrichment of herbarium of the institute by adding collections from different bio-geographical regions of India and development of databases of plant resources.
- The scientists of PDSH division of the institute are working on 21 grant-in-aid projects (GAP) sponsored by different funding agencies like SERB-DST, New Delhi; DBT, New Delhi; Assam State Biodiversity Board, Guwahati; MOEF&CC, New Delhi; Indo-US Science and Technology Forum, New Delhi; Government of Maharashtra; and CSIR, New Delhi.
- The group has significantly contributed towards bio-prospecting plant resources through collaborative research with other disciplines like Molecular Biology, Phytochemistry, Pharmacognosy & Pharmacology and Botanical Garden of the institute, which has led to

development of new varieties, processes and technologies. The scientists of the PDSH division discovered 7 new species to science, 21 new geographic records and published 42 research papers, 2 book chapters and 8 general articles in Hindi. Besides, scientists of the PDSH division are also teaching various courses to AcSIR students.

- Herbarium (LWG) of the institute is recognized as a 'National Repository' by the National Biodiversity Authority (NBA) of India. The scientists of the PDSH division are significantly contributing towards the growth and development of the herbarium, and have added 2200 specimens collected from different parts of the country during the period under report.

## Future prospects

- Plants and Lichens exploration in under/un-explored areas like Suhelwa Wildlife Sanctuary, Terrai region (Uttar Pradesh); Pachmari Biosphere Reserve; North Eastern India, Western Himalayan region and Chambal Ravines.
- Revisionary and monographic studies on Arthoniales, *Buellia*, *Pyrenocarpus*, *Rinodina* (Lichens); Mniaceae, Marchantiales (Bryophytes) *Anemone, Desmodium, Geranium* (Angiosperms).
- Molecular Systematics, phylogeny and phylogeography of *Juniperus, Ephedra, Betula Citrus*, *Commiphora, Ensete, Gymnema* and *Uraria.*
- Recovery, rescue and rehabilitation of threatened plants of India.

# HERBARIUM: A NATIONAL FACILITY

## Curator

**Dr. Lal Babu Chaudhary, Senior Principal Scientist**

Herbarium, the store house of the dried plant specimens, is the laboratory for taxonomy and biodiversity study. In addition, it also plays significant role in palynology, phenology, anatomy, embryology, ecology, conservation biology, molecular systematics and climate change studies. The herbarium of CSIR-National Botanical Research Institute (LWG), established in 1953 by the institute's first Director Prof. K. N. Kaul, is actively involved in several research activities at local and national level. Some of these activities are as follows:

## Plant Collection

The collection of plant materials from different parts of the country to assess the diversity and their preservation for long term study, is one of the core activities of the CSIR-NBRI herbarium. During the last one year plants have been collected chiefly from North-East region, Maharashtra, Uttar Pradesh and different parts of the Himalaya. Plants of some specific groups such as *Betula*, *Desmodium, Didymocarpus, Ensete, Geranium*, *Henckelia, Saxifraga*, *Uraria* and *Juniperus* have also been collected from throughout the country. Thousands of collections have been made and their processing to prepare herbarium specimen and identification are in progress. Meanwhile more than 2200 specimens have been accessioned and incorporated in the herbarium after their proper identification.

## Floristic Study

Group is also involved in the floristic study of different areas of the country, such as Chandrapur district and its surrounding areas (Maharashtra) and Suhelwa Wildlife Sanctuary and Pilibhit Tiger Reserve (Uttar Pradesh). Studies on some specific groups of plants, such as Euphorbiaceae and Asteraceae of Uttar Pradesh, Herbaceous flora of Lucknow and its adjoining districts, cultivated legumes of Uttar Pradesh and grasses of the Himalaya are in progress.

## Revisionary Study

Apart from floristic study the group is also involved in monographic and revisionary study of different groups of plants such as *Desmodium* and its allied genera (70 spp.), *Didymocarpus* (22 spp.), *Geranium* (27 spp.), *Henckelia* (36 spp.) and *Uraria* (11 spp.).

## Training Course

CSIR-NBRI herbarium organises training on plant taxonomy for researchers, students and faculties of different institutions and universities. Students/ participants are also taken to the field to demonstrate them collection and identification procedures.

## Visit of Students and Researchers to the Herbarium

Every year hundreds of students from different schools, colleges, universities and research organisations visit CSIR-NBRI Herbarium to know about the plant diversity, techniques of herbarium preparation and identification and authentication of plant materials. During 2019-2020 students from more than 10 organisations like IIT (ISM), Dhanbad; MGIMT College, Banthra; Allahabad University, Allahabad; Madras University, Chennai; CSIR-NEIST, Jorhat; and Bharathiar University, Coimbatore visited the herbarium for various purposes at different occasions like Science day, Environment day, CSIR and NBRI foundation days, etc. The researchers working in the area of taxonomy and other botanical sciences from various organisations also visit the herbarium for the study of herbarium specimen housed here.

## Plant Identification and Certification

CSIR-NBRI herbarium has been designated as 'National Repository of Indian Flora' by National Biodiversity Authority, Govt. of India. The herbarium provides services to general people and researchers in plant identification and authentication and preserving voucher specimens for future records. During this year the plant specimens received from different organisations/research personnel such as DIBER, DRDO, Haldwani; Naturex India Pvt. Ltd. Mumbai; AMITY University, Lucknow; Ramnarain Ruia Autonomous College, Mumbai; Department of Pharmaceutical Sciences, Kumaun University, Nainital and Dept. of Botany, Gorakhpur University, Gorakhpur were identified and certificates were issued.

**Tikam Singh Rana**

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**Genetic diversity and population genetics, phylogeny, phylogeography, DNA barcoding and bio-prospection of plant resources.**

## *Bergenia ciliata* (Haw.) Sternb. (Saxifragaceae)

*Bergenia ciliata* is a perennial rhizomatous herb predominantly found in temperate and sub-temperate regions of the Himalaya at an elevation of 350-4000 m from Afghanistan to eastward in Pakistan, India, Nepal and Bhutan. In India it occurs mostly in humid, damp, moist to dry and open to shady habitats; on rock surfaces, crevices, hill slopes and near water channels. It is commonly known as '*Pashanbheda*' or stone breaker because of its habitat characteristics and applications in dissolving urinary calculi in Indian System of Medicine. Traditionally, the plants of *B. ciliata* are used in asthma, boils, cuts, wounds, burns, fever, liver complaints, ophthalmia, piles, thirst, kidney stones and urinary complaints, and for diarrhoea in cattle. Due to the presence of various bioactive metabolites, *B. ciliata* is used as a chief botanical source for preparations of various Herbal and Unani medicines. It constitutes one of the major ingredients of indigenous drugs like Cystone and Calcuri used clinically to treat kidney and urinary bladder stones. The present study was undertaken to examine the pattern of genetic variability and population structure in *B. ciliata* occurring naturally in Indian Himalayan Region(IHR), using two SPAR markers namely, Directed Amplification of Minisatellite region DNA (DAMD) and Inter Simple Sequence Repeats (ISSR).A total of 11 populations comprising 111 accessions sampled from Jammu & Kashmir (15), Himachal Pradesh (28), Uttarakhand (43), West Bengal (13) and Sikkim (12) were analyzed for extent of genetic variability and population structure in *B. ciliata* (Table 1).

**Table 1. Sample sites and habitat conditions of *B. ciliata* in Indian Himalayan Region**

| Population ID | Accession No's | Site | Habitat condition | Latitude (°N) | Longitude (°E) | Elevation (m) |
|---|---|---|---|---|---|---|
| **DGF (24)** | DGF (1-15) | Dhara Mohara Nallah, Dera Gali Forest, Rajouri, J&K | Moist, shady places, on rocks, among crevices and on big boulders along the water stream | 33°35.349' | 074°21.503' | 2036 |
| **KUL (250)** | KUL (16-30) | Kothi to Rahla, Kullu, HP | Moist, shady places, on rocks, among crevices and big boulders on gentle slopes | 32°20.885' | 077°13.303' | 2277 |
| **SHM (150)** | SHM (31-37) | Shimla, HP | Dry and open slopes | 31°06.476' | 077°10.105' | 2135 |
| **KUF (250)** | KUF (38-43) | Kufri, HP | Dry and partially shady rocky slopes | 31°05.826' | 077°16.380' | 2529 |
| **GWS (100)** | GWS (44-51) | Govind Wildlife Sanctuary, UK | Moist, on rocks and gentle slopes | 31°04.498' | 078°14.955' | 2041 |
| **RNK (100)** | RNK (52-58) | Ranikhet, UK | Dry, open rocky slopes under pine trees | 29°39.917' | 079°32.148' | 1669 |
| **NTL (150)** | NTL (59-64) | Kilbury Road, Nainital, UK | Dry, on almost vertical rocky slopes | 29°25.138' | 079°25.771' | 2187 |
| **BWS (350)** | BWS (65-77) | Binsar Wildlife Sanctuary, Almora, UK | Dry, on partially shady and gentle sandy slopes under pine forest | 29°40.988' | 079°43.789' | 1923 |
| **PTH (150)** | PTH (78-86) | Dewalthal, Pithoragarh, UK | Moist, on almost vertical slopes | 29°41.089' | 080°13.091' | 1280 |
| **DRJ (70)** | DRJ (87-99) | Darjeeling, WB | Dry, among the stone wall gaps | 27°03.23.1' | 088°15.16.1' | 2081 |
| **PNL (50)** | PNL (100-111) | Penlong, East Sikkim, SK | Moist, among the stone wall gaps and on rocky slopes | 27°22.445' | 088°37.328' | 1646 |

Abbreviations: DGF = Dera Gali Forest; KUL = Kullu; SHM = Shimla; KUF = Kufri; GWS = Govind Wildlife Sanctuary; RNK = Ranikhet; NTL = Nainital; BWS = Binsar Wildlife Sanctuary; PTH = Pithoragarh; DRJ = Darjeeling; PNL = Penlong; J&K = Jammu and Kashmir; HP = Himachal Pradesh; UK = Uttarakhand; WB = West Bengal; SK = Sikkim [Source: Tiwari *et al.* (2020)].

### Detection of polymorphism using DAMD and ISSR markers

Amplification of nine DAMD primers with 111 *B. ciliata* accessions resulted into 131 bands, varied from 100 to 2000 bp in size, of which 119 were polymorphic, revealing 90.27% polymorphism. Primer FVIIex8 produced the highest number of polymorphic bands (16) along with maximum PIC (0.38) while, primer URP9F produced the least number of polymorphic bands (06) and minimum PIC (0.13). Out of nine DAMDs employed, six primers (6.2H+, 33.6, FvIIex8, FvIIex8C, HVR and URP2R) resulted in 100% polymorphic bands, whereas primer URP9F revealed the least levels of polymorphism (46.15%). The amplification of fifteen ISSR primers generated 240 bands ranging from 150 to 2000 bp in size, of which 215 were polymorphic, revealing 89.96% polymorphism. Primer UBC 807 produced highest number of polymorphic bands (20) and maximum PIC (0.44) whereas primers UBC 840 and 891 resulted into least number of polymorphic bands (10) and three primers UBC 823, UBC 836 and UBC 842 showed minimum PIC (0.26) values. Five ISSR primers UBC 807, UBC 808, UBC 811, UBC 834 and UBC 835 produced 100% polymorphic bands, whereas UBC 842 revealed least polymorphism (70%). Comparatively, ISSRs revealed slightly higher values of mean PIC (0.32) than DAMD markers (0.28). However, both DAMD and ISSR markers revealed almost similar levels of polymorphism (90.27% and 89.96%, respectively) across 111 accessions of *B. ciliata*. The cumulative analysis of (9 DAMD and 15 ISSR) marker data revealed a total 371 amplified bands, of which 334 were polymorphic with 90.11% average polymorphism and 0.30 mean PIC value. Comparative evaluation of the two marker systems in respect of polymorphic information content, diversity index, effective multiplex ratio and marker index values revealed that the ISSR markers were more informative (PIC = 0.32, DI = 5.10, EMR = 12.84, MI = 4.56) than DAMD markers (PIC = 0.28, DI = 4.18, EMR = 12.01, MI = 3.78) The pair-wise genetic distances ranged from 0.11 (Bc93–Bc94) to 0.64 (Bc04–Bc86), with an average of 0.37. Mantel correlation (*r*) test between three data sets ISSR, DAMD and cumulative, showed that cumulative v/s ISSR data (0.92) are the best fit, followed by cumulative v/s DAMD (0.73), and DAMD v/s ISSR (0.41). The correlation found was significantly high between ISSR and cumulative data, while DAMD showed a weak correlation with cumulative data as well as with ISSR data, suggesting the use and suitability of both marker systems to estimate the genetic diversity in *B. ciliata*.

### Estimation of genetic diversity

The levels of polymorphism ranged from 45.01% (SHM) to 73.05% (BWS) with a mean 56.95% among populations; whereas, estimates of polymorphism detected at species level (90.03%) were substantially higher (Table 2). Relatively, number of observed alleles ($N_a$) was found maximum in BWS followed by

**Table 2.Intra-population diversity statistics of *B. ciliata* populations were computed using POPGENE (Ver. 1.32)**

| Population* (sample size) | PB | %P | Mean $N_a$ (SD) | Mean $N_e$ (SD) | Mean H (SD) | Mean I (SD) | Mean $H_T$ (SD) | Mean $H_S$ (SD) | $G_{ST}$ | $N_m$ |
|---|---|---|---|---|---|---|---|---|---|---|
| DGF(15) | 247 | 66.58 | 1.66(0.47) | 1.38(0.38) | 0.22(0.19) | 0.33(0.28) | | | | |
| KUL(15) | 266 | 71.70 | 1.71(0.45) | 1.42(0.37) | 0.24(0.19) | 0.37(0.27) | | | | |
| SHM(7) | 167 | 45.01 | 1.45(0.49) | 1.28(0.37) | 0.16(0.20) | 0.24(0.28) | | | | |
| KUF(6) | 171 | 46.09 | 1.46(0.49) | 1.30(0.38) | 0.17(0.20) | 0.25(0.29) | | | | |
| GWS(8) | 226 | 60.92 | 1.60(0.48) | 1.35(0.37) | 0.20(0.19) | 0.31(0.28) | | | | |
| RNK(7) | 200 | 53.91 | 1.53(0.49) | 1.30(0.35) | 0.17(0.19) | 0.27(0.27) | | | | |
| NTL(6) | 184 | 49.60 | 1.49(0.50) | 1.31(0.37) | 0.18(0.20) | 0.27(0.29) | | | | |
| BWS(13) | 271 | 73.05 | 1.73(0.44) | 1.41(0.37) | 0.24(0.19) | 0.36(0.26) | | | | |
| PTH(9) | 199 | 53.64 | 1.53(0.49) | 1.35(0.39) | 0.20(0.21) | 0.29(0.29) | | | | |
| DRJ(13) | 197 | 53.10 | 1.53(0.49) | 1.31(0.37) | 0.18(0.20) | 0.27(0.28) | | | | |
| PNL(12) | 196 | 52.83 | 1.52(0.49) | 1.32(0.38) | 0.18(0.20) | 0.27(0.29) | | | | |
| Mean | 211.27 | 56.95 | 1.56(0.48) | 1.34(0.37) | 0.19(0.20) | 0.29(0.28) | | | | |
| ALL LOCI(111) | 334 | 90.03 | 1.90(0.30) | 1.49(0.34) | 0.29(0.17) | 0.43(0.22) | 0.28(0.02) | 0.19(0.01) | 0.30 | 1.16 |

*Abbreviations*: Population = population code; PB = number of polymorphic loci; %*P* = percentage of polymorphic bands; $N_a$ = observed number of alleles; $N_e$ = effective number of alleles; *H* = Nei's gene diversity; *I* = Shannon's information index; $H_T$ = total genetic diversity; $H_S$ = genetic diversity within populations; $G_{ST}$ = relative magnitude of genetic differentiation among populations; $N_m$ = gene flow among populations; SD= standard deviation of mean values.

*The numbers in parenthesis in each population are the number of accessions from that population used in the present study. [Source: Tiwari *et al.* (2020)]

KUL and DGF populations, while GWS, RNK, PTH, DRJ and PNL showed moderate and NTL, KUF and SHM the lowest numbers of alleles. A similar pattern of diversity for effective number of alleles, Nei's gene diversity and Shannon's diversity index was observed with the highest values in KUL ($N_e$ = 1.42, $H$ = 0.24, $I$ = 0.37) and the least in SHM populations ($N_e$ = 1.29, $H$ = 0.16, $I$ = 0.24). Overall genetic diversity at species level ($N_a$ = 1.90, $N_e$ = 1.49, $H$ = 0.29, $I$ = 0.43) was much higher than the mean diversity found at population level ($N_a$ = 1.56, $N_e$ = 1.34, $H$ = 0.19, $I$ = 0.29) in *B. ciliata* occurring naturally in IHR (Table 2).

**Evaluation of genetic differentiation and population structure**

Total genetic diversity ($H_T$) and genetic diversity within populations ($H_S$) were 0.28 and 0.19, respectively. The proportion of the genetic variations contributed by the differences among populations ($G_{ST}$) was 0.30, thus revealing 70% of the total genetic variations within the populations. A $G_{ST}$ derived gene flow ($N_m$ = 1.16) showed moderate level of migration of genetic material among populations of *B. ciliata* (Table 2). The higher inter-population genetic distances ranged from 0.06 (NTL v/s BWS) to 0.19 (DGF v/s PTH). The corresponding geographic distances ranged from 10.03 km (SHM v/s KUF) to 1530 km (DGF v/s PNL) among populations of *B. ciliata* sampled from different habitats in IHR (Table 3). The hierarchical partitioning of variance at three strata as determined by AMOVA revealed higher proportion of genetic variance within populations (73%) followed by among populations (17%) and least among the two Himalayan regions (10%) (Table 4). The levels of genetic diversity based on $G_{ST}$ and AMOVA are corroborating with each other, and further support the variance found within populations.

The UPGMA dendrogram based on Nei's genetic distances grouped all the 11 natural populations into two major groups (I and II) (Fig. 1). All the populations sampled from Western Himalaya grouped together in Cluster I, while both the Eastern Himalayan populations (DRG and PNL) grouped together into cluster II. PTH population clearly segregated out from rest of the Western Himalayan populations of subgroup Ia, showing its distant relationship to form an independent subgroup Ib. On the basis of spatial relationships of genetic distances, PCoA plot grouped all the 111 accessions from 11 populations into two clusters (I and II) along the three axes of the plot (Fig. 2). Cluster I grouped together 25 accessions from DRJ

**Table 3. Inter-population Nei's genetic and geographical distances of *B. ciliata* populations. Above the diagonal are Nei's genetic distance and below the diagonal are pair-wise geographic distance values (km). The values in bold are either minimum or maximum values, and cells with **** are for the identical populations***

| Population ID | DGF | KUL | SHM | KUF | GWS | RNK | NTL | BWS | PTH | DRJ | PNL |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **DGF** | **** | 0.1018 | 0.1592 | 0.1335 | 0.1082 | 0.1097 | 0.124 | 0.0973 | 0.1855 | 0.1426 | 0.1713 |
| **KUL** | 300.64 | **** | 0.0831 | 0.0711 | 0.0838 | 0.1123 | 0.0995 | 0.0896 | 0.1321 | 0.1530 | 0.1462 |
| **SHM** | 381.80 | 137.99 | **** | 0.0723 | 0.1064 | 0.1488 | 0.1150 | 0.1202 | 0.1759 | 0.1847 | 0.1818 |
| **KUF** | 389.52 | 139.19 | 10.03 | **** | 0.0823 | 0.1307 | 0.1036 | 0.0981 | 0.1772 | 0.1679 | 0.1721 |
| **GWS** | 460.15 | 171.72 | 102.98 | 93.00 | **** | 0.0773 | 0.0850 | 0.0814 | 0.146 | 0.1579 | 0.1625 |
| **RNK** | 656.06 | 370.96 | 278.01 | 269.18 | 199.51 | **** | 0.0775 | 0.0661 | 0.1615 | 0.1446 | 0.1623 |
| **NTL** | 667.76 | 387.88 | 287.09 | 278.77 | 216.24 | 29.26 | **** | 0.0600 | 0.1367 | 0.1275 | 0.1413 |
| **BWS** | 668.56 | 380.68 | 292.31 | 283.27 | 210.05 | 18.85 | 41.31 | **** | 0.0970 | 0.1099 | 0.1195 |
| **PTH** | 704.20 | 411.35 | 332.54 | 323.19 | 244.06 | 65.96 | 81.81 | 47.18 | **** | 0.1679 | 0.1804 |
| **DRJ** | 1516.75 | 1216.25 | 1166.90 | 1157.13 | 1069.53 | 900.72 | 903.18 | 883.37 | 838.52 | **** | 0.0902 |
| **PNL** | 1529.59 | 1229.64 | 1185.56 | 1175.70 | 1086.85 | 923.27 | 927.19 | 905.57 | 860.01 | 51.00 | **** |

*[Source: Tiwari *et al.* (2020)]

**Table 4. AMOVA analysis carried out using GenAlEx program (Ver. 6.5) for the cumulative* (DAMD and ISSR) data of 111 *B. ciliata* accessions***

| Source of Variations | Degrees of Freedom | Sum of Squares | Mean of Squares | Variance Component | Percentage of Variations |
|---|---|---|---|---|---|
| Among Regions | 2 | 758.510 | 379.255 | 6.101 | 10% |
| Among Populations | 8 | 1164.159 | 145.520 | 10.530 | 17% |
| Within Populations | 100 | 4395.565 | 43.956 | 43.956 | 73% |
| Total | 110 | 6318.234 | | | 100% |
| Degree of Freedom: Independent values that can be assigned to a statistical distribution | | | | | |

*[Source: Tiwari *et al.* (2020)]

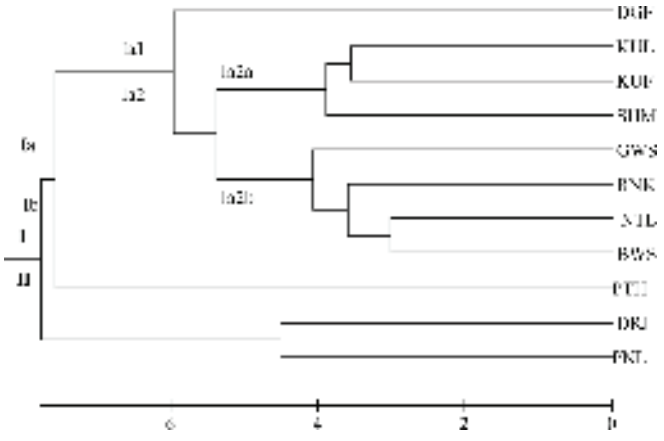


Fig. 1: UPGMA dendrogram showing relationships among 11 populations of *B. ciliata* in IHR and population codes are as given in the Table 1. [Source: Tiwari *et al.* (2020)]

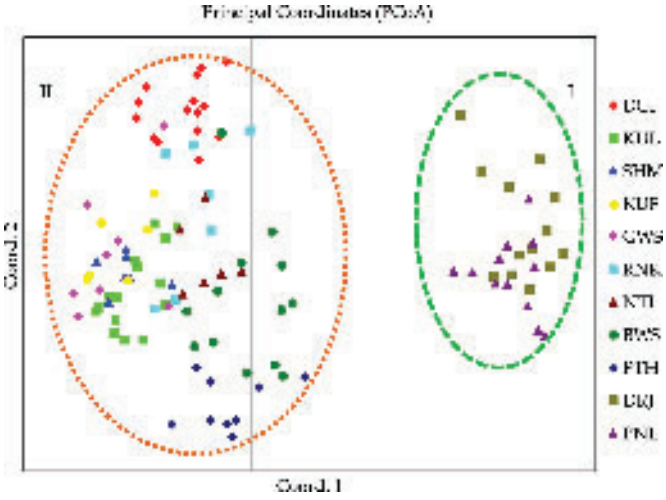


Fig. 2: Principal Coordinate Analysis showing clustering of *B. ciliata* populations in IHR. The population codes are as given in the Table 1. PCoA was performed in the program GenAlEx (Ver. 6.5) [Source: Tiwari *et al.* (2020)]

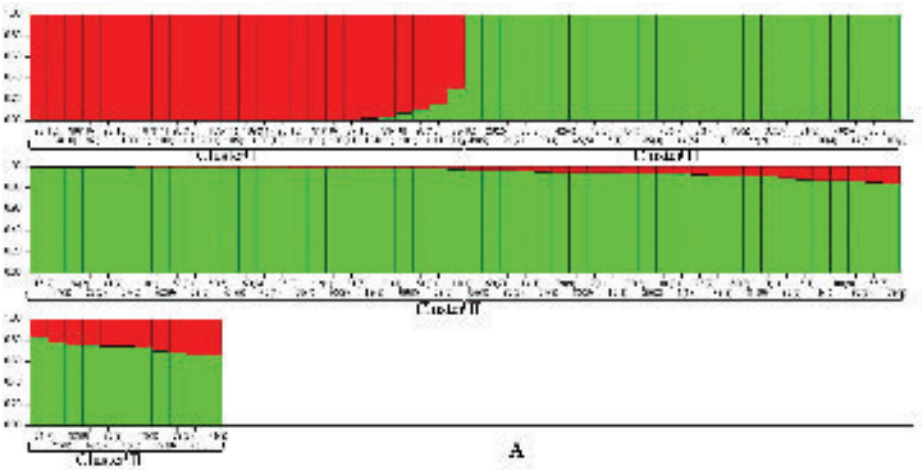
and PNL populations from Eastern Himalayas, while cluster II contained the remaining 86 accessions belonging to nine geographic populations from Western Himalayas. The three axes of the plot accounted for 27.56%, 22.13% and 16.65% of the total variations, respectively.

Analysis of population genetic structure of *B. ciliata* using Bayesian clustering revealed two genetic clusters ($k$ = 2). The cluster I contained 25 individuals from two natural populations of Eastern Himalaya (DRJ and PNL) showed an average ancestry membership participation coefficient of 96.9% (DRJ = 96.3% and PNL = 96.55%). Cluster II comprised of 86 accessions of nine populations from Western Himalaya showed an average ancestry membership participation of 93.8% (DGF = 95.9%, KUL = 98%, SHM = 99.2%, KUF = 99.4%, GWS = 99.4%, RNK = 96.8%, NTL = 92.5%, BWS = 80.5%, PTH = 88.2%). Therefore, the assignment of the assumed 11 geographic populations into two genetic clusters comprising nine populations of Western Himalayas and the two populations of Eastern Himalayas revealed the existence of two natural genetic populations of *B. ciliata* in IHR (Fig. 3). In the present study, all the three methods of clustering of populations, neighbor-joining, Bayesian clustering and PCoA were found in congruent with each other and support the admixture of individuals among the natural populations.

The isolation by distance (IBD) analysis performed using Mantel's correlation test revealed a positively significant correlation between pair-wise genetic and geographic distances of populations ($r$ = 0.662; $p$ = 0.001), indicating the role of geographic isolation in shaping the present population structure of *B. ciliata* in IHR. The analysis of genetic diversity at population level revealed that KUL and BWS populations harbour maximum levels of genetic diversity, whereas SHM population showed minimum levels of the diversity among the 11 populations. The higher levels of diversity among KUL and BWS populations may be due to comparatively larger population size and favourable habitat conditions such as availability of soil moisture, gentle slopes and shady conditions (low light intensity). The SHM population was growing at dry and exposed site, attenuated soil moisture, fragmentation and degradation of habitats and other anthropogenic pressures operating on the specific habitats could be the reasons for low genetic diversity in SHM population. The levels of genetic diversity found in *B. ciliata* were much higher at species level than the mean diversity observed at population level and these levels of polymorphism were further supported by the average genetic distances estimated among pair of accessions of the species.

## *Sapindus emarginatus* Vahl (Sapindaceae)

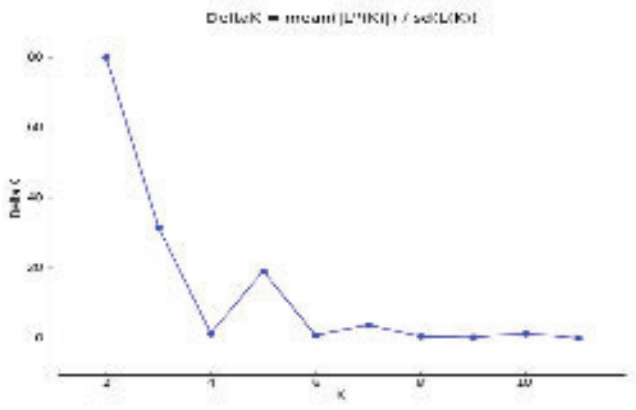
*Sapindus emarginatus*, also known as 'Indian Soap nut', is significantly important for saponin content in its fruits. However, its current population in India is heavily fragmented due to lack of sustainable harvesting practices. Moreover, changing climatic regimes may further limit its distribution and possibly compromise the survival of the species in nature. The aim of the present study was to predict the future



A

| Pop ID | Inferred Clusters | | No. of Individuals |
|---|---|---|---|
| | Cluster I | Cluster II | |
| 1 | 0.041 | 0.959 | 15 |
| 2 | 0.019 | 0.981 | 15 |
| 3 | 0.008 | 0.992 | 7 |
| 4 | 0.006 | 0.994 | 6 |
| 5 | 0.005 | 0.995 | 8 |
| 6 | 0.031 | 0.969 | 7 |
| 7 | 0.074 | 0.926 | 6 |
| 8 | 0.194 | 0.806 | 13 |
| 9 | 0.117 | 0.883 | 9 |
| 10 | 0.963 | 0.037 | 13 |
| 11 | 0.975 | 0.025 | 12 |

B



C

| K | Reps | Mean LnP(K) | Stdev LnP(K) | Ln'(K) | Ln''(K) | Delta K |
|---|---|---|---|---|---|---|
| 1 | 20 | -38141.110 | 0.808 | — | — | — |
| 2 | 20 | -35562.585 | 9.12 | 2581.525 | 728.480 | 79.946 |
| 3 | 20 | -33709.540 | 13.532 | 1853.045 | 426.605 | 31.523 |
| 4 | 20 | -32283.100 | 210.933 | 1426.440 | 332.055 | 1.578 |
| 5 | 20 | -31188.715 | 20.105 | 1094.385 | 382.765 | 19.038 |
| 6 | 20 | -30477.085 | 71.062 | 711.629 | 58.945 | 0.842 |
| 7 | 20 | -29825.320 | 125.130 | 651.775 | 467.120 | 3.733 |
| 8 | 20 | -29640.665 | 893.094 | 184.655 | 447.570 | 0.501 |
| 9 | 20 | -29018.440 | 841.859 | 633.225 | 246.650 | 0.293 |
| 10 | 20 | -28623.863 | 907.235 | 385.575 | 1217.920 | 1.342 |
| 11 | 20 | -29455.210 | 3888.792 | -832.345 | 385.305 | 0.094 |
| 12 | 20 | -29023.250 | 5662.877 | -467.040 | — | — |

D

Fig. 3: Genetic structure of *B. ciliata* inferred from Bayesian clustering, A. Bar plots representing individuals arranged according to its most likely ancestry, B. Table showing number of individuals and average membership fractions in two genetic clusters, C. Graph showing the maximum value of Δk estimated by Evanno method, D. Evanno table showing maximum value of K [Source: Tiwari *et al.* (2020)].

distribution range of *S. emarginatus*; identify the bioclimatic variables limiting this distribution and to evaluate its adaptive fitness and genomic resilience towards these variables. To determine future species distribution range and identify limiting bioclimatic variables, we applied two different ecological niche models (ENMs; BioClim and MaxEnt) on real occurrence data (n=88 locations). The adaptive fitness of the species was evaluated by quantifying the genetic variability with AFLP markers and marker-environmental associations, using AFLP-associated Bayesian statistics.

A significant correlation ($p$<0.05, $r$=0.85) was found between the predictions by both the models (BioClim and MaxEnt) for the species distribution on its range of occurrence in the baseline (the year 2030) and future (the year 2100) climatic regimes. Therefore, the species distribution prediction and output obtained from the MaxEnt was applied for all further estimations. The comparison between the species distribution patterns predicted for the baseline and future climatic regimes resulted into 77% proportion of overlapping range. The niches from Deccan peninsula biogeographic region were predicted to be the most suitable for survival of the species. The niches of species occurrence at Semi-arid biogeographical region showed comparatively less suitability for the survival of species for the year 2100 (Fig. 4). During prediction, MaxEnt resulted no change in area under curve (AUC = 0.99 ±0.0) for both climatic regimes. The prediction of limiting bioclimatic variables (by BioClim) and their responses to the probability of presence (by MaxEnt) resulted in the relative proportion of maximum temperature ($T_{MAX}$=43.10%), and annual precipitation (MAP=27.10%) with the highest contribution in the model predictions (Fig. 5, Table. 5). The species

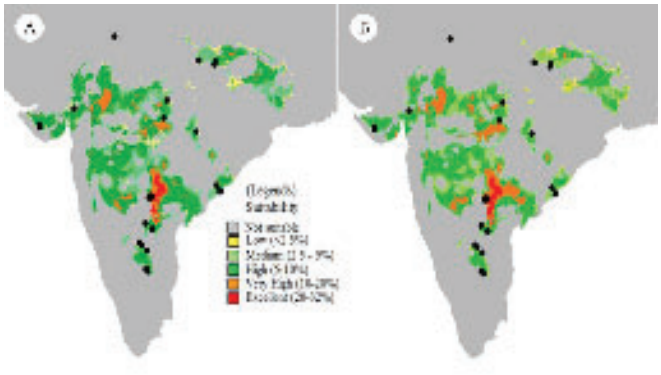


Fig. 4: Predicted suitability of ecological niches for the occurrence of *S. emarginatus* in the years (A) 2030 and (B) 2100 supported by the both BioClim and Maxent algorithm. Black dots represent the sampled locations [Source: Pal *et al*. (2020)].

niches were found with sensitive response towards $T_{MAX}$ (<10 $^0$C), temperature range ($T_{RANGE}$; >10 $^0$C) and increased MAP (<1000mm).

The AFLP primers amplified 1957 loci (103±39.37 loci/primer) with 94.79±6.43% polymorphism (1859 polymorphic loci), 0.65±0.02 major allele frequency (MAF) and 0.33±0.01 polymorphic information content (PIC) (Table. 6). The 49 loci amplified by the AFLP primers ACG/CTA and ACA/CAG were excluded from the analysis due to low numbers of amplified loci (<50) and further genetic analysis was performed with the 1908 loci amplified by the 17 AFLP markers. The Bayesian model-based analysis performed with Hickory resulted into the lowest deviance information criteria (DIC) value (35357.20) supporting the suitability of full-model (inbreeding) among the four models for the data. The average heterozygosity (Hs value) generated for the locations was 0.40±0.0. For the samples as a whole, panmictic heterozygosity (Ht) was 0.43, whereas θ-I and *f* ($F_{IS}$) values were 0.18 and 0.98, respectively. The observed heterozygosity (Ho) ranged from 0.42±0.0 to 0.44±0.0 with an average of 0.43±0.01 (Table 7) while $F_{ST}$ value was 0.048. Allahabad (AL) population revealed the highest number of common alleles<=50%, and no rare and common (<=25%) allele was found in the populations analyzed.

The Jaccard's genetic similarity coefficient among the genotypes ranged from 0.24 to 0.61 with an average of 0.38±0.05. The principal coordinate analysis (PCoA) differentiated the genotypes into three clusters (Fig. 6A). Few genotypes from AL, KA, and VS populations (Table 8) were found clustering in distinct clusters but most of them are highly admixed with the genotypes of other locations. Analyzing

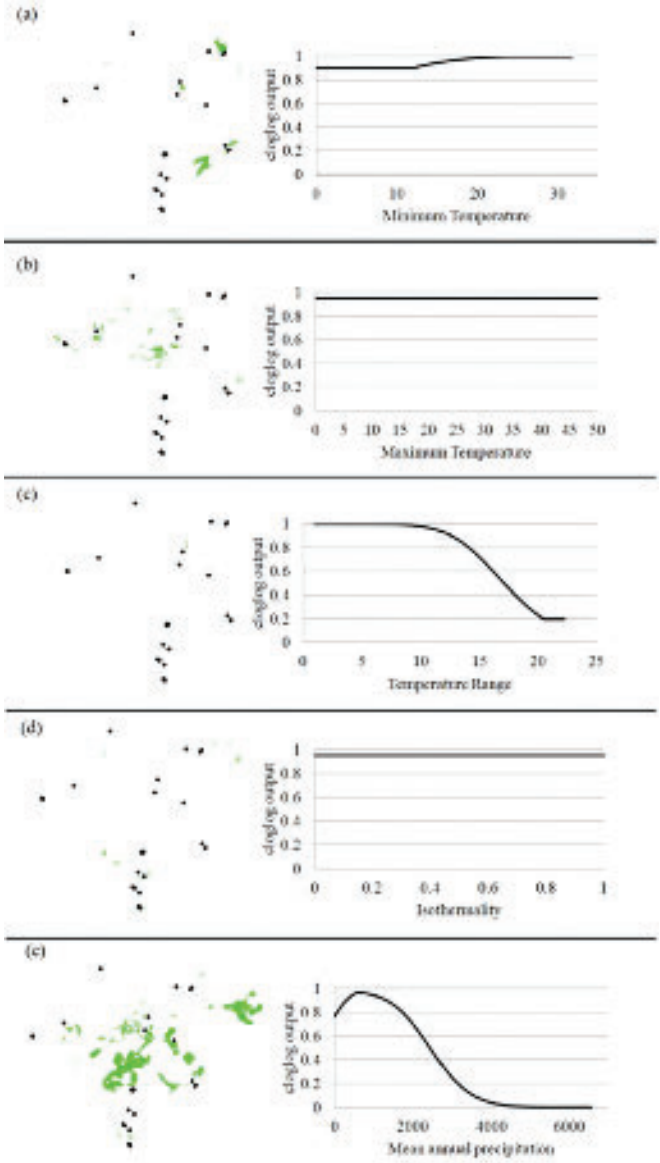



Fig. 5: Responses of climatic variables *viz*. (a) minimum temperature ($^0$C), (b) maximum temperature ($^0$C), (c) temperature range ($^0$C), (d) isothermality, and (e) mean annual precipitation (mm) as limiting factor influencing the occurrence sites of *S. emarginatus* (in left) with response curve (in right). Black dots represent the sampled locations [Source: Pal *et al*. (2020)]

**Table 5. Estimates of relative contribution (in %) of the climatic variables to the Maxent model and of AFLP loci in significant association with the climatic variables**

| Approach/Models | MAP | I | $T_{RANGE}$ | $T_{MAX}$ | $T_{MIN}$ |
|---|---|---|---|---|---|
| ENM/ Maxent | 27.10 | 11.30 | 2.20 | 43.10 | 16.40 |
| GWAS/ MLM | 7.55 | 20.75 | 39.62 | 7.55 | 24.53 |

ENM/Maxent- ecological niche modeling based on maximum entropy , GWAS/MLM – genome-wide association study based on mixed linear modeling, MAP- mean annual precipitation in mm, I- isothermality, $T_{RANGE}$- diurnal temperature range in $^0$C, $T_{MAX}$- maximum temperature $^0$C, $T_{MIN}$- minimum temperature $^0$C [Source: Pal *et al*. (2020)]

**Table 6. Genetic information revealed by the 19 AFLP primer combinations on 41 genotypes of *S. emarginatus**

| Primer Combinations *EcoRI/MseI* | AL | %P | PIC |
|---|---|---|---|
| AGC/CAT | 99 | 94.95 | 0.32±0.05 |
| AGC/CTA | 112 | 99.11 | 0.33±0.03 |
| AGC/CTG | 110 | 100.00 | 0.34±0.03 |
| ACA/CAT | 157 | 92.99 | 0.32±0.06 |
| ACA/CAG | 27 | 96.30 | 0.33±0.04 |
| ACA/CTC | 110 | 100.00 | 0.33±0.03 |
| AAC/CTG | 129 | 100.00 | 0.32±0.07 |
| AAG/CAG | 126 | 91.27 | 0.31±0.06 |
| ACT/CTG | 110 | 95.45 | 0.33±0.06 |
| ACT/CAT | 98 | 100.00 | 0.35±0.03 |
| ACT/CAA | 135 | 100.00 | 0.34±0.02 |
| ACT/CAG | 111 | 85.59 | 0.33±0.05 |
| ACT/CTT | 156 | 100.00 | 0.34±0.02 |
| ACC/CAC | 136 | 89.71 | 0.33±0.06 |
| ACC/CAT | 130 | 90.77 | 0.33±0.05 |
| AGG/CAT | 84 | 88.10 | 0.32±0.06 |
| AGG/CTA | 53 | 100.00 | 0.34±0.02 |
| AGG/CTG | 52 | 76.92 | 0.33±0.04 |
| ACG/CTA | 22 | 100.00 | 0.34±0.02 |
| Average | 103±39.37 | 94.79±6.43 | 0.33±0.01 |

AL- the number of amplified loci, %P- the percentage of polymorphism, PIC- polymorphic information content, ±- standard deviation
* [Source: Pal *et al.* (2020)]

the results in program STRUCTURE, based on the highest Delta-K value, the admixture model with independent allelic frequencies was found the most appropriate for our dataset through the program STRUCTURE HARVESTER. The most suitable cryptic population number was four (*K*=4). The bar plot showed admixture in populations, and KA population distinctly. The populations VS, GJ, AL, and RJ were admixed, whereas GJ population was

**Table 7. Genetic diversity of *S. emarginatus* based on AFLP markers**

| Regions | Location | N | He | Hs | Ho |
|---|---|---|---|---|---|
| Gangetic Plain | AL | 15 | 0.35±0.01 | 0.41±0 | 0.43±0 |
| | VS | 7 | 0.30±0.06 | 0.40±0 | 0.43±0 |
| Semi-Arid | RJ | 5 | 0.28±0.02 | 0.40±0 | 0.44±0 |
| | GJ | 9 | 0.33±0.02 | 0.40±0 | 0.44±0 |
| Deccan Peninsula | KA | 5 | 0.26±0.02 | 0.40±0 | 0.42±0 |
| **Average (±SD)** | | | 0.30 ±0.04 | 0.40 ±0 | 0.43± 0.01 |

N- the number of genotypes investigated, ±- standard deviation, He- expected heterozygosity, Hs- panmictic heterozygosity resulted from Hickory, Ho- observed heterozygosity resulted from AFLP-Surv [Source: Pal *et al.* (2020)].

found in admixing with KA population. Populations like AL and VS were also found admixed distinctly. The $F_{ST}$ values on these clusters ranged from 0.02 to 0.08. The pair-wise $F_{ST}$ values among the locations ranged between 0.015 to 0.128 and the Nm exchanged among the locations ranged between 3.39 (AL-KA) to 32.39 (GJ-VS). The Mantel's test revealed significant correlation ($p$<0.01) between genetic distances and geographical distances matrix and non-significant correlation (p>0.05) was found between the number of migrants (Nm) exchanged among locations to geographic distance matrix and altitudinal gradient ($r$=0.59). The variation among locations was 6.46±1.34% and within location among genotypes was 91.63±0.31%.

In order to detect the outlier loci with a signature of adaptation, the only locus E-AGC/M-CTG-71 ($F_{ST}$ = 0.23) was found with the posterior odd ($\log_{10}$PO) >0.5 (Fig. 6B). For the rest of the loci, their corresponding $F_{ST}$ values were found real positive. Linkage disequilibrium (LD) was confirmed to avoid

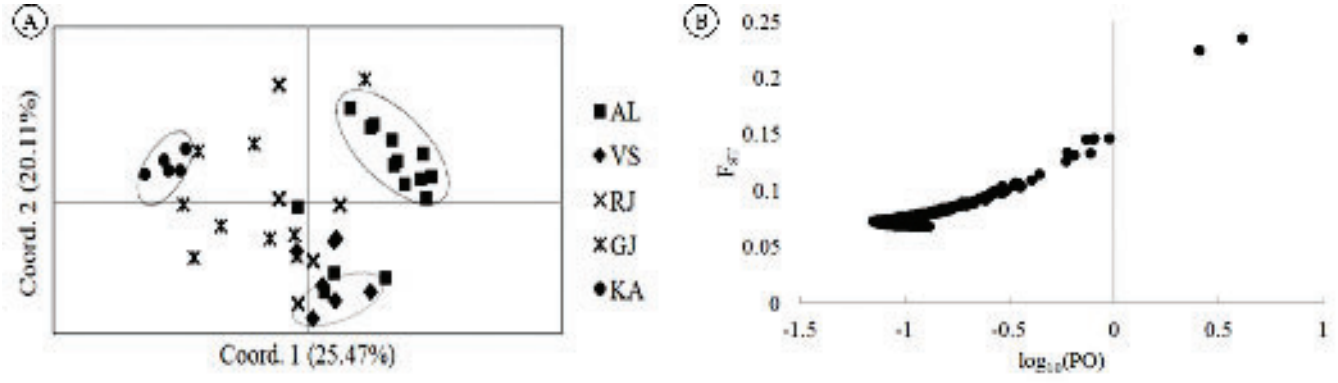



Fig. 6: A. The PCoA differentiating 41 genotypes into three clusters. Few genotypes from AL, KA, and VS were found representing distinct clusters but the most of them are highly admixed with the genotypes of other locations, B. Bayescan analysis resulting FST values on Bayes Factor, i.e. Log10 (PO) for 1859 AFLP loci, confirms only one locus namely E-AGC/M-CTG-71 as an outlier (Log10 (PO) >0.5) depicting substantial evidence to be in balancing selection [Source: Pal *et al.* (2020)].

**Table 8. Geo-climatic variables at locations of *S. emarginatus* populations in different bio-geographical regions of India**

| Bio-geographic Regions | States | Locations | N | Alt (m) | T (°C) | MAP (mm) |
|---|---|---|---|---|---|---|
| Gangetic Plain | Uttar Pradesh | Allahabad (AL) | 15[a,b] | 88±0 | 27.80±7.35 | 1090±0 |
| | | Varanasi (VS) | 7[a,b] | 78.14±1.34 | 28.14±0.05 | 1095±21.47 |
| Semi-Arid | Rajasthan | Jaipur (JP) | 5[a,b] | 416±0 | 27.10±0 | 668±0 |
| | Gujarat | Aanand (AD) | 1[a,b] | 105±30.41 | 27.70±0.53 | 1331.67±74.10 |
| | | Junagarh (JG) | 8[a,b] | 106.25±27.50 | 27.60±0.20 | 1339.25±55.50 |
| Deccan Peninsula | Karnataka | Kolar (KO) | 5[a,b] | 875±34.66 | 25.32±0.21 | 849.80±27.13 |
| | Telangana | Hyderabad (HY) | 17[b] | 547.20±24.14 | 27.80±0.2 | 1117±33.78 |
| | Andhra Pradesh | Vizag (VP) | 10[b] | 108.33±91.90 | 28.73±0.55 | 1189.67±135.50 |
| | | Kurnool (KU) | 7[b] | 271±41.61 | 29.50±0.26 | 919±30.47 |
| | | Anantpur (AN) | 7[b] | 424±110 | 28.46±0.68 | 723±56.92 |
| | Madhya Pradesh | Jabalpur (JB) | 1[b] | 361±0 | 26.80±0 | 1301±0 |
| | | Seoni (SE) | 1[b] | 608±0 | 26.50±0 | 1288±0 |
| | Chhattisgarh | Raipur (RP) | 4[b] | 281±0 | 28.5±0 | 1452±0 |
| | | | CV% | 74.40 | 3.90 | 22.51 |

N- the number of genotypes, Alt (m)- altitude in meters, T (°C)- temperature in °C, MAP (mm)- mean annual precipitation in millimeter, [a]-used for DNA profiling, [b]-used for species distribution modeling, ± - standard deviation, CV- coefficient of variation [Source: Pal *et al*. (2020)].

false-discovery in genome-wide association study (GWAS). Among all loci pairs, only 1.99% were found in significant LD ($p$<0.01). Major LD decay was observed within a distance of 100 base pair (bp) and the length of LD block extended up to 1450bp. The mixed linear model (MLM) based analysis detected a significant ($p$<0.001) association of 65 loci (3.59% out of 1810 polymorphic loci) from 15 AFLP markers with bioclimatic variables and altitude). Among these 65 loci, the highest proportion (32.30%) was found associated with $T_{RANGE}$ and the lowest proportion (6.15%) was with MAP and $T_{MAX}$. Among 1651 possible combinations of these 65 loci, only 4.54% were found in significant ($p$<0.001) LD.

We found 77% overlap between the baseline (2030) and predicted (2100) species distribution ranges, which were primarily determined by maximum temperature ($T_{MAX}$) and mean annual precipitation (MAP). The $T_{MAX}$ and MAP contributed 43.1% and 27.1%, respectively to ENM model prediction. Furthermore, AFLP loci significantly associated with bioclimatic variables, and $T_{MAX}$ and MAP represent the lowest proportion (6.15%), confirming to the severe response of the species genome towards these variables. Nevertheless, the very low Linkage disequilibrium (LD) in these loci (4.54%) suggests that the current sensitivity to $T_{MAX}$ and MAP is subject to change during recombination. Moreover, a combination of high heterozygosity (0.40-0.43) and high within-population variability (91.63±0.31%) confirmed high adaptive fitness to maintain reproductive success. Therefore, the current populations of *S. emarginatus* have substantial genomic resilience towards future climate change, albeit significant conservation efforts (including mass multiplication) are warranted to avoid future deleterious impacts of inbreeding depression on the fragmented populations.

## *Uraria* Desv. (Leguminosae)

The genus *Uraria* Desv. comprises of perennial herbs and under-shrubs and is represented by 20 species in the world, mainly distributed in tropical Africa, Asia and Australia. In India the genus has 8-12 species predominantly found in tropical and sub-tropical regions. Most species of *Uraria* are medicinally important and are used against various ailments like dysentery, diarrhoea, enlarged spleen and liver, tumours and fistulae, antipyretic, fever and inflammation. *Prishniparni* (*Uraria picta*) is one of the important constituents of the well-known Ayurvedic drug *Dashmoola*. The whole plant is medicinally important and has anti-inflammatory, anti-thrombotic, anti- viral, hepatoprotective, acaricidal, nephroprotective, vasoactive and fracture healing properties. *Uraria picta* has been reported as a rare and endangered plant in some parts of India. After the Flora of British India by J.D. Hooker (1879), the only recent account on Indian *Uraria* is in the form of a checklist (Sanjappa 1992), wherein 8 species and 2 varieties have been enumerated. In order to fill this gap and to have a comprehensive assessment

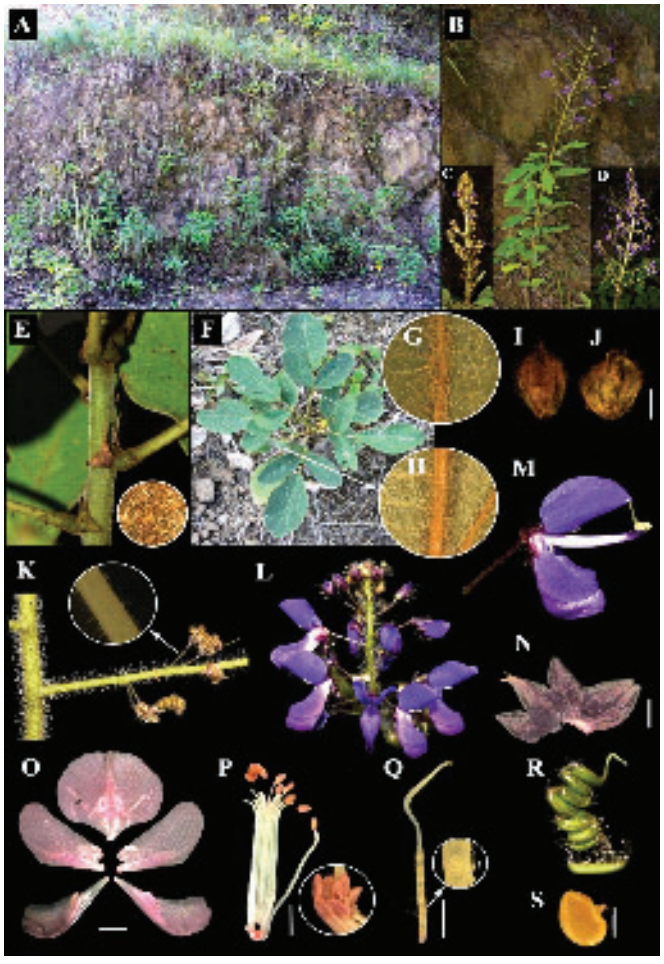



Fig. 7: *Uraria lacei* Craib A. habitat, B. habit, C. young panicle, D. mature panicle, E. stipules and magnified stem hairs, F. leaflets G. upper surface of leaf, G. lower surface of leaf, I. abaxial surface of bract, J. adaxial surface of bract, K. rachis and fruit position with magnified hairs of pedicel, L. flower position on the panicle, M. single flower, N. calyx (stained), O. petals-standard, wings, keel (stained) P. androecium with magnified anthers (stained), Q. gynoecium with magnified hairs, R. single pod S. single seed. Scale bars: 2mm (J, N, O, P, Q) 500µm (S).

of diversity and phylogenetic relationships among the species, a molecular systematic study on Indian *Uraria* has been taken up.

Over 1500 herbarium specimens of *Uraria* spp. were studied in 14 Indian herbaria (AHMA, ARUN, APF, ASSAM, BSA, BSD, BSI, BSID, CAL, DD, FRC, LWG, MH and TBGT) and various foreign virtual herbaria during the period under report. Field visits were carried out in different localities of 10 states (Assam, Arunachal Pradesh, Chhattisgarh, Gujarat, Madhya Pradesh, Maharashtra, Manipur, Mizoram, Nagaland and Uttarakhand) and about 180 samples of eight species of *Uraria* have been collected from their natural habitats. Morphological details such as flower dissections, taxonomic descriptions, keys, illustrations, pollen morphology under light microscopy and scanning electron microscope are undergoing. All the voucher specimens have been processed following standard herbarium procedures. *Uraria lacei* Craib has been rediscovered after 67 years from Bishnupur district of Manipur (Fig. 7).

Genomic DNA has been isolated from the 180 leaf samples. Polymerase chain reaction amplification was done using nuclear ITS and chloroplast *matK, rbcL, trnL-F* and *psbA-trnH* markers. Sanger sequencing for the same is in progress. De-novo transcriptome sequencing using leaf samples for *U. picta* was completed. Simple Sequence Repeats (SSR) detection and primer designing is undergoing.

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**Plant molecular systematics, phylogeography and genetic diversity**

## Phylogeny and phylogeography of Indian *Citrus* L. (Rutaceae)

Global research in *Citrus* taxonomy and phylogeography poses new questions as to the centre of origin and nativity of Indian species such as *Citrus medica* and *C. indica*. Additionally, there are still issues to be resolved regarding the true identity and taxonomic status of indigenous *Citrus* fruits like sour pomelos (*C. megaloxycarpa*) and also the phylogeny and phylogeography of the species of the papeda group, such as *C. cavaleriei, C. latipes* and *C. hystrix*. Our group has been engaged in an integrative taxonomic analysis for assessment of diversity and phylogenetic relationships among native and wild species of *Citrus*. The study primarily aims at resolving two research questions: 1) the center of origin and population evolution of *Citrus medica* and *C. indica* through phylogeographic approach, and 2) species delimitation as well as inter and intra-specific phylogenetic relationships among all species of Indian *Citrus*.

### Plant survey and sampling

During the year under report, four field trips were conducted in six states of Northeast India (Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram and Nagaland). A total of 267 samples of *Citrus* were collected. GPS co-ordinates (Longitude, Latitude and Altitude) of the locations were recorded. Each sample of *Citrus* was identified through critical studies and macro and microscopic observations. A new population of *C. medica* was recorded in Kathelbam Island in Dibru-Saikhowa National Park. Total genomic DNA from 267 accessions of eight *Citrus* species was isolated using a modified CTAB protocol.

### SSR Primer screening and Genotyping

Ninety-six microsatellite primers from 10 linkage groups in *Citrus* were synthesized and these were screened with a single genomic DNA each of *C. medica* and *C. indica* through PCR. Out of 96 SSR primers, 48 primers were amplified successfully. Each amplified SSR primer was screened across 13 selected individuals of *C. medica* and *C. indica* samples. So far, 48 SSR primers were screened in both the *Citrus* species, of which 16 SSR primers were found polymorphic. A set of 134 samples of *C. medica* from 16 populations across different North eastern states has been selected for SSR genotyping through multiplex PCR with 16 polymorphic primers. The work is in progress.

### Sequencing ITS, trnL-F, and single copy genes

Genomic DNA from 45 accessions of four species (*C. hystrix, C. indica, C. latipes, C. medica)* were amplified using the ITS primer pairs: ITS4-5'TCCTCCGCTTATTGATATGC3' and ITS5- 5'AAGTCGTAACAAGGTTTCCGTAGT3'. DNAs of the same 45 accessions of the four wild species of *Citrus* were also used for PCR amplification of the *trnL-F* intron and spacer region using the universal primers: *trnL-C* 5'-CGAAATCGGTAGACGCTACG-3' and *trnL-F* 5'-ATTTGAACTGGTGACACGAG-3'. The purified PCR amplicons were sequenced using an Automated ABI 3730XI 96 Capillary DNA Analyser. Out of 45 accessions, 37 accessions were successfully sequenced for ITS and 24 accessions for *trnL-F* region. Nine single copy genes were identified and synthesized from *Citrus* database. Three of these single copy genes were PCR amplified and sequenced in 35 accessions of four wild species of *Citrus*. Out of 35 accessions, 25

accessions were sequenced successfully. Sequencing of ITS, trnL-F, single copy genes in the rest of the citrus accessions is in progress.

## Phylogeography of *Ensete* Bruce ex Horan. (Musaceae)

The group has been working on phylogeography of two species of wild bananas in India, i.e. *Ensete superbum* and *E. glaucum*. The study aims at estimating genetic variability, genetic structure, and age and divergence of populations of *E. superbum* and *E. glaucum* through molecular phylogeographic methods.

A total of 167 accessions of *E. superbum* were collected from Western Ghats, Vidhyanchal and Satpura hills, of which 158 were from wild and nine were from home gardens. Samples of *E. glaucum* were collected from North East India, which included 114 accessions with 16 planted and 98 wild/semi wild plants. Both the species occurred in diverse habitats and showed variations in plant size, inflorescence length, fruit and seed sizes. Local uses were documented from the indigenous communities. Herbarium voucher specimens were prepared for each accession. Distribution maps for *E. glaucum* and *E. superbum* indicating the collection sites were also prepared.

Seed samples were collected from eleven *E. superbum* and seven *E. glaucum* populations. Quantitative and qualitative morphological characters of seeds were documented. Seedlings of *E. superbum* (50) and *E.glaucum* (20) were collected from different locations and planted in the botanic garden conservatory.

Genomic DNA was extracted from 227 leaf samples of both the species (*E. superbum* -73; *E. glaucum*-154) through a modified CTAB protocol using Triton-X suspension buffer to remove phenolics. PCR amplification of selected samples of *Ensete* for cpDNA (*trnL-F*, *matk, trnH-psbA*) is in progress.

Transcriptome sequencing of two diverse accessions of *E. glaucum* has been done. Transcriptome data analysis is in progress. EST SSRs will be developed *de novo* for estimation of genetic diversity and population genetic structure. In-silico primer designing is going on using sequence data from Ensete Knowledge Base (http://www.enset-project.org/).

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**Ethnobotany and floristics of angiosperms**

## Bioresources Inventory of Suhelwa Wildlife Sanctuary, Uttar Pradesh

Field surveys in different terai forests ranges of Uttar Pradesh resulted in collection and systematic documentation of the following plant species along with associated indigenous knowledge: *Aegle marmelos, Aloe vera, Asparagus adscendence*, *Bauhinia vahlii, Boerrahavia diffusa, Bombax ceiba, Buchanania lanzan, Butea monosperma, Capparis zeylanica, Carissa opaca, Chlorophytum tuberosum, Coccinia grandis, Cordia dichotoma, Cuccumis callosus, Curcuma angustifolia, Dillenia pentagyna, Dioscorea oppositifolia, Dioscorea belophylla, Dioscorea bulbifera, Diospyros exsculpta, Emblica officinalis, Ficus benghalensis, Garuga pinnata, Glycosmis mauritiana*, *Glycosmis pentaphylla, Grewia tilifolia, Helminthostachys zeylanica, Holarrhena pubescens, Holoptelia integrifolia, Ipomoea aquatica, Leucasaspera, Limonia acidissima, Marsilia minuta, Madhuca longifolia, Mommordica dioica, Murraya koenigii, Nymphea pubescens, Nelsonia canecsence, Nelumbo nucifera, Oxalis corniculata, Phyllanthus fraternus, Physalis minima, Pithecellobium dulce, Schleichera oleosa, Solanum nigrum, Spondias pinnata, Syzygium cumini, Terminalia bellirica*, *Xeromphis uliginosa* and *Zizyphus nummularia*.

## Characterization and value addition of plant-based resins, gums and waxes

Physico-chemical characterization and chemo profiling of 58 accessions of gum, dye and wax yielding plants of different phytogeographical areas were done for identification of major chemical markers through chromatographic and spectroscopic techniques. Quantification of phytochemicals was done to select the best accessions based on nutraceutical value for utilization as food/ nutraceuticals. Pre formulation studies were done in 58 accessions for synergy. Further, utilized wax source by processing with various methods as defatting, saponification, and extracted wax for preparation of different value added products like refined wax and policosanol rich fraction was carried out.

## Agro-technology development of *Aloe* species for popularization and training among farmers for cultivation on Sodic degraded lands of Uttar Pradesh

Experiments were carried out to observe the growth of the *Aloe* species and gel content in different pH level. Data on gel content on two species of *Aloe* at four intervals were recorded. In a statistical analysis it was summarised that *Aloe vera* is superior for cultivation at high sodicity level. A hand on training on cultivation of *Aloe* species on sodic land was conducted at CSIR NBRI. About 100 farmers participated and several theory and practical clases were conducted. They were demonstrated with Aloe cultivation and gel extration at extraction unit.

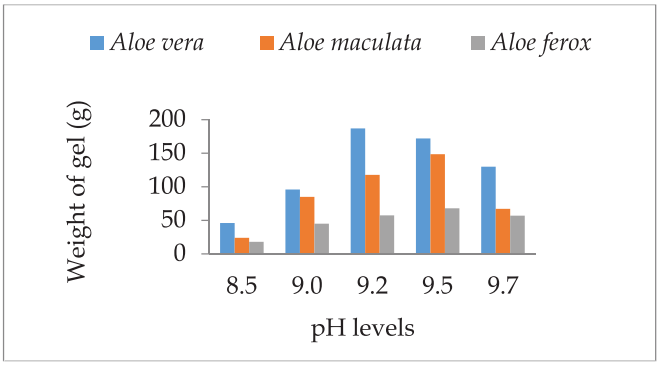


Fig.1: Gel content of *Aloe vera* and *A. maculata* at different pH level


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**Plant diversity assessment, floristic analysis, taxonomic revision, plant collection and herbarium curation**

### Floristic survey of herbaceous flora of Lucknow and its surrounding districts

Lucknow and its adjacent five districts Barabanki, Sitapur, Hardoi, Unnao and Raebareli were surveyed to assess the herbaceous flora with more emphasis on invasive alien plant species. Since these areas are chiefly covered by agriculture lands,there is a great scope of study of herbaceous and invasive species in relation to agriculture crops. The present work will also be very useful for students, teachers, scientists and concerned government departments. During the reporting period, 11 field tours to different parts of the study areas have been taken and about 175 plant species were collected. Identification and preparation of herbarium specimens of collected specimens are in progress. In addition to field surveys, plant specimens housed at Botanical Survey of India, Allahabad (BSA) and CSIR-National Botanical Research Institute, Lucknow (LWG) were also critically examined to know the correct number of herbaceous species occurring in the study areas of Uttar Pradesh. A list of all expected herbaceous plants was also prepared, that contains 457 species under 71 families and 340 genera. Some of the dominant families are Amranthaceae Asteraceae, Cucurbitaceae, Euphorbiaceae, Fabaceae, Rubiaceae (Fig. 1). Detailed taxonomic study of more than 70 species have been completed with nomenclature, description, phenology, distribution, habitat and ecology, significant uses and reference to specimens examined.

### Taxonomic Revision of the genus *Desmodium*

*Desmodium* Desv. (Leguminosae), with ca. 275 species, is almost cosmopolitan in tropical and subtropical regions of the world. The genus was established by N. A. Desvaux (1813) with five species based on its loment type of fruits. At present, the tribe *Desmodieae* comprises ca. 43 genera which are subdivided into three groups, i. e. *Desmodium*, *Phyllodium* and *Lespedeza*. The *Desmodium* group consists of 29 genera as per the recent classifications. *Desmodium* is chiefly characterized by herbs to shrubs habit, uni- to trifoliolate leaves, raceme or panicle inflorescence, pink to purple (sometimes white) flowers and loment fruits, generally covered by uncinate hairs. The plants are generally found along the roadsides, open lands, fallow lands, agriculture fields, mountain slopes, etc. The entire group exhibits tremendous variations in their morphology at generic as well as specific level.

In India, ca. 70 species were known in *Desmodium s. l.* However, according to recent classification only ca. 7 species remain under *Desmodium s. str.* and rest of the species have been shifted to other 12 allied genera (i.e., *Bouffordia*, *Codariocalyx*, *Grona*, *Huangtcia*, *Hylodesmum*, *Leptodesmia*, *Monarthrocarpus*, *Ototropis*, *Pleurolobus*, *Polhillides*, *Sohmaea* and *Tateishia*). The genus commonly occurs throughout India from sea level to 7000 ft. altitudes in the Himalaya. Within India, the genus has maximum distribution in North-East region. Plant collection tours were conducted to some parts of Assam, Meghalaya, Odisha and Uttar Pradesh and about 22 species were collected. Till date, 17 species from *Desmodium s. l.* have been critically examined with all taxonomic information. To use the micro-morphological character for identification, the SEM study of seeds and hairs has also been initiated. In the present investigation ca. 800 herbarium specimens housed at LWG, CAL & ASSAM have also been studied.

### Taxonomic study and diversity assessment of some selected plant groups

Asteraceae, Euphorbiaceae, introduced and cultivated legumes of Uttar Pradesh, and invasive

alien plant species of Sikkim Himalaya have been selected for diversity and taxonomic study. Based on exhaustive literature survey, it has been observed that Uttar Pradesh comprises about 334 species in 99 genera of legumes, of which 75 genera and 155 species have been found in cultivation among four subfamilies of Leguminosae viz., Papilionoideae (40 genera, 71 species), Caesalpinioideae (27 genera, 66 species), Detarioideae (5 genera, 7 species) and Cercidoideae (3 genera, 11 species). Out of these 155 species, 27 species belong to herbs, 33 species to shrubs, 61 species to trees, 27 species to herb climbers and 2 species to shrub climbers. Among all only 14 species are heavily cultivated for pulses, 19 species as vegetables and 12 species are used as fodder while the majority of the species are chiefly grown as ornamental. The dominant genera are *Senna*, *Vigna*, *Bauhinia*, *Cassia*, *Albizzia*, *Trifolium*, *Phaseolus*, etc. About 33 genera and 54 species have been collected during three field tours from different regions till now and all have been processed for herbarium preparation and taxonomic study. So far, detailed taxonomic studies of 22 species have been completed. Similarly, the work on Asteraceae and Euphorbiaceae is in progress.

For the first time, a list of 102 alien plant species has been prepared from Sikkim Himalaya, of which 93 species of dicots belong to 75 genera and 30 families while nine species of monocots fall under seven genera and three families. These species include 77 herbs, 11 shrubs, six grasses, four climbers and two species each in sedges and trees. The region is dominated by the members of Asteraceae (27 species), followed by Fabaceae (12 species), Solanaceae (09 species), Poaceae (06 species) and Malvaceae (05 species). Further, the detailed ecological study was also carried out on some commonly growing invasive alien species like *Ageratina adenophora, Ageratina riparia, Chromolaena odorata, Mikania micrantha* and *Lantana camara.* Frequency, density and basal cover data for target invasive alien plant species (IAPS) and its associates were measured. Phytosociological analyses of IAPS and associates were conducted by random quadrate sampling. One hundred fifty seven quadrates of 5 m x 5 m size, covering total area of 3925 $m^2$ were laid between 300 m – 2700 m elevations. Nearly 50 species have been collected and voucher specimens are under the preparation. In the present field survey, it was noticed that *Ageratina adenophora*

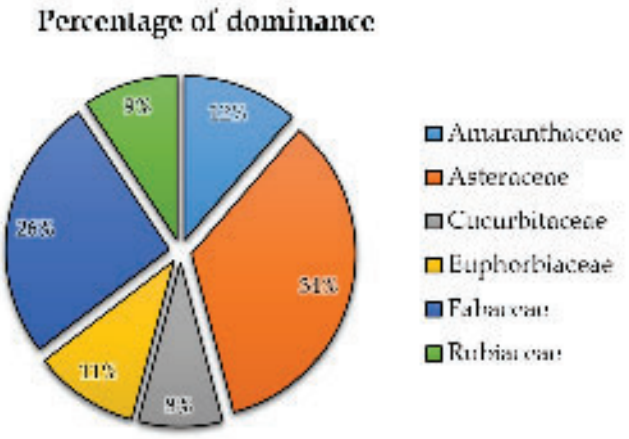


Fig. 1: Distribution of herbaceous species in some dominant families in Lucknow and its adjacent districts.

was observed in all altitudinal gradients with higher number of individuals. However, *Chromolaena odorata*, although present in almost all gradients, was found with lesser number of individuals. *Mikania micrantha* and *Lantana camara* were reported only in lower gradients between 300 m-1500 m with lowest density. *Ageratina riparia* was not found during the field study.

## Herbarium curatorial work

In the last one year, 2200 specimens were accessioned and incorporated in the herbarium. Large numbers of students and researchers from different schools, universities and organizations visited herbarium and they were explained about the herbarium techniques and the role of herbarium in taxonomy and biodiversity studies. About 25 plants were received from researchers of other organizations for identification and authentication.

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**Diversity, revisionary, floristic and bio-prospection studies of lichens and algae**

During reporting period three species of lichens were described as new to science, while one species was reported for the first time from India.

## New lichen species discovered (Fig. 1)

1. *Ioplaca rinodinoides* S. Y. Kondr., K. K. Ingle, D. K. Upreti *et* S. Nayaka
2. *Letrouitia assamana* S. Y. Kondr., G. K. Mishra *et* D. K. Upreti
3. *Rusavskia indochinensis* S. Y. Kondr., D. K. Upreti *et* S. Nayaka

## Species reported as new record for India

1. *Pyxine dactyloschmidtii* Kalb & Mongkols

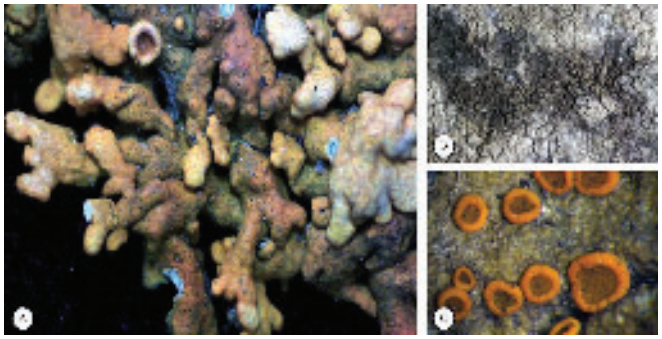

Fig. 1: New lichen species discovered. A. *Rusavskia indochinensis*, B. *Ioplaca rinodinoides*, C. *Letrouitia assamana*

## Diversity and floristic studies

During the year 2019-20 lichen and algal diversity in following areas were documented:

**Assam:** Identification of lichen samples earlier collected from five districts of Assam revealed 138 species belonging to 34 genera and 16 families. Out of these, 37 species are found to be new records to Assam. The crustose lichens exhibited their dominance with 123 species, followed by 15 foliose species. Most of the lichen species were corticolous in habitat (138 spp.). The Lichen family Graphidaceae exhibited dominance with nine genera and 59 species, followed by Arthoniaceae with four genera and 22 species, and Pyrenulaceae with two genera and 15 species. Among the different genera, *Graphis* and *Pyrenula* with 27 and 14 species, respectively, showed the maximum diversity. Among the five districts explored, Karbi Anglong exhibited the maximum diversity of lichens, represented by 112 species, followed by Nagaon, Golaghat, Goalpara and Kamrup with 74, 71, 67 and 63 species, respectively. The areas in Goalpara and Kamrup have higher anthropogenic activities, thus exhibit poor lichen diversity. The rich diversity of graphidaceous (59 spp.) and pyrenocarpous (16 spp.) lichens in the studied area indicates evergreen vegetation with abundance of trees with smooth barks and suitable conditions for their growth. Frequent encountering of previously unrecorded species from Assam indicates the lichen richness and insufficient exploration in the state.

**Meghalaya:** A field tour of 20 days was conducted to Meghalaya and 26 grids were surveyed comprising localities of Khasi and Jaintia hills. About 230 lichen samples were collected, which resulted in identification of 131 species, including 98 species as new distributional records for Meghalaya. The most dominant families in the study area were Graphidaceae and Pertusariaceae with 17 species and 11 species, respectively. Abundant species in the study area were *Cladonia cariosa* (Ach.) Spreng, *Evernisatrum cirrhatum* (Fr.) Hale, *Evernisatrum*

*nepalense* (Taylor) Hale, *Lecidella enteroleucella* (Nyl. in Nyl Crombe) Hertel and *Lepraria ecorticata* (J.R. Laundon) Kukwa.

**Suhelwa Wildlife Sanctuary, Uttar Pradesh:** A plant collection tour to Suhelwa Wildlife Sanctuary, Uttar Pradesh was conducted. The localities such as Tulsipur range, Khabri naka (Indo-Nepal border), Gurung nala, Udaipur beat, Nawalgarh beat, Baghelkhand beat, Bhaisasur beat, Hasanpur beat and Kanvi nala were surveyed. About 200 lichen and 60 algal samples were collected. The identification resulted into 30 species of lichens belonging to 20 genera and 14 families, of which 12 were new distributional records to Uttar Pradesh. The crust forming lichen exhibited their dominance in the study area represented by 24 species. Out of 14 families of lichens, members of Graphidaceae exhibited their dominance with eight species followed by Pyrenulaceae with five species. The genera *Diorygma* and *Pyrenula* were common in the study area with four species each.

The morphological identification of algal samples resulted in 35 species belonging to 22 genera under four classes– Chlorophyceae (15 spp.), Cyanophyceae (6 spp.), Bacillariophyceae (10 spp.) and Euglenophyceae (4 spp.). The genus *Cosmarium* of Cholorophyceae was most common in the study area. *Trentepohlia keralensis* G. G. Satpati and R. Pal, a terrestrial green filamentous algae, was found growing luxuriantly on the leaves and tree trunks in the dense forest. Due to its orange shades the entire forest was appearing orange red in colour. This species is reported for the first time from Uttar Pradesh (Fig. 2). Another interesting species *Gloeotrichia raciborskii* Woloszynska, was observed forming bloom in the ponds within the Sanctuary (Fig. 3).

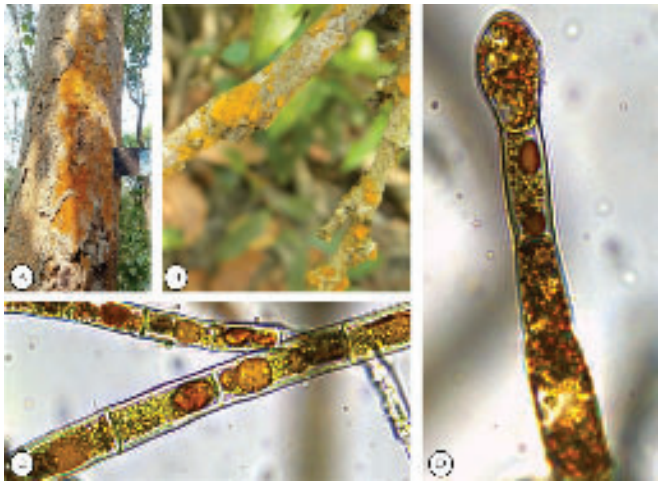

Fig. 2: *Trentepohlia keralensis* G. G. Satpati & R. Pal- a prominent algae collected from Suhelwa Wildlife Sanctuary, Uttar Pradesh. A. and B. Natural habitat, C. and D. Microphotographs

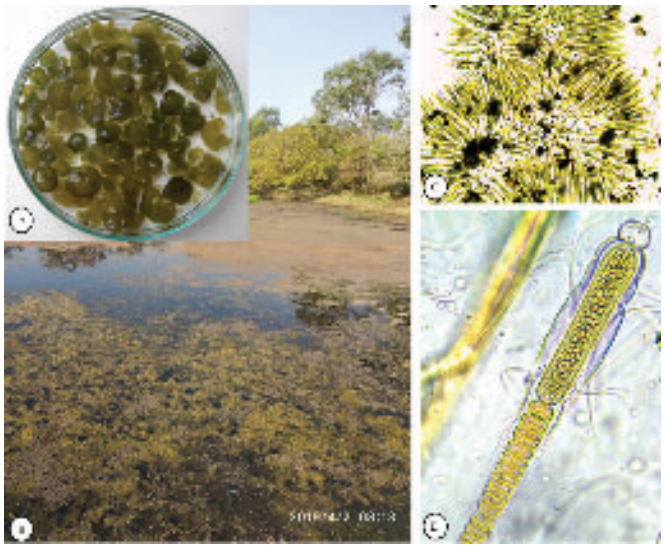

Fig. 3: *Gloeotrichia raciborskii* Woloszynska- A prominent algae collected from Suhelwa Wildlife Sanctuary, Uttar Pradesh. A. Habit B. Natural habitat, C. and D. Microphotographs

## Jim Corbett National Park, Uttarakhand:

A total of three season-based algal collection tours were conducted to the Jim Corbett National Park, Uttarakhand. The zones such as Durga Devi, Sona Nadi, Jhirna, Dhikala, Bijrani, Dhela, Sitavani were surveyed and 250 algal samples were collected. The identification of the algal samples so far resulted in 128 species belonging to class Chlorophyceae. The desmids were most common members of class represented by 52 species under 11 genera and four families. Family Desmidiaceae dominated with 37 taxa under seven genera, followed by Closteriaceae with 11 taxa and one genus. All the taxa under Desmidaceae were recorded for the first time from National Park as well as from Uttarakhand. A rare species *Oocardium stratum* Nägeli was recollected after nine decades from Indian sub-continent Maximum algal species diversity occurred in winter season followed by monsoon and least diversity was recorded in summer season.

## Revisionary and phylogenetic grouping of lichens

### Family Arthoniaceae

Taxonomic status of the lichen genus *Schismatomma* Flot. & Körb. ex A. Massal. in India was examined

in details and excluded from the country. The morphological, anatomical and chemical characters of the types of *Schismatomma atomellum* (Stirt.) Zahlbr., *S. cinereum* (Müll. Arg.) Zahlbr. and *S. gregantulum* (Müll. Arg.) Zahlbr. suggest that they should be assigned to the genus *Phlyctis* (Wallr.) Flot. Interestingly, these three species are conspecific with the recently described *Graphidastra himalayana* Jagadeesh & G.P. Sinha from West Bengal, and the earlier known *Phlyctis himalayensis* (Nyl.) D.D. Awasthi from Sikkim. *Platygrapha atomella* Stirt. (≡ *S. atomellum*) has priority over the other four names following the rule of priority. Thus, the new combination *Phlyctis atomella* (Stirt.) S. Joseph, G. P. Sinha, Jagadeesh & S. Nayaka is proposed and the other four species are synonymized under it.

**Pyrenocarpous lichens**

The Pyrenocarpous lichens of India are revised based on freshly collected samples and specimens preserved in herbarium LWG of CSIR-NBRI, Lucknow. The specimens from herbaria AHMA, ASSAM, BSA, BSHC were also studied. The study resulted in 396 species belonging to 49 genera and 12 families. The study also resulted in nine species as new distributional records to India, viz. *Anisomeridium albidoatrum* (Nyl.) R.C. Harris, *Porina atlantica* (Erichsen) P. M. Jorg., *P. exserta* Müll. Arg., *P. siamensis* P.M. McCarthy, *Pyrenula concastroma* R.C. Harris, *P. cruenta* (Mont.) Vain., *P. dissimulans* (Müll. Arg.) R.C. Harris, *P. pyrenastrospora* Aptroot and *P. rinodinospora* Aptroot. The phylogenetic study of the group is in progress.

***Buellia* and *Rinodina***

The revisionary studies of lichen genera *Buellia s.l.* and *Rinodina* are in progress. The herbarium specimens from LWG, Botanical Survey of India Eastern Regional Center, Shillong (ASSAM) and recent collections from Assam, Meghalaya and Uttarakhand have been studied. The study revealed the occurrence of new distributional records for India under both the genera *Buellia s.l.* and *Rinodina* (five each). The species include - *Amandinea efflorescens* (Müll. Arg.) Marbach, *A. incrustans* (J. Steiner) Marbach, *Baculifera orosa* Marbach, *Hafellia dissa* (Stirt.) H. Mayrhofer & Sheard, *H. reagens* Pusswald, *Rinodina archaea* (Ach.) Arnold, *R. ascociscana* (Tuck.) Tuck., *R. capensis* Hampe, *R. isidioides* (Borrer) H. Olivier, and *R. laevigata* (Ach.) Malme.

## Bio-prospection study of algae

**Screening, isolation and culture of algal samples for pure strains**

The algal samples collected from Suhelwa Wildlife Sanctuary and Jim Corbett National Park were cultured in BBM as well as BG11 media in different laboratory conditions. Optimum conditions of factors affecting the microalgal growth in cultures such as nutrient availability, temperature, pH, salinity, oxygen, inorganic carbon, light intensity, etc. were provided. Various isolation methods were used to obtain pure algal strains for producing biomass which could be exploited further for value added products of nutraceutical and pharmacological importance. From Jim Corbett National Park *Chlamydomonas* sp., *Chlorella* sp., *Oscillatoria* sp., *Scenedesmus bijugus* (Turpin) Lagerheim, *Stigeoclonium* sp., *Tetradesmus obliquus* (Turpin) M.J. Wynne, *Tetradesmus dimorphus* (Turpin) M.J. Wynne, *Ulothrix* and *Trebauxia* were isolated. All the isolated pure strains are maintained in algology laboratory of CSIR-NBRI.

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**Diversity assessment, floristic analysis, morpho-taxonomy, *in vitro* studies and conservation of Bryophytes**

## Diversity assessment

Bryophyte diversity of Meghalaya region has been assessed in the 20 grids to undertake quantitative assessment and mapping of diversity of non-flowering plants of Northeast India. Identification revealed occurrence of 173 species, including 116 species of mosses, 56 species of liverworts and one species of hornwort. The most dominant species in terms of percentage cover/density (100%/20) were *Asterella wallichiana* (Lehm.) Grolle, *Atrichum obtusulum* (Müll. Hal.) A. Jaeger, *Campylopus ericoides* (Griff.) A. Jaeger, *Cheilolejeunea imbricata* (Nees) S. Hatt, *Conocephalum japonicum* (Thunb.) Grolle, *Jungermannia mizutanii* Amak, *Marchantia polymorpha* L., *Plagiochasma appendiculatum* Lehm. & Lindenb., *P. pterospermum* C. Massal, *Rhynchostegiella humillima* (Mitt.) Broth., *Scapania angusta* Mitt. ex K. Müller, *Solenostoma fusiforme* (Steph.) R.M. Schust., *Sphagnum subsecundum* Nees, while species with lowest percentage cover/density were *Dicranodontium didymodon* (Griff.) Paris (6%/1.2) and *Campylopus aureus* Bosch. & Sande Lac. (5%/1). The most dominant moss families in the study area were Bryaceae (20 species) followed by Dicranaceae (14 taxa) and Fissidentaceae (8 species). The dominant families of liverworts were Jungermanniaceae (12 species), Lejeuneaceae (11 species) and Plagiochilaceae (05 species). According to Raunkier's law of frequency class, *Entodon rubicundus* (Mitt.) A. Jaeger, *Gammiella pterogonioides* (Griff.) Broth, *Garckea phascoides* (Hook.) Müll. Hal., *Macrothamnium macrocarpum* (Reinw. & Hornsch.), *Mesonodon flavescens* (Hook.) W.R. Buck and *Ptychanthus striatus* (Lehm. & Lindenb.) Nees belongs to E class (most frequent) followed by *Dicranodontium decipiens* (Mitt.) Mitt. ex Broth., *Floribundaria sparsa* (Mitt.) Broth., *Hyophila involuta* (Hook.) A. Jaeger, *Hyophila nymaniana* (M. Fleisch.) M. Menzel, *Marchantia emarginata* Reinw. Blume & Nees, *Racopilum orthocarpum* Wilson ex Mitt., *Thuidium glaucinum* (Mitt.) Bosch & Sande Lac. Abundant species in the study area were *Asterella wallichiana* (Lehm.) Grolle, *Atrichum obtusulum* (Müll. Hal.) A. Jaeger, *Conocephalum japonicum* (Thunb.) Grolle, *Jungermannia mizutanii* Amak., *Marchantia polymorpha* L., *Plagiochasma appendiculatum* Lehm. & Lindenb., *Plagiochasma pterospermum* C. Massal., *Rhynchostegiella humillima* (Mitt.) Broth., *Scapania angusta* Mitt. ex K. Müller, *Solenostoma fusiforme* (Steph.) R.M. Schust. and *Sphagnum subsecundum* Nees. Nine bryophyte species were reported as new to North-East India and 20 species reported as new to Meghalaya.

## Floristic analysis

Work on Bryophyte Bioresource inventory of Sohelwa Wildlife Santuary (SWLS), Uttar Pradesh has been carried out. Preliminary floristic analysis of Tulsipur range of SWLS revealed the occurrence of 20 species of bryophytes belonging to 13 genera and 10 families. Pottiaceae was found more dominant moss family in the region with 6 species. The genus *Hydrogonium* has maximum number (3) of species. *Bryum porphyroneuron* Müll. Hal., *Ditrichum tortuloides* Grout, *Fissidens zippelianus* Dozy and Molk, *Erpodium glaziovii* Hampe., and *Hydrogonium spathulifolium* (Dixon et P. Varde) Aziz et Vohra have been recorded as new to Uttar Pradesh.

## Morphotaxonomic Study

During an investigation on Bryophytes of Singalila National Park (SNP), Darjeeling, eastern Himalaya, some plants of a rare and interesting liverwort,

*Mylia taylorii* (Hook.) S. Gray, were collected. The collection of this taxon from SNP provides the authentic information about its occurrence in Indian region after a gap of about more than a century. A detailed morphological account of this taxon has been prepared.

During study on the family Mniaceae in Darjeeling and its neighbouring areas, three genera and six species (*Mnium lycopodioides* Schwägr., *Orthomnion bryoides* (Griff.) Nork., *Plagiomnium acutum* (Lindb.) T.J. Kop., *P. confertidens* (Lindb. & Arnell) T.J. Kop. , *P. rhynchophorum* (Harv.) T.J. Kop. and *P. succulentum* (Mitt.) T.J. Kop.) have been identified. Of these, *Plagiomnium acutum* is reported here for the first time from eastern Himalaya. A detailed morpho-taxonomic account of these species with their current status and a key to all the taxa of family Mniaceae has been prepared.

## *In vitro* studies and conservation of Bryophytes

*Anthoceros bharadwajii* Udar & Asthana (Anthocerotaceae) is an Indian endemic hornwort. The pattern of germination, morphogenesis of sporeling and rhizoid formation has been observed in liquid, semi-solid and solid forms of Hoagland medium using spores as explants. Spore germination rate was found maximum in semi-solid form, while solid form of Hoagland medium was found most suitable for the vegetative growth and development of mature thalli. The study has also revealed that the spore exine ruptured only in semi-solid and solid media with high germination rate in semi-solid medium, though further growth occurred only in solid medium. Based on the results and observation a standardized protocol has been established for raising the pure population and bulking up the germplasm of this important endemic hornwort. (Fig. 1).

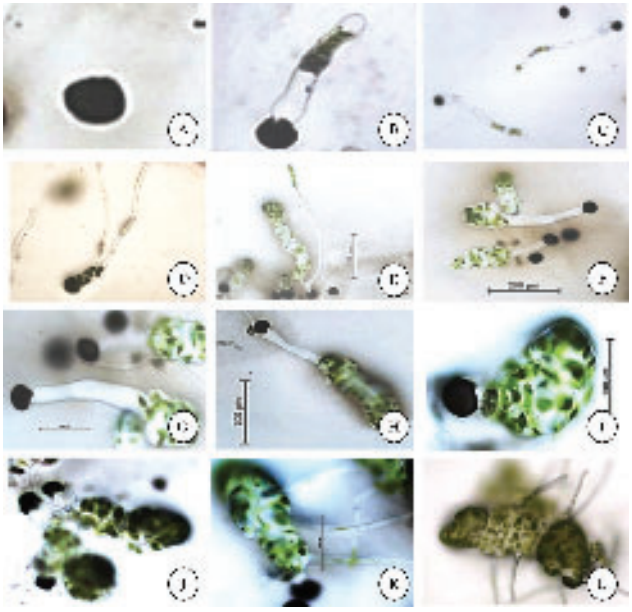

Fig. 1: Stages during *in-vitro* propagation of *Anthoceros bharadwajii* Udar & Asthana. (A-C): Germ tube emerging from spore, (D-F): Earlier stage of spore germination with primary rhizoid appearing, (G-H): Sporeling protuberance with formation of multicellular globose protonema at apex., (I): Globose protonema with single chloroplast per cell, (J-L): Early stages of thallus and rhizoid formation.

## New plant taxa discovered

A new species of a liverwort, *Cololejeunea lobulopapillata* A.K. Asthana, V. Sahu & D. Gupta (Lejeuneaceae) has been discovered from Govind Wild Life Sanctuary (GWLS), Uttarakhand and described. The new species was found growing on leaves of *Porella plumosa* (Mitt.) Parihar and is characterised by its distant, ovate–triangular leaves with arched antical and postical margins of leaf lobe, leaf cells dorsally unipapillose, lobules covering nearly 1/2 the leaf length, cells characteristically uni-

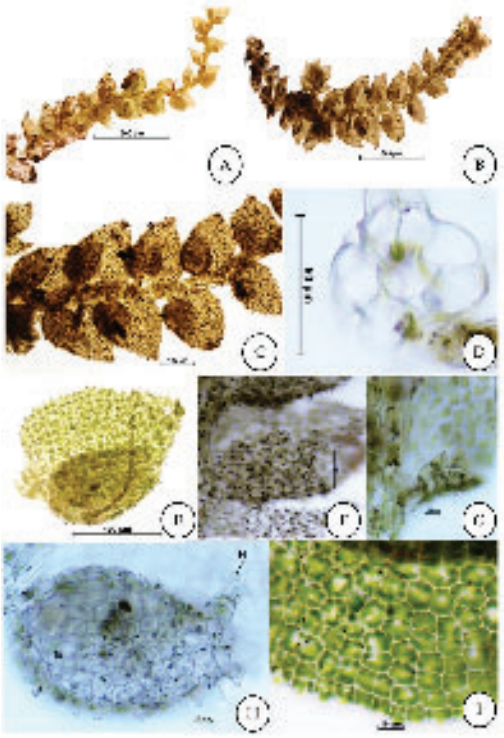

Fig. 2: *Cololejeunea lobulopapillata* Asthana, Sahu & Gupta**.** A-B. Plants, C. A enlarged portion of plant, D. Cross section of stem, E. Leaf lobe and lobule, F. Larger lobule, G. Reduced lobule, H. Leaf lobule showing dorsal papillosity and hyaline papilla, I. Leaf cells.

papillose, first tooth large distinct, 1-celled, hyaline papilla present, second tooth indistinct (Fig. 2).

During bryophyte exploration in Govind Wild Life Sanctuary, Uttarakhand, some interesting specimens of *Paraleucobryum* (Lindb. ex Limpr.) Loeske have been collected and identified. A critical morpho-taxonomic study of these plants showed their close resemblance with *P. enerve* (Thed.) Loeske. However, they differed from *P. enerve* in having smaller size of plants, larger leaves and strongly falcato-secund rather hooked leaves with ragged appearance. Hence these interesting plants were designated as a new variety of *P. enerve* namely: *Paraleucobryum enerve* var. *secundum* A.K. Asthana & V. Sahu (Fig. 3).

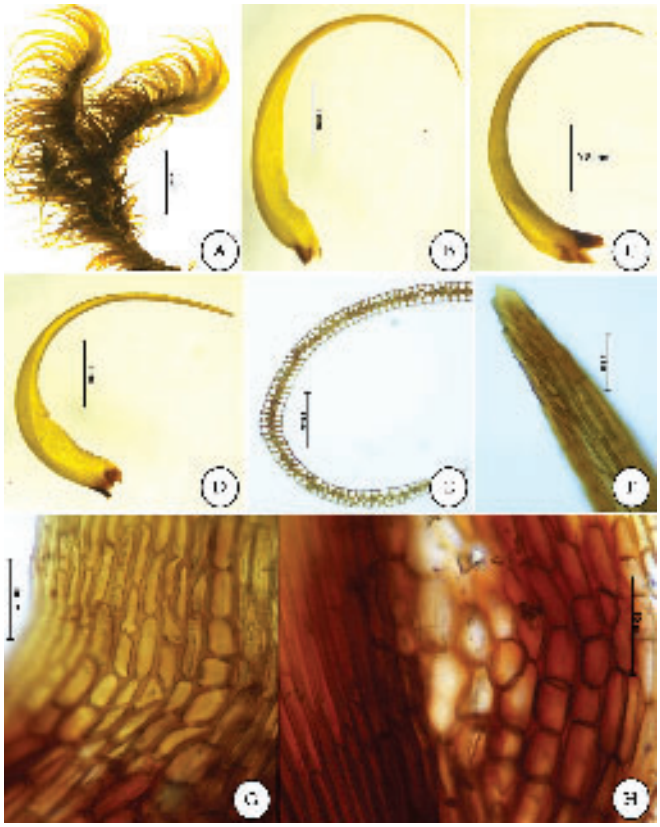

Fig. 3: *Paraleucobryum enerve* var. *secundum* var. nov. (A): Plant; (B-D): Leaves, (E): Cross section of leaf, (F): Leaf Apex, (G): Leaf Basal cells; (H): Leaf alar cells.

## New plant distributional records

During studies on family Mniaceae in India, *Orthomnion javense* Koponen have been reported as a new record for India and East Nepal. Earlier it was known from China, Indonesia, Japan, Laos, Papua New Guinea, Philippines and Vietnam. *Orthomnion javense* is characterized by its fragile leaves, costa ending below the leaf apex, 1–3 cells wide border extending near leaf apex. Morpho–taxonomic details of Indian plants of *O. javense* and paratype of *O. noguchii* Koponen have been critically investigated (Fig. 4).

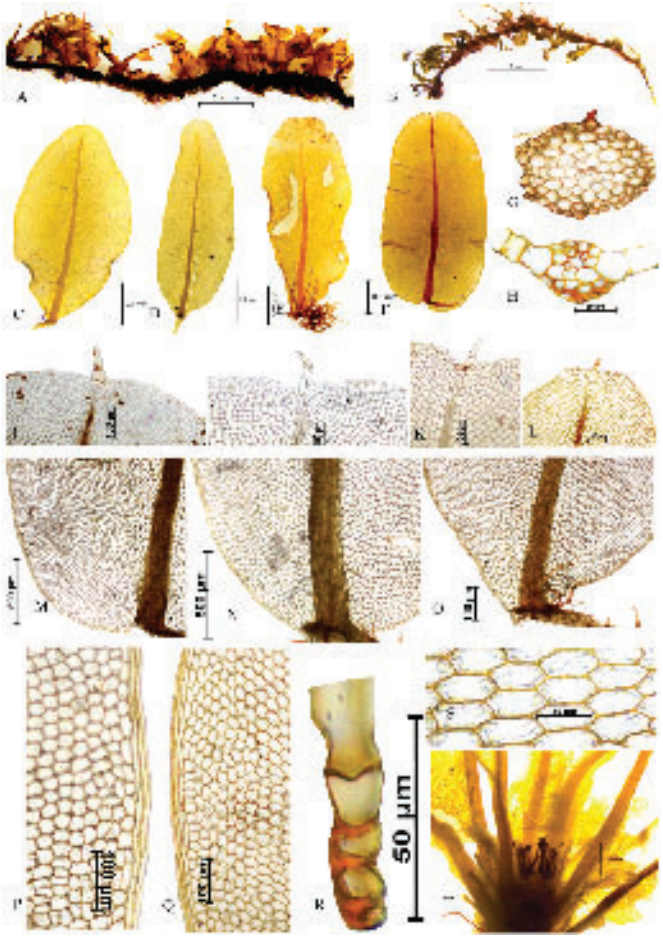


Fig. 4: *Orthomnion javense* Koponen A-B. Fragile plants, C-F. Leaves, G. Cross section of stem, H. Cross section of leaf costa, I–L. Different variations in apex of leaves, M-O. Bordered base of leaves, P-Q. Leaf showing 2-3 stratose border, R. Cross section of leaf border, S. Middle laminal cells of leaf, T. Perichaetial leaves showing archegonia

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**Floristic survey, biodiversity assessment, reproductive biology, mass-multiplication, conservation & prospection of Indian Pteridophytes**

## Floristic Survey & Biodiversity Assessment

Survey and collection of pteridophytes from different localities *viz.* Gurughat, Jankipur, Mohanawa Ghat, Navalgarh, Khabri Naka, Bhagwanpur beat, Nawa Nagar, Baghelkhand and near Forest Rest House of Tulsipur Forest Range in Suhelwa Wildlife Sanctuary (SWLS), Uttar Pradesh was made in December 2019.

About 25 pteridophytes samples belonging to six species *viz. Adiantum philippense* L., *A. incisum* Forssk., *Ampelopteris prolifera* (Retz.) Kopel, *Cheilanthes farrinosa* (Forssk.) Kaulf., *Equisetum ramosissimum* Desf., and *Lygodium flexuosum* (L.) Swartz. (Fig. 1) were collected, with the record of their localities, habit, habitat, altitude, longitude, latitude, etc.

Fig. 1: Pteridophytes collected in Suhelwa Wildlife Sanctuary (SWLS), Uttar Pradesh. A. *Adiantum philippense* L., B. *Adiantum incisum* Forssk., C. *Ampelopteris prolifera* (Retz.) Copel, D. *Cheilanthes farrinosa* (Forssk.) Kaulf. E. *Equisetum ramosissimum* Desf., F. *Lygodium flexuosum* (L.) Swartz.

Extensive survey and collection of the pteridophytes from different geographical areas in Meghalaya during June-July 2019 was made for preparation of inventory and quantitative assessment of the Pteridophytes using grid-based sampling method. A total 26 grids (40 $km^2$) and 5 macro plots (10x10 $m^2$) were laid-down in each grid. Total 130 such macro-plots (10x10 $m^2$) were laid-down in the entire surveyed areas, and 285 samples of pteridophytes were collected from these macro-plots. Study for preparation of inventory and baseline data (including mapping of the ecosystems and species distribution) has provided information about the locality, coordinates, altitude, date of plant/data collection, vegetation type, site characteristics, numbers of quadrate, name of the plants, numbers of individuals, habitat, families with their ecological parameters. Study related to density, relative density, frequency, relative frequency, frequency classes, abundance, relative abundance, diameter of root collar (drc), basal area cover, relative basal area cover, importance value index (IVI), and ecological diversity indices *viz.* Simpson Index, Shannon-Wiener Index, Pielou's evenness, Menhinicks Index, Whittaker evenness, Margalef index, Berger–Parker index, Odum Index and Number of occurrence (NOI), is under progress. Taxonomic study on 285 herbarium specimens revealed the occurrence of 67 species of pteridophytes belonging to 52 genera under 28 families in the sample plots surveyed.

Survey and collection of Pteridophytes from Pachmarhi Biosphere Reserve (PBR), Madhya Pradesh was carried out during November-December 2019. Atotal 190 specimens of pteridophytes were collected. Preliminary study of these specimens revealed the occurrence of 52 species and 41 genera.

Besides, 32 samples of spore of tree ferns (*Cyathea spinulosa* and *Cyathea gigantea*) were collected from three localities *viz.* Handi Khoh, Baari Amm and Jalgali in PBR with their ecological data to perform *in-vitro* investigation on the reproductive biology including viability of spores, germination pattern,

gametophyte development, mating system and sporophytes development. The average germination percentage of *C. spinulosa* was observed as 96.36%. The spore germination pattern was of *Cyathea*-type and the prothalial development was of *Adiantum*-type in *C. spinulosa*. Study on gametophytes in isolate culture revealed that the antheridia emerged first followed by the archegonia, revealing a sexual gap. It was also observed that the gametophyte led to a monoecious or bisexual trend in composite culture, and the sporophyte primordium emerged on 80$^{th}$ day (Fig. 2 and Fig. 3).

**Mass Propagation:** Mass propagation of 2500 individuals (replicates) of 13 ornamental species of pteridophytes was made for sale.

***In-vitro* culture & Conservation:** About 67 species of ferns, including some threatened species, have been maintained and conserved in the Fern house of CSIR-NBRI. Besides, large scale propagation of *Microsorum scolopendria* (Fig. 5) has been made for screening for potential molecules.

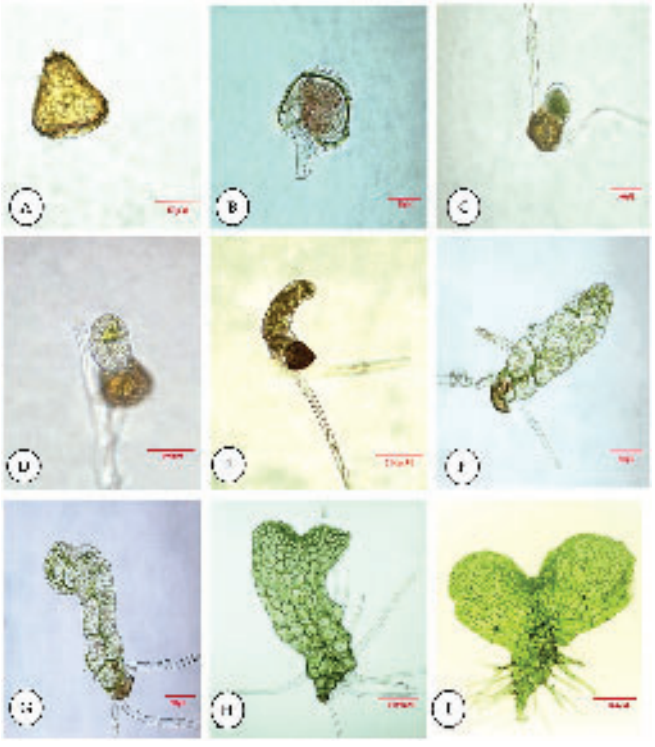

Fig. 2: Spore germination and development of *Cyathea spinulosa* Wall. ex Hook. in composite culture. A.Trilete spore, B. Rhizoid initial germination, C. One-celled prothallus, D. Two-celled filamentous gametophyte, E. 4-5-celled filamentous gametophyte, F. 2-dimensional semi-spatulate gametophyte, G. Spatulate gametophyte, H. Semi-cordate gametophyte, I. Cordate gametophyte with deep notch.

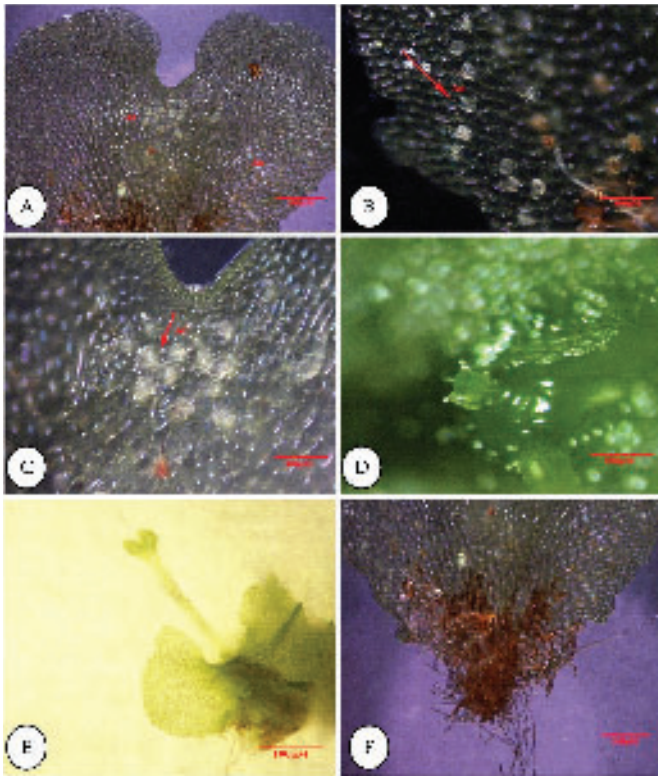

Fig. 3: Mating system and development of *Cyathea spinulosa* Wall. ex Hook. in composite culture. A. Cordate gametophyte showing anthredia (An) and archegonia (Ar) with an apical notch, B. Portion of a lobe with anthredia (An), C. Portion of a deep notch with archegonia (Ar), D. Close view of sporophyte primordium, E. Sporophyte primodium, F. Enlarged view of rhizoids.

## New Introduction

*Asplenium nidus* (Fig. 4) has been multiplied through *in-vitro* spore culture and have been introduced in the Fern house.

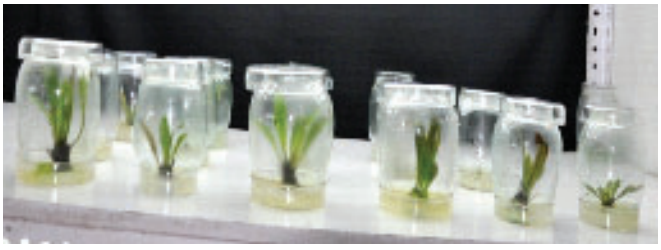

Fig. 4: *In-vitro* culture of *Asplenium nidus* L.

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**Plant diversity assessment, systematic and molecular studies**

## Floristic Studies

Vidarbha region constitutes the north-eastern part of the Maharashtra state sharing its borders with Madhya Pradesh to the north, Chhattisgarh to the east and Telangana to the south and Marathwada and Khandesh regions of the state to the west. The region is an upland plateau with elevation ranging from 457 to 548.6 m asl and is marked by a tropical rainy climate. Vidarbha region lacks a comprehensive systematic documentation of its rich plant diversity; therefore a study to document floristic diversity of the region and establishing a herbarium at Botanic Garden Chandrapur has been initiated. Different forest regions (Koka, Tumsar, Gobarwahi, Nakadongri, Sitasoangi, Salekasha and Arjuni forests) as well as field under cultivation and fallow lands in Nagpur, Bhandara, and Gondia districts were surveyed and 625 specimens were collected. Critical study and identification of the collected plant materials resulted in 324 species belonging to 242 genera and 79 families. Among the families Leguminosae (48) was found to be the most species rich family, followed by Poaceae (32), Euphorbiaceae (21), Malvaceae (15), Cyperaceae (13) and Asteraceae (11) Among the genera, *Ficus* L. with 6 species (*F. amplissima*, *F. beddomei*, *F. benghalensis*, *F. hispida*, *F. mollis* and *F. racemosa*) was the dominant genus, followed by *Acacia* and *Terminalia* represented by 5 species each. Further work is in progress.

## Molecular systematic studies on *Juniperus* L. (Cupressaceae)

*Juniperus* L. is the second most diverse genus of the conifers, consisting approximately 70 species and 40 varieties, widely distributed over Northern Hemisphere from the Arctic, to Mexico, West Indies, Azores, Canary Islands, Ethiopia, Sudan, the mountains of East Tropical Africa, Himalaya, Tibet, China and Taiwan. *Juniperus* species are an important source of food, spice and flavour, wood, fuel wood and the Juniper essential oil, commonly known as 'Cedar-wood oil' used in perfumery and cosmaceuticals as well as therapeutics.

The taxonomy of *Juniperus* is still not clear despite it being a highly important plant resource. Therefore, a study to investigate the taxonomy and phylogeny of the genus *Juniperus* in IHR using both morphological and molecular markers has been initiated.

So far, 53 samples from different localities in Arunachal Pradesh and Himachal Pradesh were collected and four taxa (*J. communis* L. var. *saxatilis* Pall., *J. indica* Bertol., *J. semiglobosa* Regel and *J. recurva* Buch.-Ham ex D. Don have been identified. Specimens of *Juniperus* housed in the herbaria of LWG, IIIM, DD, ASSAM and K (Images) were also studied. The isolation of genomic DNA from all 53 samples has been accomplished and quality and quantity of the DNA samples have been determined. Seven primer sequences specific to *Juniperus* species available in public domain have been synthesized for phylogenetic analysis. Optimization of PCR amplification conditions to screen ISSR and DAMD markers for diversity analysis is also in progress.

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**Angiosperm systematics, floristic diversity assessment, taxonomic monograph/ revision and plant conservation**

## Taxonomic Revisionary Studies

***Saxifraga* L. (Saxifragaceae)**

Arctic-alpine plants in the genus *Saxifraga* L. provide an excellent material for investigating the process of diversification in Himalayan regions. *Saxifraga* comprises of *ca.* 440 species worldwide, which are generally known as Saxifrages. It derives its name from the latin word 'Saxifraga', which means stone braker. As its name indicates it is medicinally used for treatment of renal calculi and has several other ethnobotanical uses. *Saxifraga*, divided into several sections, subsections and series, has a rather controversial taxonomic status as at times the genus is divided into subgenera with several infra specific complexes. Several taxa of *Saxifraga* share similar anatomical and morphological characters and polyploidy. Thus, critical micro-morphological and ecological studies along with molecular phylogenetic analysis may be of great help for a better understanding of the character evolution in *Saxifraga* and generic as well as species delimitation.

In India, *Saxifraga* is represented by *ca.* 64 species (with 4 subspecies and 5 varieties), abundant in western and eastern Himalayan alpine scrubs and meadows. Out of these 64 species, 23 are confined to western Himalaya and 17 in eastern Himalaya while 40 species are common to both the regions. The maximum diversity has been observed between 4000-4500 m asl. Although the genus is confined to Himalayan region, one species *S. stolonifera* has been reported in cultivation from Western Ghats. Few species such as *S. ramulosa* and *S. punctulata* are found at 6000-6500 m. asl, the maximum elevation attained by flowering plants. *Saxifraga* includes species with diverse life forms, mostly perennial to biennial and annual herbs. Morphological variations include, a habit that ranges from compact cushions to single stemmed herbs, roots that ranges from axonomorphous to fasciculate emerging from bulblets, leaves that ranges from compound to entire, flowering stems that develop from terminal to axillary rosette buds, flowers that are solitary or arranged in many flowered inflorescence, an ovary position that varies from semi-inferior to inferior, hairy to glabrous petals and chromosome numbers ranging from 2n=20 in *S.exarata* to 2n=210 in *S.androsacea*.

Field surveys were conducted to Uttarakhand, Himachal Pradesh and Jammu & Kashmir in Western Himalaya to collect the samples of *Saxifraga*. Eight species, namely *S. parnassifolia* D. Don, *S. jacquemontiana* Decne., *S. sibirica* L., *S. brunonis* Decne., *S. pulvinaria* H. Smith, *S. brachypoda* var. *fimbriata* (Wall. ex Ser.) Engel, *S. stolonifera* Curtis and *Saxifraga* sp. were collected from natural habitat. International Herbarium databases were consulted on line and images of 'TYPE' specimens of the different taxa of *Saxifraga* were down loaded. Specimens of *Saxifraga* housed in Indian herbaria such as BSD, DD, and CAL were also studied. Species such as *S. Jackmontiana* and *S. duthiei* are on the IUCN Red List. During the field surveys very small, scattered populations of 2 or 3 individuals of *S. Jackmontiana* was found in the Himalayas. Habitat destruction and other developmental activities in the Himalayan region are the main causes of threat. One interesting taxon of *Saxifraga* has been collected from Kedarnath Wild Life Sanctuary and is under study. Taxonomic studies on seven species of *Saxifraga* have been completed.

## Taxonomic studies on grasses of Western Himalaya

Poaceae, the grass-family, is the fifth largest family comprising ca. 793 genera and 10,000 species with cosmopolitan distribution. In India, the family is represented by ca. 268 genera and ca. 1300 species. Grasslands form an integral part of ecosystem, rendering vital services and act as reservoirs of the crop gene pool. Himalayan ecosystem supports enormous number of grasslands at different altitudes, which harbour a variety of grass species of great economic value. The rich diversity of grasses present in the Himalayan region is of both intangible value and direct value for the livestock and grassland dependent mountain communities. Grasses are diverse in taxonomic diversity and exhibit wide range of tolerance against the environmental factors qualifying as a pioneer species of an ecological community. In mountain ecosystems, grasses are redundant element with huge functional roles in purification of soil quality and acting as organizers of macro-invertebrate communities. Keeping in view the role of grasses in mountain ecosystem, the present study was initiated to assess the diversity of grasses in different altitudinal zones of western Himalaya. The purpose of the study is to document the taxonomic diversity of grasses, its functional role and prospective uses.

To fulfill the above objectives, field tours were conducted to different localities of Himachal Pradesh, Jammu & Kashmir and Uttarakhand. Approximately, 600 specimens comprising about 170 species belonging to 55 genera of grasses were collected. At higher altitudes, species of subfamily Pooideae were of common occurrence whereas members of Panicoideae were generally found at lower elevations. As Western Himalaya has not been extensively explored for grasses earlier, various novelties in different groups of grasses are expected. Apart from new species, three new records for India have been identified in the genera *Agrostis* and *Calamagrostis*. Tribe *Paniceae* and Triticeae which comprise of millets and cereals are nutritionally important groups of grasses. About 50 species belonging to 16 genera of these groups have been collected and identified. Pooideae represents one of the taxonomically complex groups of grasses. Approximately, 55 species belonging to 15 genera of Pooideae have been collected and identified. The study is in progress.

## New plant species discovered

***Heterostemma barikiana*** P. Agnihotri, D. Husain, P. Katiyar, D. Sahoo, Rodda & T. Husain (Apocyanaceae).

*Heterostemma barikiana* is similar to *Heterostemma xuansonense* Tran & Kim because both species have no or very reduced peduncle and have a pubescent staminal corona; they can be separated on flower size and colour (c. 20 mm diam. and purple in *H. xuansonense* vs. 8–12 mm and yellow or orange, rarely pink with dark red spots in *H. barikiana*) (Fig. 1).

*Heterostemma barikiana* occurs in Manipur, India, in Chin State, Myanmar as well as in North and West Thailand. It grows between 775 and 2400 m in open evergreen forest (India, Myanmar), and in dry evergreen forest (West Thailand).

Fig. 1: Newly discovered plant species: *Heterostemma barikiana* P. Agnihotri, D. Husain, P. Katiyar, D. Sahoo, Rodda & T. Husain.

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**Floristic inventory, documentation of bioresources, plant conservation and systematic studies of flowering plants**

### Plant diversity assessment and conservation

In India, still many areas are floristically unexplored or underexplored. These areas are rich in plant diversity harboring several important medicinal as well threatened plant species. Floristic studies required extensive field survey works that can result into discovery of new species, new distributional record, reveal population size and the current status of the plant diversity of the particular region. The government, academicians or scientists can use this data for the formulation of conservation policies especially for the threatened group of plants. In India, 2704 plant species are facing various kinds of threats in their habitat and most of the plant species are traded for various purposes and harvested unscientifically. If it continues, many plants will be extinct in the near future; hence their conservation is of utmost priority. For *ex-situ* conservation, germplasm of these threatened plants will be collected from different localities of the country and planted in our Botanical Gardens.

Seventeen field trips were conducted in different parts of the country *viz*. Maharashtra, Madhya Pradesh, Uttar Pradesh, Gujarat, Uttarakhand, Kashmir, and Meghalaya and more than 3000 samples of different plant groups were collected.

For the development of herbarium at Botanical Garden in Chandrapur district, Maharashtra, field surveys were conducted in Western Ghats and Vidarbha region of Maharashtra. A total 2100 samples were collected, of which more than 250 species have been identified so far.

The gum and resin are minor forest produce of the forest and the tribal communities collect and sell these produce in markets to get some income. Detailed study is required to assess the role of these minor forest produce in the livelihood of the tribal community and also to study the potential of these produce for product development. A total of 70 samples of gum and resin were either procured or collected from different states of country viz. Maharashtra, Meghalaya, Madhya Pradesh, Uttar Pradesh, Gujarat and Uttarakhand for the development of value added products.

### Plant systematic studies

Revisionary studies provide comprehensive taxonomic information of taxa, which can be used to solve taxonomic ambiguities related to identification, nomenclature, classification, phylogeny, distribution, variation pattern and several other aspects. Genera such as *Geranium* L. and *Rhynchosia* Lour., and the tribe *Boehmerieae* of Urticaceae are very complex morphologically and only scanty information of these groups is available from India. We have taken up the above two genera and the tribe *Boehmeriae* for comprehensive taxonomic revisions.

### *Geranium* L. (Geraniaceae)

*Geranium* L. (Geraniaceae), commonly known as 'Cranebills', includes plants with beautiful brightly coloured (pink, purple, blue, white and red) flowers. The distribution of ca. 350 species of *Geranium* in the world is confined to temperate regions and the tropical mountains. Three subgenera of *Geranium,* i.e. subg. *Geranium,* subg. *Erodioidea* (Picard) Yeo and subg. *Robertium* (Picard) Rouy, have been recognized based on the fruit dispersal mechanism. The first systematic account of *Geranium* in India was given by Edgeworth and Hooker (1875), wherein they recorded 18 species. Recent work of Malhotra (1997) reported

27 species under two subgenera (i.e. *Geranium* and *Robertium*) and eight sections. No comprehensive revision for *Geranium* in India is available, apart from the species enumeration in some regional Floras of the Indian Himalayan Region. A large number of herbarium specimens were studied from Indian herbaria physically as well as virtually from international herbaria (BSD, DD, LWG, ASSAM, K, BM, L. GDC, M, P). Four field tours were conducted to collect the fresh samples from Gangotri National Park, Bageshwar and Govind Wildlife Sanctuary of Uttarakhand, and Shillong, Dawki and Cherapunji in Meghalaya. About 348 samples were collected and 12 known species were identified, *viz. Geranium clarkei* P.F. Yeo, *G. donianum* Sweet, *G. kishtvariens* Knuth., *G. nepalense* Sweet, *G. polyanthes* Edgew. & Hook. f., *G. pratense* L., *G. pusillum* L., *G. robertianum* L., *G. rotundifolium* L., *G. sibiricum* L., *G. wallichianum* D. Don ex Sweet, and *G. swatense* Schonb.-Tem. (Fig.1. A-D). Nomenclature has been updated and lectotypes were designated for *Geranium erianthum* f. *leucanthum* H. Takeda and *G. arnottianum* Steud.

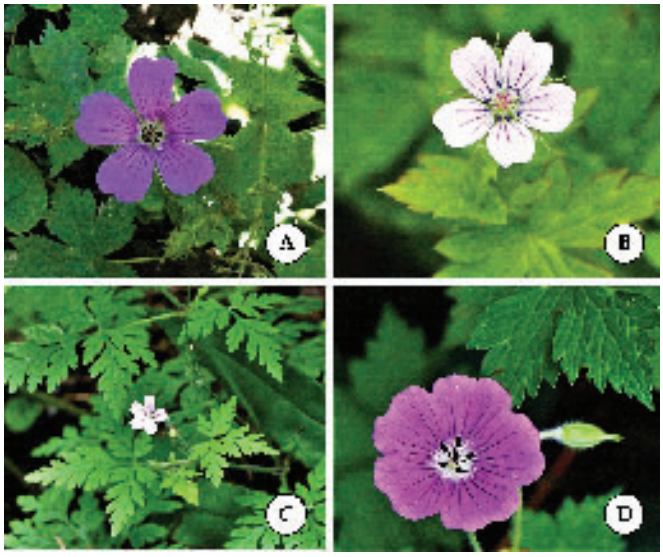


Fig. 1: Some of the interesting species of *Geranium*-(A) *G. kishtvariens* Knuth., (B) *G. nepalense* Sweet, (C) *G. robertianum* L., (D) *G. wallichianum* D. Don ex Sweet

## *Rhynchosia* Lour. (Leguminosae)

The genus *Rhynchosia* Lour. belongs to the subtribe *Cajaninae*, tribe *Phaseoleae*, in the family Leguminosae. It is the largest genus of the subtribe *Cajaninae*, comprising about 232 species, distributed throughout the tropics and subtropics and extending to North America from Mexico to some parts of the United States as well as Africa and Madagascar where it is most diverse. In India, the genus is represented by 25 species with one subspecies and one variety. Out of these, 7 species are endemic to India. *Rhynchosia* is having a lot of morphological plasticity which causes lot of confusion in the identification of the species. For the study of *Rhynchosia* specimens three Indian herbaria were consulted (LWG, ASSAM, CAL) and three field tours were conducted in Maharhashra, Uttarakhand and Meghalaya. A total of 70 samples were collected and three species have been identified so far:, *R. suaveolens*, *R. minima* and *R. maxima*, while the identification of the remaining specimens is in progress. *R. suaveolens* shows an extended distribution in Vidarbha region of Maharashtra as this species was earlier known only from Mumbai area. Nomenclature ambiguity of *R. suaveolens* has also been resolved.

## Tribe *Boehmerieae* (Urticaceae)

Urticaceae Juss., commonly known as the Nettle family, comprise of about 53 genera and 2600 species distributed in both temperate to tropical parts of the world. In India, Urticaceae are represented by 153 species in 29 genera. On the basis of characters of indumentum, stigma, and female perianth, the family is classified into 5 tribes: Urticeae, Lecantheae, Boehmerieae, Parietarieae, and Forsskaoleae. The tribe Boehmerieae is taxonomically very complex, as most of the genera are difficult to distinguish morphologically from one another. Moreover, there is no comprehensive taxonomic account of Boehmerieae available in India. Boehmerieae consist of 19 genera and nearly 250 species in the world. Genera in this tribe can be identified on the basis of nonstinging hairs, well developed, membranous and dry female perianth, free ovary and persistent or deciduous stigma. In India, *Boehmerieae* is represented by 10 genera and nearly 60 species.

As part of revisionary study on Indian *Boehmerieae,* four field tours were conducted in Bageshwar, Govind Wildlife Sanctuary, Gangotri National Park of Uttarkhand and Shillong in Meghalaya. Specimens of *Boehmerieae* housed in national and international herbaria were examined physically as well as virtually (LWG, CAL, BSD, K, BM, P). A total of 250 samples were collected and so far 8 species were identified, *viz. Boehmeria penduliflora* Wedd ex. D.G. Long, *B. clidemioides* Miq, *B. macrophylla* Horn., *B. nivea* (L.) Goud., *B. malabarica* Wall ex. Long, *Pouzolzia hirta* (Blum) Hussk., *P.rugulosa* (Wedd) Kravastova and *Debregeasia longifolia* Wedd. Further identification

is in progress. *Boehmeria clidemioides* Miq. was collected for the first time from central Himalaya i.e. Bageshwar district, Uttarakhand. This species has been known earlier only from North east India. Lectotypes were designated for *Urtica penduliflora* Wall., *Boehmeria penduliflora* Wedd. ex D.G. Long and *Boehmeria densiflora* var. *intermedia* (Wedd. ex D.G. Long) Acharya and Yonek.

## Bioresource documentation

The traditional communities of India largely depend on the forest bioresources for their livelihood; using these resources not only for food and medicine but also for their economic upliftment. For the documentation of traditional knowledge, field tours and one to one interviews will be conducted with traditional healers and other knowledgeable persons. For the quantitative assessment of ethno-medicinal data, cultural indices can be used *viz,* Fidelity level (FL), Use Value (UV) and Informant Consensus Factor (ICF). Indigenous knowledge provides very useful information for treating different diseases. Bio-prospection of these plants results into the isolation of the novel molecules for treating many life threatening diseases and development of various healthcare products. Detailed study is required to document the indigenous knowledge, diversity of medicinal plants, their status and role of these forest resources in the livelihood of the local tribal community.

The Yavatmal district of Maharashtra is rich in floristic and ethnic diversity. The tribal community of this region conserves the forest patches by means of their belief and faith i.e. sacred groves. The sacred groves of this region are still unexplored from floristic as well as ethnobotanical point of view. Many tribal people of the study area are dependent on these groves not only for medicinal uses but also for their livelihood. Yavatmal district was surveyed for the identification of the sacred groves. During these explorations eight new sacred groves were discovered, namely Amba, Ralinama, Bhawani mata, Jagdamba mata Kesurli, Kawadashi, Pandhara Devi, Usad Devi Bhudkeshwar and Dapora. The eight sacred groves were studied thoroughly for documentation of floristic and medicinal plant diversity. In the preliminary survey, we collected more than 300 samples of flowering plant species from these sacred groves and prepared herbarium specimens by using standard method and identified 154 species. The dominant family observed in the area was Leguminosae with 34 species. Based on the use, 126 plant species were documented as medicinally important whereas 22 were found ornamental, 17 wild edible, 6 oil yielding and 15 species were used as Fodder. Herbs were found dominant (38%) followed by trees (37%) in the study sites. The mostly preferred plant part for preparation of medicine was leaf, followed by root and stem bark. The decoction was the most favored practice used by the local tribal community. Nine threatened plant species were also reported from these groves.

Similarly Jhabua district of Madhya Pradesh was surveyed to collect information from the Bhil and Bhilala tribes on the use of medicinal plants in the treatment of dermatological diseases. The ethnobotanical data was collected from local traditional healers in 39 villages within the Jhabua district of western Madhya Pradesh, using standard methods. The Use Value (UV), Fidelity Level (FL) and Informant Consensus Factor (ICF) were calculated in order to analyse the data collected and results were compared to prior ethnobotanical surveys relating to dermatological treatments conducted within India. A total of 116 plant species of 103 genera, belonging to 58 families were identified, which are used in the treatment of 21 different dermatological disorders. The highest UV (2.41) was recorded for *Punica granatum* and the lowest UV (0.11) in *Rumex dentatus*. The highest FL of 100% FL was found for 17 plant species, and the ICF was found to range from 0.20 (leucoderma) to 1 (mouth ulcers). The survey enabled us to identify and record a broad range of medicinal plants and practices used by the Bhil and Bhilala tribes for the treatment of dermatological conditions. The data collected is valuable, not only as part of the process of documenting and preserving the traditional knowledge and culture that is in danger of being lost, but also in its provision of a broad selection of medicinal plants that could be subjected to further pharmacological and clinical investigation for their potential role in the treatment of dermatological conditions.

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# Pharmacognosy, Phytochemistry and Product Development

# PHARMACOGNOSY, PHYTOCHEMISTRY AND PRODUCT DEVELOPMENT

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- Phytochemistry
- Product Development

## Research Scholars Statistics

| Sr. No. | Position Name | Numbers |
|---|---|---|
| 1. | Research Associate | 01 |
| 2. | Young Scientist | 01 |
| 3. | JRF/SRF Fellow | 17 |
| 4. | Project Staff | 12 |

## R&D Highlights

**Development of quality standards for important phytomolecules**

- Galactomannan was extracted and isolated from leguminous seeds, purified and characterized through, UV, IR, NMR. Characterization through gel permeation chromatography (GPC) for mol. wt. and polydispersity index was standardized.
- Sennosides rich fractions were isolated from the leaves of *Cassia* species and Quantified using HPTLC.

**Pharmacognostic evaluation and pharmacological validation**

- The Indian pharmaceutical industry constantly faces the problem of the adulteration and substitution of raw drugs. To develop identification and quality control markers of aforesaid drugs and their substitutes/ adulterants, pharmacognostic evaluation of several drugs especially, the bark drugs is being carried out using organoleptic characters, macro-microscopic details, physicochemical parameters and HPTLC/ fingerprint profiles along with the chemical markers.
- Variations in quinic acid content in different accessions of *Commiphora wightii* and *Commiphora agallocha* were investigated using RP HPLC. Quinic acid was detected as a major metabolite in aqueous extracts of leaves of *Commiphora wightii* and *C. agallocha*.
- *Sphaeranthus indicus* is an important medicinal plant in Ayurveda which grows as weed in rice fields throughout India. A simple, rapid, sensitive and reproducible method was developed for simultaneous HPTLC quantification of two bioactive compounds eugenol and β-sitosterol from *S. indicus*.
- *Elephantopus scaber* (L.) is a widely used traditional medicinal plant. It grows in hotter parts of the Indian subcontinent. Four important phenolic compounds, i.e chlorogenic acid, ferulic acid, gallic acid and protocateuchine, were identified and quantified with the help of developed RP-HPLC method.

**Pharmacological studies of lichen species, *Usnea longissima* used in peptic ulcer**

- Four compounds, 18R-hydroxy-dihydroallopro-tolichesterinic acid, neuropogolic acid, barbatic acid, and usnic acid were extracted from *Usnea longissima*. These compounds were identified through mass spectrometry and NMR spectroscopy. All four compounds displayed cytotoxic activity. The potential leads from *U. longissima* were validated in rats.

**Search for elite germplasms of *Gymnema sylvestre* with respect to Gymnemagenin, Deacyl gymnemic acid, Lupeol and Stigmasterol**

- Studies were conducted on *Gymnema sylvestre* samples collected from different states of India with the aim of identifying the best elite germplasm based on content of their major metabolites.
- Chemical reference marker Mangiferin was isolated from the leaves of *Mangifera indica*. Mangiferin possesses several health endorsing properties such as antioxidant, antimicrobial, antiaging, anticancer, hepatoprotective and many more.

**Anti-termite activity from oil of *Artemisia absinthium***

- Essential oil from *Artemisia absinthium* leaves, stem and seeds were evaluated for termite repellency and mortality. The leaves essential oil showed most significant termite repellency comparative to stem and seed and can be used for termite repellency.

**Herbal Gulal from temple waste flowers**

- *Tagetes* flowers (yellow and red) collected from temples of Lucknow and Varanasi were used for standardization of colour extraction process and chemical profiling of the colour molecules. The colours extracted were mixed with natural ingredients. The prepared synergistic mixture of colored dry powder has good sticking capacity to skin and can be easily removed by soft mop.It is non-toxic to skin.

**Characterization and value addition of plant based resins, gums and waxes**

- For separation and isolation of various products of rice bran wax like oil, wax and policosanol (By product of rice bran oil processing industries), different methods like solvent extraction saponification and transesterification were standardized.

**Preparation of certified reference materials**

- Institute has taken initiative to prepare some of the commercially important Cerified Reference Materials (CRMs)/Reference Materials (RMs) of medicinal and aromatic nature.

**Aroma Mission**

- Various samples of turmeric leaf oil collected from farmers were analyzed using GCMS for Quality Assessment. The major chemical compounds present are α-phellandrenes (32%), terpinolene (26%), p-cymene (5.9%) and 1, 8 cineole (6.5%).
- A Shodhan protocol and preparation of standardised cannabis extracts based on AYUSH formulation was developed from Hemp (*Cannabis sativa*).

**Endolichenic fungus inhibits quorum sensing and biofilm formation of *Pseudomonas aeruginosa* PAO1**

- Along with the mycobiont, numerous non-obligate microfungi live in lichen thalli. These microfungi are called endolichenic fungi (ELF). The extracted metabolites of ELF (MELE) were investigated for anti-quorum sensing activity using the biomarker strain *Chromobacterium violaceum*. The effect of MELE was also evaluated on the production of virulence factors and biofilm formation of *Pseudomonas aeruginosa*. Our study for the first time showed that the ELF, *Aspergillus quandricinctus* possesses potential to inhibit quorum sensing and biofilm formation of *P. aeruginosa* and can be further exploited for hospital and healthcare facilities.

**Nanoparticles for antimicrobial activity**

- Formulation of herbal nano emulsion against dermal pathogens was developed.

**Herbal product against urolithiasis & nephrolithiasis**

- A herbal formulation was developed to alleviate urolithic and a patent on this is being filed in India. This product is more efficacious and cost effective than existing herbal brands against Urolithiasis & nephrolithiasis.

**Herbal formulation for management of dandruff**

- An oil based formulation was developed consisting of three ingredients. Promising anti microbial activity was found in the formulation developed. Further validation studies are in progress.

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**Chemical investigation of medicinal and aromatic plants and products for various applications**

## Preparation of certified reference materials/ reference materials

CSIR-NBRI has taken initiative to prepare some of the commercially important Cerified Reference Materials (CRMs)/Reference Materials (RMs) of medicinal and aromatic nature. CRMs/RMs of high purity active molecules are required for quality assessment of products and calibration of equipments.

The fractionating column and reaction vessels of 5 litre capacity each have been installed and work for conversion and isolation of desired molecules of aromatic nature is under progress.

CRMs/RMs will be prepared as per the requirments of ISO-17034-2016 and accordingly following documents have been prepared for accreditation:

- Quality Manual
- Quality System Procedures

Preparation of Standard Operating Procedures for aromatic reference materials is in progress.

## Aroma Mission

- Various samples of turmeric leaf oil collected from different farmers were analyzed using GCMS for Quality Assessment. The major chemical compounds present are α-phellandrenes (32%), terpinolene (26%), p-cymene (5.9%) and 1, 8 cineole (6.5%).
- Facilitated marketing of turmeric leaf oil of farmers with industries.

## Technologies and Products for reduced emission fire works

- Testing of fire crackers substituted with plant materials and added essential oils was completed. Results are very promising in reducing the air pollution.

## Characterization and value addition of plant based resins, gums and waxes

- For separation and isolation of various products of rice bran wax like oil, wax and policosanol (By product of rice bran oil processing industries), different methods like solvent extraction saponification and transesterification have been carried out. Following products were prepared:
- Product-1-Oil, without wax
- Product-2- wax, without oil
- Product-3-Upgraded wax
- Product-4- Policosanol rich fraction

## Breeding and genetic improvement of Hemp (*Cannabis sativa*) for industrial and medicinal purposes

HPLC method was established for the quantification of Cannabinoids (Tetrahydrocannabivain, Cannbidiol, Cannbidiolic acid, Cannabinone, Delta-9 Tetrahydrocannabinol, Delta-8 Tetrahydrocannabinol, Tetrahydrocannabinolic acid) in various samples of *Cannabis sativa* (Fig. 1).

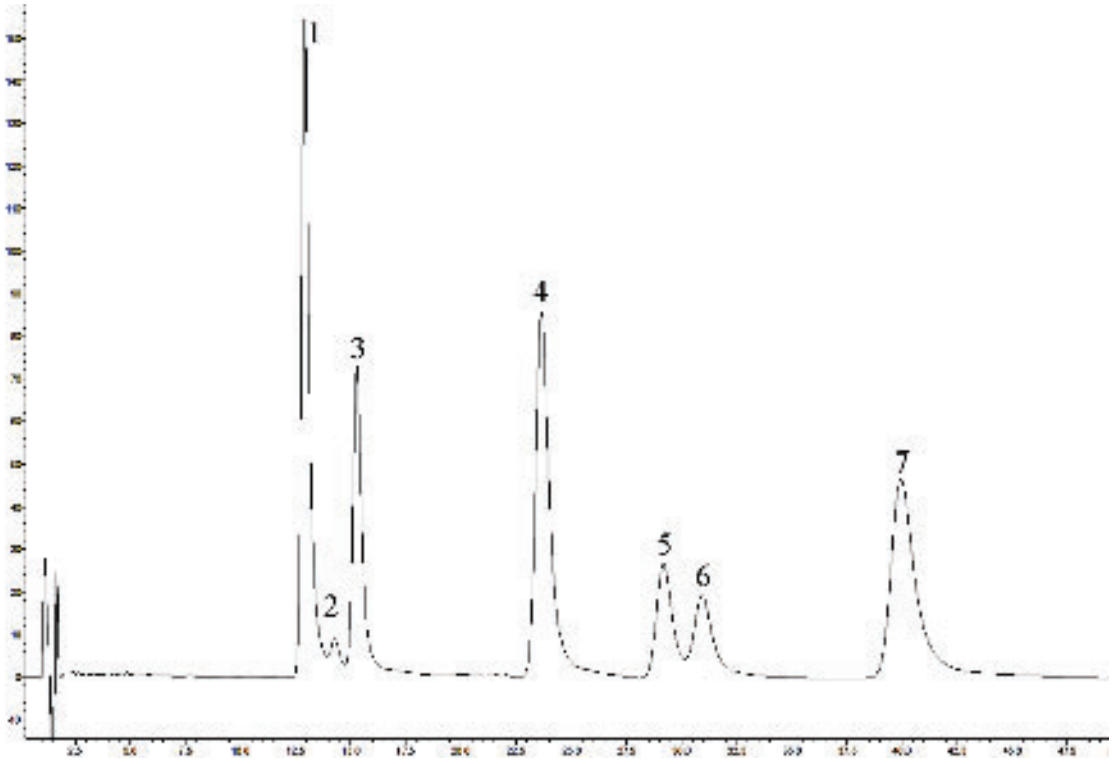


Fig. 1: HPLC chromatogram of Cannabinoids. 1 = Tetrahydrocannabivain, 2 = Cannbidiol, 3 = Cannbidiolic acid, 4 = Cannabinone, 5 = Delta-9 Tetrahydrocannabinol, 6 = Delta-8 Tetrahydrocannabinol, 7 = Tetrahydrocannabinolic acid

## Quantification and identification of volatiles and nonvolatile secondary metabolites of cotton leaves at various developmental stages

Quantification and identification of volatile and nonvolatile secondary metabolites of cotton leaves samples of various stages were carried out using GCMS, GLC, GCHS and HPLC. Different extraction methods like Hydro distillation, Soxhlet Method and Cold extraction were used. The work is under progress.

## Study on variation in oil content and chemical composition of different *Citrus* species of north east region

Study on variation in oil content and chemical composition of various *Citrus* species of north east region was carried out (sample analysed-37). The oil content using hydro-distillation varied between the different locations. The major chemical compounds and essential oils present in citrus peel were identified as D-Limonene, β Linalool, Citronellal, β Pinene, β Citral, α Citral, Caryophyllene, Eugenol and Eugenol acetate.

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**Pharmacological evaluation of herbal drugs/formulations and their safety in Rodent Models**

Safety of herbal products provides the base to determine the effectiveness of the medications. The short and long term study of herbal medicaments avoids the risk of adverse reactions.

### Pharmacological studies of lichen species *Usnea longissima* and *Cladonia furcata* used in peptic ulcer

Our study focused on the identification of secondary metabolites in acetone extract of the lichen, *Usnea longissima,* using ultra-performance liquid chromatography-electrospray ionization-quadrupole time of flight-tandem mass spectrometry (UPLC-ESI-QTOF-MS/MS) hyphenated techniques. From our study, 19 compounds were tentatively identified through comparison of exact molecular masses from their MS/MS spectra, mass fragmentation studies and compared with literature data. In addition, potent cytotoxic activity of *U. longissima* extract prompted us to isolate four compounds, 18R-hydroxy-dihydroalloprotolichesterinic acid, neuropogolic acid), barbatic acid, and usnic acid from this extract, which were adequately identified through mass spectrometry and NMR spectroscopy. All four compounds displayed cytotoxic activity. Barbatic acid manifested doxorubicin equivalent activity against A549 lung cancer cell line with IC50 of 1.78 µM and strong G0/G1 accumulation of cells. Poly ADP-ribose polymerase (PARP) cleavage confirmed that it induced cytotoxic activity via apoptosis. Our work has discerned the depside barbatic acid from crude extract as a candidate anti-cancer molecule, which induces cell death by stepping up apoptosis. The potential leads from *Usnea longissima* and *Cladonia furcata* were subjected to test against peptic ulcer and gastroesophageal reflux disease (GERD) model in rats (Fig. 1).

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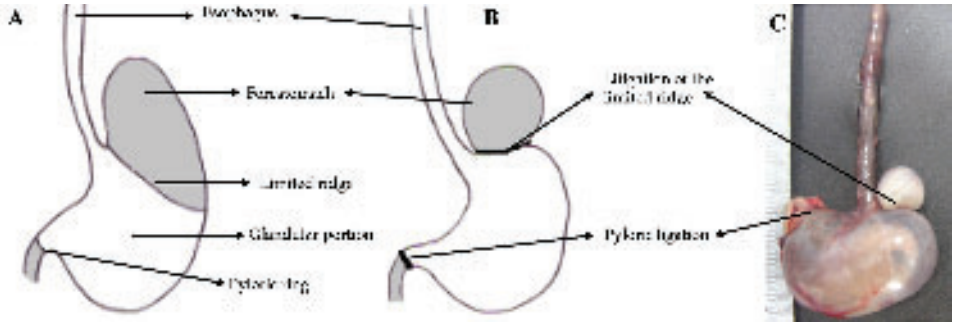


**Fig. 1**: Preparation of reflux oesophagitis model in rats; A. Illustration of stomach, B. and C. Ligation between the fore stomach and glandular portion followed by pylorus –induced oesophagitis

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**Herbal product development for industrial application**

## Bark Drugs

The Indian pharmaceutical industry constantly faces the problem of the adulteration and substitution of raw drugs. Therefore, the pharmacognostic evaluation of the drugs, especially the bark drugs viz. *Acacia arabica, A. nilotica, A. catechu, Aconitum heterophyllum, Anthocephalus cadamba, Artocarpus heterophyllus, Betula utilis, Bombax ceiba, Buchanania lanzan, Butea monosperma, Caesalpinia bonduc, Calotropis procera, C. gigantea, Carissa carandas, Cassia fistula, Commiphora mukul, Dalbergia sissoo, Delonix regia, Ficus bengalensis, F. carica, F. glomerata, F. religiosa, F. retusa, Helictrus isora, Lannea coromandelica, Lawsonia inermis, Leptadenia reticulata, Madhuca longifolia, Mallotus philippinensis, Mangifera indica, Melia azedarach, Mimusops elengi, Moringa oleifera, Millettia pinnata, Punica granatum* (two varieties), *Quercus glauca, Q. leucotrichophora, Rhododendron indicum, Syzygium cumini* (two cultivars), *Tinospora cordifolia*, *Ulmus wallichiana* and *Zyziphus jujuba* are being compiled using organoleptic characters, macro-microscopic details, physicochemical parameters and HPTLC/ fingerprint profiles along with the chemical markers. This study has been done with the aim to develop identification and quality control markers of aforesaid drugs and their substitutes/adulterants.

## Macro-microscopy of *Aconitum*

*Aconitum heterophyllum* belongs to the family Ranunculaceae, commonly known as 'Ativisha'. Dried tuberous roots of *A. heterophyllum* are used as expectorant, anti-diarrhoeal, anti-inflammatory agent. *A. heterophyllum* was collected for macro-microscopical studies. *A. heterophyllum* is an annual plant with erect shoot and biennial root. Branches are absent or 1 or 2 in number. Leaves are glabrous, sessile, and variable in shape and size. The tubers are up to 3 cm long, conical at ends. Microscopy of tuberous root of *A. heterophyllum* has also been done. It shows the four peculiar vascular bundles in the ground tissues.

## CSIR-Phytopharmaceutical Mission

Male and female plants of *Tinospora cordifolia* have different leaf shapes, petiole shapes and length. Quantitative anatomical features also provide basis to distinguish between male and female plants. The size of cortical region, presence of starch grains and mucilage canals were significantly different between the male and female plants. Total sugar, starch and tannin were also high in female plants. Four markers viz. as berberine, magnoflorine, jatrorrhizine and palmatine were estimated through HPTLC. Our studies demonstrated a gender based differences in morphology, anatomy and physico-phytochemical profiles. This study underscores the importance of gender in *Tinospora cordifolia* for quality control.

## Evaluation of seasonal effect on anti-hypertensive indole alkaloid of *Rauvolfia* spp. from northern India and development & validation of physicochemical and molecular markers

*Rauvolfia serpentina* (L.) Benth. ex Kurz. and *Rauvolfia tetraphylla* L. were collected in different seasons. The detail of the seasonal variation of phytochemical markers viz. Reserpine and Ajmalicine in different seasons in roots of *R. serpentina* and *R. tetraphylla* were performed. The HPTLC Chromatograms under UV 254nm and UV 366nm showing the methanolic

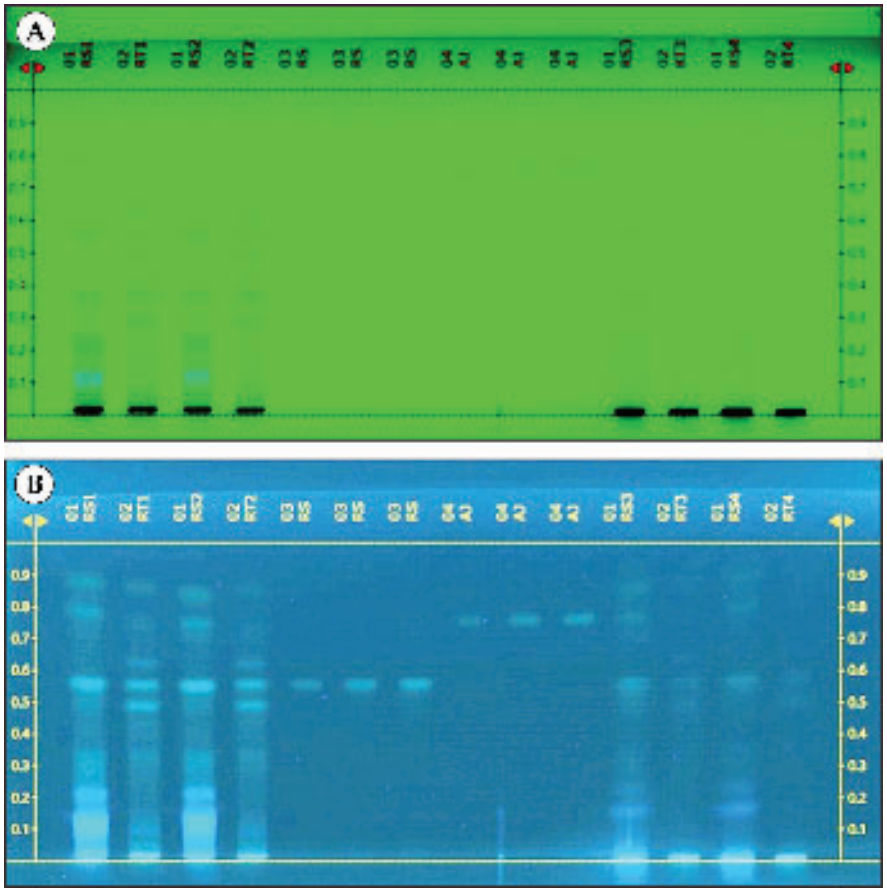


Fig. 1: HPTLC Chromatoplate; A. under UV 254nm, B. under UV 366nm showing the methanolic extract of the sample of *R. serpentina* (RS1) March, (RS2) May, (RS3)July, (RS4) September and *R. tetraphylla* (RT1) March, (RT2) May, (RT3) July, (RT4) September, (RS) Reserpine (at Rf 0.56) and (AJ) Ajmalicine (at Rf 0.76).

extracts of the different seasons of *R. serpentina* [(RS1) March, (RS2) May, (RS3) July, (RS4) September and *R. tetraphylla* (RT1) March, (RT2) May, (RT3) July, (RT4) September] are presented in Fig. 1. The Reserpine (RS) and Ajmalicine (AJ) were observed at Rf 0.56 and Rf 0.76 respectively.

## Evaluation and optimization of nanoparticles using natural polymers

Characterization of naturally isolated mucilage which is used for the preparation of polymeric nanoparticle as a natural polymer (Carrier) was carried out. The isolated mucilage was characterized for its various properties by performing the following evaluation parameters such as organoleptic evaluation, phytochemical characterization, physicochemical characterization, NMR Spectroscopy and flow properties of the mucilage.

The studies conformed that *Hibiscus cannaabinus* L. is a novel source of mucilage with great functional value and can be used as a natural polymer for pharmaceutical formulations in both conventional and novel drug delivery systems.

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**Herbal product development for industrial application, stable herbal food colours**

## Chemical composition and anti-termite activity of essential oil from *Artemisia absinthium* growing in Kashmir valley of India

*Artemisia absinthium* is an aromatic and medicinal plant containing essential oil commonly known for the use in variety of human diseases, cosmetics as well as in pharmaceutical industry. Essential oil extracted from leaves, stem and seeds of *A. absinthium* were 0.429±0.034%, 0.148±0.006%, and 0.072±0.007% respectively. Chemical constituents of essential oil from all three parts were identified and compared by gas chromatography–mass spectroscopy. Total 16 compounds were identified in the essential oil of leaves, stem and seeds in which boronyl acetate was present in major amount (Table 1). L-terpenen-

**Table 1. Comparative essential oil composition of *Artemesia absinthium* leaves, stem and seed.**

| S.N. | Compound Name | R.T. | Method of Identification | % Composition | | | RI Values | |
|---|---|---|---|---|---|---|---|---|
| | | | | Leaves | Stem | Seed | Experimental | Literature |
| **Monoterpens-07** | | | | | | | | |
| 1. | α-Pinene | 6.49 | S,RI | 1.74 | 1.79 | 2.2 | 925 | 933 |
| **2.** | Camphene | 7.34 | MS,RI | 1.77 | 1.63 | 2.01 | 935 | 948 |
| **3.** | Sabinene | 8.49 | MS,RI | 5.39 | 5.14 | 6.83 | 966 | 975 |
| **4.** | D-Limonene | 10.85 | MS,RI | 1.74 | 1.58 | 1.91 | 1006 | 1025 |
| **5.** | p-Cymene | 12.01 | MS,RI | 14.14 | 12.86 | 14.87 | 1070 | 1059 |
| **6.** | γ-Terpinene | 12.64 | MS,RI | 1.05 | --- | 1.17 | 1098 | 1102 |
| **7.** | δ-Terpinene | 13.83 | MS,RI | 1.15 | --- | 1.16 | 1110 | 1106 |
| **Total** | | | | 26.98 | 23.00 | 30.15 | | |
| **Monoterpene Alcohol-04** | | | | | | | | |
| **8.** | p-Cymen-3-ol | 14.34 | MS,RI | 1.12 | 1.45 | --- | 1130 | 1114 |
| **9.** | Nerol | 14.87 | MS,RI | --- | 1.15 | --- | 1155 | 1164 |
| **10.** | L-terpinen-4-ol | 18.58 | MS,RI | 18.24 | 17.07 | 17.3 | 1190 | 1176 |
| **11.** | α-Terpineol | 19.49 | MS,RI | 5.37 | 6.07 | 5.56 | 1230 | 1222 |
| **Total** | | | | 24.73 | 25.74 | 22.86 | | |
| **Terpenoid-01** | | | | | | | | |
| **12.** | Bornyl acetate | 22.20 | MS,RI | 26.59 | 27.17 | 26.63 | 1270 | 1284 |
| **Sesquiterpenes-04** | | | | | | | | |
| **13.** | Caryophyllene | 25.06 | MS,RI | 7.59 | 9.07 | 6.96 | 1410 | 1425 |
| **14.** | Humulene | 26.50 | MS,RI | 1.03 | --- | 0.8 | 1434 | 1459 |
| **15.** | trans-α-Bisabolene | 29.26 | MS,RI | --- | 1.35 | --- | 1474 | 1499 |
| **16.** | Caryophyllene oxide | 32.05 | MS,RI | --- | --- | 0.14 | 1570 | 1550 |
| **Total** | | | | 8.62 | 10.42 | 7.9 | | |
| **Total Identified Compounds-16** | | | | 86.92 | 86.33 | 87.54 | | |
| **Total Unidentified** | | | | 13.08 | 13.67 | 12.46 | | |

4-ol was also found in higher amount in leaves (18.24%), stem (17.07%) and seeds (17.3%). Many other compounds such as α -pinene, camphene, sabinene, limonene, cymene, β-linalool, terpinen-4-ol, α-terpeneol, caryophyllene present commonly in all parts of plant like leaves, stem and seeds. γ-terpinene, terpenolene and humulene are present in leaves and seeds but not in stem part of the plant. Nerol and trans-α-bisabolene are present only in stem and caryophyllene oxide is present only in seeds.

The essential oils of *A. absinthium* leaves, stem and seeds were evaluated for termite repellency as well as termite mortality at five doses. The leaf essential oil showed most significant termite repellency compared to stem and seed. Leaf oil was found to have significant mortality as well as repellency along with the highest oil yield. Significant percentage repellency has been seen at a dose 10mg/g and 20 mg/g after 40h (Fig. 1). Leaf essential oil showed highest repellency % with $ED_{50}$ 2.44 mg/g whereas $ED_{50}$ for

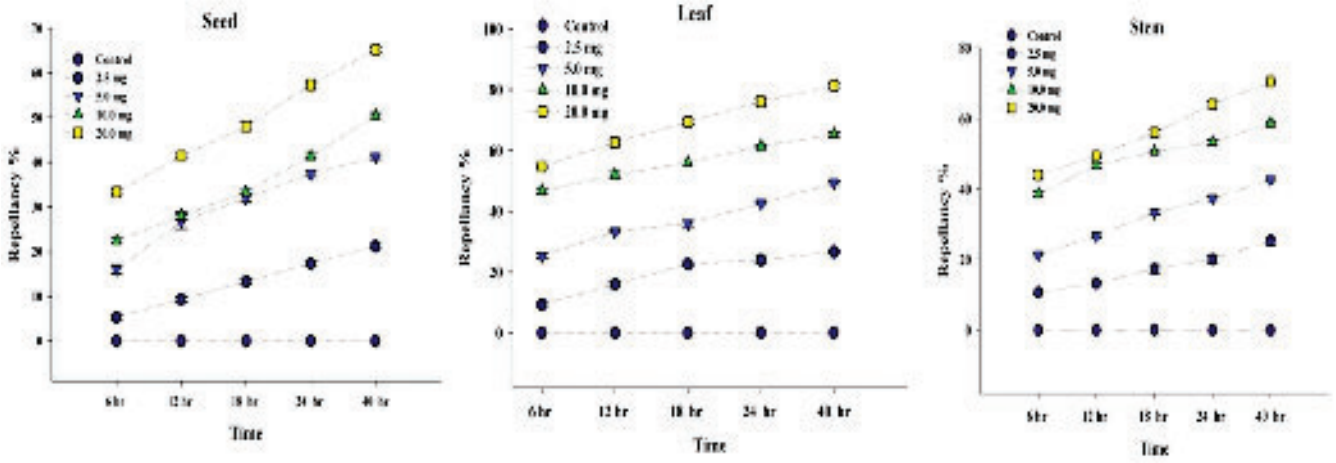


Fig. 1: Termite repellency of *Artemesia absinthium* leaf, seed and stem essential oil.

**Table 2. Regression equation and $ED_{50}$ values of leaf, stem and seed essential oil of *Artemesia absinthium***

| Samples | Leaf | | Stem | | Seed | |
|---|---|---|---|---|---|---|
| | Regression equation | $ED_{50}$ mg/gm | Regression equation | $ED_{50}$ mg/gm | Regression equation | $ED_{50}$ mg/gm |
| EOR | y=17.468x + 7.32<br>$R^2$ = 0.9969 | 2.44 | y =15.1x + 6.16<br>$R^2$ = 0.9927 | 2.9 | y=12.904x +4.32<br>$R^2$ = 0.9928 | 3.55 |
| EOM | y=9.704x - 9.18<br>$R^2$ = 0.9952 | 6.10 | y=8.408x - 6.36<br>$R^2$ = 0.9948 | 6.7 | y=6.668x-7.34<br>$R^2$ = 0.992 | 8.59 |

EOR: essential oil repellency; EOM essential oil mortality

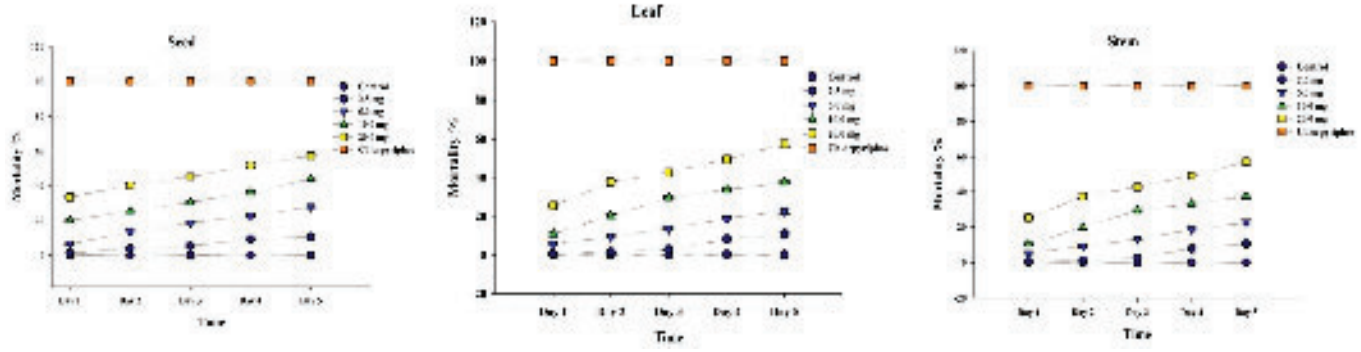


Fig. 2: Termite mortality of *Artemesia absinthium* leaf, seed and stem essential oil.

seed and stem essential oil was 3.55 and 2.9 mg/g, respectively (Table 2). In case of termite mortality essential oil was not found much significant where as it shows somewhat mortality at a dose of 20mg/g after 5 days (Fig. 2). In case of termite mortality for $ED_{50}$ leaf, stem and seed essential oil was found 6.09, 6.7 and 8.59 mg/g respectively. Chlorpyriphos 20% TC was taken as standard and ethanol was taken as positive control and no repellency or mortality has been found in control. 0.5 % does of Chlorpyriphos was used, which was sufficient for 100 % mortality of termites within 24 h. Thus the present study proved essential oil of *A. absinthium* leaf can be used for termite repellency.

## Herbal Gulal from temple waste flowers

At present, 90% colours available in market are based on synthetic dyes, which are usually of non-standards specification and are harmful to skin and other body parts. Colours from flowers are good alternative to chemical dyes based gulal. About 50 kg flowers of *Tagetes* (yellow and red) collected from temples of Lucknow and Varanasi were used for standardization of colour extraction process and chemical profiling of the colour molecules. The colours extracted from waste flowers were mixed with natural ingredients. The prepared synergistic mixture of colored dry powder has good sticking capacity to skin and can be easily removed by soft mop. It is non-toxic to skin. The technology of making herbal gulal from temple floral waste has been developed at lab scale (Fig. 3).

Fig. 3: Herbal Colors developed by CSIR-NBRI

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**Chemoprofilling of medicinal plants for herbal product development**

## Pharmacognostic evaluation and pharmacological validation of *Sphaeranthus indicus* DC.

*Sphaeranthus indicus* is an important medicinal plant in Ayurveda which grows as weed in rice fields throughout India, Sri Lanka, Australia and Africa. The present study was aimed at pharmacognostical evaluation and pharmacological validation of this high-value medicinal species. All the pharmacognostical parameters were done as per the API guideline. A simple, rapid, sensitive and reproducible method was developed for simultaneous HPTLC quantification of two bioactive compounds, eugenol and β-sitosterol, from *S. indicus*. The HPTLC was performed on silica gel 60 F254 by using toluene/ethyl acetate/glacial acetic acid (8:2:0.2) as a mobile phase for eugenol and b-sitosterol at Rf value 0.64 and 0.48, respectively (Fig. 1). *In vitro* activities viz. antioxidant, antidiabetic and anti-inflammatory were done to evaluate the pharmacological potential of *S. indicus*. Four antioxidant models viz. DPPH, ferric reducing power, 2-deoxyribose assay and antioxidant capacity were used to determine the free radical scanning. Antidiabetic and anti-inflammatory potential was determined by using starch–iodine colour assay and inhibition of protein denaturation model. IC50 value of *S. indicus* extract in DPPH and 2-deoxyribose assay was 328.96 ± 0.003 µg/ml and 30.36 ± 0.004 µg/ml respectively. The present study will be helpful for quality check of the raw material and monitoring batch-to-batch consistency of herbal drugs, wherein *S. indicus* is used as an ingredient.

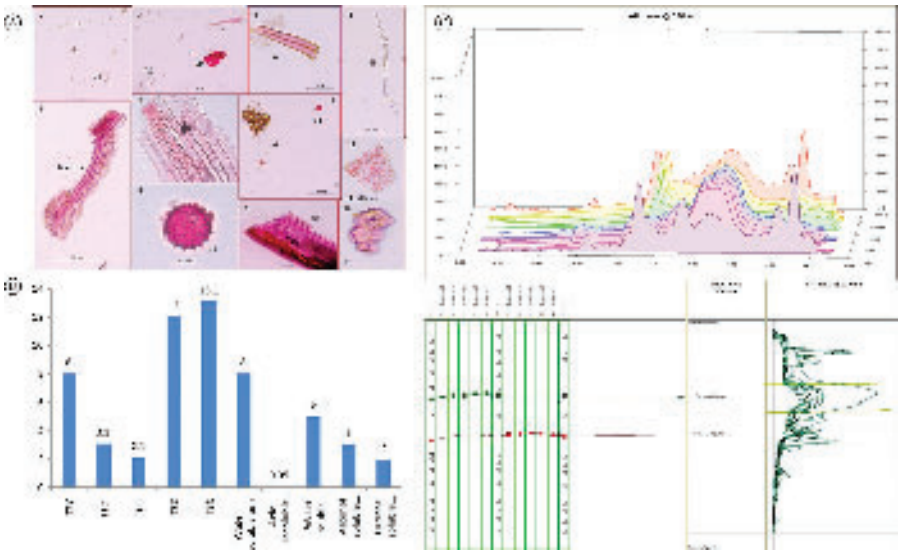

**Fig. 1(A-C)**: A. Powder microscopy of *Sphaeranthus indicus*. pc, prismatic calcium oxalate crystal (×20); og, oil globules (×20); ep, epidermal cell (×20); te, tracheary element (×20); fi, fibre (×20); tr, tracheid (×100); cs, cellulosic structure (×20); pg, pollen grain (×100); ve, vessels (×20); st, stone cells (×40); ol, oil globule cells (×20), B. Physicochemical parameters of *Sphaeranthus indicus*. *TFC* total flavonoid content, *TTC* total tannin content, *TPC* total phenolic content, *TSC* total sugar content, *TSC* total starch content, C. HPTLC 3D densitometric and substance assignment diagram of *Sphaeranthus indicus*, eugenol and β-sitosterol.

## Simultaneous RP-HPLC quantification of four phenolics in *Elephantopus scaber* L. and their *in vitro* pharmacological validation

*Elephantopus scaber* L. is a widely used traditional medicinal plant. It grows in hotter parts of the Indian subcontinent, Tropical Africa and East Asia. The present study aimed at RP-HPLC quantification of phenolics in *Elephantopus scaber* and their pharmacological validation (Fig. 2). The chromatographic

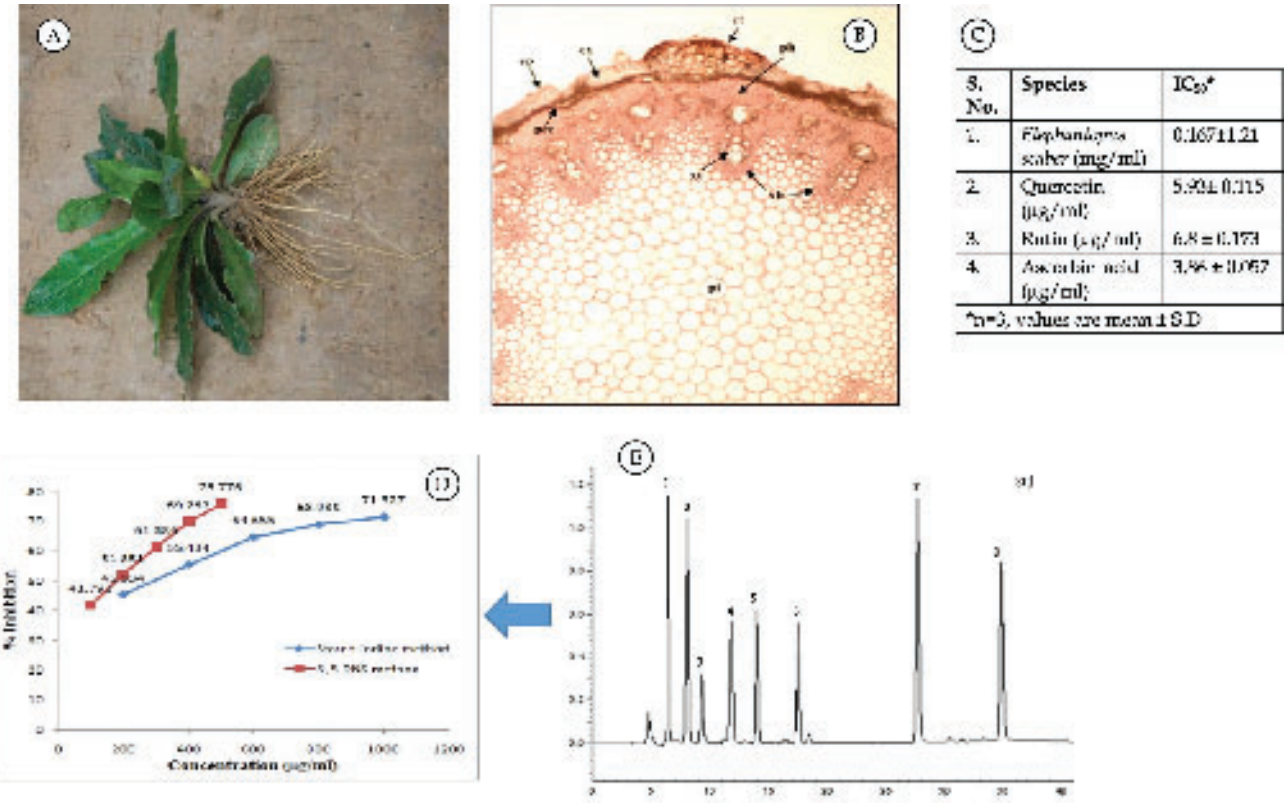


Fig. 2: A. *Elephantopus scaber* Linn herb, B. T.S of stem (Abbreviation: ep- Epidermis, cx- Cortex, pec- Pericycle, ph- Phloem, xy- Xylem, pi- Pith region.), C. $IC_{50}$ value of *Elephantopus scaber* Linn. in DPPH radical scavenging assay, D. *In vitro* anti diabetic activity of *E. scaber* extract by α- amylase inhibition methods. Graph point on the line represents the inhibition exhibited by sample (Y axis) with corresponding concentration (X axis) and standard deviation (S.D; trend lines represent S.D on x axis and y axis), E. HPLC chromatograms obtained from standard solutions at 254 nm: 1- Gallic acid; 2- Protocatechuic acid; 3- Chlogrgenic acid; 4- Caffeic acid; 5- Rutin; 6- Ferulic acid; 7- Quercetin; 8- Kampferol

separation was obtained using RP-C18 column, using mobile phase acetic acid: water (1.0: 99.0 V/V) as solvent-A and acetonitrile as solvent-B and 0.6ml/min flow rate was used for proper separation. HPLC method was developed and validated according to ICH guidelines. Four important phenolic compounds i.e chlorogenic acid, ferulic acid, gallic acid and protocateuchine were identified and quantified with the help of developed RP-HPLC method. Result reveals the presence of chlorogenic acid (3.48mg/g), ferulic acid (0.84 mg/g), gallic acid (0.67 mg/g) and protocateuchic acid (0.086 mg/g). Total phenolic and flavonoid content in the methanolic extract was found to be 16.24±1.61 mg/g GAE and 12.87±0.043 mg/g QE. *In vitro* antioxidant and antidiabetic assays were performed as per standard protocols. The IC50 value for the *in vitro* DPPH method was found to be (0.167±1.21 mg/ml), in DNS assay 0.522±0.04 mg/ml and 0.364±0.03 mg/ml for the starch-Iodine method in methanolic extract of *E. scaber*. This study may be helpful for the selection of *Elephantopus* species and to establish the importance of medicinal properties of plants by correlating with the traditional uses and scientific knowledge to discover the active potential medicine. Further, the identified marker compounds can be used to evaluate the batch to batch consistency of the herbal products made out of this plant.

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**Pharmacological evaluation of herbal drugs/formulations for antidiabetic and antioxidant activities. Primarily working on herbal/ ayurvedic formulations, validation of traditional knowledge, developing novel compositions / formulations for better health care as well as income generation through plant wealth**

## Preliminary *in vitro* screening of extracts for Antioxidant and Anti-diabetic properties

Radical scavenging activity of the extracts is measured using the stable radical DPPH. The antioxidant activity of the extracts is expressed as the percentage of DPPH radical inhibition and the IC-50 was calculated for comparing the obtained results.

***In-vitro* anti-diabetic activity:** Following methods were used to check anti-diabetic activity of plant extracts:

i) **α-Glucosidase Inhibitory Assay:** The α-Glucosidase inhibitory activity is monitored using the substrate p-Nitrophenyl α-d-glucopyranoside (pNPG), which is hydrolyzed by α-Glucosidase to release p-Nitrophenyl. The results are expressed as percentage inhibition.

ii) ***In-vitro* α-amylase inhibitory assay:** The α-amylase inhibitory activity is monitored by using the starch solution (1% w/v).

iii) ***In-vitro* DPP-4 inhibitory assay:** DPP-IV activity was analyzed using a DPP-IV inhibitor screening assay kit, which provided a fluorescence-based method for screening DPP-IV inhibitors.

## Development of Shodhan protocol and preparation of standardised cannabis extracts based AYUSH formulation

A plant native to India, Cannabis has many medicinal benefits. Cannabis industry worldwide is a much regulated industry. In India, Cannabis medicine is allowed under AYUSH category, but quality of medicine remains questionable due to non-standard raw material. We Developed Shodhan protocol and prepared standardised cannabis extracts based AYUSH formulation:

- Standardisation of raw material, and shodhan process, using pharmacognostic and phytochemical tools.
- Protocol for shodhan process has been developed, and *shodhan* has been performed, chemical analysis and studies are further in progress.

The pharmacognostical and phytochemical studies on various part of *Cannabis sativa* L. were conducted for quality evaluation of species. The parameters were studied on leaves, flower buds and aerial part as per standard protocols of Ayurvedic pharmacopeia of India. The pharmacognostical parameter viz. foreign organic matter, loss on drying, total ash and extractive values (alcohol soluble and water soluble) were also estimated. The sample was collected after thorough identification and hence foreign organic matter was nil. The moisture content among the samples varied from 9.05 to 12.08% and ash value was highest in Cannabis leaves followed by aerial part and flower buds. The water soluble extractive was highest in leaves; similarly alcohol soluble extractive was higher in leaves (9.80%) as shown in Fig. 1.

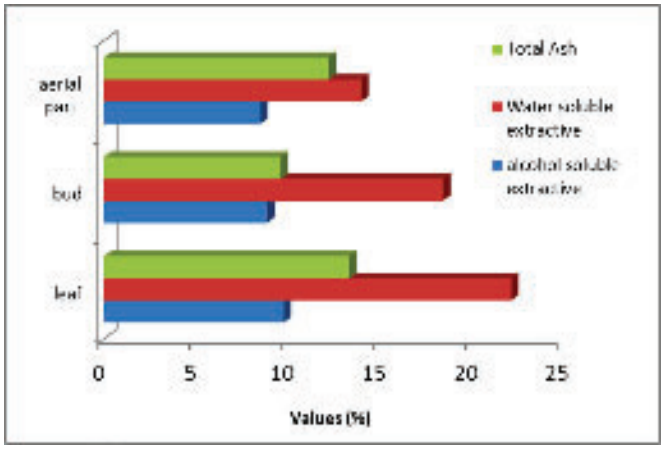


Fig. 1: Pharmacognostical parameters of *Cannabis sativa*

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**Non-targeted metabolite profiling of medicinal plants for bio-prospection**

## Variability in *Commiphora* species with respect to Quinic acid content

Quinic acid (1,3,4,5-tetrahydroxycyclohexane-carboxylic acid) is an alicyclic organic acid, a hydrolysis product of chlorogenic acid, and is a good source of nutraceuticals (Fig. 1A). Quinic acid has been reported to have many biological properties such as DNA repair enhancement, anti-aging, anti-inflammation, immune function enhancement, anti-oxidant and neurogenic effects.

Variations in quinic acid content among different accessions of *Commiphora wightii* and *Commiphora agallocha* was investigated using RP HPLC. Quinic acid was detected as a major metabolite in aqueous extracts of leaves of *Commiphora wightii* and *C. agallocha*. Quinic acid content varied significantly amongst *Commiphora* accessions (Fig. 1B and C). It varied from 34.36 mg $g^{-1}$ in *C. agallocha* (CHT 165) to 217.62 mg $g^{-1}$ dry wt. leaves in *C. wightii* (NBRI-103), respectively.

## Chemical profiling of *Commiphora wightii* for enhanced markers and value added compounds

Latex samples of various accessions of *C. wightii* (Guggul) were collected from Rajasthan, Gujarat and Madhya Pradesh and investigated for variability in their androsterone and androst-5,7-diene-3-ol-one content using GC-MS. Androgens are steroids group of hormones that play a role in male hormone therapy traits and reproductive activity. Chemical structure of androsterone a steroidal hormone is presented in Fig. 2A. The concentration of androsterone and androst-

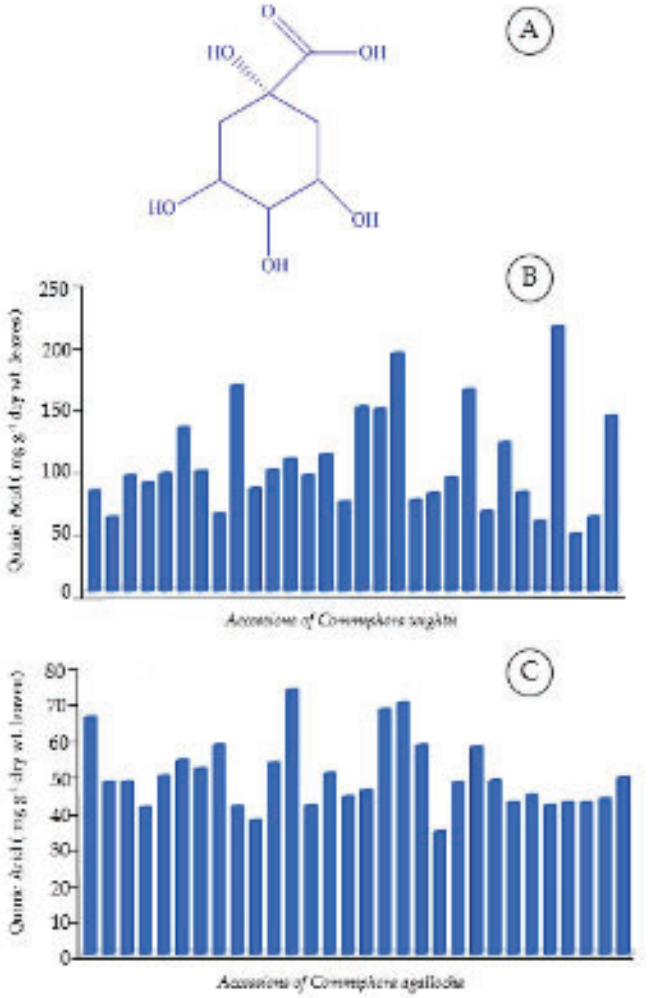


Fig. 1: A. Chemical structure of Quinic acid and Variations in quinic acid content among different accessions B. *Commiphora wightii*, C. *Commiphora agallocha*

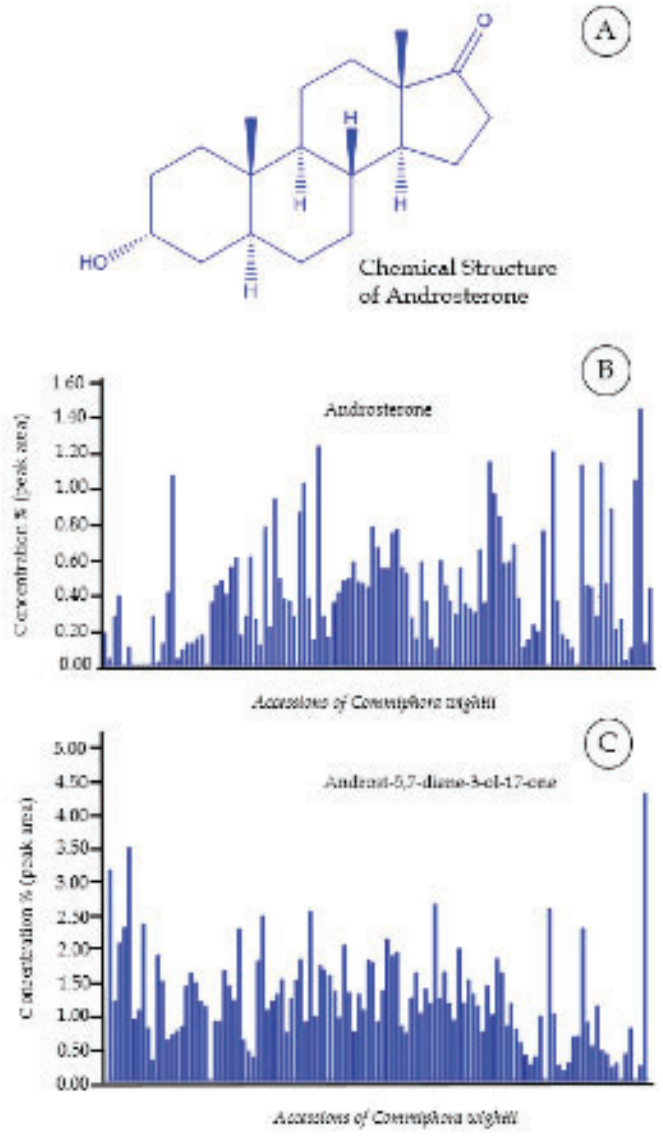


Fig. 2: A. Chemical structure of Androstane, B. variations in Androstane among different accessions of *Commiphora wightii* C. variations in Androstane derivative among different accessions of *Commiphora wightii*

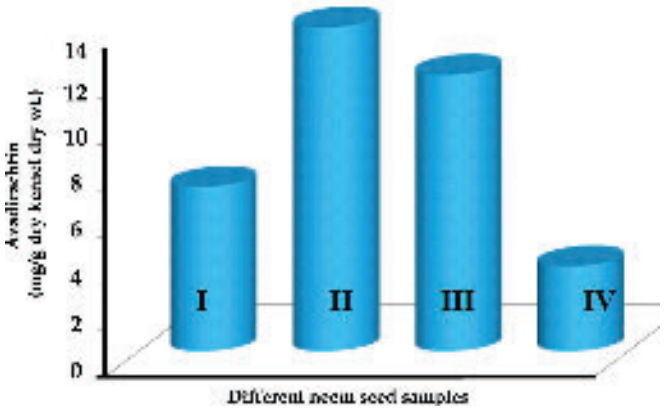


Fig.3: Showing azadirachtin content among different neem seed samples.

5,7-diene-3-ol-one varied significantly amongst accessions. Peak area of androsterone varied from 0.01% to 0.47% (Fig. 2B). Peak area of androst-5,7-diene-3-ol-one varied from 0.00 to 4.55% (Fig. 2C).

## Variations in *Azadirachta indica* (Neem) with respect to seed morphology and azadirachtin content

Seed weight, oil content, ethanol soluble content and azadirachtin content was investigated in four neem seed samples. Seed weight, oil content, ethanol soluble content and azadirachtin content varied significantly among different neem seed samples investigated. Average seed weight varied from 71 mg/seed in sample #1 to 111.9 mg/seed in sample #2 with an average of 92.9 mg/seed, respectively. Percent oil content ranged from 38% in sample # 3 to 43.9% in sample # 2 with an average of 40.2%. Azadirachtin content ranged from 3.65 mg/g dry wt. kernel to 13.94 mg/g dry wt. kernel in sample # 2 with an average of 9.14 mg/g (Fig. 3).

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**Phyto-constituents analysis and their content variation; Phytochemical investigation; Isolation of important phytomolecules**

## Search for elite germplasms of *Gymnema sylvestre* in samples collected from different locations in India, with respect to Gymnemagenin, Deacylgymnemic acid, Lupeol and Stigmasterol

Under the CSIR-Phytopharmaceutical Mission project, studies were conducted on *G. sylvestre* samples collected from different states of India with the aim of identifying the best elite germplasm based on content of their major metabolites. A total of fifty three samples (88 collections) of *G. sylvestre* were studied for their physicochemical parameters (ethanol soluble extractives, water soluble extractives, total ash and acid insoluble ash) as well as for the content of gymnemagenin, deacylgymnemic acid, lupeol and stigmasterol. Earlier thirty samples (56 collections) had been studied. In the samples studied, the percentage of ethanol soluble extractives was from 2.22% to 21.50% while the percentage of water soluble extractives was from 23.52% to 41.57%. Both, the ethanol extractives as well as the water soluble extractives were highest in sample no. 39 (21.50% and 41.57% respectively). All the samples were subjected to acid-alkaline hydrolysis as well as acid hydrolysis and the samples were subjected to HPLC analysis for the estimation of gymnemagenin and deacylgymnemic acid respectively. The lupeol and stigmasterol contents were determined in the methanolic extracts of all the samples using HPTLC analysis. In the samples studied, the content of gymnemagenin was found to be highest in sample no. 32 while deacylgymnemic acid was found to be highest in sample no. 30 (23.38 and 35.42 µg/mg plant material respectively) (Fig. 1A). Sample nos. 2 and 46 were found to contain the lowest amount of

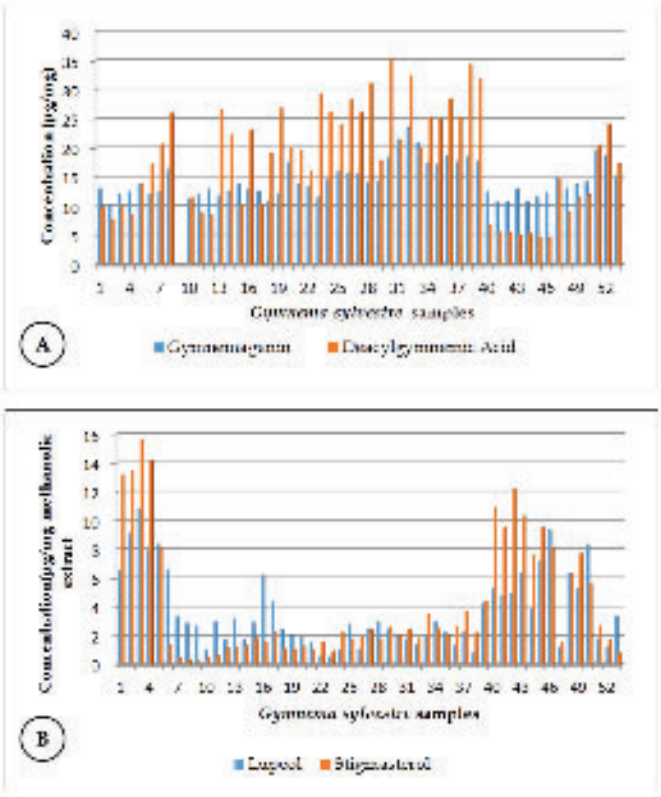


Fig. 1: A. Content of Gymnemagenin and Deacylgymnemic acid in *Gymnema sylvestre*, B. Content of Lupeol and Stigmasterol in Gymnema sylvestre

gymnemagenin and deacylgymnemic acid (10.19 and 4.70 µg/mg plant material), respectively. The content of Lupeol ranged between 0.57 and 10.8 µg/mg methanolic extract (sample no. 23 and 3 respectively) while Stigmasterol was found to range between 0.25 and 15.6 µg/mg methanolic extract (sample no. 9 and 3 respectively) (Fig. 1B).

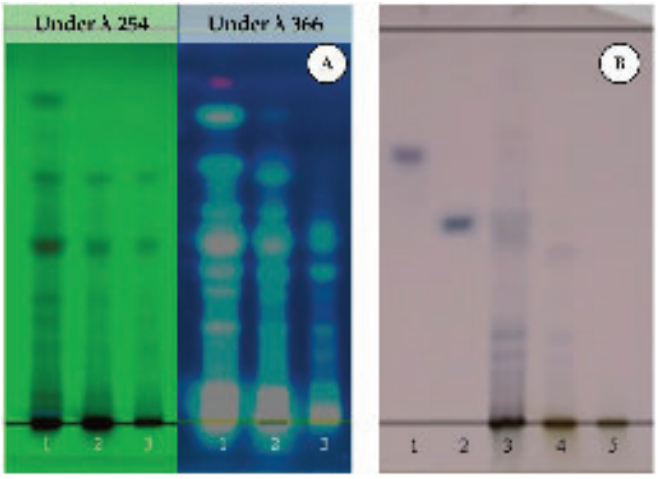


Fig. 2: A. HPTLC fingerprint profiles of *A. excelsa* stem bark (Track 1- Methanolic extract, Track 2- 50% Aqueous methanolic extract, Track 3- Aqueous extract, B. HPTLC profiles of A. excelsa stem bark using Lupeol and Stigmasterol as standards (Track 1- Lupeol, Track 2- Stigmasterol, Track 3- Methanolic extract, Track 4- 50% Aqueous methanolic extract, Track 5- Aqueous extract; as seen under visible light after derivatization)

## Phytochemical investigation of *Ailanthus excelsa*

Investigation of the stem bark of *Ailanthus excelsa* Roxb. for its physicochemical parameters, HPTLC fingerprinting and phytochemical analysis and assessment of its antioxidant potential was undertaken. The stem bark of *A. excelsa* known as Aralu, is commonly used as a substitute in trade and raw drug market for several other important medicinal plants like *Oroxylum indicum* and *Holarrhena antidysenterica*. The different extracts were analyzed for their total phenolic and flavonoid contents and subjected to phytochemical analysis using HPTLC (Fig. 2A and 2B) and the chemical markers lupeol and stigmasterol were quantified. Lupeol and stigmasterol were found to be present only in the methanolic extract (5.3 µg/mg and 8.1 µg/mg extract respectively). Results indicated that the 50% aqueous methanolic extract contained the highest content of phenolics and flavonoids. The methanolic extract exhibited the best antioxidant potential in both the *in vitro* test models used *viz*. DPPH radical scavenging activity as well as the Total Antioxidant Capacity. These results may thus be used for the routine analysis of the raw drug samples and formulations for the presence of *A. excelsa*. The HPTLC fingerprint profiles are especially useful as they provide a fingerprint of the various phytoconstituents present in the crude drug and can be essentially used for quality control and assessment. They may also be used for confirming the presence of authentic plant material and monitoring the consistency of different batches of finished products where *A. excelsa* has been used as an ingredient.

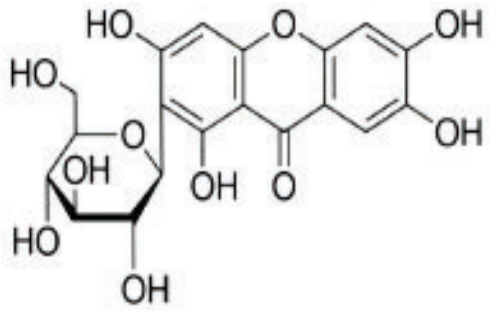


Fig. 3: Chemical Structure of Mangiferin

## Isolation of Mangiferin

Mangiferin is a xanthone C-glycoside present in significant levels in different parts of the mango fruit, such as the peel, stalks, leaves, barks, kernel, and stone. It possesses several health endorsing properties such as antioxidant, antimicrobial, antiaging, anticancer, hepatoprotective, hypocholesterolemic, immunomodulatory, cardiotonic, hypotensive, wound healing, antidegenerative and antidiabetic activities. Chemical reference marker Mangiferin (Fig. 3) was isolated from the leaves of *Mangifera indica*. Further studies are under progress.

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**Phytochemical investigation, value addition and natural product development for plant based technologies**

## Herbal product development for industrial application

Two best plant sources (Biopol-1 and Biopol-2) from fifteen screened plants were selected on the basis of phytochemical investigation, physicochemical characteristics and markers to prepare plant based bioplastics. Physical testing was done and the data produced comply as per BIS standards *(density-1.33 gm/cc, thickness- 126 micron, tear resistance- 320.6 g)* for its application prospects.

Eight plants (NBR Pl-11, 13, 14, 16, 17, 18, 21 and 25) were evaluated physicochemically on the basis of pH, moisture and viscosity. Based on studies NBR Pl-13 was found to be a potential source to prepare 100% water soluble synergistic cleansing formulation.

Plant based biodegradable cutlery was developed using safe BC-RM-1 and BC-RM-2 for dry food packaging, eating and serving.

Galactomannan from seed gums of *Sesbania glandulifera* and *S. sesban* were isolated, purified and analysed. Carboxymethyl derivatives of *S. glandulifera* and *S. sesban* galactomannan were prepared. Gum was evaluated for its use as a thickener and tablet binder.

Chemoprofiling of leaves and seeds of four *Cassia* species was done to identify and characterize two markers i.e. Aloe emodin and Sennosides. Purification of the compounds was also done for *in-vitro* cyto-toxicity against colorectal and breast cancer cell lines. Methanolic extracts of *Cassia suratensis* leaves showed the best activity.

Six lichen acids, Usnic, Fumarprotocetraric, Salazinic, Caffeic, Protocetraric and Collatolic acids isolated and purified from three lichen species (*Cladonia, Usnea, Evernestrium* spp.) for antidiabetic activity.

Seeds and isolated gums of *Acacia nilotica* and *Leucaena leucocephala* were investigated for phytochemicals and secondary metabolites. GC-MS studies revealed the presence of D-Pinitol, Sucrose, Maltose, Palmitic acid, Linoleic acid and Myo-inositol as major identified markers for anti-inflammatory activity.

## Technologies and products for reduced emission fireworks

Synergistic combinants of two types of less polluting fire crackers formulated with selected safe plant materials to substitute high emitting carbon fuel, antioxidants and additives in commercially used fireworks. Preformulation and formulation studies carried out to ascertain flow, uniformity and binding properties.

## Development of food colours

Three plant seed and exudate gums (NBRg-11, NBRg-16 and NBRg-21) at different variables were utilized to stabilize extracted colouring principles from two potential sources and standardized to obtain four stable food colours (Red, Orange, Yellow and Blue). Colour value, anthocyanin content, total phenolics, flavonoids, antioxidants and heavy metals were estimated. Temperature and pH studies carried out in different food matrices to explore plant based food colours as safer technology in food and beverage industries.

## Phytopharmaceutical mission

Chemoprofiling and quantification of *Dioscorea deltoidea* tubers for four chemical markers i.e. Diosgenin, Dioscin, Beta Sitosterol and Stigmasterol

was carried out in 92 germplasms through HPLC and GC-MS. Maximum Dioscin content i.e. 213.93 mg/g was detected in germplasm (304453) from Uttarakhand). Diosgenin, Stigmaserol and Beta sitosterol content was maximum in germplasm (315771) from Sikkim. The two best selected germplasms are under cultivation, and propagation for identification of elite chemotypes.

## Bioresource and sustainable livelihoods in North East India

Nutraceutical characterization and chemical profiling of seeds of *Parkia roxburghii, Psophocarpus tetragonalobus* and *Erythrina* sp. along with solution properties were determined. GC-MS profiling reveals the presence of Glucose, Erysodine, sucrose and Myo-Inositol as major markers. Oil is found to be rich in squalene, stigmasterol and tocopherol. Tannin and protein estimations in different processed samples carried out for utilization prospects as nutraceuticals.

## Characterization and value addition of plant-based resins, gums and waxes

Sixty two accessions of gum, resin and wax plant materials from fourteen states of different geographical zones of India was estimated for physicochemical characteristics and chemical markers to develop synergistic combinants and hydro-stable products.

Quantification of phytochemicals in fifty accessions was done to select best one on the basis of nutraceutical parameters and markers for its utilization as for food/ nutraceuticals.

One selected wax producing plant source was processed by de-fatting, saponification to prepare specific marker rich value products. Policosanol (yield-6.6%) from edible wax rich fraction was isolated to develop nutraceutical products.

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- Mr. Rachit Mohan, Research scholar
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**Molecular pharmacology, herbal nano-biotechnology, herbal product development**

The broad research interests of our laboratory are in the area of herbal pharmacology. Our ongoing research broadly comprises:

- Deciphering molecular mechanisms of wild medicinal plant extracts/phytochemicals for their anti-quorum sensing, anti-diabetic and anti-inflammatory activities.
- Developing efficient nanomaterials-based delivery systems for drug phytochemicals
- Developing innovative herbal products

## Endolichenic fungus inhibits quorum sensing and biofilm formation of *Pseudomonas aeruginosa* PAO1

Lichens are composite organisms, comprising of a fungus (mycobiont) and a blue-green alga (photobiont). Along with the mycobiont, numerous non-obligate microfungi live in lichen thalli. These microfungi are called endolichenic fungi (ELF). In recent years, the ELF's have emerged as promising natural sources because of their capability to produce unique drug molecules. The present study was aimed at isolating the ELF from the lichen, *Usnea longissima* Ach., to control biofilm formation and quorum sensing phenomenon in *Pseudomonas aeruginosa* PAO1, an opportunistic multidrug resistance pathogen that uses quorum sensing network to produce an array of pathogenic agents. Therefore, inhibiting quorum sensing to manage the infection caused by PAO1 could be an alternative approach to conventional antibiotics. The isolated ELF was identified by amplifying the long subunit region of the fungal genome. The extracted metabolites of ELF (MELE) using the acetone solvent was further investigated for anti-quorum sensing activity using the biomarker strain, *Chromobacterium violaceum* 12472, which exerts violacein pigment via the AHL mediated quorum sensing signalling. Moreover, the effect of MELE was also evaluated on the production of virulence factors and biofilm formation of *P. aeruginosa* PAO1. The molecular identification revealed that ELF (accession number MN171299) exhibited 100% similarity with *Aspergillus quandricinctus* strain CBS 135.52. The MELE showed significant anti-quorum sensing activity at the concentration of 4 mg/mL without affecting the cell viability of *P. aeruginosa* PAO1. The MELE diminished the production of virulence factors, including pyocyanin, protease, elastase, rhamnolipids, and extracellular polysaccharides of *P. aeruginosa* PAO1 in a concentration-dependent manner. The MELE also disturbed biofilm formation of *P. aeruginosa* PAO1. The 3-D analysis of biofilm architecture showed that the thickness and surface area covered by microcolonies was decreased as the concentration of MELE was increased. The GC-MS analysis of MELE exhibited that organic acids and fatty acids are major constituents of the MELE. The present study is the first report to show that the ELF, *A. quandricinctus* possesses potential to inhibit quorum sensing and biofilm formation of *P. aeruginosa* and can be further exploited for hospital and healthcare facilities.

## Anthraquinone-functionalized nanoparticles for anti-fouling and anti-quorum sensing potentials to prevent urinary catheter associated bacterial infections

Antibiotic resistant bacterial biofilms are responsible for most catheter-associated infections in hospitals. Recently, nanoparticles (NPs) have been considered as strong antibacterial agents that can be used as an alternative treatment approach. However, their

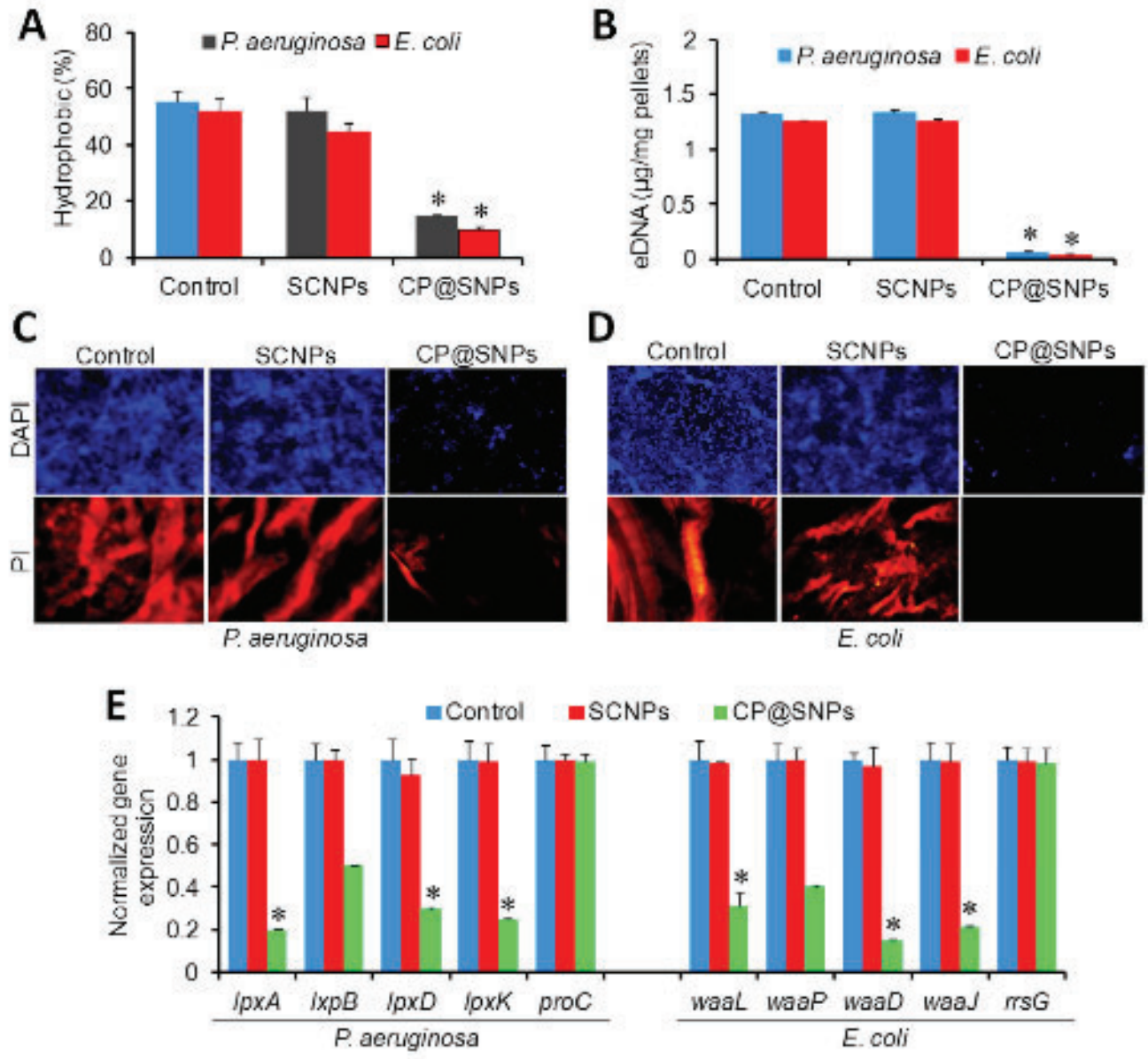


Fig. 1: A-E. Possible mechanism of CP@SNPs on combating bacterial biofilm. A. Impact of CP@SNPs on the hydrophobicity of the *P. areuginosa* and *E. coli* with the treatment of 24 h, B. The eDNA content of bacterial biofilm matrix with treatment for 24 h. The results were presented as mean; bar: SE. All experiments were performed at least thrice in independent experiments having six replicates. *P<0.001 versus control, C-D. The fluorescence microscopic observation of eDNA in *P. areuginosa* and *E. coli* biofilms after staining with DAPI and PI, E. The genes involved in the expression of virulence factors controlled by QS measured by RT-qPCR in *P. aeruginosa* and *E. coli* with the treatment of 24 h. proC and rrsG were used as housekeeping genes for *P. aeruginosa* and *E. coli*, respectively. The results were presented as mean; bar: SE. All experiments were performed at least thrice in independent experiments having six replicates. *P<0.001 versus control.

continuous use could induce drug resistance and recurrence of biofilms which makes it difficult to eradicate. Moreover, they are also toxic at higher concentrations. To address such challenges, the current work presents one approach by decorating NPs with an anthraquinone, chrysophanol (CP@SNPs) to increase their cellular internalizations and interactions with QS signalling of the bacterial pathogens. The advantage of this strategy lies in superior prevention of commercially available urinary catheters (UCs) from bacterial adhesion and subsequent bacterial colonization long-term use by a

single coating of CP@SNPs through inhibition of QS as compared to NPs. The anti-adhesion and antibiofilm effects of the CP@SNPs-coated UC surface were assessed for the growth of *Pseudomonas aeruginosa* and *Escherichia coli* under both static and flow conditions. The CP@SNPs-coated latex and silicone UCs showed > ~9-fold higher antiadhesion effect in comparison to the NPs-coated UCs which show the practical applicability of this strategy. The strong anti-QS activity of CP@SNPs influenced surface hydrophobicity, eDNA content, lipopolysaccharide production, and virulence gene expression of bacterial biofilm cells, which reduced biofilm invasion and formation (Fig. 1). Besides, the CP@SNPs-coated UCs did not provoke hemolytic effect and are resilient to the attachment of blood-circulating cells, allusive of massive biocompatibility. Eventually, the CP@SNPs system is applied to prevent bacterial colonization on UCs *in vivo* without inducing toxicity in liver, lungs, and kidneys. Overall, the present anthraquinone-functionalized NPs are potentially useful as anti-QS and antifouling coating materials that render existing medical UCs resilient to bacterial colonization.

## Development of innovative herbal products

### Alcohol-based herbal hand sanitizer gel

Plants are known for their pharmacological properties, particularly antimicrobial to prevent and treat infections caused by human pathogenic bacteria, fungi and viruses. CSIR-National Botanical Research Institute, Lucknow has identified potential herbal antimicrobial that has been used to develop an innovative herbal hand sanitizer along with isopropyl alcohol (IPA) (Fig. 2). Thus, it is a unique combination of herbal antimicrobial and IPA for killing 99.9% germs on skin and palms. This herbal hand sanitizer contains Tulsi essential oil as herbal constituent, which is a strong natural antimicrobial agent and 60 percent of isopropyl alcohol for killing germs. The product is validated scientifically for its strong germ killing activity. The know-how technology of the Alcohol-based Herbal Hand Sanitizer was transferred to M/s. Sadguru Biologicals Pvt. Ltd., Lucknow.

Fig. 2: Newly developed herbal hand sanitizer

## ZANTHODENT: A plant based toothpaste for oral care

Nowadays demand for herbal toothpaste is very high. CSIR-National Botanical Research Institute, Lucknow has developed a novel formula for herbal toothpaste, which contains herbal ingredients to treat periodontal problem and yellowing/staining of teeth. It is very effective to prevent cavity formation. It does not contain triclosan (carcinogen) and synthetic chemical preservatives. It is safe to use without any adverse effects.

### Research Group

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- Mr. SK Chaudhary, CSIR-SRF
- Mr. S Sharma, CSIR-SRF
- Mr. V Sharma, CSIR-SRF
- Mr. N Nagpore, Project Assistant

# Plant Ecology and Environmental Technology

# PLANT ECOLOGY & ENVIRONMENTAL TECHNOLOGY

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- Dr. Suchi Srivastava, Principal Scientist
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- Dr. Sumit Yadav, Senior Technical Officer
- Ms. Rekha Kannaujia, Technical Assistant
- Dr. Shashank K Mishra, Technical Assistant
- Mr. Sri Pal, Senior Technician

## Research Scholars Statistics

| Sr. No. | Position Name | Numbers |
|---|---|---|
| 1. | NPDF | 01 |
| 2. | Research Associate | 01 |
| 3. | Young Scientist | 02 |
| 4. | JRF/SRF Fellow | 24 |
| 5. | Project Staff | 14 |

## Plant Ecology and Climate Change Science

- Plant eco-physiological and biochemical processes and adaptation in response to abiotic stresses, air pollution and climate change.
- Forest ecosystem structural and functional analysis, forest biomass, and forest carbon sequestration.
- Monitoring of fluoride and arsenic in environmental matrices, Fe and Zn bio-fortification of rice using siderophore secreting microbes.

## Research Highlights

- Two varieties of wheat were assessed for effect of ethylenediurea (EDU) on apoplast and chloroplast proteome under high ambient ozone. Several chloroplast proteins involved in photosynthesis, carbon metabolism, protein synthesis assembly degradation, defense, and energy metabolism-related proteins were identified.
- Adaptation strategies were studied on twenty three rice varieties of Indo-Gangetic Plains to elevated $CO_2$, Ozone, and temperature. NDR-359 showed better yield in all the treatments. Azad basmati performed very well in elevated $CO_2$, NDR-3112 was better under elevated $O_3$, while, Sarju-52, Shambha sub-1 and Pant 12 did well at elevated temperature.
- Studies in cotton showed that, in cotton leaves endogenous levels of abscisic acid predominantly maintains the stomatal behavior and regulates its physiology by antagonizing 6-Benzylaminopurine to coordinate with water deficit signals.
- In *Cyamopsis tetragonaloba* (Guar) plants under restricted water supply, it was demonstrated that the variability in the gene expression of carbon metabolising enzymes modulates the accumulation of carbohydrate.
- Soil $CO_2$ efflux in three forest communities, dry mixed, Sal mixed and teak plantation, were studied in summer season. Significant increase in soil $CO_2$ flux was observed with increasing air and soil temperature in dry mixed and Sal mixed forest.
- The quality and quantity of litter and associated factors influence soil properties in different ways in a forest ecosystem. The litter chemistry, and soil properties have specific relation among them despite unique species composition in each forest community.
- A baseline data on cryptogamic plant diversity was generated with a standard protocol adopted from Global Observation Research Initiative in Alpine Environments (GLORIA). This data will be utilised to understand the functional role of microclimate on community structure and functioning at Alpine ecotones in Indian Himalayas.
- The level of $F^-$ was estimated in the crops cultivated in the agricultural fields of Unnao district, which were collected during three distinct seasons, pre-

monsoon, monsoon, and post monsoon.

- A comparative assessment of Zn and Fe uptake in four rice cultivars was carried out using four microbial inoculums under two regimes of Zn treatments.

## Microbial Technology

The group focuses on disease management of commercially valuable crops and developing sustainable eco-friendly remedies, development of economical and efficient bio-inoculant formulations both for agricultural lands and stressed soils and elucidation of molecular mechanism(s) of microbe mediated abiotic and biotic stress tolerance in different crop plants.

## Research Highlights

- Six antagonistic bacterial endophytes, *Bacillus tequilensis* (PBE1) (MTCC25188) have been identified to be most effective and eco-friendly substitute of chemical fungicides against *Fusarium oxysporum* for tomato wilt disease management.
- Supplementation of *Trichoderma reesei* has been investigated and identified as a biofertilizer (BF) to ameliorate nutrient stress in different rice cultivars at physiological, biochemical and molecular levels.
- A simple and facile technique for biogenic silver nanoparticles (BSNP) was developed for wound healing acceleration and suppression of wound infections. The BSNP is formulated in an ointment base, and the study to accelerate the wound healing process was conducted in rat model.
- A study was conducted to demonstrate the use of bioengineered silver nanoparticles in combating black spot disease caused by necrotrophic fungus *Alternaria brassicicola* in *Arabidopsis thaliana* via foliar spray.
- A study was conducted with the aim to identify and characterize Chlorpyrifos (Chlp) degrading soil microbes. *Alcaligenes faecalis* (NBRI OSS2-5), a potent bacterial strain, was identified for Chlp degradation. This strain can be used for plant growth promotion and bioremediation in pesticide contaminated sites.
- Studies were carried out to show the efficacy of a *Trichoderma* consortium comprising *T. koningiopsis* NBRI-PR5 and *T. asperellum* NBRI-K14 to overcome salt stress in paddy. The microbial application improved the anatomical and morphological features of the rice roots under salt stress and also improved the yield and seed size and weight.
- A plant growth promoting rhizobacteria (PGPR), *Paenibacillus lentimorbus* NRRL B-30488, on inoculating chickpea plants, grown under nutrient stress condition showed better growth and development by modulating its metabolic pathways.
- The *Bacillus amyloliquefaciens*-SN13 in rice (*Oryza sativa*) grown under salt stress showed extensive alterations in gene expression in root transcriptome, and a significant increase in biomass, and total soluble sugar was observed.
- A comparative roots proteomic analysis of chickpea seedlings grown under drought stress was performed. Data generated can be utilised for genetic improvement programs to develop drought tolerant chickpea lines.
- Molecular mechanism of a silicon solubilising rhizospheric microbe (NBRISSM) and root associated microbe, *Pseudomonas putida* (MTCC 5279) was elucidated.
- *Bacillus amyloliquefaciens* (NBRISN13) was studied as to how it modulates plant metabolite system under biotic stress conditions of *Rhizoctonia solani*. Twenty one compounds related to antimicrobial activity and defense signalling were identified.
- A yeast strain *Debaryomyces hansenii* was identified for amelioration of arsenic stress in rice. *D. hansenii* reduced arsenic content in grain and also showed plant growth promotory traits.
- A microbial formulation was developed for faster *in situ* rice straw decomposition and soil health improvement and also enhancement of the subsequent wheat crop productivity.

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**Eco-physiological and biochemical responses and adaptation of plants to abiotic stresses**

## Synchronization of the endogenous phytohormones, stomatal behaviour and physiology promotes intrinsic water use efficiency in cotton under water stress

The coordination between phytohormones regulation, stomatal behavior (stomatal index and opening/closing) and physiology are potent determinants of plant survival to drought stress. However, the mechanism regulating fine-tuning among these features during drought remains little explained. Here, during water deficit conditions, gas exchange, stomatal behavior and endogenous phytohormones

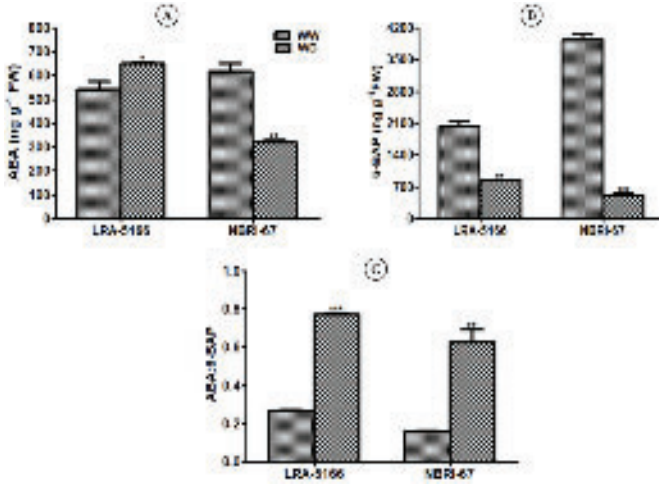

Fig. 1(A-C): Effects of water deficit on endogenous phytohormones content (ng $g^{-1}$ FW) in leaves of LRA-5166 and NBRI-67. Variation in (A) Abscisic acid; ABA, (B) 6-Benzylaminopurine; 6-BAP and (C) ABA and 6-BAP ratio (ABA: 6-BAP). Values are means ± SD of two replicates tested for significance using Student's *t*-test at**P*<0.05; ***P*<0.01, ****P*<0.001 level

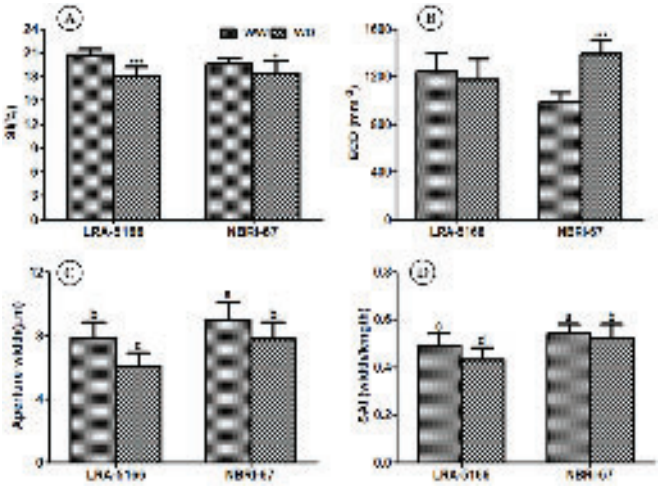

Fig. 2(A-D): Effects of water deficit on behavior (Stomata index and Aperture; openness) in leaves of LRA-5166 and NBRI-67. Changes in (A) Stomatal index; SI, (B) Epidermal cell density; ECD,(C) Aperture width, and (D) Stomatal aperture index (SAI). Values for (A-B) are means ± SD (n=12 leaf impression images in four different leaves). Significance was determined by *t*-test at **P*<0.05, ****P*<0.001 level. One-way ANOVA was conducted for (C-D). The letters above the bars determine significant variation between two varieties under two water treatments at *P*<0.05 level. Values are means ± SD (n=150 stomata in three different leaf from each treatment; one leaf/plant)

content were evaluated in the two cotton varieties (LRA-5166 and NBRI-67) differing in drought sensitivity. Water deficit significantly reduced photosynthesis rate and stomatal conductance in both varieties, being less in drought tolerant LRA-5166 than drought sensitive NBRI-67. The abscisic acid (ABA) accumulation was significantly increased in LRA-5166 while reduced in NBRI-67 by water deficit, which was accompanied with relatively less reduced

6-Benzylaminopurine (6-BAP) level in LRA-5166 than NBRI-67. Thus, improved ABA/6-BAP ratio was observed in both varieties of cotton (Fig. 1). Critically, LRA-5166 showed reduced stomatal index (Fig. 2) and opening and significantly higher intrinsic water use eficiency ($WUE_i$) and drought tolerance than NBRI-67. Furthermore, we found that endogenous ABA predominantly maintains the stomatal behavior and regulates its physiology by antagonizing 6-BAP to coordinate with water deficit signals, our findings describe new insight, and how drought modulates endogenous ABA and 6-BAP homeostasis in cotton leaf and mechanism of stomatal regulation by ABA and 6-BAP in cotton.

## Effect of water stress on carbon metabolism and its partitioning in *Cyamopsis tetragonaloba (Guar)*

Drought being a major stress factor responsible for yield penalty in legumes, there has always been a high

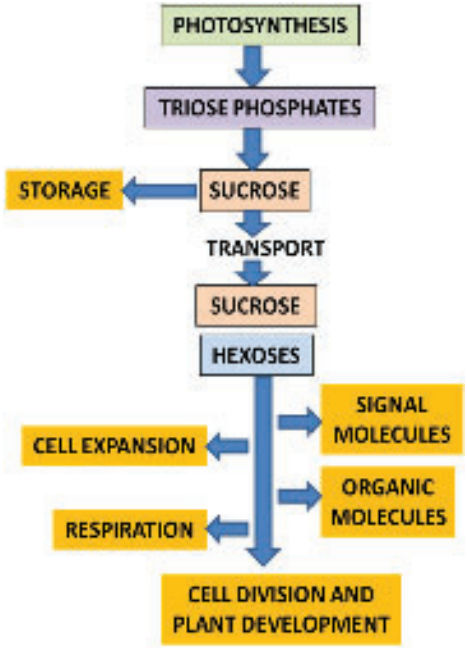


Fig. 3: Sugar signalling under drought conditions in guar varieties

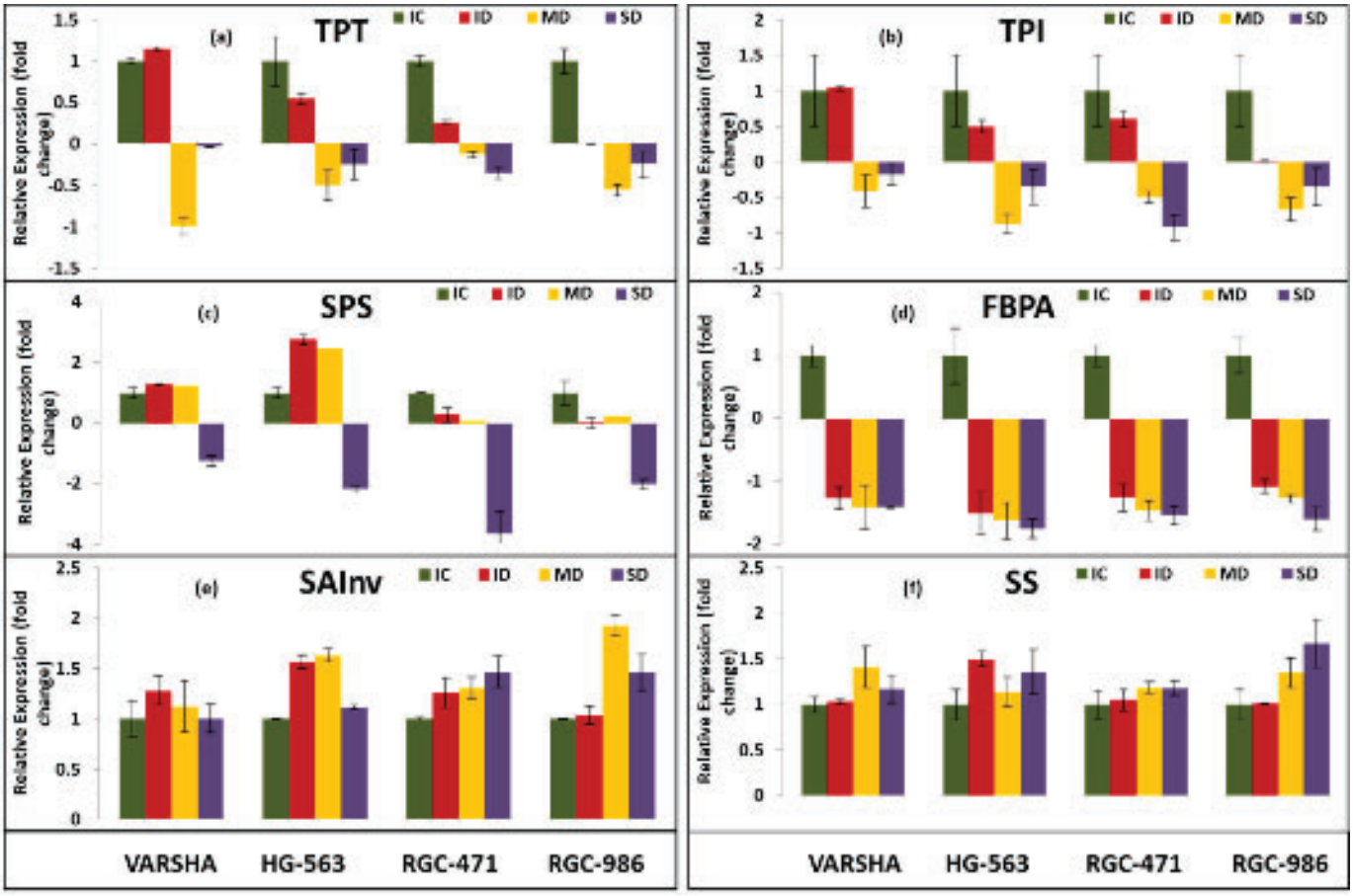


Fig. 4: Carbon partitioning in guar plants

priority to generate knowledge on adaptation and tolerance of guar. To elucidate underlying mechanism, transcript level of the genes that are putatively responsible for regulation of carbon partitioning in plants were analyzed in four contrasting varieties of guar viz., HG-563, RGC-986, RGC-471 and VARSHA during drought stress. We demonstrate the alteration in the expression levels of many drought responsive genes accompanied by decrease in carbon assimilation rate (Fig. 3). Interestingly, the genes encoding *TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR (TPT*) enzyme showed down regulation in all varieties, however, significant down regulation in mid and severe stages of drought-stressed leaves was seen in RGC-986 and VARSHA variety (Fig. 4a). This suggests the reduced demand for triose-phosphate export under drought stress. *TRIOSE-PHOSPHATE ISOMERISE (TPI)* is an enzyme that catalyzes the reversible inter-conversion of the triose phosphate isomers Dihydroxy acetone phosphate and D-glyceraldehyde 3-phosphate. The *TPI* also shows the same level of gene expression as that of *TPT* in all the four varieties of guar (Fig. 4b). Markedly, glucose content increased in all the four varieties in severe drought. However, the glucose content was higher in HG-563 than other three varieties under drought condition. Moreover, leaf *SUCROSE PHOSPHATE SYNTHASE (SPS)* level was decreased in severe drought stress in all varieties (Fig. 4c). *SPS* content decreased in RGC-986 by 2.1 fold, RGC-471 by 3.6 folds and HG-563 by 2.1 fold as compared to control plants under severe stress (Fig. 4c). Furthermore, genes encoding enzymes involved in the production of glucose-1-phosphate from triose-phosphates such as *FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE (FBPA)* were down-regulated, which results into alteration in triose-phosphates synthesis and translocation in the leaves of all guar varieties during drought stress (Fig. 4d). However, genes encoding enzymes responsible for sucrose hydrolysis and synthesis *(SUCROSE-PHOSPHATE SYNTHASE(SPS), ACID INVERTASE(SAInv)* and some isoenzymes of *SUCROSE SYNTHASE (SuSy)*) showed increase in mRNA levels in the drought stressed leaves (Fig 4c, 4e & 4f). Although under all the stages of drought *SUCROSE SYNTHASE (SuSy)* gene showed up regulation in all the varieties of guar (Fig 4f). Collectively, our results reveal two possible mechanism for regulation of glucose level in guar plants, first by increasing level of sucrose synthase transcripts and secondly, higher transcript accumulation of invertase during drought stress. Eventually, due to elevated glucose level the guar varieties RGC-986 and HG-563 were better able to sustain drought condition than RGC-471 and Varsha. Based on these results, we demonstrate that the variability in the gene expression of carbon metabolising enzymes modulates the accumulation of carbohydrate in guar plant under restricted water supply.

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**Plant eco-physiological and biochemical processes in response to air pollution and climate change**

## Effects of ethylenediurea (EDU) on apoplast and chloroplast proteome in two wheat varieties under high ambient ozone

Rising tropospheric ozone ($O_3$) is a significant threat to plants and animals. High tropospheric $O_3$ can disrupt cellular organelles leading to impaired photosynthesis as well as yield reduction. Apoplast and chloroplast are two crucial cellular components in a plant leaf. Their proteomic response under tropospheric $O_3$ stress is less explored. Ethylenediurea (EDU, an organic chemical) protects plants exclusively against harmful $O_3$ effects through activation of antioxidant defense mechanism in several crops. The present study investigated mode of action of EDU (hereafter MAE) through protein abundance pattern in apoplast and chloroplast isolates. Two varieties of wheat viz. Kundan and PBW 343 (hereafter K and P respectively) and three EDU treatments (0= control, 200 and 300 ppm) have been used for the study.

The levels of intracellular contamination in the vacuum infiltrated apoplast (VIA) fluid were quantitatively evaluated from the enzyme activity of glucose-6-phosphate dehydrogenase (G6PDH). On this basis, contamination of VIAs with other intracellular proteins was negligible. The isolation of chloroplast was done using Percoll gradient method. The intactness of the chloroplast was found to be in the range 85-90% as estimated by ferricyanide-dependent $O_2$ evolution. Light microscopy reconfirmed the intactness of isolated chloroplasts.

### *SDS-PAGE analysis for apoplast proteins*

Image quant analysis result showed significant differentially abundant protein bands in the gel ($P< 0.05$). Twenty-six bands were detected by the image quant software at the vegetative stage in each lane. In Kundan variety, Catalase, Aminomethyl transferase (AMT), Serine glyoxylate aminotransferase (SGAT), Superoxide dismutase (SOD) proteins were more abundant at both stages whereas, in PBW 343, Germine like protein, SOD and Thioredoxin-dependant peroxidase (TPX) were also more abundant at both developmental stages under two doses of EDU. In Kundan, Germin like protein was less abundant at both stages whereas, in PBW 343, Catalase, AMT, SGAT, Ascorbate peroxidase (APX) and TPX were less abundant at both developmental stages under EDU treatment.

### *2D gel analysis for chloroplast proteins*

Three representative gels were analysed for each treatment with each variety. In total, more than 332 protein spots were reproducibly detected on Sypro ruby stained gels within each treatment in Kundan, whereas in PBW 343, 283 spots were reproducibly detected. Several significantly differentially abundant proteins ($P < 0.05$) were observed under EDU treatment in both the varieties.

Several chloroplast proteins involved in different functions were identified by mass spectrometry. It included photosynthesis, carbon metabolism, protein synthesis assembly degradation, defense, and energy metabolism-related proteins (Fig 1). Prevailing tropospheric ozone and given EDU doses were enough to induce changes in chloroplast protein abundance.

***Photosynthesis related proteins*** included Rubisco LSU, oxygen evolving enhancer protein 1 (OEE), Cytochrome b-6-f complex, Light-harvesting a/b binding protein, FNR protein, Crystal structure of Psbp. Based on the abundance of proteins related to photosynthesis, it can be said that EDU treatment resulted in limited damage to photosynthetic proteins in both wheat varieties, thereby maintaining optimum photosynthesis under prevailing $O_3$ stress.

***Carbon metabolism related proteins*** included Rubisco activase, TPI protein PRK protein, Enolase, FBPase, GAPDH, and RPI protein. Carbon metabolism under EDU treatment may have controlled stomatal movement, RuBP regeneration and regulation of different biosynthetic pathways protecting membranes, enzymes and other structures against $O_3$ induced damage thus providing more ozone tolerance in Kundan as compared to PBW 343.

***Energy metabolism related proteins*** plants respond to stress conditions by triggering a network of events linked to energy metabolism. ATP synthase subunit α, β, ε ADP glucose pyrophosphatase, Vacuolar proton ATPase, F0-F1 ATPase Chloroplast proteins related to energy metabolism revealed the underlying molecular mechanism of EDU induced protection by providing an optimum supply of energy in Kundan than PBW 343.

***Protein synthesis, assembly and degradation*** included Rubisco LSU-binding protein, Trigger factor protein, Elongation factor, 30S Ribosomal protein, 70 kDa heat shock protein, 20kDa chaperonin, Peptidyl-prolyl cis-trans isomerase, ATP dependent Clp proteases, ATP dependent Zinc metalloproteases, EDU protection of proteins synthesis and folding may have contributed towards photosynthetic and stomatal adjustment and prevention of proteins from membrane degradation under EDU treatment.

***Amino acid metabolism related proteins*** included Thioredoxin H-type, Ser/Thr kinase, Glutamine synthase, Glycine dehydrogenase.

***Defense related proteins*** included Peroxiredoxin, Germin like protein, APX.

## Adaptation strategies of rice varieties of Indo-Gangetic Plains to climate change

Twenty three rice varieties were exposed to elevated $CO_2$ ($eCO_2$), elevated Ozone ($eO_3$), elevated temperature (eTemp) alone, $eCO_2$ + $eO_3$ and $eCO_2$ + $eO_3$+ eTemp throughout their growing period. During the experimental period the average ambient $CO_2$ concentration was 396 ppm and that of elevated $CO_2$, 519 ppm. Average ambient $O_3$ concentration was 41 ppb and that of elevated 66 ppb. The elevated temperature was kept at + 2° C above ambient temperature.

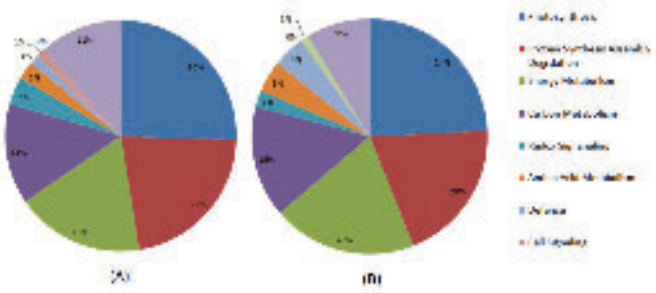

Fig. 1: Pie chart showing different functional categories among identified proteins in chloroplast in response to two EDU concentrations. (A- Kundan, B- PBW 343).

### Plant height and total biomass

Out of 23 rice varieties, Shambha sub-1 was the only variety to perform well in all the treatments, in terms of biomass accumulation. Varieties such as CSR-27, DRR-42 and Sarju-52 also had better biomass in $eCO_2$, $eO_3$, and $eCO_2$+$eO_3$ but were not responsive to $eCO_2$+$eO_3$ + eTemp treatment. Three varieties CSR-27, PB-1, Azad Basmati showed significant biomass accumulation in eTemp while three varieties NDR-359, NDR-3112, NDR- 8002 showed decreased biomass accumulation.

Out of the twenty three varieties screened for physiological efficiency, highest $CO_2$ assimilation rates were observed in variety NDR -8002 followed by CSR -43 and CSR-27 in ambient condition while lowest rate was observed in Lalmati. In $eCO_2$ condition CSR-27 performed well with value of (30.02 µmol $m^{-2}$ $sec^{-1}$), followed by NDR-2065 (29.43 µmol $m^{-2}$ $sec^{-1}$) and CSR-43 (28.51 µmol $m^{-2}$ $sec^{-1}$) while lowest rate was observed in BPT 5204 (20.25µmol $m^{-2}$ $sec^{-1}$) and Lalmati (20.58 µmol $m^{-2}$ $sec^{-1}$). In $eO_3$ treatment variety NDR -2064 and NDR- 2065 performed well while variety BPT 5204 and Lalmati had low photosynthetic rates. Under eTemp, photosynthetic rates were down in almost all the varieties (Fig. 2).

### Yield parameters

Of all the 23 varieties, NDR-359 had better grain weight/plant in all the treatments. Azad basmati

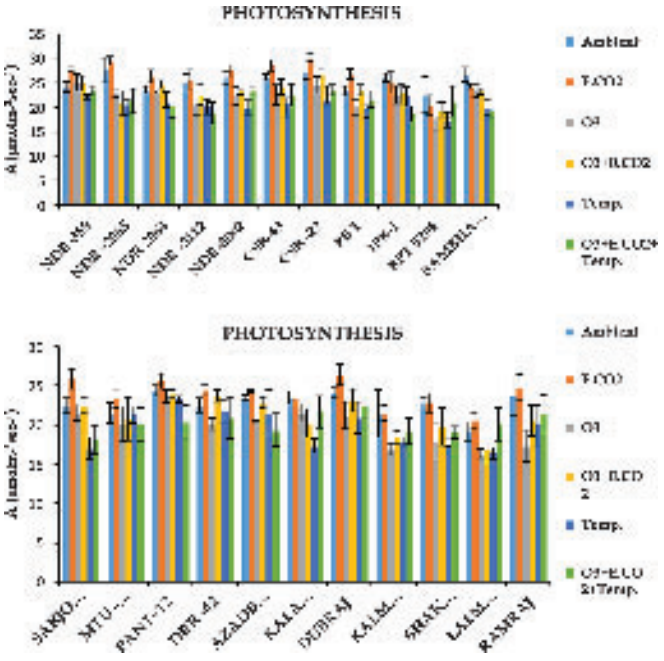


Fig 2: Photosynthesis and stomatal conductance of different rice varieties under different treatments.

performed very well in elevated $CO_2$ and its grain weight was significantly increased. Variety NDR-3112 had better grain weight per plant under $eO_3$ (Fig 3). Grain weight per plant increased significantly in most of the varieties in combined treatments of $CO_2$ and $O_3$.Varieties Sarju-52, Shambha sub-1 and Pant 12 had better grain weight in eTemp treatment.

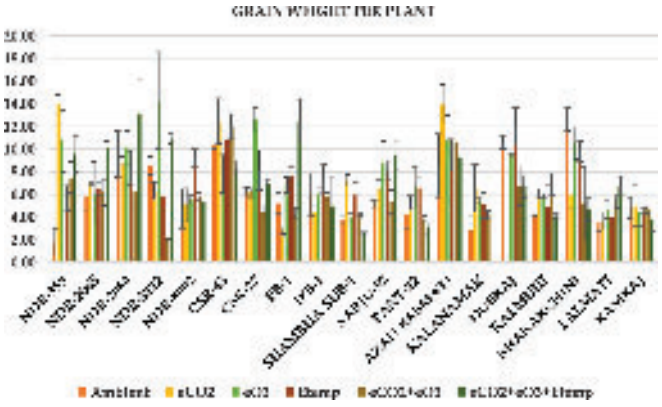


Fig. 3: Grain weight (g) of rice varieties under different treatments

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**Monitoring of fluoride and arsenic in environmental matrices, Fe and Zn bio-fortification of rice using siderophore secreting microbes**

The contaminants of toxic elements i.e. fluoride and arsenic are silently and constantly entering human body through various environmental matrices i.e. water and food. Thus the contamination of vegetables and cereals in the contaminated region needs a constant monitoring. Moreover, co-occurrence of fluoride and arsenic in groundwater and thereafter in farm soils aggravates the problem, as not only the health of the consumers is affected, but also the productivity of crop plants declines.

Although several transgenic approaches are available for bio-fortification of cereals, these are not permitted for release by the regulatory authorities. Siderophore secreting soil microbes and the ligand exchange between plant roots and microbes hold potential for bio-fortification.

## Temporal monitoring of $F^-$ levels in different crop plants in Unnao district

The level of fluoride ($F^-$) was estimated in the crops that were cultivated (2017-2018) in the agricultural farms of Unnao district, three distinct seasons i.e. pre-monsoon (March-May), monsoon (July - Sep) and post monsoon (Nov-Jan).

Among the 12 sampling sites, seven sites, i.e., *Pathakpur, Jajmau, Atwah, Asoha, Jargaon, Meethitikur* and *Sarukheda* are agricultural sites from where different plants (n = 18) including crops (n = 13) were collected. The crops included *Piper betle (*betle leaf), *Legenaria siceraria* (bottle Gourd), *Coccinia grandis* (ivy gourd), *Zea mays* (maize), *Beta vulgaris* (beet-root), *Pennisetum glaucum* (pearl millet), *Capsicum annum* (capsicum), *Gossypium arboreum* (cotton), *Oryza sativa* (rice), *Trichosanthes diocia* (pointed gourd), *Vigna mungo* (moong), *Momordica charantia* (bitter gourd) and *Luffa acutangula* (ribbed loofa), Fruits (n = 3) like *Punica granatum* (pomegranate), *Psidium guajava* (guava) and *Syzygium cumini* (black plum) and grasses (n = 2) *Parthenium hysterophorus* (Parthenium) and *Cymbopogon nardus* (lemongrass) (Table 1).

*Pathakpur* and *Asoha* had diverse crops (n = 7) while *Meethitikur, Sarukheda* and *Jargaon* had less diversity of crops. Rice was found to be cultivated commonly in all the sites and was also cultivated during monsoon and post-monsoon season, while *Capsicum annuum* was observed in four sites, i.e., *Pathakpur, Jajmau, Atwah* and *Asoha* among seven sites. Most of the crops/ plants were grown during monsoon (n = 12) and post-monsoon (n =12) while least was observed during pre-monsoon (n = 7).

Highest $F^-$ content (1.8 µg $g^{-1}$) was found in a grass, *Cymbopogon nardus* followed by 1.58 µg $g^{-1}$ in leaves of *Coccinia grandis* and 1.47 µg $g^{-1}$ *Trichosanthes diocia* and *Momordica charantia.* Range of $F^-$ content in plants were 0.21-1.58 µg $g^{-1}$ during pre-monsoon, 0.16-1.21 µg $g^{-1}$ for monsoon and 0.23-1.8 for the post-monsoon season (Table 1). Accumulation of $F^-$ in the leaves of trees i.e. *Punica granatum, Psidium guajava, Syzygium cumini*, exhibited not much variation across the seasons, which was 0.44, 0.47 and 0.25 µg $g^{-1}$, respectively during monsoon and 0.46, 0.27 and 0.25 µg $g^{-1}$, respectively during post-monsoon.

Range of $F^-$ content in leaves of rice plants was 0.23-0.64 µg $g^{-1}$. The highest value of $F^-$ content in rice leaves was observed for pre-monsoon (0.66 µg $g^{-1}$) and post-monsoon (0.64 µg $g^{-1}$) at *Jajmau* and *Pathakpur* sites, respectively. Generally, it was observed that $F^-$ content in the agricultural crop was maximum during the pre-monsoon season followed by post-monsoon and lowest during monsoon. The leaves of *Zea mays*

contained higher $F^-$ level (0.68 µg $g^{-1}$) than rice (0.27 µg $g^{-1}$) for the same site (*Asoha*) during pre-monsoon season. The range of $F^-$ in leaves of *Capsicum annuum* ranged between 0.27-0.7 µg $g^1$ and 0.36-0.77 µg $g^{-1}$ for monsoon and post-monsoon seasons, respectively. The highest accumulation of $F^-$ in capsicum was recorded for *Pathakpur* (0.77 µg $g^{-1}$) and *Jajmau* (0.7 µg $g^{-1}$). Similarly, *Vigna mungo* was found growing in two sites, i.e., *Jajmau* and *Atwah,* whereas, a higher level of $F^-$ was recorded from crops cultivated in *Atwah*. Among the seven sites, the highest F- level in collected crops was recorded from Pathakpur (0.34-1.58 µg g-1) followed by Atwah (0.29-1.45 µg g-1).

**Table 1. Fluoride accumulation (µg $g^{-1}$) in leaves of plants collected from various villages of Unnao district during different seasons.**

| S. No. | Location | Plant species | Fluoride concentration in Leaf (µg $g^{-1}$) | | |
|---|---|---|---|---|---|
| | | | Pre-Monsoon | Monsoon | Post-Monsoon |
| 1. | *Pathakpur* | *Piper betle* (betel leaf ) | $0.77^{d}$±0.03 | | |
| | | *Trichosanthes diocia* (Pointed gourd ) | $1.47^{g}$±0.32 | $1.21^{i}$±0.06 | $0.41^{c}$±0.00 |
| | | *Legenaria siceraria* (White flower gourd) | $1.20^{f}$±0.00 | | |
| | | *Coccinia grandis* (Ivy Gourd ) | $1.58^{h}$±0.02 | | |
| | | *Capsicum annuum* (Capsicum) | | $0.54^{f}$±0.03 | $0.77^{e}$±0.03 |
| | | *Momordica charantia* (Bitter gourd ) | | $0.97^{h}$±0.04 | $1.47^{f}$±0.02 |
| | | *Oryza sativa* (Rice) | | $0.34^{d}$±0.03 | $0.64^{d}$±0.03 |
| 2 | *Jajmau* | *Oryza sativa* (Rice) | $0.64^{b}$±0.03 | | |
| | | *Vigna mungo* (Split green gram) | $0.97^{e}$±0.03 | | |
| | | *Beta vulgaris* (Beet) | | $0.16^{a}$±0.01 | |
| | | *Capsicum annuum* (Capsicum) | | $0.70^{g}$±0.08 | $0.65^{d}$±0.04 |
| | | *Pennisetum glaucum* (Millet) | | | $0.26^{a}$±0.01 |
| 3. | *Atwah* | *Vigna Mungo* (Split black gram) | $1.45^{g}$±0.57 | | $0.65^{d}$±0.04 |
| | | *Capsicum annuum* (Capsicum) | | $0.46^{e}$±0.02 | $0.36^{bc}$±0.00 |
| | | *Gossypium arboreum* (Cotton) | | $0.49^{e}$±0.02 | $0.29^{ab}$±0.01 |
| 4. | *Asoha* | *Luffa acutangula* (Dishcloth Gourd) | $0.21^{a}$±0.00 | | |
| | | *Oryza sativa* (Rice) | $0.27^{a}$±0.02 | | |
| | | *Zea mays* (Maize) | $0.68^{cd}$±0.05 | | |
| | | *Capsicum annuum* (Capsicum) | | $0.27^{c}$±0.02 | $0.43^{c}$±0.04 |
| | | *Gossypium arboreum* (Cotton) | | $0.34^{d}$±0.4 | $0.59^{d}$±0.34 |
| | | *Cymbopogon nardus* (Citronella grass) | | $0.19^{ab}$±0.68 | $1.80^{g}$±0.68 |
| 5. | *Jargaon* | *Oryza sativa* (Rice) | | | $0.23^{a}$±0.02 |
| | | *Parthenium hysterophorus* (Parthenium) | | $0.48^{e}$±0.01 | $0.61^{d}$±0.01 |
| 6. | *Meethitikur* | *Oryza sativa* (Rice) | $0.28^{a}$±0.01 | | |
| | | *Punica granatum* (Pomegranate) | | $0.44^{e}$±0.13 | $0.46^{c}$±0.11 |
| 7. | *Sarukheda* | *Oryza sativa* (Rice) | $0.38^{b}$±0.01 | | |
| | | *Psidium guajava* (Guava) | | $0.47^{e}$±0.02 | $0.27^{ab}$±0.02 |
| | | *Syzygium cumini* (Black plum) | | $0.22^{bc}$±0.04 | $0.25^{a}$±0.04 |

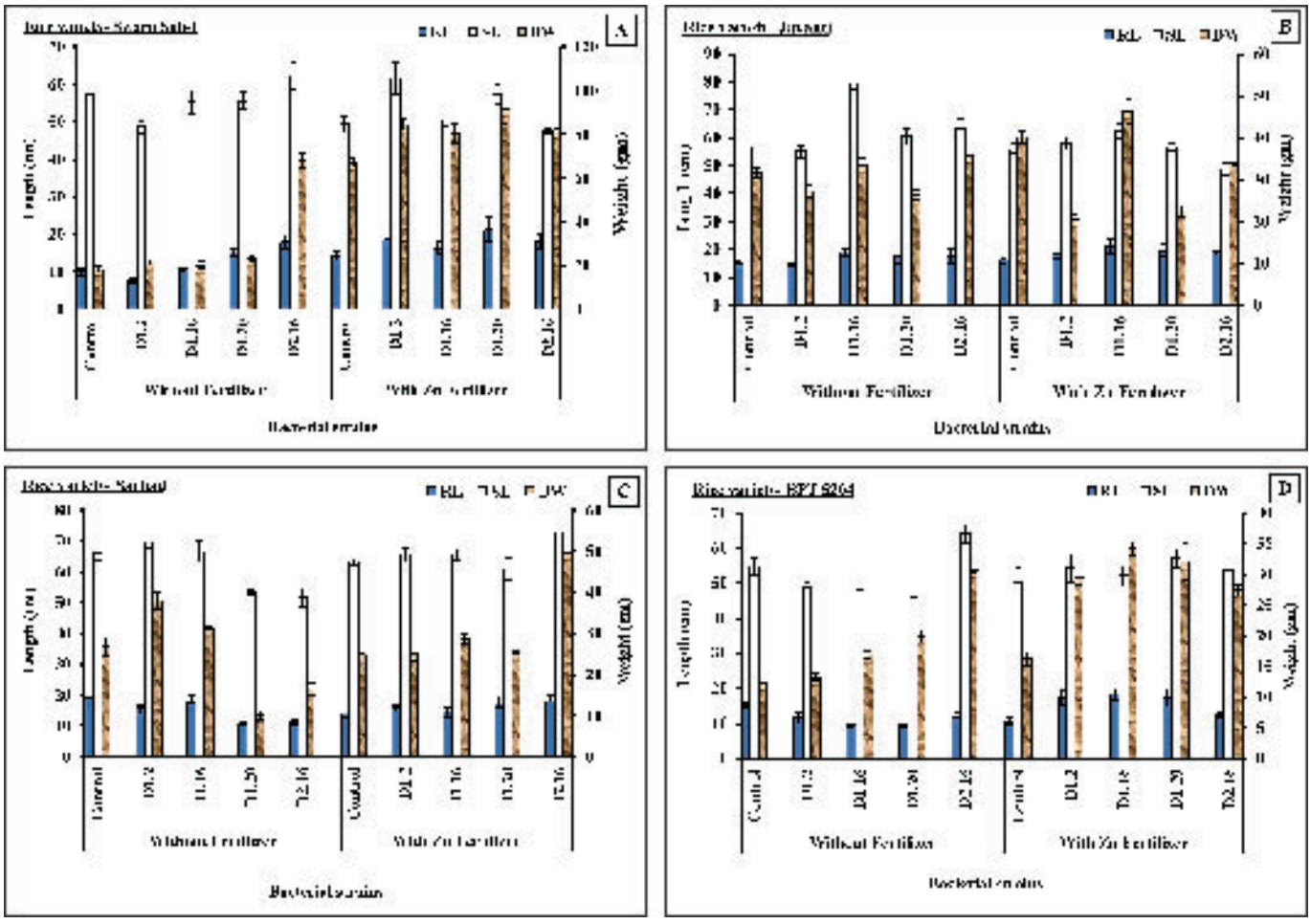

Fig. 1: Morphological change; root length (RL), shoot length (SL) and dry weight (DW) of rice cultivars Swarn Sub-1 (A), Jayanti (B), Sarbati (C) and BPT 5204 (D) when grown with D1.2, D1.16, D1.20 and D2.16

## Comparative assessment of Zn and Fe uptake in four rice cultivars using four microbial inoculums under two regimes of Zn fertilization

In order to evaluate the enhancement of Fe and Zn in rice plants, an elaborate experiment was performed involving four rice cultivars (*Swarn sub-1, Jayanti, Sharbati and BPT-5204*) and four siderophore secreting microbial strains viz, NBRI-D1.2, NBRI-D1.16, NBRI-D1.20, NBRI-D2.16 (*Pseudomonas putida, Pseudomonas mohnii, Pseudomonas spp. and Pseudomonas fluorescens*, respectively). The four rice cultivars consisted of two contrasting pairs of rice cultivars, with respect to Zn accumulation. The selection was made by screening cultivars, based on their Zn accumulation levels when grown on garden soil.

In order to assess the enhancement of Fe and Zn with microbial inoculums, an outdoor experiment was performed with application of the microbes and $ZnSO_4$ till the maturity of the grains (~120 days) and eventually the analysis of grain Fe and Zn content, along with other physiological parameters, soil CFU count of the inoculated microbes, expression of the root Fe and Zn transporters in the rice plants, soil physio-chemical parameters, morphological parameters, were carried out.

The root length (RL), shoot length (SL) and dry weight (DW) increased significantly in presence of all the four microbial inoculums, applied in the Zn amendment soil. Interestingly growth parameters did not show any increase when these microbial inoculums applied in garden soil (Fig. 1). The RL increased with an average percentage of 29.19%, 21.87%, 18.92% and 52.33% in cv. *Swarn-sub-1, Jayanti, Sarbati* and *BPT-5204*, respectively. The SL increased by 10.04%, and 8.65% in cv. *Swarn sub-1,* and *BPT5204*, respectively. Similarly, the DW

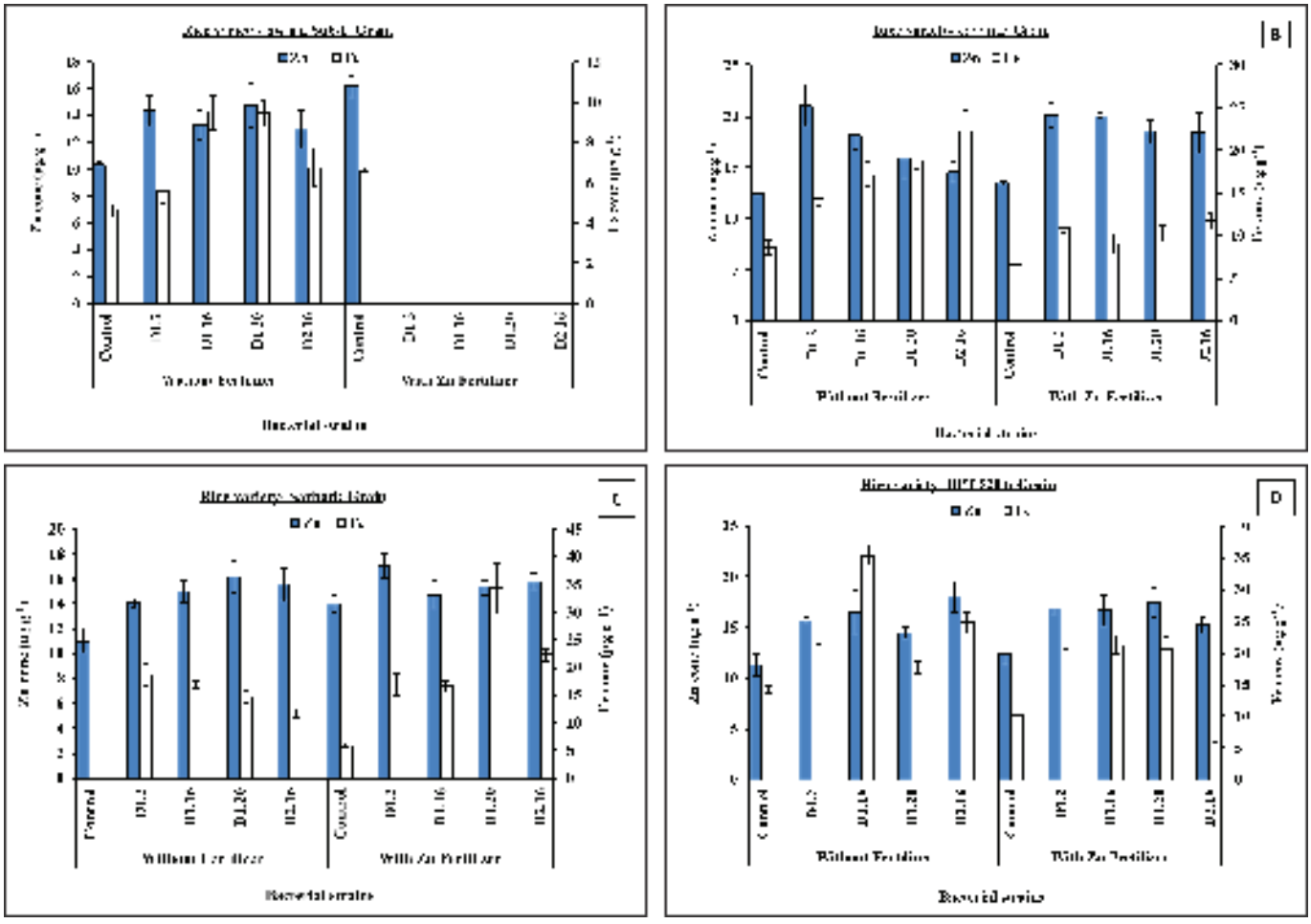

Fig. 2: Zn and Fe levels in grain of rice cultivars Swarn Sub-1 (A), Jayanti (B), Sarbati (C) and BPT 5204 (D) when grown with D1.2, D1.16, D1.20 and D2.16

increased by 25.6%, 54.3% and 88.8% in cv. *Swarn sub-1*, *Sarbati* and *BPT 5204*, respectively when grown in Zn amended soil. In case of plants cultivated on normal soil, the highest RL, SL and DW were observed against *P. fluorescens* in cv. *Swarn-sub 1*. Similarly, in cv. *Jayanti* the highest RL (18.7±1.5), SL (62.3±3.5) and DW (79.7±2.5) was observed against *P. mohnii*. In cv. *Sarbati* highest SL (69.7±2.5) and DW (38±2.2) was observed against *P. fluorescens*. On the other hand, in plants cultivated on Zn amended soil, the highest RL (21.6±2.6), SL (62.3±2.5) and DW (46.2±3.0) was observed in cv. *Jayant*i against *P. mohnii*. In cv. *Sarbati* highest RL (18.3±1.5), SL (62.3±2.5) and DW (46.2±3.0) was observed in cv. *Jayanti* against *P. mohnii*. In cv. *Sarbati* highest RL (18.3±1.5), SL (73.0±3.6) and DW (49.8±0.4) was observed against *P. fluorescens* and in cv. *BPT 5204*, highest RL (18.3±1.5) and DW (34.2±1.1) was observed against *P. mohnii*.

In grains, the percentage increase in the Fe level, against the different inoculums ranged between 52.2% to 111.6% in cv. *Sarbati* and cv. *Jayanti*, respectively (Fig. 2). The highest level of Fe content in grain (µg $g^{-1}$) was observed against *P. mohnii* in cv. *Swarn sub-1* (9.5±0.8) and in *BPT5204* (35.4±1.5). In the rest two other cultivars, the highest level of Fe was observed against *P. mohnii* in cv. *Jayanti* (22.3±2.4) and against *P. putida* in cv. *Sarbati* (18.7±2). Alternatively, the grain Fe content when cultivated with Zn amendment ranged between 59.31% to 28.3% in cv. *Jayanti* and *cv. Sarbati*, respectively. The highest Fe content was observed against *P. fluorescens* in cv. *Jayanti* (11.8±1) in cv. *Sarbat*i against *Pseudomonas spp* (34.2±4.5) and in cv. BPT 5204 (23.1±2.7) against *P. putida*.

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**Plant ecology, forest ecosystem structural and functional analysis, forest biomass, forest carbon sequestration, ecosystem physiology, climate change**

The role of forests in carbon sequestration has become an important means of mitigating the impact of increase in atmospheric carbon dioxide concentrations. Tropical deciduous forest plays an important role in carbon sequestration and storage, with complex regulation mechanism by local environment (microclimate) and community structure. Our group has been working in the field of forest productivity and carbon sequestration assessment, and modelling using field measurements. The group is primarily focusing on long-term studies for understanding the ecosystem functioning and carbon dynamics at tree community level, thereby providing inputs for better model simulation in tropical deciduous forest.

## Soil $CO_2$ efflux in three forest communities in tropical deciduous forest

Tropical forests contain 30% of global soil carbon and play a fundamental role in global carbon budgeting. It helps in sequestrating the atmospheric $CO_2$ into soil carbon pool. Interaction of soil carbon to environmental processes plays a key role in controlling the future concentrations of $CO_2$ in the atmosphere. However, carbon sequestration potential in tropical forests soil pool is poorly assessed. Soil $CO_2$ flux is extremely dynamic, and is controlled by spatio-temporal changes in soil temperature, water content, pH, and carbon in soil. The soil $CO_2$ efflux is also controlled by type of vegetation cover, under-canopy microclimate and soil physico-chemical quality. The present study aims to analyse the soil $CO_2$ efflux patterns in three forest communities (dry mixed, sal mixed and teak plantation) in an Indian tropical deciduous forest site at Katerniaghat Wildlife Sanctuary located in Terai region of Uttar Pradesh. We studied the diurnal soil $CO_2$ efflux in above three forest communities.

The three forest communities i.e. dry mixed (DMF), sal mixed (SMF) and teak plantation (TPF) were selected for measuring soil $CO_2$ efflux in summer season using automated LI-COR 8100 soil $CO_2$ flux system. Soil physico-chemical parameters were also studied. We measured the different microclimatic variables at forest understorey in all three communities during same time to investigate the interaction of microclimate on soil $CO_2$ efflux (Fig. 1). Total day time soil $CO_2$ efflux of 827, 1089 and 829 (µmol $CO_2$ $m^{-2}d^{-1}$) were observed in TPF, SMF and DMF, respectively. Soil $CO_2$ efflux showed significant differences ($P<0.01$) among the three forest communities for summer season. Average soil $CO_2$ efflux rate (µmol $CO_2$ $m^{-2}s^{-1}$) of 4.06±0.36, 5.03±0.45, 4.37±0.79 was observed in TPF, SMF and DMF, respectively, which is positively correlated with total organic carbon (TOC) and water holding capacity among soil physico-chemical variables. Among microclimatic variables (Fig. 1), soil temperature (ST, $^0$C) and air temperature (AT, $^0$C) observed strong positive correlation with day time soil $CO_2$ efflux in all three communities. Significant increase in soil $CO_2$ flux was observed with increasing air and soil temperature (AT and ST) in DMF and SMF.

### *Interaction of microclimate on soil $CO_2$ efflux*

The soil $CO_2$ efflux was positively correlated with soil temperature and atmospheric temperature, as soil temperature influence the activity of microbes positively which lead to increased rate of soil organic matter decomposition resulting in more soil $CO_2$ efflux. Diurnal variations in soil temperature were

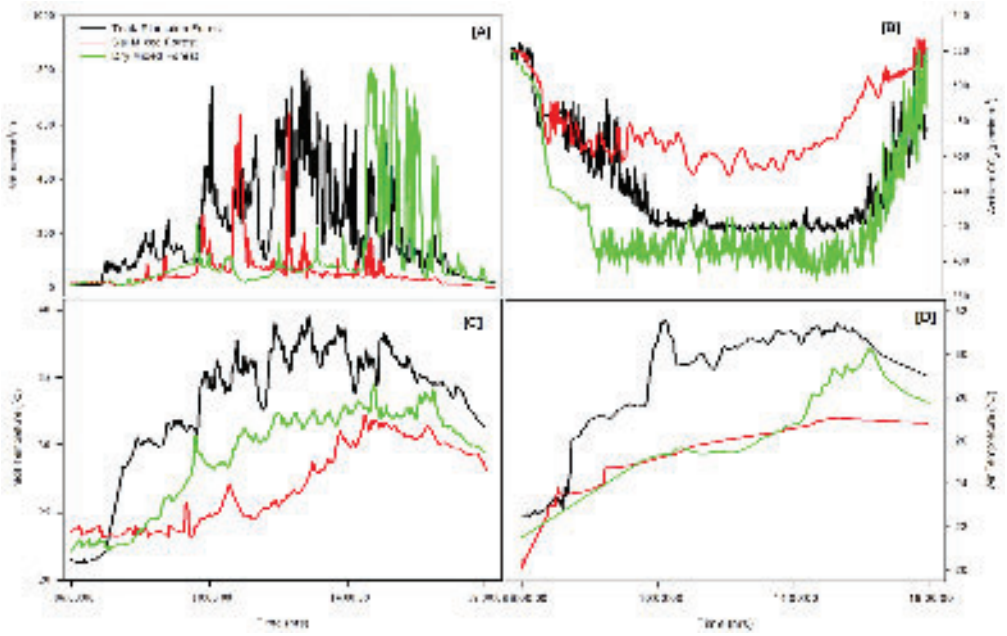

Fig. 1 (A-D): Diurnal trend of four microclimatic variables during summer season in three forest communities in tropical deciduous forest from North India. A. Photosynthetically active radiation (PAR µmolm$^{-2}$s$^{-1}$), B. Ambient $CO_2$ (µmolmol$^{-1}$), C. Soil Temperature (°C), D. Air Temperature (°C).

more in comparison to air temperature in all forest communities, may be diurnal fluctuations in radiation has larger impacts on soil surface temperature. The average daytime PAR (06 h to 18 h) at forest understory was 210, 61 and 123 in (µmol m$^{-2}$s$^{-1}$) in TPF, SMF and DMF, respectively. Multiple linear regression analysis observed weak positive relationship between soil $CO_2$ efflux with soil temperature and air temperature in all forest communities (Fig 2). No significant positive relationship was observed for soil $CO_2$ efflux against PAR and ambient $CO_2$ (Fig 2). However, PAR is negatively correlated with soil $CO_2$ efflux (r= -0.81) among all forest communities, PAR may be indirectly controlling soil $CO_2$ effluxes by heating ambient air and soil surface layer. We may conclude that, AT and ST are two most significant microclimatic factors regulating forest canopy physiology, which is also regulating below ground soil $CO_2$ efflux. Further detailed investigation for understanding spatio-temporal variations of soil $CO_2$ efflux along with its interaction with canopy cover, tree diversity, physiological processes of dominant tree species, and litter dynamics is needed.

### *Relationship between soil properties and litter chemistry*

The quality and quantity of litter and associated factors can influence soil properties in different ways in a forest ecosystem. Therefore, understanding the relationship between soil properties and litter chemistry in tropical forests is one of the high priority research areas by plant ecologists. We investigated the relationship between soil properties and litter chemistry in three forest communities i.e. Sal mixed forest (SMF), dry mixed forest(DMF) and Teak plantation forest (TPF), in tropical deciduous forest ecosystem in North India. Fresh leaf litter and soil samples were collected at two soil depths (0-15 and 15-30 cm) from all these three forests. Litter bag experiments were also conducted to know differences in litter nutrients after its decomposition. The concentration (mg Kg$^{-1}$) of different nutrients such as sodium (Na, 2.6), potassium (K, 38.5), calcium (Ca, 425) and carbon (C, 45.54 %) were highest in DMF fresh litter (Table 1). Total organic carbon (TOC) (g Kg$^{-1}$) was significantly higher in SMF (19.23) in comparison to DMF (18.41) and TPF (13.61) in surface soil (0-15 cm depth). Na, K, Ca, available P, total P, available N, total N were highest in DMF surface soil. We observed significant positive correlation between all nutrients of litter vs. soil. Although soil bulk density (BD) and particle density (PD) showed their significant negative correlation with litter C, total porosity was positively correlated. Similarly, litter Na had significant negative correlation with BD and positive correlation with PD. The litter chemistry

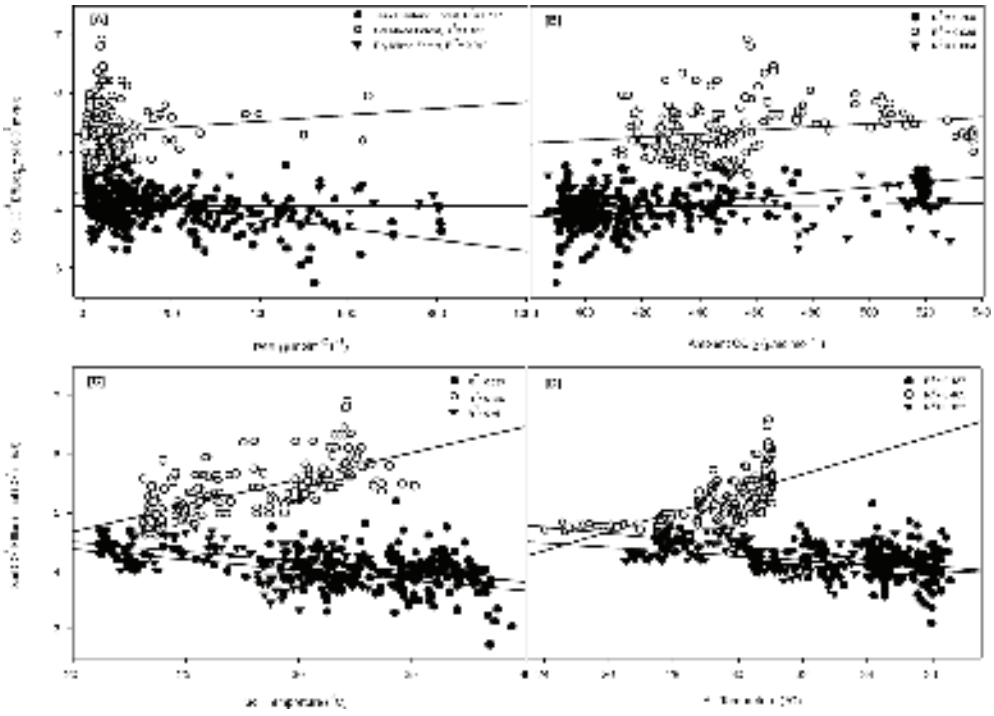

Fig. 2 (A to D): Multiple linear regressions of soil $CO_2$ efflux against microclimatic variables in different forest communities in tropical deciduous forest from North India.

played a significant role in changing soil pH and TOC. All litter nutrients, except total P, have their significant positive correlation with soil pH. Total P, C and N of litter have strong positive correlation with total soil organic carbon. This indicates that litter chemistry, and soil properties have specific relation among them despite unique species composition in each forest community.

## Characterizing patterns and processes of alpine ecosystem in Indian Himalaya

Due to the compression of thermal zones and isolation caused by low temperature, the alpine landscape has the highest level of sensitivity to climatic changes. The alpine ecosystems can be considered as "natural laboratories" for observing climatic changes. A long-term monitoring network known as HIMADRI (Himalayan Alpine Dynamics Research Initiative) was established by Space Application Centre (SAC), Indian Space Research Organization (ISRO) in collaborations with other participating national organizations during 2013-2016 of which CSIR-NBRI is one of the participating institute. Under HIMADRI initiatives, six long-term monitoring sites were established having 20 summits in Indian Himalayas. Baseline data on plant diversity have been collected with a standard protocol adopted from GLORIA (Global Observation Research Initiative in Alpine Environments).

In the alpine ecosystems, the ecotones are the most sensitive transition zones for monitoring the micro-scale variations to understand the ecological processes in response to climatic changes. The present study primarily focuses on understanding the alpine ecotone structure and function through space based and *in-situ* observations in close collaboration with SAC, ISRO.

Microclimate is a crucial determinant of ecological patterns in both vascular and non-vascular plant communities and also determines ecosystem functioning. The present study primarily focused on microclimate characterization of Alpine ecosystem ecotone *vis-a-vis* cryptogam diversity assessment in Indian Himalayas, jointly with the plant diversity division.

Microclimate data were collected at HIMADRI long-term monitoring sites at Tungnath (Uttarakhand) and Chansal pass (Himachal Pradesh) to understand the site specific micro-meteorological patterns to understand how vegetation structure affects microclimate and vice-versa at alpine ecosystems.

**Table 1.** The concentrations of different nutrients in fresh and degraded litter of Teak plantation (TPF), Sal mixed forest (SMF) and dry mixed forest (DMF) (Mean ± SD)

| Litter nutrients | Teak plantation forest | Sal mixed forest | Dry mixed forest |
|---|---|---|---|
| Sodium (mg $Kg^{-1}$) | 1.34 ± 0.23 | 1.57 ± 0.42 | 2.6 ± 0.78 |
| Potassium (mg $Kg^{-1}$) | 24.2 ± 7.52 | 28.2 ± 10.54 | 38.5 ± 20.34 |
| Calcium ( mg $Kg^{-1}$) | 200 ± 54.32 | 313 ± 102.23 | 425 ± 119.57 |
| Phosphorus (%) | 0.45 ± 0.024 | 0.51 ± 0.017 | 0.56 ± 0.023 |
| Carbon (%) | 33.52 ± 10.54 | 40.53 ± 18.35 | 45.54 ± 20.34 |
| Nitrogen (%) | 1.24 ± 0.41 | 1.45 ± 0.57 | 1.65 ± 0.47 |
| C/N | 27.03 | 27.95 | 27.6 |
| (LD) Carbon (%) | 29.41 ± 10.31 | 32.64 ± 19.24 | 34.75 ± 18.35 |
| (LD) Nitrogen (%) | 0.46 ± 0.054 | 0.86 ± 0.041 | 0.91 ± 0.056 |
| (LD) C/N | 64 | 37.95 | 38.19 |

*LD=Degraded litter

Diurnal (daytime only) variations in five microclimatic variables (photosynthetically active radiation (PAR), air temperature, soil temperature, ambient $CO_2$ and air absolute humidity) were measured with Li-Cor 850 $CO_2/H_2O$ gas analyzer along with quantum and temperature sensors. All the above variables were measured diurnally in treeline/timberline (under-canopy) and immediately after the treeline/timberline (in open areas without any canopy cover) in the ecotone of alpine ecosystems. The results showed wide variations among Tungnath and Chansal sites. The PAR at Chansal ranged from 900 to 3686 (µmol $m^{-2}s^{-1}$) in open areas and 46 to 552 (µmol $m^{-2}s^{-1}$) under canopy of treeline/timberline. The air temperature (AT) ranged from 14.1 to 22.8 $^0$C in open areas and 10.9 to 13.9 $^0$C under canopy of treeline at Chansal. Soil temperature ranged from 18.6 to 38.6 $^0$C in open areas and 10.9 to 16.6 $^0$C in treeline at Chansal. The results will be further compared with other HIMADRI sites to have a detailed suit of microclimate across Indian Himalayas in Alpine ecosystems. The study will be utilized to understand the functional role of microclimate on cryptogams (particularly lichens and bryophytes) community structure and functioning at Alpine ecotones in Indian Himalayas.

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**Plant microbe interaction, microbial genetics, bio-remediation, agri-waste management**

Our group is mainly working on elucidation of molecular mechanism(s) of microbe mediated abiotic and biotic stress tolerance in different crop plants. Microbial intervention for environmental sustainability has also been one of the emerging areas, where group has developed some important leads.

### Elucidation of molecular mechanism of Silicon solubilisation and functional diversity of Silicon solubilizes

Rhizospheric microbes are known to play vital role in improving plant growth and productivity by dissolution of minerals like silicates and phosphates. Hence, a Si-solubilizing P discriminating media (NBRISSM) for efficient screening of Si solubilizers with minimum P interference was developed earlier. Further on, elucidation of molecular mechanism of silicon solubilisation in number of strains showed close clustering of Si solubilisation with acidic phosphatase activity and production of organic acids *viz*. tartaric acid, succinic acid, fumaric acid and maleic acid , whereas gluconic acid and P solubilization in NBRIP media are distantly placed. Functional diversity of the microbes through 16S ribosomal DNA sequencing based study showed that the silicon solubilizers mainly belong to the genera of *Pseudomonas* and *Bacillus* (Fig. 1).

### Elucidation of molecular mechanism of abiotic stress amelioration

Root associated microbiota are known to improve phosphate availability through alteration in root architecture for improved plant growth. Role of *Pseudomonas putida* (MTCC 5279) for alleviating the phosphate starved salinity stressed condition has been demonstrated earlier. Working on the insight of the molecular mechanism shows that enhanced ROS metabolism and modulated expression of P transporters can be one of the probable mechanisms for alleviation of phosphate starved salinity stressed conditions.

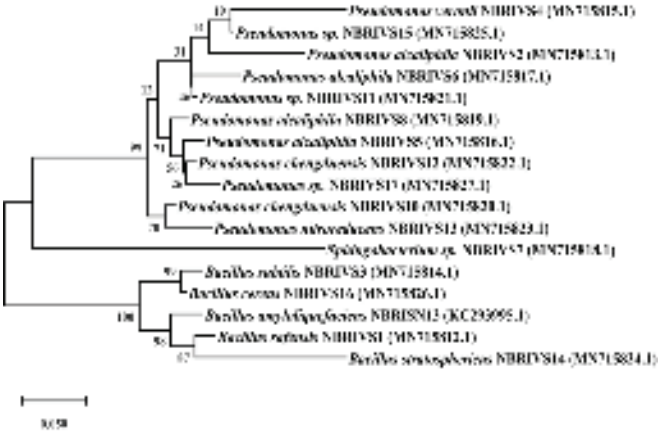

Fig. 1: Functional diversity of silicon solubilizing microbes based on 16S rDNA (partial) sequencing

### Characterization of microbes for arsenic biotransformation

Microbes were characterized for arsenic biotransformation in rice and wheat. To elucidate the role of microbes in amelioration of arsenic, their physiological and molecular mechanism was studied. Number of microbes (bacteria, yeast and fungi) were characterized for different arsenic biotransformation potential *i.e.* arsenate reductase, arsenite oxidase and methyltransferase through biochemical assays and PCR amplification of respective genes. A yeast strain *Debaryomyces hansenii* was identified for amelioration of arsenic stress in

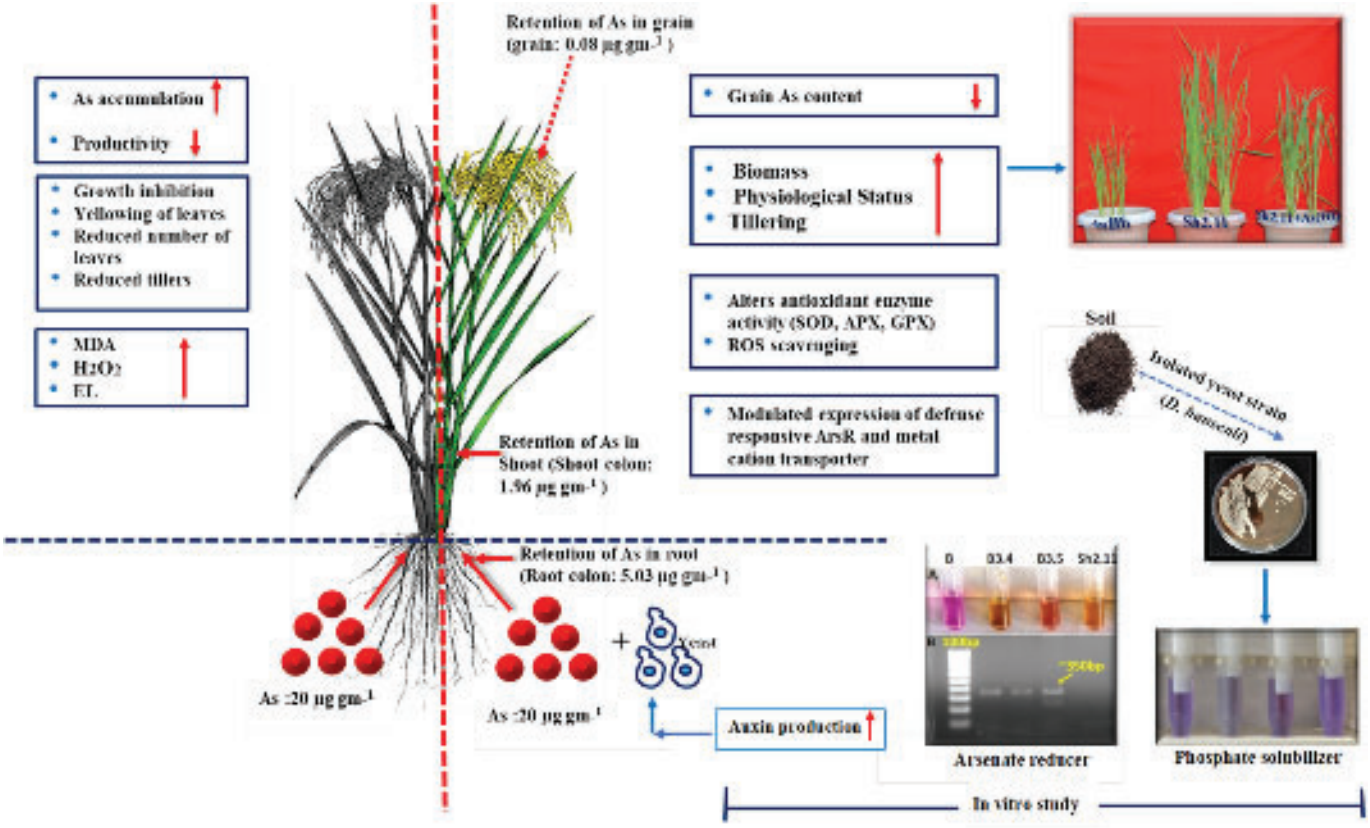


Fig. 2: Yeast strain *Debaromyces hansenii* for reduced arsenic uptake in rice

rice. Rice plants inoculated with *D. hansenii* under arsenic stress conditions were able to reduce grain arsenic content along with other plant growth traits (Fig. 2).

## Characterization of microbes for rice straw decomposition

Development of microbial consortia for *in situ* decomposition of rice straw for soil recarbonization and better productivity of subsequent crop has been reported earlier. To minimize the yield compromise in absence of chemical fertilizer, field trial with different agricultural practice was performed at Faizabad research farm of agriculture department. Microbial formulation after mulching of rice straw were subjected to the field along with half and full dose of fertilization practices. Microbial formulation showed great potential of rice straw decomposition and soil health improvement and also enhanced the productivity of the subsequent crop wheat. The average yield of wheat with different doses of fertilization improved the yield of wheat in presence of applied formulation as compared to control. Thus utilization of microbial formulation results in faster *in situ* decomposition of rice straw, which ultimately enhances nutrient assimilation in the soil resulting in low requirement of chemical fertilization.

### Research Group

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**Abiotic-Biotic stress management of plants, phyto-pathogenic microbes management, green nanotechnology**

The group focuses on disease management of commercially valuable crops and developing sustainable eco-friendly remedies. The microbial techniques are also explored to combat with rising $CO_2$ conditions. Green nano-technological approach is involved in suppression of human and phytopathogens by herbal lipid based nanomaterials.

## Biocontrol efficacy of endophyte *Bacillus tequilensis* against *Fusarium* infected tomato plants

Plants in their natural environment face various biotic stresses due to invading phytopathogens. Their control measure primarily involves large scale applications of chemical fungicides. Excessive use of chemicals lead to the contamination of the environment by entering the food web. To address the above concern, in the present study six antagonistic bacterial strains were screened from 344 isolates and identified through 16S rRNA sequencing. Out of these six antagonistic bacterial endophytes, *Bacillus tequilensis* (PBE1) (MTCC25188) has proved to be most effective and eco-friendly substitute of chemical fungicides against *Fusarium oxysporum* for tomato wilt disease management. The antagonistic effect of PBE1 was well corroborated by dual culture plate assay and SEM micrographs (Fig. 1). The PBE1 also showed efficient plant growth-

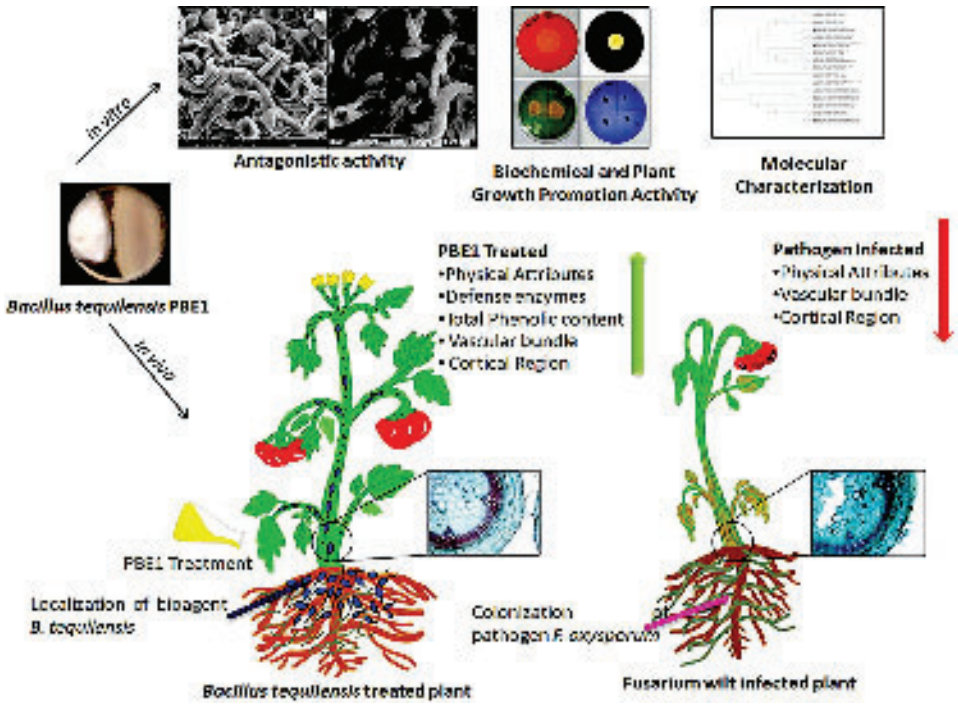


Fig. 1: Graphical presentation of biocontrol efficacy of endophyte *Bacillus tequilensis* against Fusarium wilt infection in tomato plants

promoting traits as it produced indole acetic acid (31.89 µg $ml^{-1}$), hydroxymate type siderophore (5.00 µg $ml^{-1}$) along with phosphate solubilizing (9.09 µg $ml^{-1}$) ability. The bio-protective intervention of PBE1 demonstrated 60.0% reduction of disease incidence in comparison to the pathogen infected plants. Simultaneously, enhanced morphological parameters such as root length, shoot length, number of branches, fresh weight and dry weight by 1.73, 1.43, 1.71, 5.35 and 2.74 folds, respectively, were also observed. All the studies were performed under greenhouse conditions at 25 ± 2 °C for 30 days. Plants were grouped into six different treatments. The pathogen infection was given to 30 days old seedlings post-transplantation and PBE1 treatment was given at 7 days post-infection. The prevention of vascular bundle disruption and uniform thickness of parenchymatous cortical layer was observed in PBE1 treated plants. The changes were distinguished in transverse sections of the collar region of tomato stems (Fig. 1). Moreover, PBE1 also enhanced various antioxidant and defense-related responses including enzymes like superoxide dismutase (77.22 U/mg protein), phenol peroxidase (0.04 U/mg protein), and catalase (1099 U/mg of protein). The lipid peroxidation was found to decreased in PBE1+P treated plants as compared to all other groups. Whereas, the secondary metabolites including total phenolics and flavonoids content were higher in PBE1+P treated plants than all other treatments. By virtue of obtained results, the study may provide an efficient eco-friendly bio-protective tool for the *Fusarium* wilt disease management by replacing widely used chemical fungicides.

## Supplementation of *Trichoderma* improves the alteration of nutrient allocation and transporter genes expression in rice under nutrient deficiencies

Nutrients are essential for rice productivity and their deficiency cause compromised yield along with reduced immunity against several biotic and abiotic stresses. In this study, the potential of *Trichoderma reesei* has been investigated as a biofertilizer (BF) to ameliorate nutrient stress in different rice cultivars at physiological, biochemical and molecular levels. The results indicated that cultivar Heena is much more beneficial with BF as compared to cultivar Kiran at 50% nutrient limiting condition. Enhancement in physiological attributes and photosynthetic pigments were observed in BF treated Heena seedlings. The localization of biofertilizer in treated roots was further validated by scanning electron micrographs (Fig. 2). This result correlated well with the higher levels of Indole acetic acid and Gibberellic acid in biofertilizer treated rice. Similarly, the uptake of micro-nutrients such as Fe, Co, Cu and Mo was found to be 1.4–1.9 fold higher, respectively in BF treated Heena seedlings under 50% nutrient deficient condition. Furthermore, different stress ameliorating enzymes Guaiacol peroxidase, Superoxide

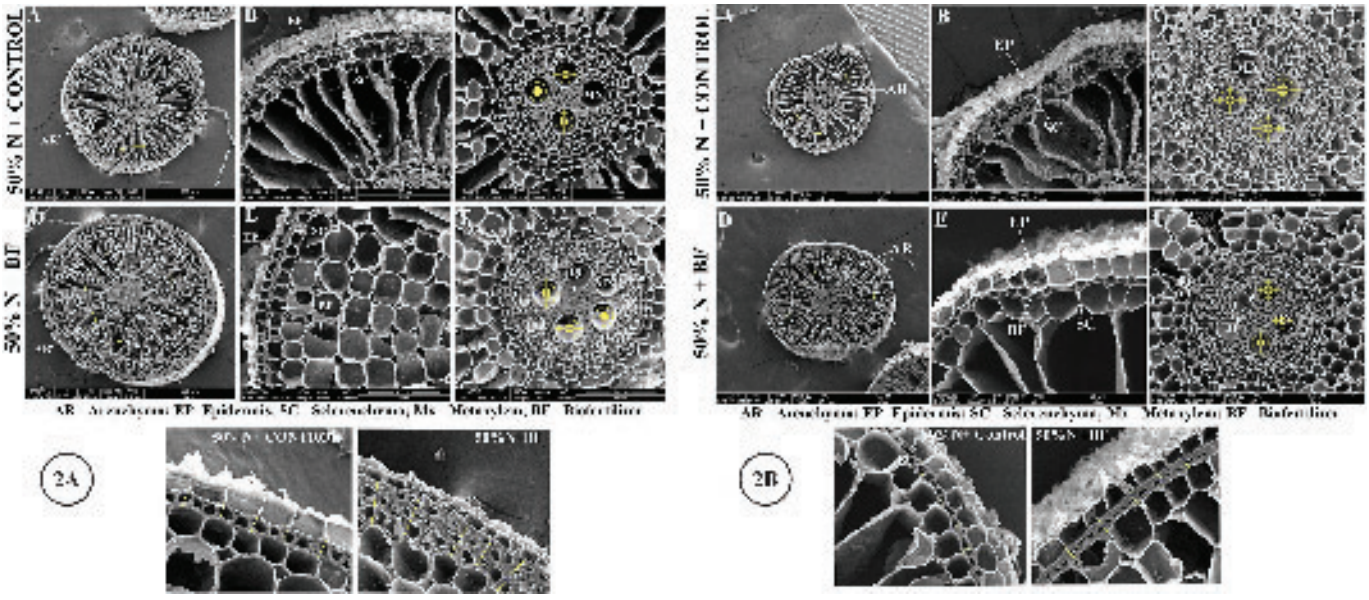


Fig. 2 (A and B): Scanning electron micrograph of two drought resistant rice cultivars in 50% control and 50 %N treated with *Trichoderma reesei* (BF) treatment under hydroponic condition. (A)- 'Heena' (B)- 'Kiran'

dismutase, Phenol Peroxidase, Phenylalanine ammonia lyase and Ascorbate peroxidase in Heena seedlings were also increased by 1.8, 1.4, 2.4, 1.2, and 8.3-fold, respectively, at 50% nutrient deficient condition. The up-regulation of different micro and macro-nutrients allocation and accumulation; metal tolerance related; auxin synthesis genes in BF treated Heena as compared to 50% nutrient deficient condition was further supported by our findings that the application of biofertilizer efficiently ameliorated the deficiency of nutrients in rice.

## Biogenic silver nanoparticles as an efficient contrivance for wound healing acceleration than common antiseptic medicine

A simple and facile way of using biogenic silver nanoparticles (BSNP) (10–20 nm) was developed for wound healing acceleration and suppression of wound infections. The BSNP were formulated in an ointment base, and the study to accelerate the wound healing process was conducted in a rat (Fig. 3). The pH of the BSNP ointment, pH 6.8 ± 0.5, lies in normal pH range of the human skin, with good spreadability and diffusibility. The wound closure rate, as a percentage, was highest at day 3 for a BSNP ointment-treated wound at 22.77 ± 1.60%, while in an untreated control the rate was 10.99 ± 1.74%, for Betadine 14.73 ± 2.36% and for Soframycin 18.55 ± 1.37%, compared with day 0. A similar pattern of wound closure rate was found at days 7 and 11. The antibacterial activity of BSNP was evaluated against wound-infection-causing bacteria *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Escherichia coli* by the agar diffusion method. The total bacterial counts in the wound area were enumerated by the colony forming unit method. The lowest number of bacterial counts was found in the BSNP-treated wound compared with the other groups. BSNP treatment at 7.5% concentration enhanced migration of fibroblasts in a scratch assay. These findings reveal BSNP as an efficient contrivance for wound healing acceleration and as an eco-friendly alternative therapeutic antimicrobial agent.

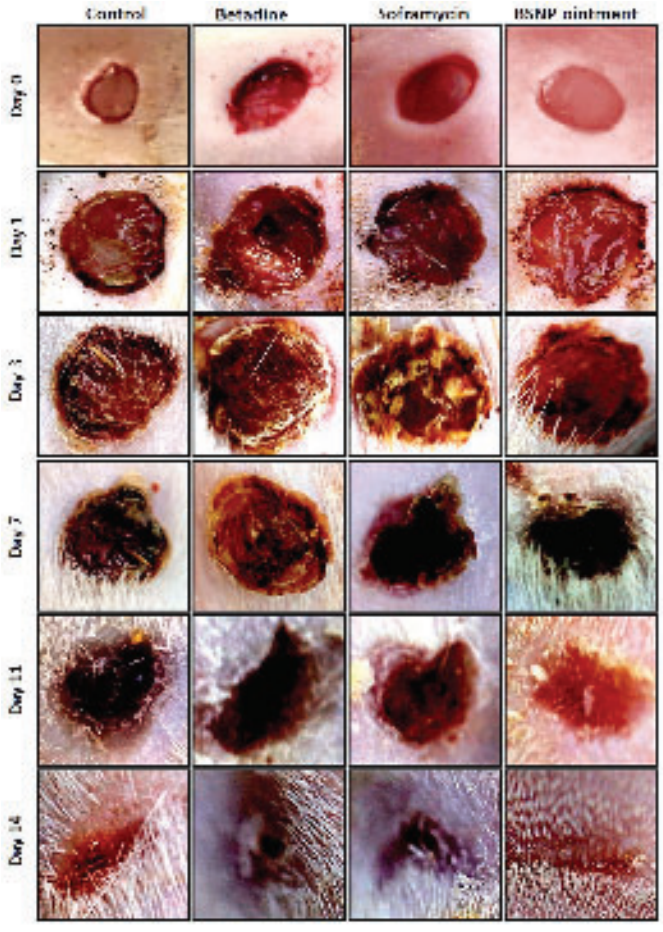


Fig. 3: Representative images of wound healing in rats at days 0, 1, 3, 7, 11 and 14. Topical administration of different wound dressing materials: untreated control, Betadine, Soframycin and BSNP ointment.

## Omics based mechanistic insight into the role of bioengineered nanoparticles for biotic stress amelioration by modulating plant metabolic pathways

Bioengineered silver nanoparticles (SNP) emerge as a facile approach to combat plant pathogen, reducing the use of pesticides in an eco-friendly manner. The plants' response during tripartite interaction of plant, pathogen, and nanoparticles remains largely unknown. This study demonstrated the use of bioengineered silver nanoparticles in combating black spot disease caused by necrotrophic fungus *Alternaria brassicicola* in *Arabidopsis thaliana* via foliar spray (Fig. 4). The particles reduced disease severity by 70–80% at 5 µg/ml without showing phytotoxicity. It elicited plant immunity by a significant reduction in reactive oxygen species (ROS), decrease in stress enzymes by 0.6–19.8-fold, and emergence of autophagy. Comparative plant proteomics revealed 599 proteins expressed during the interaction, where 117 differential proteins were identified. Among different categories, proteins involved in bioenergy and metabolism were most abundant (44%), followed by proteins involved in plant defense (20%). Metabolic profiling by gas

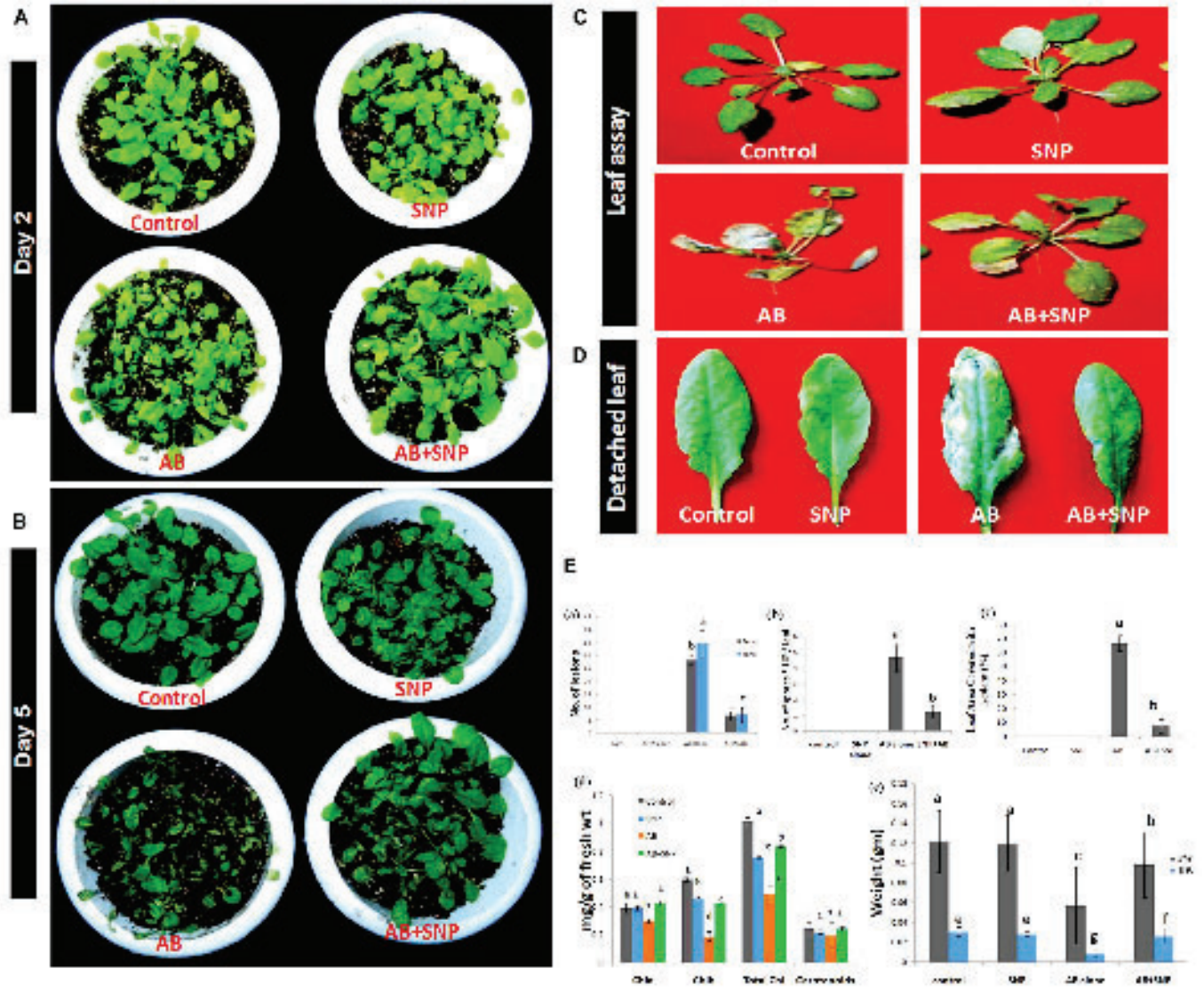


Fig. 4(A-E): Effect of silver nanoparticle (SNP) on reducing disease severity after- (A) 48 h(day2) post infection, (B) Day 5 post infection, (C) reducing in necrosis of leaves, (D) reducing in number of lesion formed per leaves, (E) Assessment of disease parameter in term of (a) number of lesion, (b) number of spore, (c) leaf area covered with lesion, (d) chlorophyll content, (e) fresh and dry weight in silver particle pre-treated plants as compared to other treatments.

chromatography–mass spectroscopy yielded 39 metabolite derivatives in non-polar fraction and 25 in the polar fraction of plant extracts. It was observed that proteins involved in protein biogenesis and early plant defense were overexpressed to produce abundant antimicrobial metabolites and minimize ROS production. Bioengineered silver nanoparticles performed dual functions to combat pathogen attack by killing plant pathogen and eliciting immunity by altering plant defense proteome and metabolome.

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**Sustainable agricultural production, food safety, bio-inoculant formulations, abiotic/biotic stress amelioration, soil fertility, soil ecology**

## *Paenibacillus lentimorbus* alleviates nutrient deficiency-induced stress in chickpea

Nutrient deficiency in soil is one of the limiting factors responsible for stunted growth and poor flowering/fruiting of crops which result in decline in overall agricultural productivity. One important strategy to overcome the problem of nutrient deficiency and to avoid use of chemical fertilizers is the use of plant growth promoting rhizobacteria (PGPR). *Paenibacillus lentimorbus* NRRL B-30488 (hereafter B-30488), an efficient PGPR has been reported to have various plant growth promoting traits that help crops to mitigate various environmental stresses. The present work was designed to examine the application of B-30488 on chickpea growth under nutrient stress condition. Plants inoculated with B-30488 showed positive modulation in physio-biochemical behavior and mineral nutrient uptake for better growth and

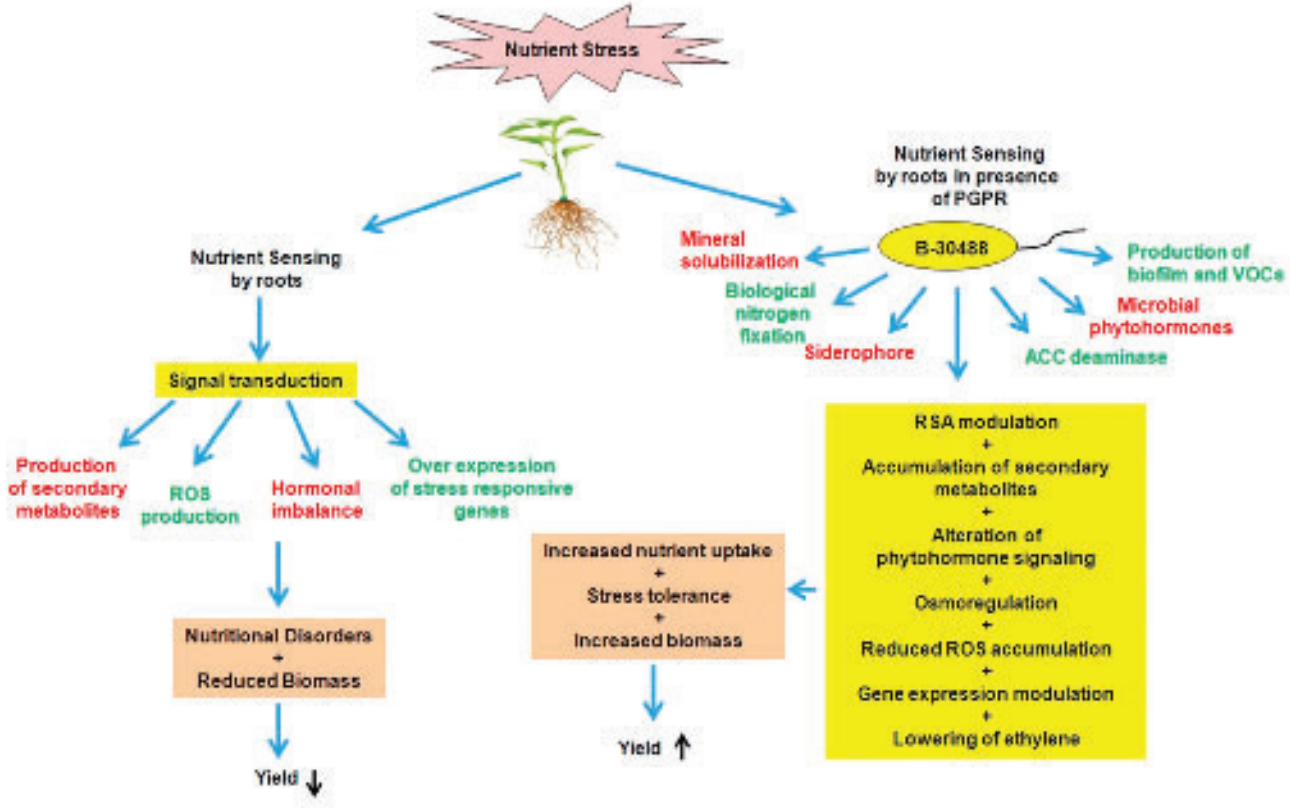


Fig. 1: A hypothetical model depicting the differential response of the enzyme assays, physiological, and molecular analysis under nutrient deficient condition in chickpea in presence and absence of PGPR and other well-known concepts

development. Alteration in gene expression and metabolic profile under nutrient stress condition in chickpea also supported the stress amelioration capability of B-30488. Principal component analysis statistically proved that improved growth performance of chickpea plants under nutrient stress was mainly due to B-30488 induced modulation of metabolic pathways (Fig. 1).

## Transcriptional alterations reveal *Bacillus amyloliquefaciens*-rice cooperation under salt stress

The *Bacillus amyloliquefaciens*-SN13 and rice (*Oryza sativa*) were chosen to understand the complex regulatory networks that govern plant-PGPR interaction under salt stress. During stress, inoculation with SN13 significantly increased biomass, relative water content, proline and total soluble sugar in rice while it decreased lipid peroxidation and electrolyte leakage. Extensive alterations in gene expression were also observed in rice root transcriptome under stress in the presence of SN13. Rhizobacteria induced changes in expression of number of photosynthesis, hormone, and stress-responsive genes, in addition to cell-wall and lipid metabolism-related genes under salt stress indicating its potential role in reducing the harmful effects of salinity. To validate RNA-seq data, qRT-PCR was performed for selected differentially expressed genes representing various functional categories including metabolism, regulation, stress response, and transporters. Results indicate qualitative and quantitative differences in SN13 treated roots under stressed and unstressed conditions. Functional expressions of *OsNAM* and *OsGRAM* in yeast showed enhanced tolerance to various abiotic stresses, indicating crucial SN13-rice interaction in imparting beneficial effects under stress. This is first detailed report on understanding molecular mechanism underlying beneficial plant-microbe interaction in any economically important model crop plant under abiotic stress (Fig. 2).

## Revealing the complexity of protein abundance in chickpea root under drought-stress using a comparative proteomics approach

The irregular rainfalls and land degradation are significant consequences of climatic change causing a decrease in crop productivity. To elucidate effect of drought and its tolerance mechanism, a comparative roots proteomic analysis of chickpea seedlings grown under hydroponic conditions

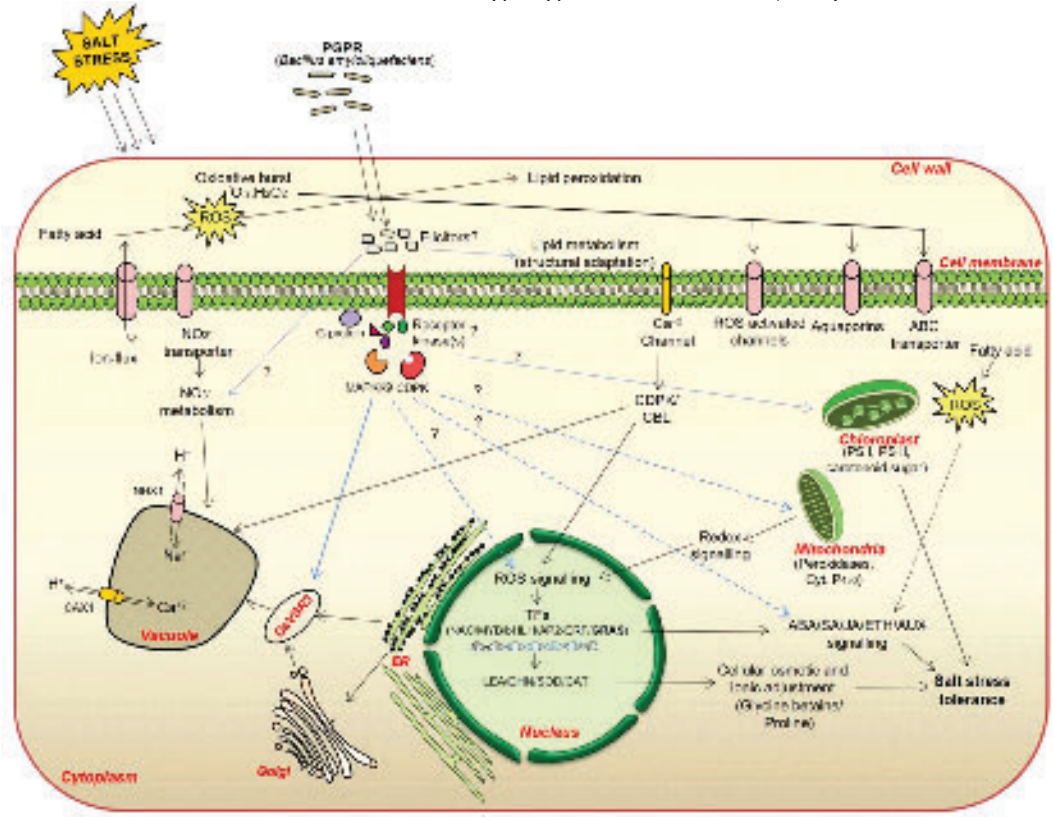


Fig. 2: A model depicting SN13-mediated salt stress regulation in rice seedlings. Solid and dashed blue lines indicate stress regulation based on uniquely found genes in SN13 treated seedlings under salt stress while solid and dashed black arrows indicate stress regulation based on commonly found genes in both salt and salt + SN13 seedlings according to well-known concepts reported earlier. Dashed arrows indicate the existence of not well characterized signalling pathways. The SN13-mediated salt stress regulation shown here is only a fraction of stress signalling occurring in plants and different other signalling and crosstalk points are yet to be discovered and characterized.

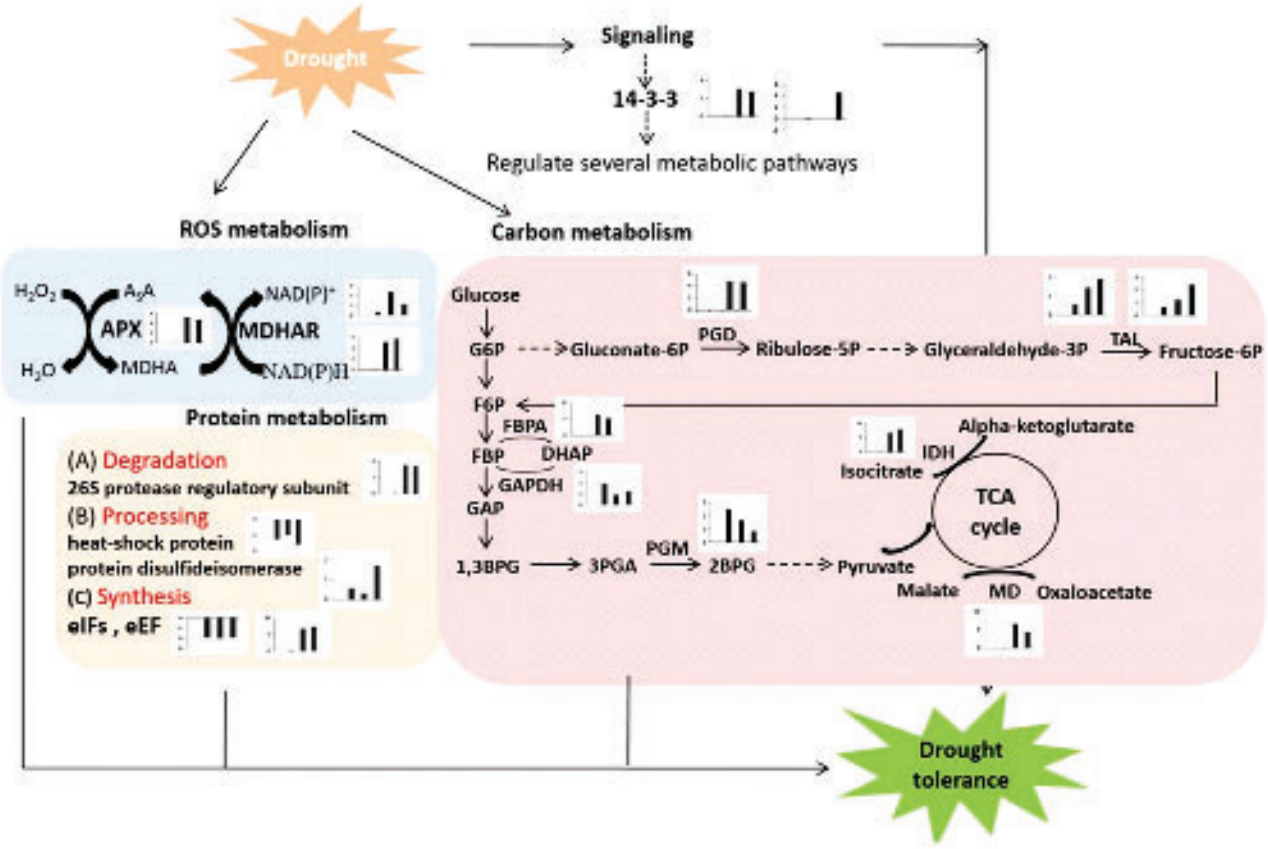


Fig. 3: Model depicting the role of differentially regulated proteins involved in diverse pathways and providing sustainable growth during drought stress. The graphs are indicative of individual protein expression profiles.

for three weeks, was performed at different time points using 2-Dimensional gel electrophoresis (2-DE). After PD-Quest analysis, 110 differentially expressed spots were subjected to MALDI-TOF/TOF and 75 spots were identified with a significant score. These identified proteins were classified into eight categories based on their functional annotation. Proteins involved in carbon and energy metabolism comprised 23% of total identified proteins including, mainly glyceraldehyde-3-phosphate dehydrogenase, malate dehydrogenase, transaldolase, and isocitrate dehydrogenase. Proteins related to stress response (heat-shock protein, CS domain protein, and chitinase 2-like) contributed 16% of total protein spots followed by 13% involved in protein metabolism (adenosine kinase 2, and protein disulfide isomerase). ROS metabolism contributed 13% (glutathione S-transferase, ascorbate peroxidase, and thioredoxin), and 9% for signal transduction (actin-101, and 14-3-3-like protein B). Five percent protein identified for secondary metabolism (cinnamoyl-CoA reductase1 and chalcone-flavononeisomerase 2) and 7% for nitrogen (N) and amino acid metabolism (glutamine synthetase and homocysteine methyltransferase) (Fig. 3). The abundance of some proteins was validated by Western blotting. The detailed information for drought-responsive root protein(s) through comparative proteomics analysis can be utilized in the future for genetic improvement programs to develop drought tolerant chickpea lines.

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**Study of the role of microbes in plant protection and growth and soil health, development of microbial formulations for agricultural applications**

Enhanced agriculture production and productivity are required to cater food and nutrition requirements of growing population of our country. Our goal is to reduce crop losses due to fungal diseases, improve plant and soil health with the use of microbes while reducing the agrochemical use. Development of microbial formulations for agricultural applications will help in increasing the productivity in a sustainable way.

The research areas of the group include biological control; plant microbe interactions and sodic soil reclamation; study on applications of *Trichoderma*, *Bacillus subtilis* and other microbes for sustainable agriculture.

## Chlorpyrifos degradation by plant growth promoting *Alcaligenes faecalis* bacteria isolated from oil contaminated soil:

Chlorpyrifos (Chlp) is one of the major organophosphates extensively used in agriculture

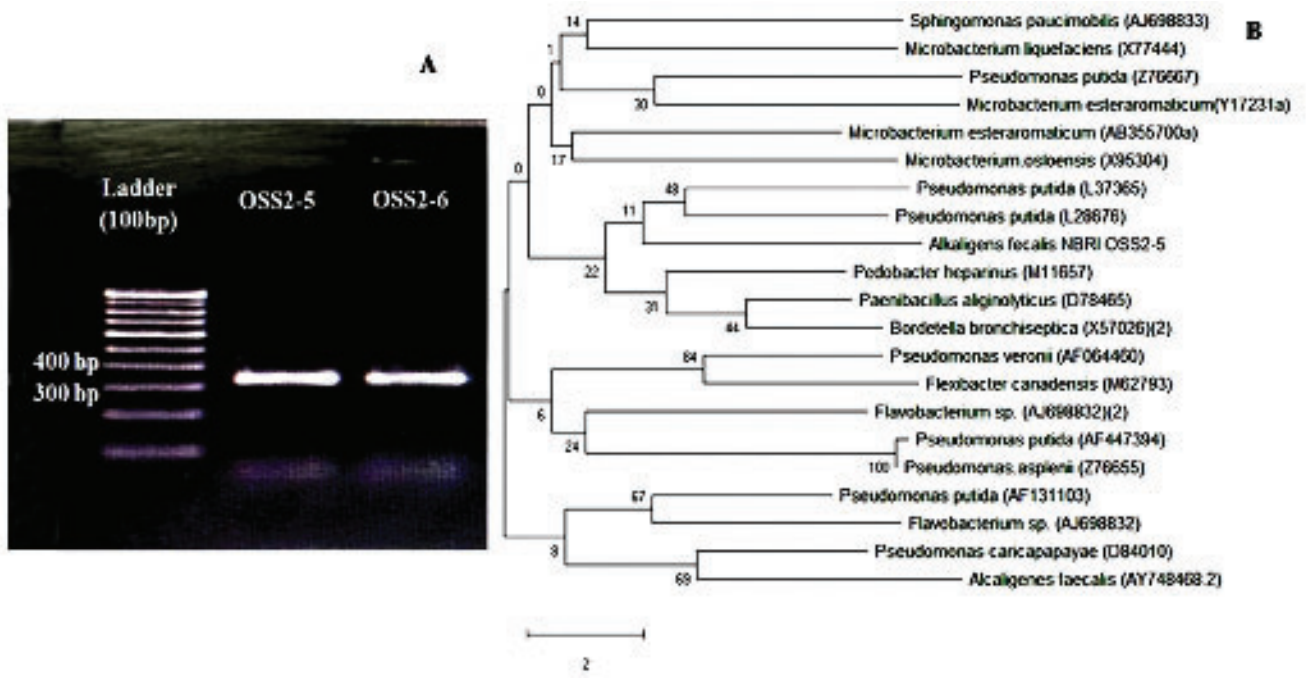


Fig. 1: A. Agarose gel showing amplified product with opd primers amplified in two bacterial isolates, NBRI-OSS2-5 and NBRI-OSS2-6, B. The phylogenetic tree of *Alkaligen faecalis* strain NBRI-OSS2-5 showing its phylogenetic relation with other bacteria reported for Chloropyriphos degradation.

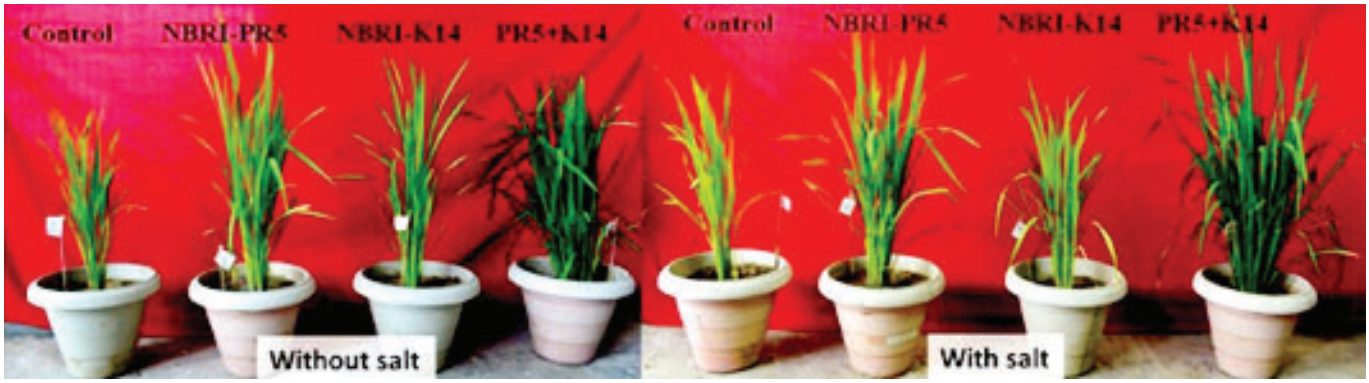


Fig. 2: Synergistic impact of *Trichoderma* consortium on plant growth promotion in salt stress (25 mM) condition.

to control pests. With a half-life of 7-120 days, it may persist for up to one year in soil depending on the soil conditions, affecting the soil microflora. Chlp degradation by soil microbes proves to be an effective and environment friendly method to remove it from the soil. A study was conducted with the aim to identify and characterize Chlp degrading soil microbes. Total 173 bacteria isolated from different soil samples were screened for Chlp degradation. Characterization of 10 selected samples showed that all the strains produced excessive exo-polysaccharides, which positively correlated with the Chlp degradation under *in vitro* conditions. Among these 10 bacterial strains, the most potent Chlp degrading bacteria was identified as *Alcaligenes faecalis* (NBRI OSS2-5) which paired with the Chlp degrading *Pseudomonas* in the phylogenetic tree prepared with different Chlp degrading microbes (Fig. 1). From the study it was concluded that sites contaminated with complex, polycyclic aromatic hydrocarbons such as oil spill sites are a rich source of isolating microbes for degradation of recalcitrant anthropogenic chemicals such as organophosphate pesticides. *Alcaligenes faecalis* strain NBRI-OSS2-5 was identified as a potent Chlp degrading microbe showing the involvement of exopolysaccharide in the bacterial tolerance and degradation of Chlorpyriphos. The strain can be used for plant growth promotion and bioremediation in pesticide contaminated sites.

## Efficacy of *Trichoderma koningiopsis* and *T. asperrelum* consortia to overcome salt stress in paddy

Studies were carried out to show the efficacy of a *Trichoderma* consortium comprising *T. koningiopsis* NBRI-PR5 and *T. asperellum* NBRI-K14 which has been developed for utilization of residual rice straw in sodic soil reclamation. The study was taken up to show the non-phytotoxicity of the two strains on rice plants and also their efficacy to perform under salt stress conditions. Rice was grown in presence of salt stress (25 mM NaCl) under net house conditions. Improved plant growth (Fig. 2) along with enhanced plant physiological and biochemical properties and soil microbial activity were observed in presence of the consortium. The microbial application improved the anatomical and morphological features of the rice roots to overcome the salt stress. Along with the increased yield, seed size and weight were also improved. Hundred seed weight of consortium treatment increased from 2.3g (control) to 3.1 g in presence of the stress. Total organic carbon (TOC%) and microbial biomass carbon were significantly increased in presence of the consortium.

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- Ms. Anshu, Research Scholar
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- Ms. Isha Varma, JRF

# Molecular Biology and Biotechnology

# MOLECULAR BIOLOGY AND BIOTECHNOLOGY

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## Technical Staff

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- Mr. Om Pal Sharma, Sr. Technician

## Research Scholars Statistics

| Sr. No. | Position Name | Numbers |
|---|---|---|
| 1. | Ramalingaswami Fellow | 01 |
| 2. | NPDF | 02 |
| 3. | Consultant | 04 |
| 4. | Research Associate | 08 |
| 5. | Young Scientist | 02 |
| 6. | JRF/SRF Fellow | 79 |
| 7. | Project Staff | 29 |

## Divisions

- Molecular Biology
- Biotechnology

## Aims and Objectives

Yield, quality and nutritional value of crops and produce are dependent on various biochemical processes and networks. These processes are under tight spatial and temporal regulation of gene expression. Studies suggest that modulation in expression of genes affects various processes leading to genotype-dependent changes in specific crops. Understanding changes at genetic level in existing germplasm/ cultivars through various approaches and utilization of information generated to develop improved varieties can lead to enhancement in the yield to meet demand of increasing population. There is need to develop new strategies for engineering crops for better yield, stress tolerance and enhanced nutritional quality preferably using genes of plant origin.

In Molecular Biology and Biotechnology Division, major objective is to understand various genetic determinants for yield and quality and develop superior plant varieties for enhanced yield and quality using plant genes for the benefits of farmers and consumers. To fulfill this objective, gene-mining, transgenic plant development and genome-editing technologies are being used on various crops.

## Major R&D Highlights

- We have obtained 1000 genotypes of cotton from Tierra Agrotech, Hyderabad under an MoU. This large genotype collection will boost cotton genomics activity in the group and help us in identification of key genes regulating important agronomical traits in cotton.
- In the area of cotton genomics, a total 15 HDACs homologs were identified in each of the A and D sub-genomes of *Gossypium hirsutum*. Among them, GhHDA5 expressed significantly at the time of fiber initiation. The *in-vitro* assay for histone deacetylase activity indicated that GhHDA5 primarily deacetylate H3K9 acetylation marks. The down-regulation of GhHDA5 in the RNAi lines resulted in H3K9 hyper-acetylation on the promoter region of few DEGs assessed by ChIP-assay. The results showed that HDA5 interact with Histone Methyl Transferases (HMTs), HSPs and other HDACs. The results indicate involvement of large suppressive complex which regulate cotton fiber initiation. We have now characterized involvement of GhHSP70 and GhHSP90 in cotton fiber development. The functional genomics of these selected genes are under progress. Besides we have also cloned GhHMT probably involved in the complex formation and its characterization is under progress.
- To develop aphid resistant cotton transgenic lines, 18 transgenic lines expressing Dhi31

constitutively downstream of the CaMV35Es double enhance promoter were developed. Fourteen transgenic plants expressed Dhi31 from low to high levels. Insect bioassay was carried out with leaf-discs and TSP of moderate to high expressing transgenic plants and 30-80% mortality was recorded. However, these plants could not advance to next generation due to abnormalities in the reproductive structure. Therefore, it became necessary to express Dhi31 in tissue specific manner. The gene was cloned at the downstream of *Arabidopsis thaliana* sucrose synthase 1 (AtSuS1) promoter for tissue (phloem) specific expression. Transformed cotton explants showed callus induction to ~50-60% on hormone selection media. These calli will subsequently form somatic embryos which will develop into transgenic plants in next 6-7 months.

- In the area of pathway elucidation and engineering of secondary plant products, *Papaver somniferum* and *Withania somniferum* have been studied and characterized in detail. Recently a Short-chain dehydrogenase/reductase, PsDeHase, which might participate in the dehydrogenation in the papaverine biosynthesis has been functionally characterized and has shown to be involved in the synthesis of papaverine. The miRNA and miPEPs involved in the flavonoid biosynthesis pathway have been functionally characterized in *Arabidopsis thaliana* using the CRISPR/Cas approach. Further to elucidate the role of various genes that are involved in Arsenic stress, two Arabidopsis thaliana accessions Koz2-2 (tolerant) and Ri-0 (sensitive) to sulphur limitation and As(III) stress have been identified and characterized in detail.
- Total 46 PME genes were identified in *Withania somnifera* with the help of available transcriptomic data. WsPME-26 was found to be the most potential putative active PME gene during biotic stress. Transgenic *Nicotiana tabacum* using this gene were developed using constitutive and inducible promoter systems. Constitutive expression system shows 75-85% mortality against both the chewing (*Spodoptera litura* & *Helicoverpa armigera*) and sap sucking (Aphid and Whitefly) insect pest at 4th day of experiment whereas inducible system show mortality at 6th day of the experiment.
- The tomato *SlWRKY23* gene identified as root up-regulated gene was found to govern root growth under stress conditions. It is strongly induced in roots by 300 mM mannitol and its expression ameliorates the inhibition of lateral root growth in transgenic Arabidopsis by mannitol and both primary and lateral root growth by NaCl. The gene is specifically induced in lateral root primordia in tomato hairy root and is strongly enhanced by mannitol suggesting its role in regulation of lateral root growth. In order to improve root growth and architecture, two genes *SlWRKY75* and *SlWRKY23* that alter root growth were chosen. About 10-15 CRISPR lines for each have been developed and validated.
- In order to facilitate expression of multiple insecticidal protein genes under different wound-inducible promoters in important crops like cotton and chickpea, several strong early-acting wound-inducible genes were indentified from chickpea. Their expression was validated in response to simulated herbivory by *H. armigera* and in response to other defense cues like JA, ethylene, SA, $H_2O_2$. Promoters ranging in length from 1.7-2 kb have been isolated and are being studied.
- The *SlERF6* gene from tomato, associated with altering the onset of fruit ripening by ABA responses, was found to regulate the expression of *SlCYP707A3* and *SlUGT75C1* –both involved in reducing ABA levels and thereby ABA responses. In mango two ripening related MAPK genes have been identified and shown to be involved in regulation of aroma. Further studies are underway to understand how these MAP kinases regulate aroma production in mango or in other fruits.
- The significance of Me-JA induced molecular signaling and tolerance towards arsenic toxicity in rice was studied. The arsenite (AsIII; 25µM) stress hampered the overall growth and development of the rice seedling. However, the co-application (25µM AsIII+0.25µM Me-JA) resulted in increased biomass, chlorophyll content, enhanced antioxidant enzyme activities as compared to AsIII treated plants. The co-application also demonstrated marked decrease in malondialdehyde content, electrolyte leakage and accumulation of total AsIII content (root + shoot) as compared to AsIII treated plants. The

co-application was also found to modulate the expression of genes involved in downstream JA signaling pathway (*OsCOI,OsJAZ3,OsMYC2*), AsIII uptake (*OsLsi1*, *OsLsi2*, *OsNIP1;1*, *OsNIP3;1*), translocation (*OsLsi6*, and *OsINT5*) and detoxification (*OsNRAMP1*, *OsPCS2* and *OsABCC2*) revealed the probable adaptive response of the rice plant to cope up arsenic stress. Our findings reveal that Me-JA alleviates AsIII toxicity by modulating signaling components involved in As uptake, translocation and detoxification and JA signaling in rice.

- In the area of functional characterization of genes involved in abiotic stress metabolism, various approaches were used. A number of genes were functionally characterized using different approaches. Analysis strongly suggest that the hormonal crosstalk of wound inducible and stress-responsive OsMYB-R1 transcription factor in combating abiotic [Cr(VI) and drought/PEG] as well as biotic (*Rhizoctoniasolani*) stress. OsMYB-R1 over-expressing rice transgenics exhibit a significant increase in lateral roots, which may be associated with increased tolerance under Cr(VI) and drought exposure. In contrast, its loss-of-function reduces stress tolerance. Higher auxin accumulation in the OsMYB-R1 over-expressed lines further strengthens the protective role of lateral roots under stress conditions. RNA-seq. data reveals over-representation of salicylic acid signaling molecule calcium-dependent protein kinases, which probably activate the stress-responsive downstream genes (Peroxidases, Glutathione S-transferases, Osmotins, Heat Shock Proteins, Pathogenesis Related-Proteins). The results suggest that OsMYB-R1 is part of a complex network of transcription factors controlling the cross-talk of auxin and salicylic acid signaling and other genes in response to multiple stresses by modifying molecular signaling, internal cellular homeostasis and root morphology.
- Two rice glutaredoxin (*OsGrx*) genes (*LOC_Os02g40500* and *LOC_Os01g27140*) were over-expressed in *Arabidopsis thaliana* to reveal their role in drought stress. The relative expression of both *OsGrx* genes was higher in the transgenic lines, which showed longer roots, higher seed germination, and survival efficiency during drought stress. The physiological parameters ($P_N$, $g_s$, *E*, WUE, *q*P, NPQ and ETR), antioxidant enzymes (GRX, GR, GPX, GST, APX, POD, SOD, CAT, DHAR, and MDHAR), antioxidant molecules (ascorbate and GSH) and stress-responsive amino acids (cysteine and proline) levels were additionally increased in transgenic lines of both *OsGrxs* to provide drought tolerance. A chickpea glutaredoxin (*CaGrx*) gene (*LOC101493651*) was over-expressed in *Arabidopsis thaliana* to reveal its role in heavy metal stress (AsIII-25µM, AsV-250µM, Cr(VI)-300µM, and Cd-500µM). The relative expression of *CaGrx* gene was higher in the transgenic lines. Transgenic plants showed longer roots, higher seed germination, and survival efficiency during metal stress. The levels of stress markers, TBARS, $H_2O_2$, and electrolyte leakage were found to be less in transgenic lines as compared to WT, revealed less toxicity in transgenic lines. In all the heavy metal treatments, accumulation of AsIII, AsV, and Cr(VI) was significantly reduced in all the transgenic lines except Cd, which was slightly reduced. The physiological parameters ($P_N$, $g_s$, *E*, WUE, *q*P, and ETR), antioxidant enzymes (GRX, GR, GPX, GST, APX, SOD, CAT, DHAR, and MDHAR), antioxidant molecules (ascorbate, GSH) and stress-responsive amino acids (proline and cysteine) levels were significantly increased in the transgenic lines. The outcome from this study strongly indicates that the *CaGrx* gene participates in the moderation of metal stress in *Arabidopsis*.
- In the area of genome-editing to improve yield and stress tolerance, group initiated studies on different crops. To delay the post-harvest life, two genes [á-mannosidase (á-Man) and â-D-N-acetylhexosaminidase (â-Hex)] were selected for genome editing in tomato. Constructs were transformed in tomato and putative lines have been selected for further analysis. To functionally characterize miR858 for its function in plant development and synthesis of molecules of nutritional importance, mature and fold back region of this miRNA have been edited and developed mutants plants have been analyzed in detail. In cotton, three genes, MYB1, SELF PRUNING (SP) and SINGLE FLOWER TRUSS (SFT), have been selected for genome editing with objective to develop determinate/semi-determinate sympodial cotton varieties. To meet

this objective, *in-silico* analysis of the promoter and gene sequences of both the GhSP and GhSFT genes has been carried out and gRNA from the potential regions has been designed. To develop rice varieties with low arsenic accumulation in grain, sgRNAs for genes involved in arsenic transport and accumulation (Lsi1, Lsi2, Inositol phosphate transporter, NIP3 and NRAMP) have been utilized to develop constructs, rice plants have been transformed and edited lines have been raised. Further analysis is under progress. We were also interested to develop short duration mustard variety development using genome editing tools. It was based on our earlier lead from natural mutant we identified in Indian *A. thaliana*. We developed gRNA guided construction to target the locus responsible for early maturity and cloned in a plant transformation vector and transformed into Mustard. Three putative transgenic lines were generated during this period.

- In the area of computational biology the whole genome sequence of *Gossypium herbaceum* cultivar wagad was assembled and annotated and compared with the genome of *G. arboretum* and the sub-genome of *G. hirsutum*. The miRNAs responsible for flower-anthesis and stress in *Cestrum nocturnum* L. (CS1) and *Cestrum diurnum* L. (CS2) were identified by *in-silico* means. Homology-search based computational analysis was employed for the identification of responsible miRNAs and their targets. The evolution and divergence of MADS box gene family in *Musa acuminata* and *Musa balbisiana* was also carried out. In this context the evolution of the Two component system module as also studied in the two species with special reference to the evolution of HPT gene family in plants.

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**Pathway elucidation and engineering of the secondary, plant products, miRNAs and associated factors, environmental biotechnology**

## Pathway elucidation and engineering of the secondary plant products

Plants have developed very efficient approaches to magnetize pollinators or seed-dispersing animals and their defence against herbivores, micro-organisms and other plants. In natural growth conditions, one of the major strategies adopted by plants for these purposes, is based on the production of secondary metabolites. Some of these secondary plant products are known to be beneficial for human health. Accumulation of these products in plants also fluctuates depending upon cellular, climatic and developmental conditions that limit their proper industrial utilization and drug development. There is an urgent need to scale up biosynthesis of these secondary plant products in homologous system or develop strategies for the synthesis of these molecules in heterologous systems through pathway engineering.

Our group has been working on plants synthesizing various bio-medically important phytoceuticals. These plants include *Papaver somniferum*, *Withania somniferum* and those synthesizing flavonoids. In *P. somniferum*, a large number of germplasm lines through breeding have been generated and mutants with modulated synthesis of specific alkaloids have been identified. In similar context, different chemotypes of *Withania* synthesizing specific withanolides have also been identified in New Millennium Indian Technology Leadership Initiative (NMITLI) supported project at CSIR level. To generate knowledge about pathways and regulatory factors leading to biosynthesis of specific alkaloid as well as to decipher changes at molecular level in different chemotypes of *Withania*, our group has established transcriptomes of different chemotypes. Detailed analysis of established transcriptomes has been helpful in deciphering biosynthetic pathways of these important molecules. We have used several approaches to decipher possible involvement of identified genes in biosynthesis of important molecules. Recently, we have identified and functionally characterized one Short-chain dehydrogenase/reductase, PsDeHase, which might participate in the dehydrogenation in the papaverine biosynthesis. The expression analysis and metabolite profiling suggested a correlation between transcript and papaverine content. *In silico* investigation predicted tetrahydropapaverine as the possible substrate that formed a stable complex with PsDeHase. Repression of PsDeHase transcripts in opium poppy plants exposed to VIGS treatment led to a comparable decrease in the accumulation of papaverine (Fig. 1). In addition to pathway elucidation, group is also involved in engineering of tobacco and tomato plants with enhanced flavonoid biosynthesis using transcription factors and other structural genes. To carry out this, our group has overexpressed and mutated genes using CRISPR/Cas9 approach.

## miRNAs and Associated Factors

MicroRNAs (miRNAs), small non-coding RNAs, are processed product of primary miRNAs (pri-miRNAs) and regulate target gene expression. Recently, through overexpression and target mimic lines, we functionally characterized Arabidopsis miR858a and established the potential role of miR858a in flavonoid biosynthesis and plant growth and development. To establish role of miRNAs and associated factors, we used CRISPR-based approach and edited pre-miR858, mature miR858 as well as

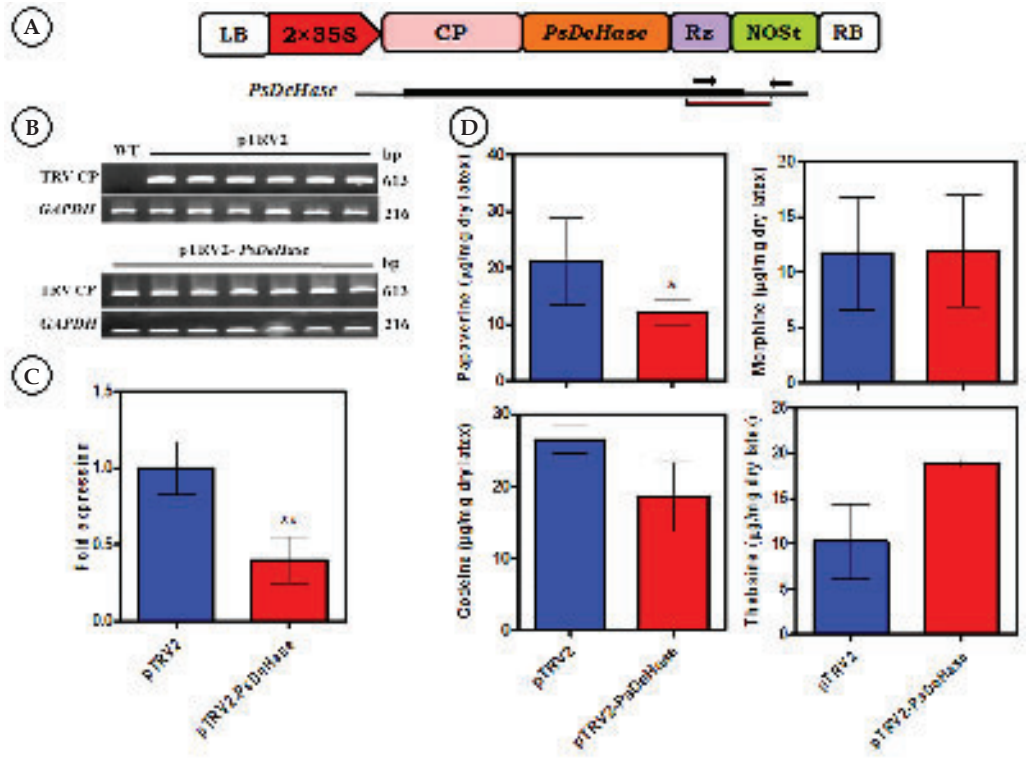


Fig. 1: Virus-induced gene silencing (VIGS) confirms the involvement of *PsDeHase* in papaverine biosynthesis. (A) Assembly of the VIGS construct used to silence *PsDeHase*. Thicker lines represent coding regions of cDNA, whereas flanking lines indicate non-coding 5′ and 3′untranslated regions. Red fragments show the unique regions on each cDNA used to construct gene-specific VIGS vectors. Solid arrows show the annealing locations of primers used to amplify cDNA fragments. (B) Ethidium bromide-stained agarose gel showing the detection of TRV2 coat protein transcripts amplified by reverse transcription-PCR using total RNA extracted from infiltrated control (pTRV2) and *PsDeHase*-silenced (pTRV2-*PsDeHase*) plants. *GAPDH* was used as the positive control. (C) qRT-PCR analysis at the peduncle stage of *PsDeHase*-silenced plants compared to control plants using actin as the reference transcript. *PsDeHase* transcript level in control (pTRV2) and *PsDeHase* silenced (pTRV2-*PsDeHase*) plants (***indicates P < 0.001). Values represent means ± SD of three technical replicates performed on each of six infiltrated plants. Asterisks represent significant differences determined using an unpaired, two-tailed Student *t* test. (D) Abundance of major alkaloids (morphine, codeine, thebaine) and papaverine in *PsDeHase*-silenced and control plants at the peduncle stage (**indicates P < 0.01, * indicates P < 0.05).

miRNA-encoded peptide (miPEP858a). miPEP-edited plants showed altered metabolite content **(Fig. 2)** and phenotypes similar to that of pre-miRNA- and mature miR858-edited plants. miPEP858a-edited and miPEP858a overexpressing lines showed altered plant development and accumulated modulated levels of flavonoids due to change in the expression of regulatory and structural genes associated with phenylpropanoid pathway and auxin signaling. To understand, miR858s-dependent plant development, extensive transcriptome analysis was carried out. Analysis suggests that interaction of miPEP858a/miR858-AtPSK plays important role in plant growth and development. In addition to miR858a, our group is characterizing other miRNAs (miR408, miR775, miR397, miR15, miR172) through overexpression and developing their knock-out mutants using CRISPR based approach.

## Environmental Biotechnology

The presence of heavy metals in groundwater poses a threat as it not only affects crop productivity but also contaminates food chain. Therefore, it is essential to understand molecular mechanisms underlying uptake, transport and accumulation of arsenic in plants. Our group identified and characterized a number of genes involved in heavy metal uptake, accumulation. In recent years, natural variation in *Arabidopsis thaliana* has been utilized to understand molecular and genetic adaptation under different stresses. We used *Arabidopsis* accessions and analyzed at biochemical and molecular levels towards arsenic stress. On the basis of reduction in root length, accessions were categorized into tolerant and sensitive ones towards arsenic stress. We identified two contrasting accessions Koz2-2 (tolerant) and Ri-0

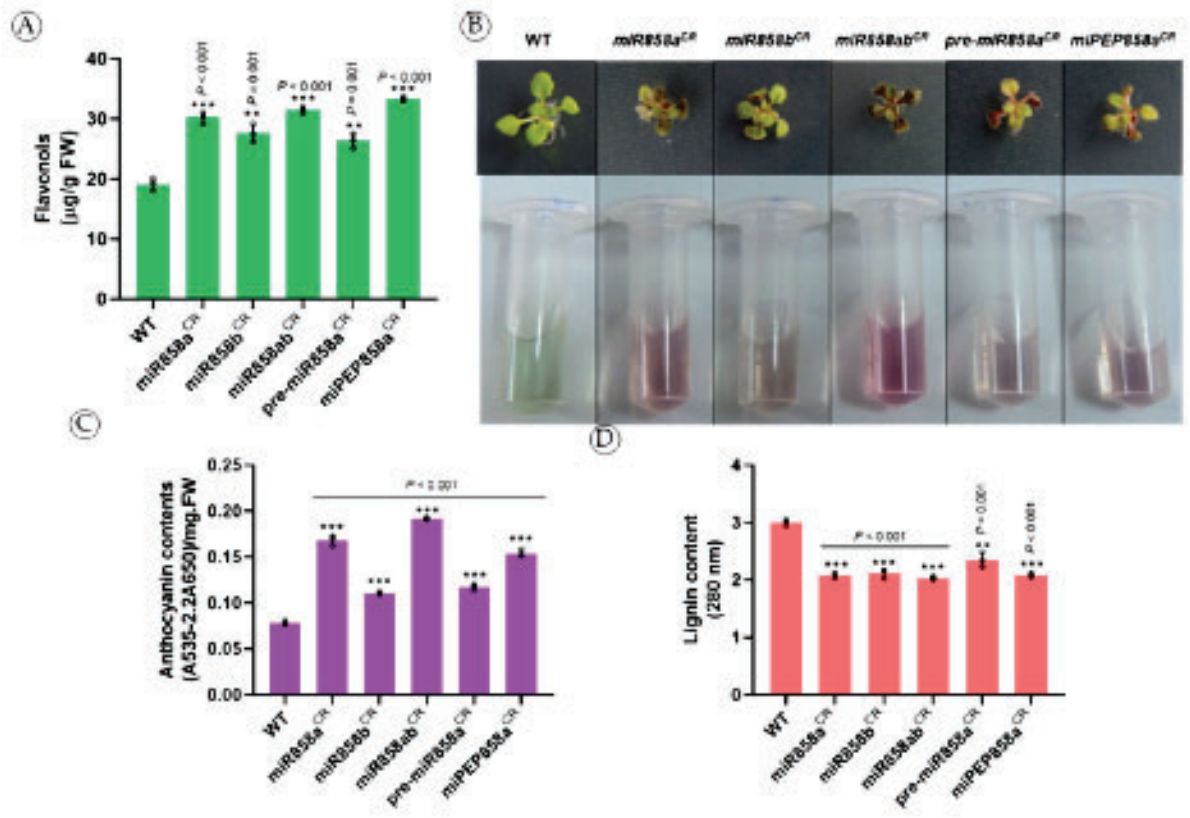


Fig. 2: Editing of miR858 leads to differential accumulation of metabolite levels. (A) Quantification of total flavonol in 10-day old seedings of WT, *miR858a*$^{CR}$, *miR858b*$^{CR}$, *miR858ab*$^{CR}$, *pre-miR858a*$^{CR}$, *miPEP858a*$^{CR}$ plants. (B) Representative image of anthocyanin accumulation in 10-day old seedlings of WT, *miR858a*$^{CR}$, *miR858b*$^{CR}$, *miR858ab*$^{CR}$, *pre-miR858a*$^{CR}$, *miPEP858a*$^{CR}$ lines. (C) Quantification of anthocyanin in 10-day old seedlings of WT, *miR858a*$^{CR}$, *miR858b*$^{CR}$, *miR858ab*$^{CR}$, *pre-miR858a*$^{CR}$, *miPEP858a*$^{CR}$ lines (D) Quantification of lignin in 35-day old stem of WT, *miR858a*$^{CR}$, *miR858b*$^{CR}$, *miR858ab*$^{CR}$, *pre-miR858a*$^{CR}$ lines (for a, c and d, small open circles represent individual values). The experiments were repeated three times independently with similar results. Statistical analysis was performed using two-tailed Student's t-tests. Data are plotted as means ±SD. Error bars represent standard deviation Asterisks indicate a significant difference, *P < 0.1, **P < 0.01, ***P < 0.001).

(sensitive) towards sulphur limitation and As(III) stress. To have in depth knowledge of the pathways modulated in such stresses, RNA-Seq of the two accessions under these treatments was carried out. Various genes were differentially expressed in the contrasting accessions which included most of the genes related to growth and development, stress or sulphate metabolism. Further, transcriptome analysis also revealed differences in nucleotide arrangement of several genes in these two accessions. Thus, transcriptome analysis carried out using these natural accessions would further enrich strategies to cope with nutrient limitation and heavy metal stress.

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**Transcription and epigenetic regulation**

The progress of genomics and epi-genomics has allowed rapid improvements in our understanding of plant biology to accelerate crop trait improvement in challenging environmental conditions. Both fields have been demonstrated remarkable visions into the mechanisms associated with growth, development, and stress responses and could be applied for the achievement of the modification of plant traits by genetic or physiological changes.

## Cotton genome editing to develop determinate/ semi-determinate sympodial varieties for synchronized fiber yield and quality

In cotton, SELF-PRUNING (*GhSP*) and SINGLE FLOWER TRUSS (*GhSFT*) gene induce vegetative growth (indeterminate) and transition to flowering (determinate state), respectively. Modulation in the expression pattern and protein's structure of these genes may lead to the development of a cotton variety with determinate/semi-determinate growth habit and synchronous flowering. To achieve this goal, the gene and promoter sequences of above two genes from Coker 312 (*Gossypium hirsutum*) are cloned and sequenced. Based on *in silico* study of the promoter and gene, specific gRNAs against several targets have been designed, and *in vitro* validation is under progress.

## Investigation of the biological roles of MYB1 transcription factor and its regulatory microRNAs in secondary cell wall biosynthesis in cotton (*Gossypium* sp.) fibers

The secondary cell wall (SCW) biosynthesis stage in cotton fiber development plays a key role in determining fiber quality and quantity. To investigate the roles played by the *GhMYB1* transcription factor and its regulatory microRNAs (miRNAs) in cotton fiber SCW biosynthesis, various approaches such as chromatin immunoprecipitation (ChIP)-sequencing, virus-induced gene silencing (VIGS), genome editing, etc., are being used. To identify the interacting partners of *GhMYB1* in cotton genome, ChIP experiment was performed by using the GhMYB1-specific antibody. ChIP-qPCR was performed to check the fold-enrichment of promoter regions of selected cotton fiber development-associated genes. Next, the ChIP-sequencing will be performed to get the clear view of GhMYB1 binding and interaction across the *G. hirsutum* genome. The effect of VIGS and artificial miRNA-mediated silencing of *GhMYB1* on cotton fiber is under investigation. In CRISPR/ Cas-based editing experiment, the sgRNAs were synthesized to edit the *GhMYB1* in cotton genome. Two sgRNAs efficiently cleaved the target genomic DNA under *in vitro* conditions. To observe the *in vivo* efficiency of the *in vitro* tested and confirmed *GhMYB1* sgRNA vector constructs, the cotton plants were transiently transformed by using the vacuum–infiltration method. The genomic DNA was isolated from the transformed plants and finally two constructs were shown to target the *GhMYB1* under the *in vivo* conditions. Further, work is under progress to investigate the role of *GhMYB1* in cotton fiber SCW biosynthesis.

## Transcriptional biomarker in Cotton: Initiation, elongation and commitment specific

Molecular markers are loci/regions/genes in the genomic regions that have a close link with the biological process and are associated with the

expression of particular traits. For cotton breeders, many molecular markers were available to identify the genomic regions that underpinning the economic trait. The availability of genome-wide transcriptional data of many tissues (Fig. 1A) in different cultivar (Fig. 1B) and refined genome sequences of cotton [*Gossypium hirsutum* ($AD_1$)] facilitated the development of transcriptional biomarkers for a particular trait or different fiber developmental stages. More than 350 RNAseq datasets of different cultivars were used for data mining the initiation, elongation and secondary cell wall specific transcriptional biomarkers. Using the machine-learning approach, the informative features of high coverage (~400X) transcriptome data were retrieved and top-scoring (RReliefF score) important genes were plotted with their z-score value. The Positive z-score value of Alpha/beta hydrolases superfamily protein, IQ domain 26, Aquaporin transporter, Gibberellin regulated protein and peroxidase gene family (Fig. 1C) at initiation stages indicates them as a transcriptional biomarker for fiber initiation. Similarly, several genes show higher Z-score value at the elongation/SCW stage such as HAD like superfamily, Phospholipases A2A protein, Prolin transporter 1, SWEET sugar transporter and some uncharacterized genes (Ghir_A05G0105660, Ghir_A06G004130, Ghir_D09G009930, Ghir_D07G020490) show positive Z score value at elongation stages and thus these are considered as transcription biomarkers for this elongation and SCW stage.

## Cotton TFIID Complex: identification and putative roles in fiber development

The rate limiting step of transcription is binding of the TFIID complex to the core promoter elements and thereby recruit RNA Polymerase II for progressing the transcription cycle. In plants, the role of TFIID complex is not clear, therefore, we examined the role of TFIID complex in cotton fiber development. In order to address the importance of the component of TFIID complex in the cotton, four *Gossypium* species were studied: two tetraploid species, *G. hirsutum* and *G. barbadense*, and their two potential ancestral

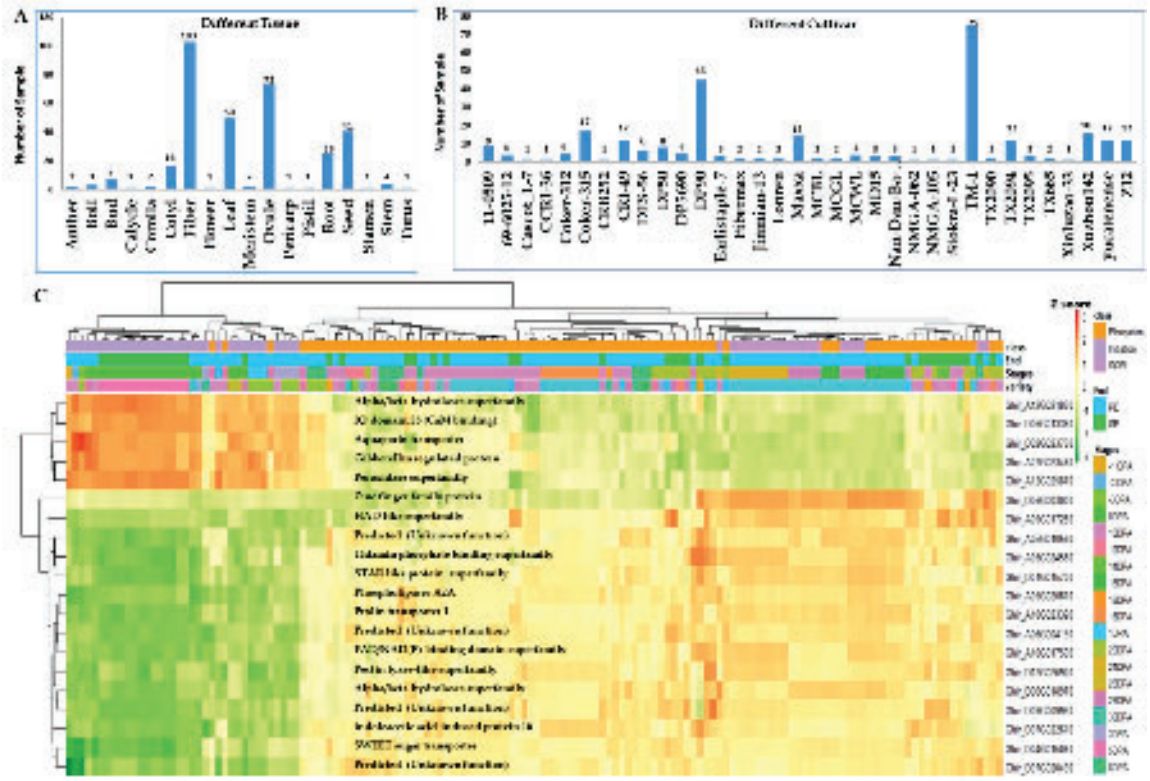


Fig. 1: (A) Number of samples of different tissues, (B) In different cultivars, downloaded from online repositories and lab generated RNA-Seq data of *Gossypium hirsutum*, (C) Transcriptional biomarker for initiation, elongation and secondary cell wall stage specific. The higher Z-score value represents the higher expression of gene and lower value represents the relatively lesser expression in that particular stages.

diploids, *G. raimondii* and *G. arboreum.* In the present study, TFIID complex genes in cotton were identified (Fig. 2) and functional characterization of each component of the cotton TFIID complex is under progress.

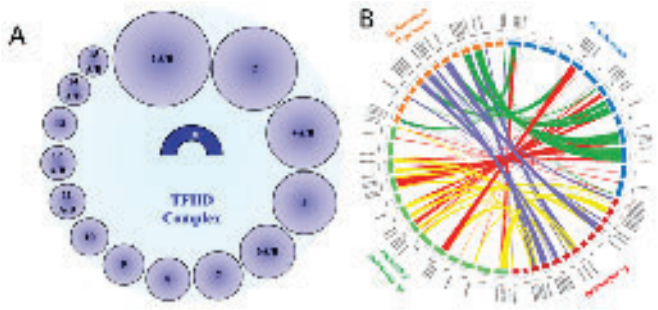


Fig. 2: (A) Representation of the TFIID complex subunits according to the size of each component and (B) Collinearity analysis of TFIID genes in *Gossypium hirsutum*, *G. arboreum*, and *G. raimondii*

## Role of GhHDA5 in cotton fibre development in *Gossypium hirsutum*

*GhHDA5* is a histone deacetylase that removes acetyl group from histone and its expression is higher during initiation of cotton fibre development (-1 and 0 DPA). The RNAi cotton transgenic lines were generated to assess the role of GhHDA5. These RNAi transgenic lines showed decreased lint fibre production and increased fuzz fibre. The decreased lint fibre production was due to higher accumulation of reactive oxygen species (ROS). So, overall results showed that the *GhHDA5* is important for the fiber initiation. We also tried to further validate these results by developing overexpressing lines of GhHDA5 (Fig. 3). These lines will be used to identify

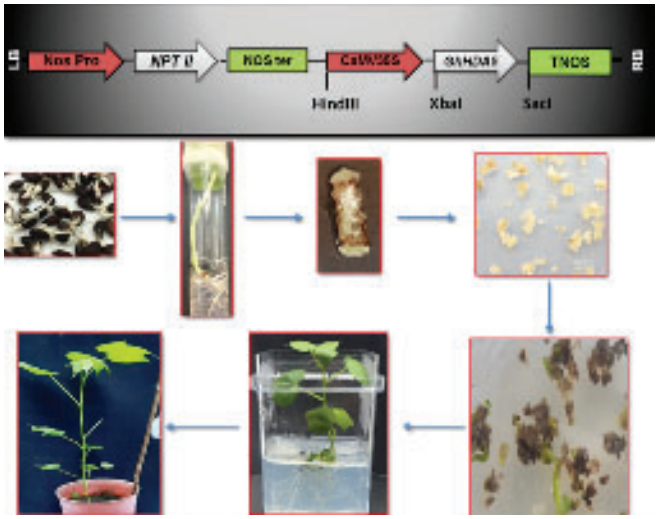


Fig. 3. Development of *Gossypium hirsutum* HDA5 construct and transgenic plant.

mechanism(s) that how GhHDA5 regulates cotton fibre development. We are also trying to identify the mechanistic details of GhHDA5 by yeast 2 hybrid assay and Chromatin immune precipitation assay.

## Exploring the role of alternative splice variants of *CAMTA1* in stress physiology of *Arabidopsis thaliana*

Several calcium dependent transcription factors are implicated in diverse stress signaling in plants. Calmodulin binding transcription activators (CAMTAs) are one of the widely studied calcium/ calmodulin dependent TFs in *Arabidopsis thaliana*. During the cloning of the CAMTA1 gene, we identified several novel splice variants of *CAMTA1* and two of them were implicated in diverse stress signaling pathways. Further, high depth targeted amplicon sequencing of CAMTA1 was performed under various developmental stages and treatments to understand the alternative splice events in more precision. The expression analysis indicated the relative distribution across all the stages. Both the CAMTA1_VS and VL variants possess 27 and 25 nucleotide intron retention (IR), respectively. Col-0-VS transgenic lines had enhanced root laterals as well as higher LR density, which were also depicted by microscopic observation. These higher root laterals might be crucial during stress tolerance Fig. 4A. In another study of CAMTA5 shown to be involved in root development as it knockdown mutant *camta 5.2* (SALK_120516C) had significant reduced root development. However, its over expression lines had higher root length as depicted in Fig. 4B.

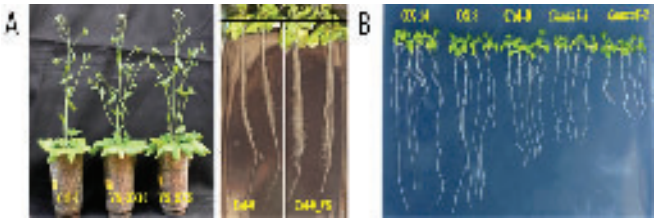


Fig. 4: (A) AtCAMTA1 _VS transgenic lines had enhanced shoot and root biomass and (B) Phenotypic differences of AtCAMTA5 over expression and knockdown mutant lines.

## Exploring the role of Calmodulin-binding transcription activators (CAMTA) in Cotton Fiber Development

CAMTA (calmodulin (CaM)-binding transcription activators) genes conserved from plants to animals that play important role in development and stress

biology. Nine CAMTAs are identified in *Gossypium hirsutum* through genome analysis. Out of these, two CAMTAs (CAMTA 2A.2 and CAMTA 7A) are highly expressed during fiber development. The expression pattern of these CAMTAs in fiber developmental stages indicated their strong correlation with fiber strength and elongation. This result indicated involvement of CAMTAs in regulation of fiber development in cotton. The functional characterization through overexpression and suppression of these two genes and target identification are under progress.

## Development of F1-Hybrid Cotton using Novel Male Sterility-Fertility Restoration System

Most of the hybrids under cultivation have been developed by conventional method (hand emasculation and pollination) and their seed is very costly which cannot be afforded by small and marginal farmers. The use of male sterility reduces the cost of hybrid seed by eliminating the process of emasculation. We successfully demonstrated this novel method of male-sterility and fertility-restoration in tobacco (Fig. 5). To achieve complete male sterility and reverse the male sterility in F1 hybrid cotton, we expressed Arabidopsis *BECLIN1* and *COP1* genes in anther tapetum of cotton plants.

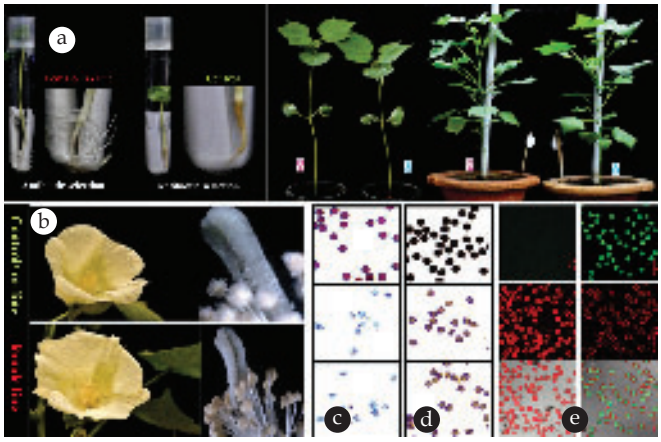


Fig. 5: Transgenic male sterility and fertility restoration in cotton. (a) cotton male and female transgenic plants (b) flower and anther morphology (c, d, e) pollen viability assay using Alexander, Iodine and FDA/ PI methods in control and transgenic female cotton plants.

## Demystifying a new transcriptional regulatory network involved in seed development of *Arabidopsis thaliana*

Seed development is a complex process, requires a coordinated development of embryo, endosperm and seed coat. Transcription is a key regulatory step in the control of tissue specific gene expression in various developmental processes through the recruitment of various factors. We observed that mutant of one of the factor, *tafx*, has smaller seed than wild type Col-0 due to the reduced endosperm cavity and smaller integument cell length. Y2H and BiFC results confirmed that TAFx interact with endosperm specific transcription factor, bZIP, that has a similar phenotype as *tafx*. Further, the double mutant of *tafxXbzip* has smaller endosperm cavity, decreased integument cell expansion as well as delay in embryo formation. Interestingly, we found that bZIP interact with AGL which is involved in endosperm celluarization and auxin signalling in seed coat. Our findings reveal that AGL interact with bZIP which recruit the preinitiation complex via interaction with TAFx and regulate the transcription of genes involved in various processes of seed development (Fig. 6.)

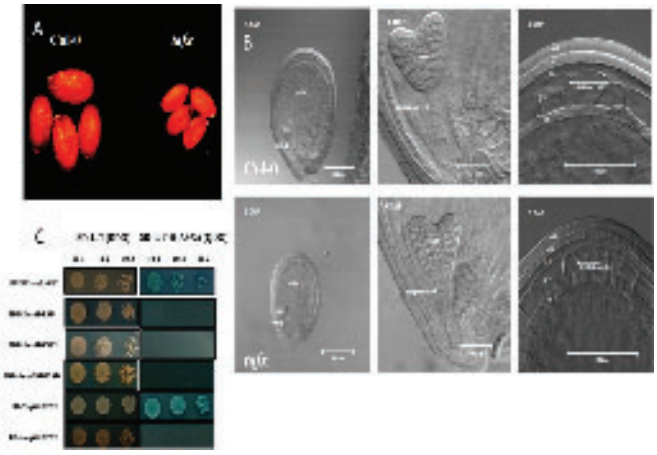

Fig. 6: (A) *tafx* mutant produce smaller seeds (B) Differential interference contrast microscopy of Col-0 and (C) Y2H assay of tafx and bZIP interaction.

## Exploring the molecular details of Sub-genome dominance during endoreduplication in F1 hybrids

Hybrids are imperative in enhancing the crop productivity through increase in biomass, seed yield and adaptive fitness. Heterosis is a phenomenon wherein the superiority of F1 hybrid over its parents with respect to different heterotic traits. Heterosis has been in the center of attraction to the geneticists and molecular biologist to elucidate the underlying mechanism. Heterosis has been studied and implemented successfully in various crop plants,

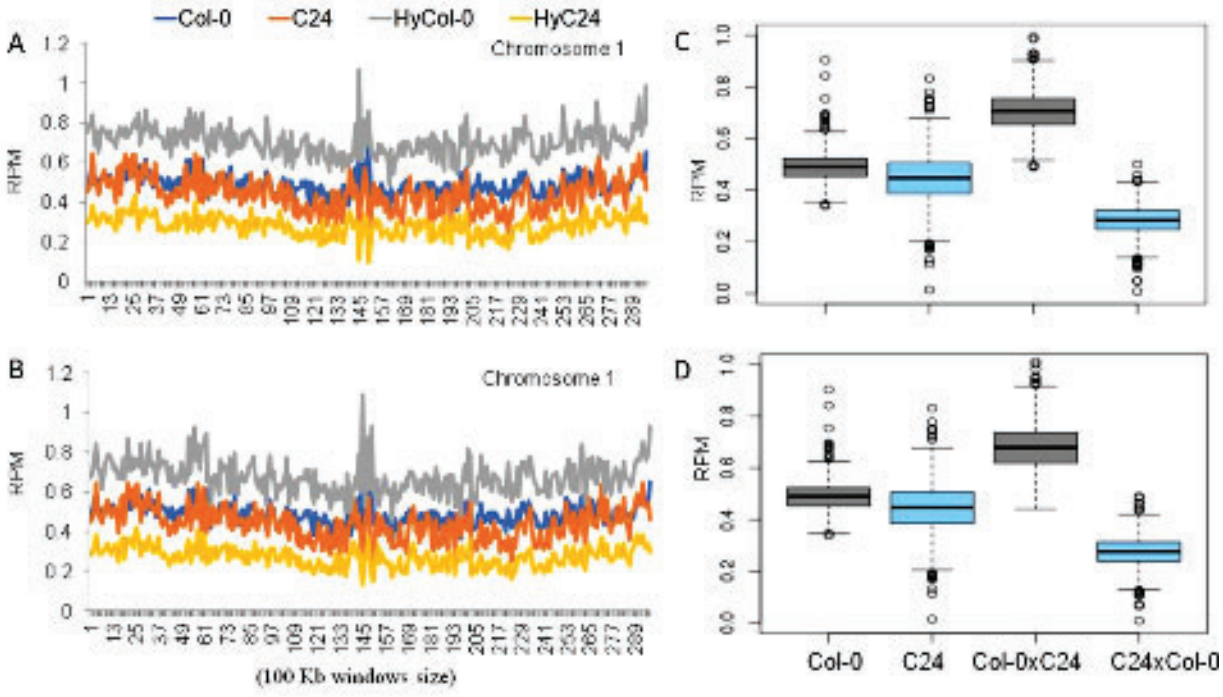


Fig. 7: Impact of sub-genome dominance at genome level. The distribution plant of SNP containing normalized whole genome reads at 100Kb bins in (A) Col-0 x C24 (B) C24x Col-0 and their parents. Box-plots showing enrichment and depletion of Col-0 sub genome and C24 sub genome, respectively for all chromosome in (C) Col-0 x C24 (D) C24x Col-0 with respect to their parents.

but the molecular mechanism behind heterosis is still elusive. In plants, whole-genome duplication is an essential feature of genome polyploidization and can produce functionally different sub-genomes. During evolution, sub-genome dominance has evolved as a specific phenomenon in which one of the parental sub-genome is dominated over the counterpart genome. To understand the impact of sub-genome dominance during endoreduplication on heterosis, we performed whole-genome sequencing in parents and their reciprocal F1 hybrids. Distribution plots suggest that Col-0 and C24 parents showed almost similar distribution with the minor differences across all chromosomes may be due to genotype-specific differences. Interestingly, in case of Col-0 X C24 F1, we could observe a significant increase in genomic reads of Col-0 sub-genome and significant decline in C24 sub-genome (Fig. 7), these changes were consistent throughout a chromosome and across all the chromosomes. The result clearly indicates that during an endocycle, the replication of Col-0 dominates replication of C24 sub-genome. The sub-genome dominance in endocycle to augment DNA content of one parent over the other is novel and interesting. Thus, it can be safely interpreted that Col-0 sub-genome has an ability to perpetuate its own sub-genome over its partners in an F1 cross.

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**Hormonal crosstalk in root architecture and development, petal abscission in rose, fruit growth and ripening, wound-inducible promoters**

## Role of SlERF6 in fruit growth and ripening

We had previously identified *SlERF6* as a ripening up-regulated gene that reduced ABA responses when constitutively expressed. Its suppression increased ABA responses across tissues and in different processes. The onset of fruit ripening (both on-vine and off-vine) was prominently affected and early upon *SlERF6* suppression while *SlERF6* over-expression delayed ripening and reduced fruit size. Fruit growth was faster in suppression lines and the onset of breaker stage was at 35 DPA compared to 39 DPA in control fruit. In contrast, over-expression lines showed a delay in onset of ripening with the breaker stage being attained at 43-44 DPA. The progression of ripening, however, did not undergo much of a change taking about ten days in control, *SlERF6* suppression

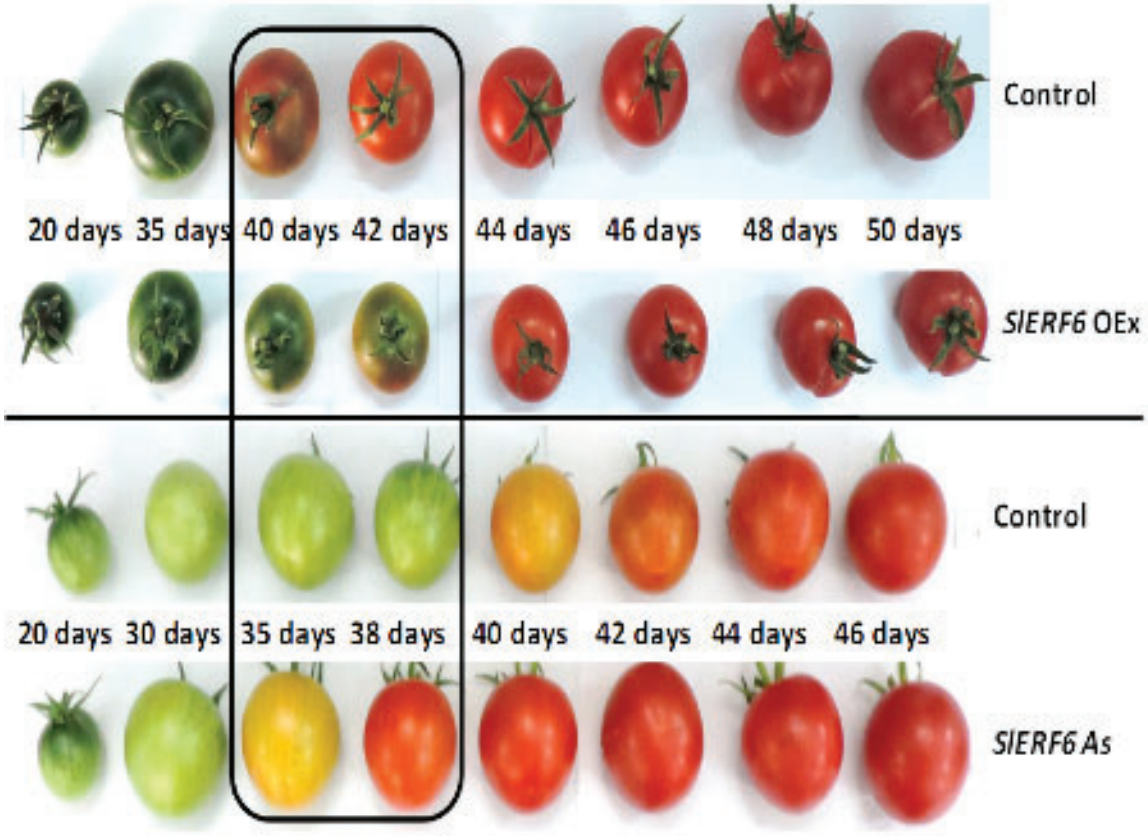


Fig. 1: Changes in the onset of ripening of tomato fruits over-expressing (top panel) and under-expressing (bottom) *SlERF6*. Days denote days post- anthesis.

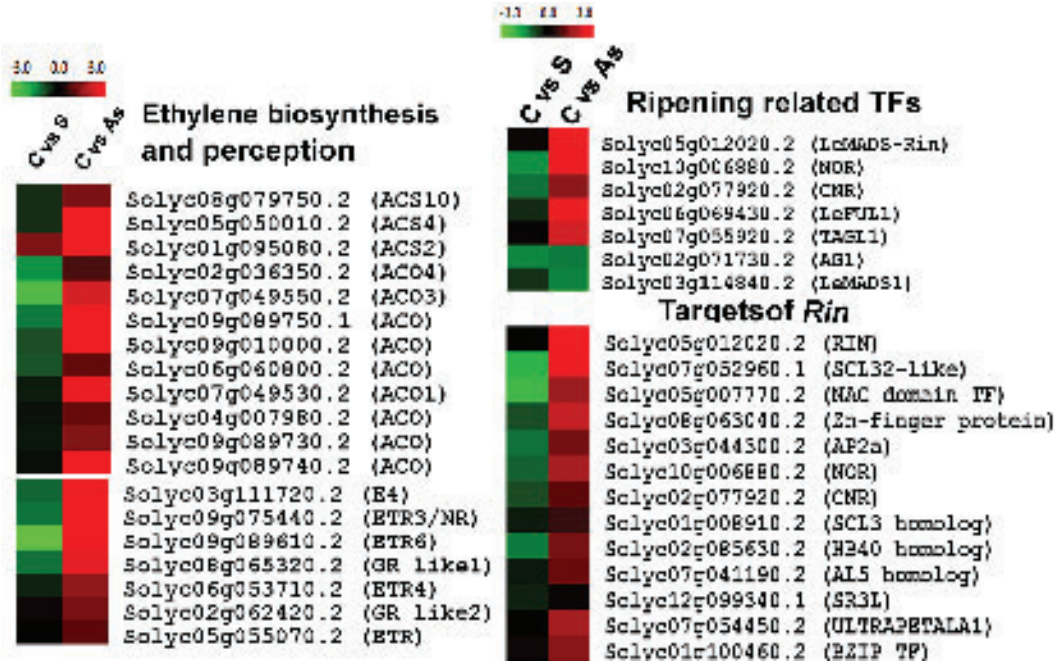


Fig. 2: Changes in expression of ethylene biosynthesis and perception genes (left panel and key transcription factors associated with ripening (right panel) in a comparison between control and SlERF6 over-expression (C vs S) and control and suppression lines (C vs AS)

and *SlERF6* over-expression lines (Fig1). Fruit size was also affected in over-expression lines with fruits showing a reduction of ~20% in size. To obtain further insight into these changes, a transcriptomic analysis of fruits was carried out (Fig 2). *SlERF6* manipulation affected large scale changes in the fruit transcriptome with suppression lines showing early activation of most ripening pathway genes that govern ethylene biosynthesis and signaling, lycopene and carotenoid accumulation, ABA and softening. Key transcription factors like *CNR, NOR, RIN, FUL1* etc., governing ethylene-dependent and ethylene-independent aspects of ripening, were activated early in *SlERF6* suppression lines suggesting a direct/indirect control of these by ABA (Fig 3). ABA altered only the timing of ripening and not its progression. The studies suggest that manipulation of the ABA pathway through *SlERF6* may be used for control of fruit ripening and fruit size. The finding of ABA responses controlling ripening by regulating the expression of key ripening TFs is a major finding with wide application in the horticulture and processing industry. It would allow industrial ripening in processing industries to proceed with ABA instead of ethylene which uncouples the softening process from other aspects of ripening often leading to off-colour, off-flavour fruits that are ripe but lack flavour.

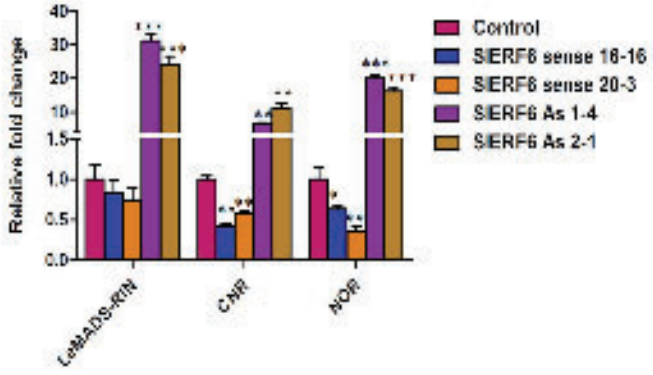


Fig. 3: Validation of expression of key transcription factors governing onset and progression of ripening

## Molecular basis of petal abscission in rose

Fragrant roses are ethylene sensitive and abscise early unlike non-fragrant hybrid roses. Transcriptomic analysis of petal abscission zones of the early-abscising fragrant rose *R. bourboniana* and the late abscising *R. hybrida* revealed a large scale up-regulation of the ethylene pathway but prominent suppression of the JA, auxin and surprisingly the light-regulated pathways. The down-regulation of the JA and light pathways appeared to be a unique feature in rose abscission since jasmonic acid is known to activate

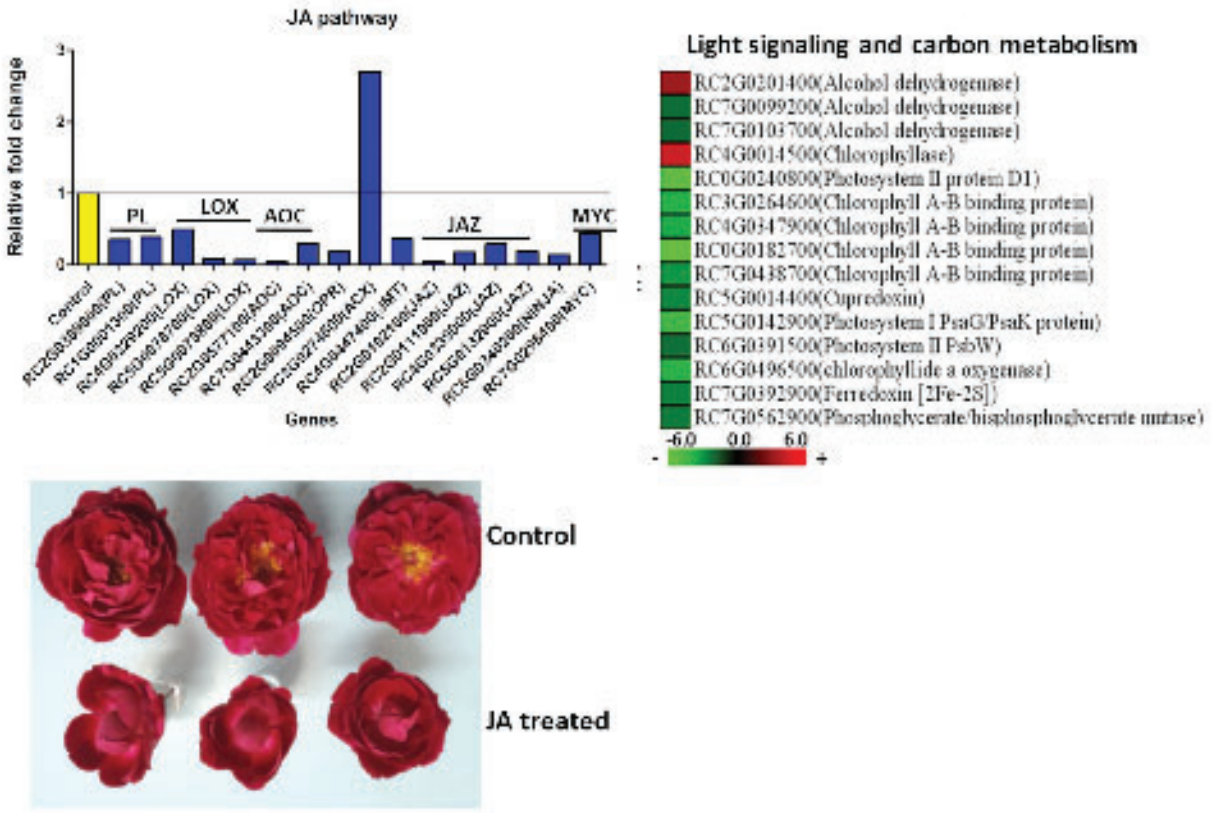


Fig. 4: Down-regulation of the JA pathway (top left) and light pathway (top right) components upon ethylene-induced abscission in *R. bourboniana*. Inhibition of flower opening and abscission by Jasmonic acid (lower panel).

abscission and senescence in Arabidopsis and other plants. The ethylene mediated down-regulation of the JA pathway occurred at the level of biosynthesis as well as signaling and included genes like PLA, LOX, ACX and JMT that govern biosynthesis and signaling-associated genes like COI, JAZ and MYC (Fig 4). The decrease in expression was rapidly induced by ethylene within 4 h of ethylene treatment for most genes interestingly, treatment with JA delays flower opening in fragrant roses and delays abscission, further pointing towards a negative role of JA in petal abscission.

Surprisingly, the core set of genes obtained from a comparison of Rb petal AZ, Rb petals and Rh petal AZ contained a large number of photosynthesis/ photosystem-related genes that were strongly down-regulated as a group. Regulatory genes encoding kinases/phosphatases/F-box proteins and transcription factors formed the major group undergoing differential regulation besides genes for transporters, wall modification, and defense and phenylpropanoid pathways. Further comparisons with ethylene-treated petals of *R. bourboniana* and 8 h ethylene-treated AZ (*R. hybrida*) identified a core set of 255 genes uniquely regulated by ethylene in *R. bourboniana* AZ. Almost 23% of these encoded regulatory proteins largely conserved with Arabidopsis AZ components. Most of these were up-regulated while an entire set of photosystem genes was prominently down-regulated.

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**To explore transcription factors involved in prickle development in *Solanum viarum* and their correlation to secondary metabolite production**

The group is mainly involved in *in vitro* propagation of economically important plants, genetic transformation and functional characterization of genes

## Exploring a novel role of *Sk*MSM1 and *Sk*R2R3-Myb315-like transcriptional regulators in the development of prickle in *Solanum khasianum*

Both the selected transcriptional regulators *Sv*MSM1 (MADS box like) and *Sv*R2R3-MYB315-like, are well known for the regulation of developmental pathways. R2R3 TFs are involved in the positive regulation of trichome cell fate determination and members of the MADS box transcription factors family also play a key role in plant development. In the present work, the function of two prickle specific potential TFs, *Sv*MSM1 (MADS box like) and *Sv*R2R3-MYB315-like, is being explored in prickle formation. We are trying to develop transgenic lines of prickly WT plants, using RNAi technology. Silencing of these TFs may interrupt the pathway of prickle differentiation and complete loss of prickle phenotype. We are successful in developing the RNAi constructs of both the TFs and one of the promoters of *Sv*R2R3-MYB315-like TF. The experiments for regeneration of transformants in homozygous system of *S. viarum* are continuously being done but till date no transgenic plant of *S. viarum* could be obtained.

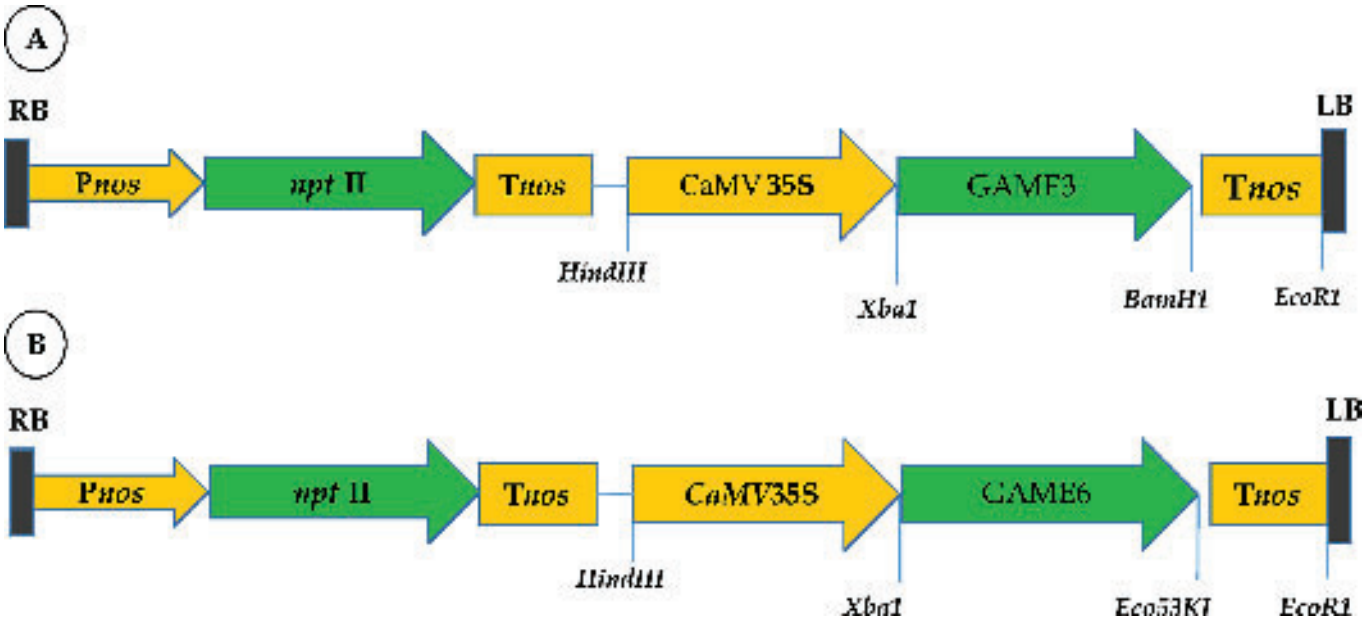


Fig. 1 (A-B): A. *SvGAME6* gene construct in pBI121 vector with *CaMV35S* promoter, B. *SvGAME3* gene construct in pBI121 vector with *CaMV35S* promoter

## Identification and functional characterization of gene/s involved in glycoalkaloids biosynthesis in *Solanum viarum* Dunal

Secondary metabolites are helpful for plants due to their protective nature towards environment; these metabolites play very important roles in pharmaceutical industries because of their medicinal properties. Metabolic engineering can cause improvement in the contents of these valuable compounds.

Glycoalkaloids are found in the Solanaceae family and used as defensive agent against insect and fungi. Glycoalkaloids showed some harmful effects to humans when used at high concentration although they exhibited anticancer and anti-inflammatory activity in humans. *Solanum viarum* is an important medicinal plant and contain important secondary metabolites such as solasodine, alpha- solanine and solanidine. In this study GAME genes (Glycoalkaloid Metabolism related genes) were isolated and cloned. These genes will be functionally characterized in *S. viarum* plant. *SvGAME3* and *SvGAME6* were selected and isolated from *S. viarum* plant. These genes were further cloned in over expression vector (Fig. 1A and 1B). *Agrobacterium tumefaciens* mediated transformation is under process.

## Metabolite profiling of *Solanum viarum*

To study the metabolite (alkaloids and phenolics) profiling of both the genotypes, *in vitro* derived tissues (leaf, stem and root) and field-grown plant parts (leaf, stem, root and berries) were used for extraction and chromatographic analysis. Methanolic extract of different plant parts of both the genotypes of *S. viarum* showed the presence of phenolic acids (gallic, caffeic, coumeric, sinapic, ferulic and benzoic acid) and flavonoids (rutin, catechol and qurecitin) in varying amounts. HPLC analysis results showed, overall phenolic contents were obtained significantly higher in prickleless (mutant) genotype as compared to prickly genotype. Among the secondary metabolites, phenols commonly act as defensive compounds not only against herbivores but also against microorganisms and competing plants. They have antioxidative properties and are capable of scavenging free radicals, resulting in reduction of cell membrane peroxidation.

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**Hormonal crosstalk in root architecture ripening and aroma in mango, seed oil regulation, abiotic stress responses in cotton**

## Effect of SlWRKY23 on plant architecture

The tomato *SlWRKY23* gene identified previously as root up-regulated gene was found to govern root growth under stress conditions. It is strongly induced in roots by 300 mM mannitol by up to 150 fold although treatment with NaCl only marginally increased transcript levels. Yet, transgenic Arabidopsis expressing *SlWRKY23,* which had previously displayed altered lateral root (LR) and aerial architecture, also showed differences in growth in response to mannitol and NaCl treatment. Seeds of transgenic lines germinated early on 150 mM mannitol and 100 mM NaCl compared to control with more than two fold increase in germination in both. This suggested that the inhibition of germination by mannitol and NaCl was suppressed by *SlWRKY23* (Fig 1). Further, expression of *SlWRKY23* suppressed the inhibition of lateral root growth by mannitol. Transgenic lines showed a 50% increase in lateral root number compared to control when grown in mannitol. Primary root was however, not affected. Treatment with 100 mM NaCl affected both primary and lateral root differently in control and transgenic lines (Fig 2). A time course study of root growth on 100 mM NaCl revealed a strong inhibition by NaCl in controls after seven days of continuous growth following germination. In contrast, transgenic lines continued to grow linearly after seven days with root length being twice as long as control by day 15. The number of lateral root was also less affected by NaCl with transgenic lines showing twice as many lateral roots on NaCl compared to controls (Fig 3). The results suggest that *SlWRKY23* expression was able to largely overcome the inhibitory effects of both mannitol and NaCl on root growth. The activation of the ethylene responses by *SlWRKY23* may be associated with amelioration of the stress effects. To obtain further insights into the role of *SlWRKY23* in tomato, hairy roots of tomato expressing the *SlWRKY23* promoter-GUS fusions were subjected to treatment with mannitol and NaCl. The gene was primarily induced in lateral root primordia in tomato hairy root. This expression was not only strongly enhanced by mannitol (as seen by the intense blue colour) but also led to an increase in the number of LR primordia (a seen by an increase in number of blue spots) upon treatment with mannitol suggesting its role in regulation of lateral root growth. Treatment

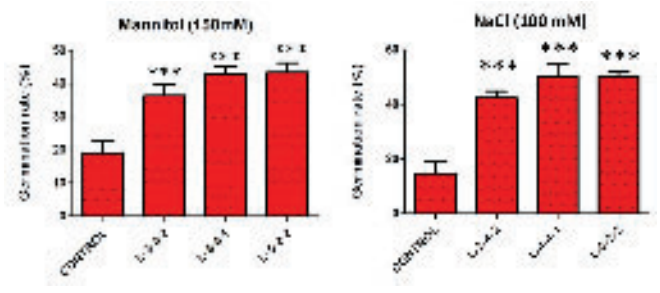


Fig 1: Effect of *SlWRKY23* expression on seed germomation in transgenic lines in presence of Mannitol and NaCl

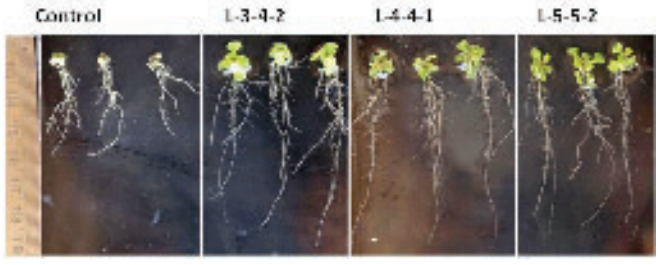


Fig 2: Pictorial representation of effect of NaCl (100mM) on three independent lines of transgenic Arabidopsis roots expressing *SlWRKY23*

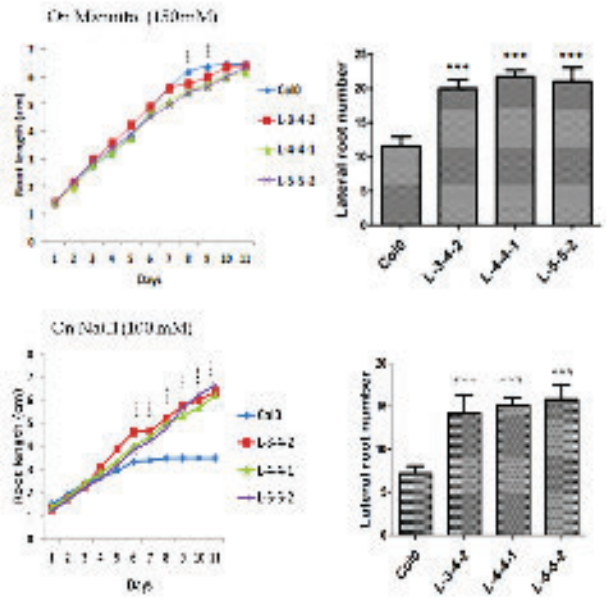

Fig 3: Effect of NaCl and Mannitol of root length and lateral root number in transgenic lines expressing *SlWRKY23*

with NaCl strongly activated *SlWRKY23* expression in the root tips of LRs. The studies show that SlWRKY23 may regulate root growth in response to different stresses.

## Role of MAP kinases in mango ripening

Fruit ripening is a complex process which involves several developmental changes such as change in fruit texture, colour and aroma. Ethylene affects ripening in climacteric fruits. Mitogen activated Protein kinases (MAPKs) have been reported to have a crucial role in ethylene signalling pathway. Different MAPKs have been reported to play role in various biotic as well as abiotic stresses that the plant experiences in its life time however; their role in fruit ripening is not very well defined. We are trying to understand role of MAP kinases in ripening and aroma formation in mango.

Sixteen differentially expressing contigs belonging to MAPK family were found in mango (Dashehari) transcriptome. Three contigs c21555_g1_i2, c21568 g1_i3 were full length. Other contigs were partial in sequence. In order to decipher their roles in fruit ripening, the full length contigs were chosen for the study.

Both c21555_g1_i2and c21568g1_i3 encode proteins of 375 amino acids. Database search with BLAST-p at NCBI (www.ncbi.nlm.nih.gov) showed that protein sequence of c21555_g1_i2 had 71% identity with Arabidopsis *MAPKinase3* (NP_190150) and c21568g1_i3 had 87% identity with Arabidopsis *MAPKinase4* (NP_192046.1) at amino acid level. Due to their similarity with *AtMPK3* and *AtMPK4* respectively we named c21555_g1_i2 as *MiMPK3* and c21568_g1_i3 as *MiMPK4* in this study. Bioinformatics analysis by Expasy tool (https://web.expasy.org/compute_pi) showed that putative *MiMPK3* and *MiMPK4* proteins had predicted molecular weight of 43.09 kDa and 43.3 kDa respectively. Domain analysis using PROSITE (https://prosite.expasy.org) suggested that the deduced amino acid sequence of both *MiMPK3* and *MiMPK4* contained a Protein kinase domain in the region from position 43-329 amino acid. Both these proteins contain a Map kinase signature domain spanning a region from 79-181 amino acids. Serine/ Threonine Protein kinase active site signature domain is present from 165-177 and Protein kinase ATP binding region structure spans from 49-72 amino acids. Transcript abundance of both the genes was checked in different tissues like leaves, flower, peel, pulp and stem. We observed significantly higher expression of *MiMPK3* in flower (30 fold), stem (27 fold) and peel (13 fold) whereas in pulp and seed gene expression level was (2-3 fold) as compared to leaf, *MiMPK4* also expressed in all tissues. In order to determine whether *MiMPK3* and *MiMPK4* are ripening related and ethylene inducible genes, we treated the harvested fruits with exogenous 100 ppm ethylene for 24 h, which caused early ripening of fruits. *MiMPK3* levels increased after day 4 in control samples whereas *MiMPK4* levels declined with the progression of ripening. When transcript levels of *MiMPK3* and *MiMPK4* were analyzed in ethylene treated fruits, *MiMPK3* transcript levels were significantly high on Day 2 and Day 3 (3-4 fold) whereas *MiMPK4* transcript level was down-regulated (0.2-0.9 fold) as compared with Day1. Both the genes were cloned in pER vector series for protein expression and work is under progress to decipher their roles in mango ripening

## Characterization of *GhNAC2* promoter for tissue and cell specific expression in *Arabidopsis* and cotton hairy roots

In order to understand regulation of *GhNAC2 in vivo*, *GhNAC2* promoter was isolated from cotton (Wagad) and characterized by expressing promoter::GUS construct in *Arabidopsis* T2 lines and cotton hairy roots.

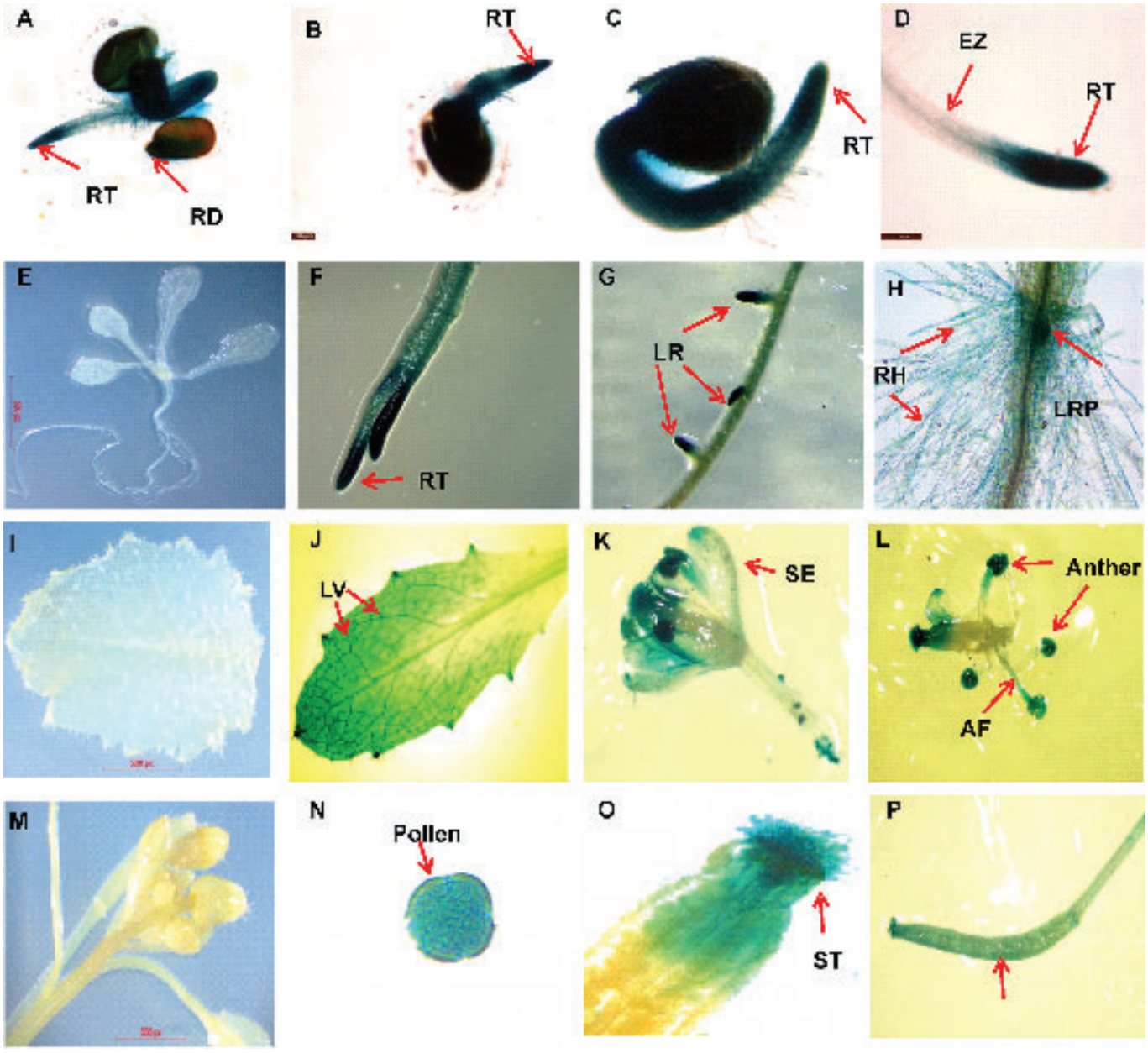


Fig 4.Histochemical GUS activity in transgenic *Arabidopsis* plants containing $PRO_{GhNAC2}$::GUS constructs. (A-D) *Arabidopsis* seedling after 2 DAS; (F-H) *Arabidopsis* seedling after 5 DAS; (I-P) *Arabidopsis* grown in soilrite under long day condition; (E, L, & M) negative control showing whole seedling, leaf, and floral part, respectively. Soilrite grown plant (J) mature leaf (K) Mature flower; (L) Anther; (N) Pollen; (O) Stigma; and (P) Immature sillique (Q & R) Treatment with 100 mM NaCl and 150 mM mannitol. Plants were grown in agar media plate supplemented with 100 mM NaCl and 150 mM Mannitol for 5 days. (E, I&M) plants transformed with pBI101 used as negative control. RD, Redical; LRP, Lateral root primordial; LR, lateral root; RT Root tip; EZ, Elongation zone; LV, leaf vein; IS, Immature silique; ST, Stigma tip; RH, root hairs; SE, sepal; AF, Anther filament; All arrows show strong GUS activity. Image (A-E & N-R) were taken under light microscope Leica MC170 HD and rest of images were taken under stereo microscope Leica MC 190 HD.

For the functional characterization of *GhNAC2* promoter, 870 bp promoter region was isolated from the genome walking library of cotton and cloned in pBI101.2 and transformed in *Arabidopsis* and cotton hairy roots.

The GUS activity was seen in the roots of 2 and 5 days old transgenic *Arabidopsis* seedlings. GUS expression was primarily seen at the root tip of the primary and lateral roots and root hairs (Fig. 4). These results correlated with the presence of several motifs related

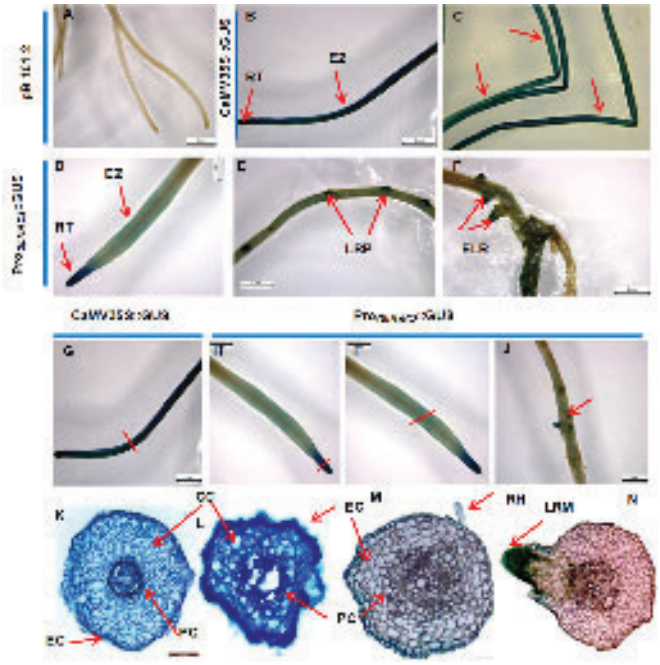

Fig. 5: Histochemical localisations of GUS activity in transgenic cotton hairy roots containing $PRO_{GhNAC2}$::GUS construct. (D-F) Hairy roots transformed with $PRO_{GhNAC2}$::GUS; (K) T.S of the GUS stained hairy root transformed with CaMV35S::GUS; (L-N) T.S of transgenic hairy root transformed with $PRO_{GhNAC2}$::GUS; (L) Root tip; (M) Elongation zone; (N) lateral root primordia. (A) Hairy roots transformed with pBI101.2; (B-C) Hairy roots transformed with CaMV35S::GUS used as negative and positive control, respectively. PR, Primary root; LR, Lateral root; ELR, Emerging lateral root; RT, Root tip; EZ, Elongation zone; LRP, Lateral root primordial; EZ, Elongation zone; EC, Epidermal cell; PC, Pericycle cells; CC, Cortical cell; RH, Root hair. All arrows show strong GUS activity. Images (A-J) were taken under stereo microscope Leica MC 190 HD and images (K-N) taken under light microscope Leica DM2500.

to root expression like ROOTMOTIFTAPOX1, ACGTROOT1, and ROOTMOTIFTAPOX1 in promoter sequence. No blue colour was observed in the root differentiation zone. In mature transgenic plants, GUS activity was found in different plant parts. Intense blue colour was seen in the leaf veins, leaf trichomes, and immature siliques. GUS activity was observed in the reproductive tissues like anther, pollen and stigma. Interestingly, no blue colour was detected in sepal, petals, mature siliques and mature seeds.

To see the salt and osmotic regulation of the *GhNAC2* promoter, transgenics were grown on agar plate for 5 days containing 100 mM NaCl and 150 mM Mannitol. GUS expression in these plants was enhanced in primary and lateral roots tips compared to control. These results indicated that *GhNAC2* promoter was induced by salt and osmotic stress. To find out the promoter activity of *GhNAC2* in homologous system, transgenic cotton hairy roots expressing $Pro_{GhNAC2}$::GUS were generated. Transgenic cotton hairy roots showed strong GUS expression in the primary and lateral root tip and lateral root primordial and diffused expression in the elongation zone (Fig. 5). However, no GUS activity was seen in differentiation zone of the root. The images of microtome cut TS of the GUS stained hairy roots were taken under light microscope. All root cells expressing CaMV35S::GUS were stained blue. Interestingly, $Pro_{GhNAC2}$::GUS activity was observed in all the cells of the meristematic zone (Fig. 5) while only epidermal cells of the elongation zone were stained suggesting cell specific expression of GhNAC2.

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**Genetic engineering of cotton for insect tolerance**

## Mutant GM cotton line with high yield potential

Cotton *(Gossypium hirsutum)* is one of the most important commercial crops and is cultivated in tropical and subtropical regions of world for fiber, oil, and protein-rich feed. India has the largest cotton cultivation area (37% of the world) which is around 12.2 million hectares. India is also the largest cotton producer (approximately 22% of the world cotton). However, our productivity (501 kg/ha) is significantly lower in comparison to world average cotton productivity (789 kg/ha), Australia holding the top-most position (2028 kg/ha) and India ranking 37$^{th}$. Indian public institutions and biotech seed companies are trying to fill the gap of land usage *vs* production. Cotton productivity can be improved by combining superior yield traits, high-density plantation, and better protection of the crop from pest infestation.

Our group is working on the development of insect tolerant GM cotton lines with a few new insecticidal genes. Insertion of a gene in the genome of cotton cells, developing transform cells into somatic embryos and then into transgenic plants is a long process. Explants are maintained on agar medium for over six months. We often see several phenotypic abnormalities in GM plants and reject them in T1 or T2 generations after transgenic expression analysis. The abnormalities occur primarily due to somaclonal and antibiotic induced variations, insertion of transgene in a functionally important regions of genome leading its rearrangement and change in gene expression profile. However, there is also a possibility of getting a transgenic event with superior agronomic traits. Theoretically, this can happen if T-DNA insertion or somaclonal variation disrupt the negative regulators of yield trait. Such mutant plants can be good by-products in crop genetic manipulation endeavours and might be useful in yield trait improvement program. We are testing our own hypothesis on cotton genetic engineering using Coker 312 as a variety.

We have developed more than 200 transgenic cotton lines with various anti-insect genes under regulation of constitutive and tissue specific promoters. We grow 6-9 plants of each transgenic lines having the desired gene (tested with gene specific PCR) in T1 generation in a polyhouse and evaluate them for transgene expression, insect tolerance and yield associated traits. We have identified an interesting transgenic line (Event384$_{NBRI}$); 3 plants (out of 9) showed higher growth and yield as compared to hundreds of other T1 plants. The mutant cotton line was expressing anti-whitefly protein Tma12 (Nature Biotechnology, 2016) in a tissue specific fashion. Seven seeds of each of three mutant plants (total 21 plants) were grown to T2 generation; one plant showing exceptional growth and yield was selected. Six seeds of the selected T2 mutant plant were germinated and grown at the various locations of polyhouse. All of them showed superior yield trait. The mutant cotton line was further advanced to T4 generation and all the plants (28 in number) showed superior yield as compared to other transgenic lines and non-transgenic control.

The selected mutant showed robustness, having more branches and number of bolls. The bolls were bigger in size and were covered with long bracts. The mutant line also had higher number of glands in their bracts. The root architecture was also different. The yield of the mutant cotton was 16-20% higher

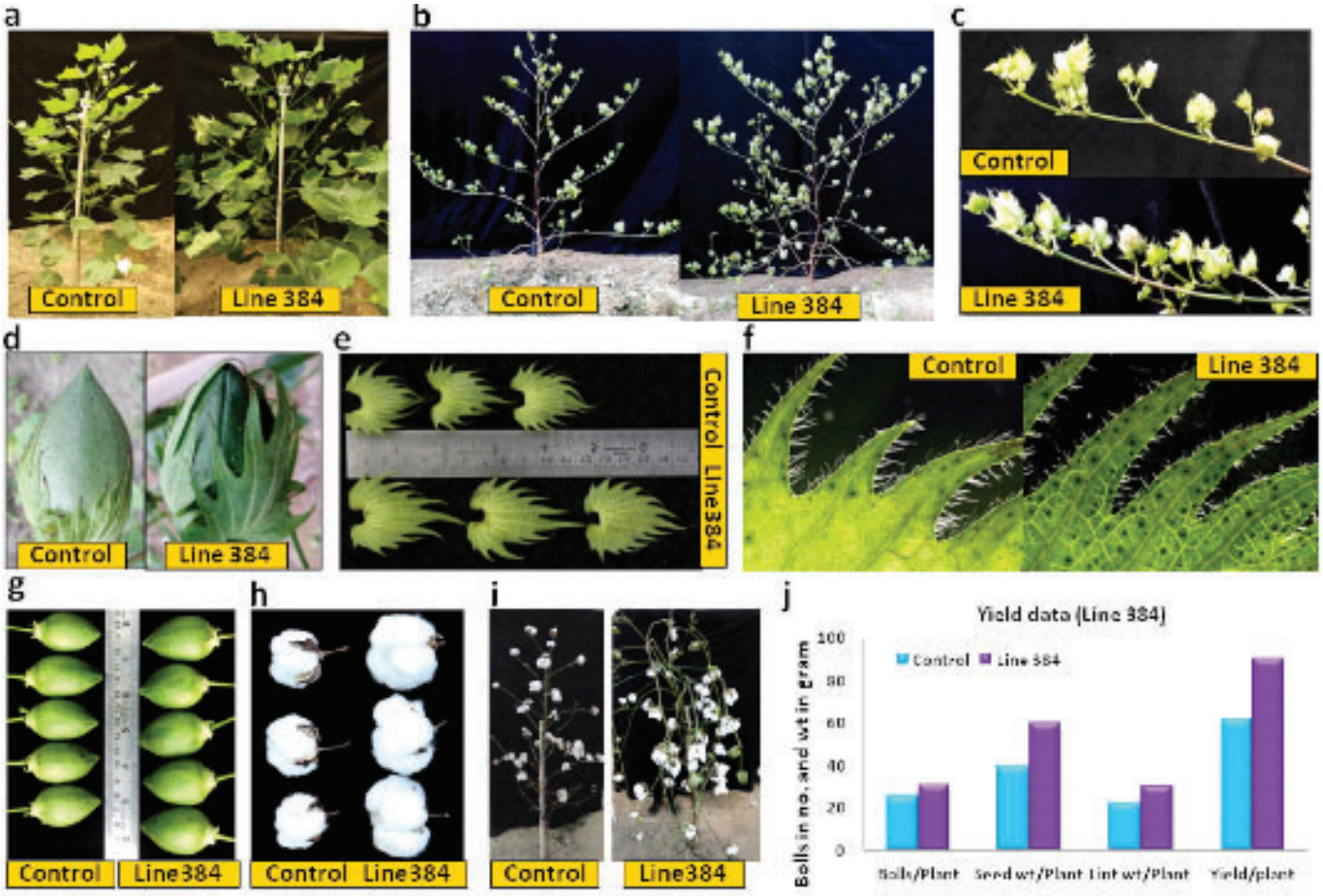


Fig. 1: Mutant cotton line and comparison with its patent (Coker 312). a-b. Vigour of mutant line 384 with more branching, c. more flowers per branch, d-e. larger bract, f. higher number of glands in bract, g-h. boll size, i. superior yield of cotton before harvesting, j. boll number and yield per plant are shown in figure.

in comparison to the Coker 312 (the non-transgenic control) and other transgenic lines, across the generations. The trait is stable and inherited (tested up to 4 generations). It is shown by representative photographs in Fig. 1.

In cotton, respiration rate of fruits (bolls) is reported to be significantly higher as compared to leaves. It enhances the concentration of $CO_2$ locally. Bract plays important role in fixing $CO_2$ and contributes to the fibre development. Larger surface area of bracts seemingly plays significant role in mutant line 384 for producing cotton balls with more fibers.

We have determined the site of integration of T-DNA in mutant cotton line. The T-DNA is inserted at three loci in chromosome ChA6, ChD1 and ChD9. Insertion in ChA6 has interrupted a transmembrane gene (T), ATP binding receptor gene in ChD1 (Y) and F complex gene in CHD9 (F). We have segregated the three insertion and found that the T and Y insertions have improved the vigour of plants and their productivity. F insertion, however, shows negative trait in plants growth. Disruption of the two loci is not reported for any role in yield enhancement.

We have crossed homozygous line of T and T & Y with a popular Indian cotton variety (Khandwa-2). F1 plants with T mutation showed superior plant growth in comparison to both the parents. The growth was much superior when T+Y mutant was crossed with Khandwa-2. The result was suggestive of dominant nature of both the mutants. Early results also show that disruption of T gene on chromosome A6 gives characters of plant growth with more branch and boll number, and Y mutant compliments these characters (Fig. 2).

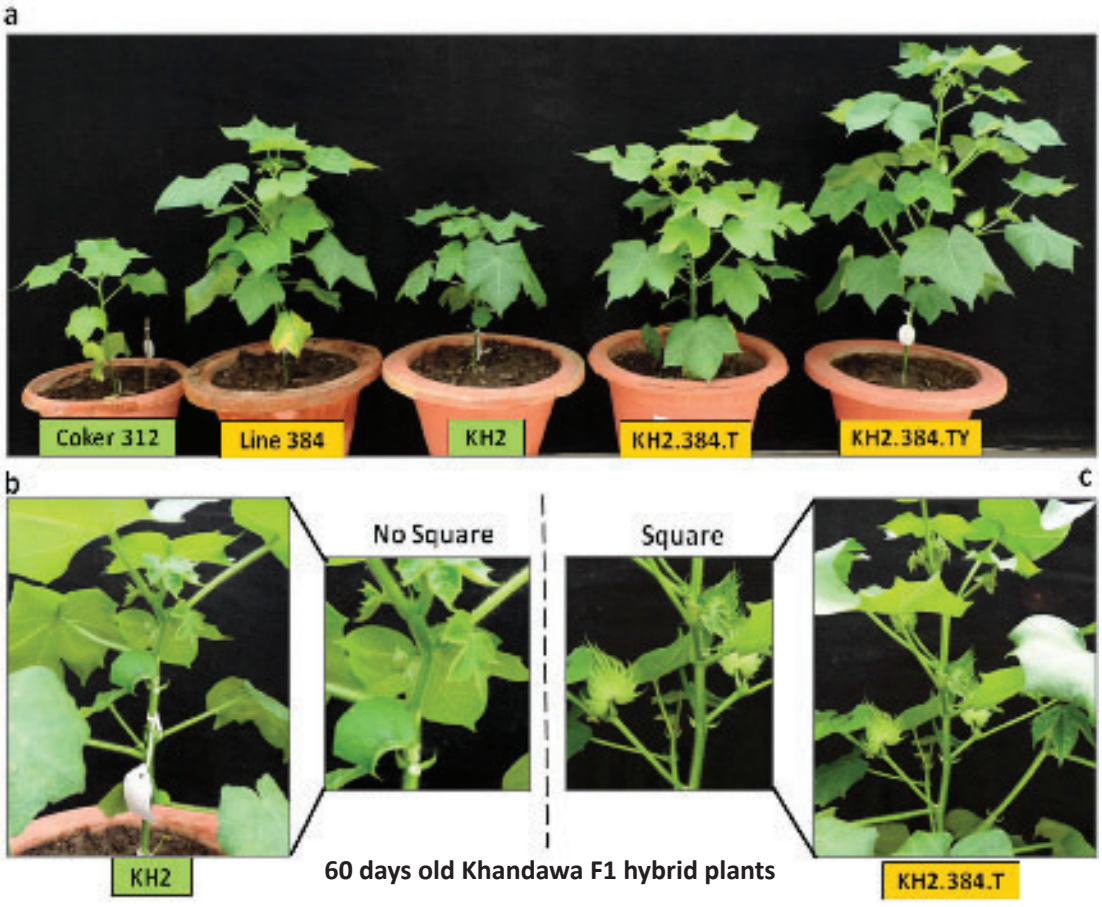


Fig. 2: F1 cotton plant from crossing of mutant lines 384-T and 384-TY with Khandwa 2. a. Figure showing Coker 312, mutant line 384TY parent, Khandwa 2 parent and F1 plant of Khandwa 2 X Coker 312-384.T and Khandwa 2 X Coker 312-384.TY, b. No square formation in 60-day-old plants of Khandwa 2 parent, **c.** Square formation in 60-day-old F1 hybrid (Kh2.384.T)

T and Y knockouts are dominant characters. It can be safely assumed that the mutant lines would show desired phenotype in other backgrounds as F1 hybrids. We are also trying to understand molecular network behind the phenotypes (higher cotton yield) in the two mutant lines using back-crossing strategy and genomic tools. The lead can be useful in enhancing productivity of cotton in India especially of low yielding varieties that are naturally tolerant to biotic and abiotic stresses. It is also notable that "bract size" has never been used as a trait for yield improvement in Cotton Breeding Program in India.

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Drought tolerance in chickpea and *Arabidopsis*, metal tolerance in *Arabidopsis*

## Drought tolerance in *Arabidopsis*

Glutaredoxins (Grxs) are small (10–15 kDa) glutathione (GSH) - dependent redox proteins. The role of Grxs is well documented in tolerance to heavy metal stress in prokaryotic and mammalian systems and a few plant genera, but poorly understood in plants against drought. A rice glutaredoxin (*OsGrx*) gene (*LOC_Os02g40500*) responsible for tolerance against heavy metal stress has been studied for investigating its role against drought. This glutaredoxin gene was over-expressed in *Arabidopsis thaliana* to understand its role in drought stress (Fig. 1). The presence of transgenes was confirmed by qRT-PCR. Transgenic lines of *OsGrx* showed longer roots, higher seed germination, and survival efficiency during drought stress. Additionally, these lines showed increase in physiological parameters ($P_N$, gs, E, WUE, qP, NPQ and ETR), antioxidant enzymes (GRX, GR, GPX, GST, APX, POD, SOD, CAT, DHAR, and MDHAR), antioxidant molecules (ascorbate and

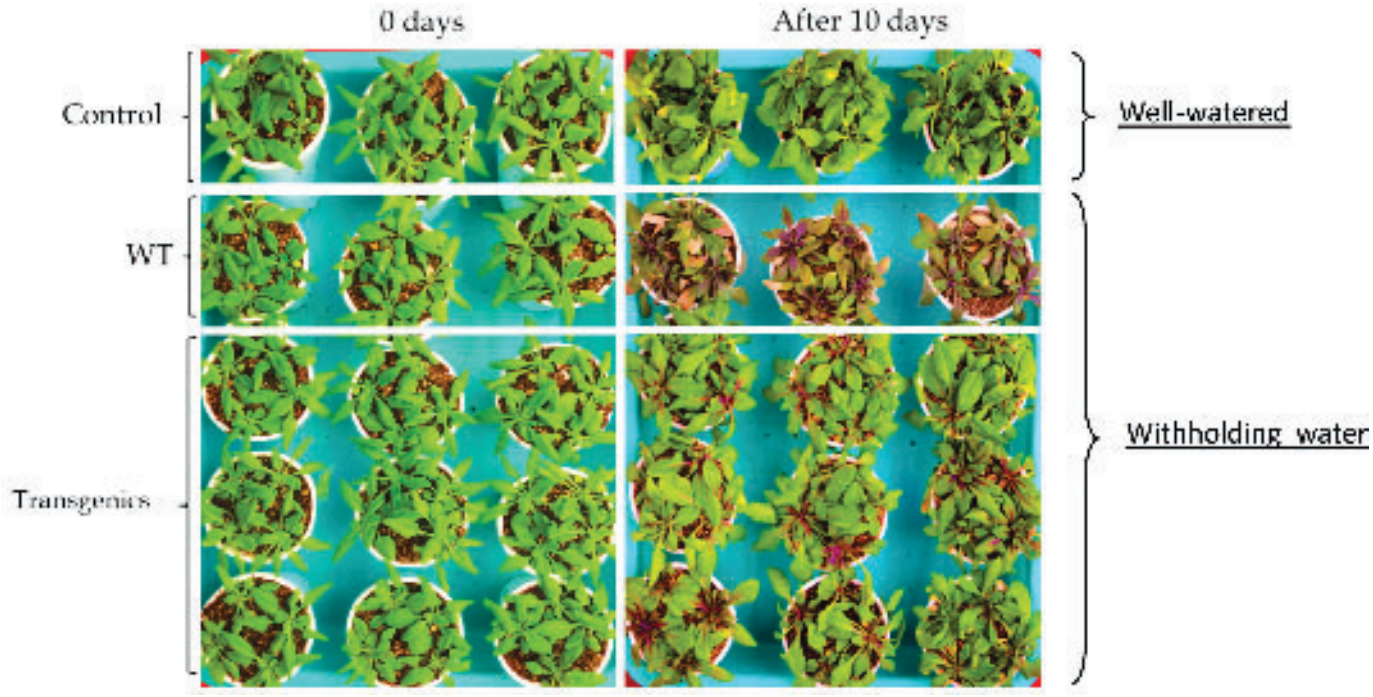


Fig. 1: Drought tolerance in *Arabidopsis* by water withholding due to the over-expression of *OsGrx* gene leading to enhanced growth of transgenic *Arabidopsis* plants expressing rice *Grx* (*OsGrx*) as compared to WT (Col-0) after 10 days drought stress

GSH) and stress-responsive amino acid (cysteine and proline) levels. Our study strongly suggests that *OsGrx* gene participated in the moderation of drought and might be a potential candidate to overcome drought conditions in different crops using biological engineering strategies (Fig. 2).

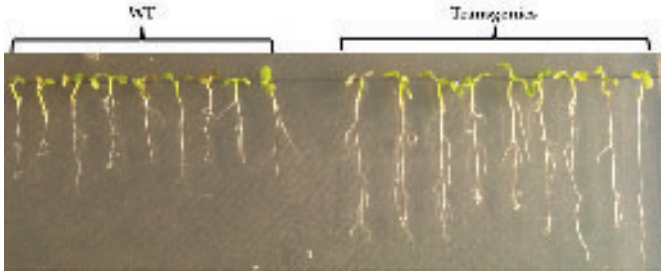


Fig. 2: Enhancement in root growth in *Arabidopsis* during drought by the over-expression of *OsGrx* gene

## Metal tolerance in *Arabidopsis*

The chickpea glutaredoxin (*CaGrx*) gene has been investigated against metal stress, based on its primary screening in chickpea which revealed higher up-regulation of *CaGrx* gene under various heavy metals (AsIII-25 µM, AsV-250 µM, Cr(VI)-300 µM, and Cd-500 µM). The *CaGrx* gene was over-expressed in *Arabidopsis thaliana* and various biochemical and physiological parameters were investigated under each metal stress. Transgenic plants showed

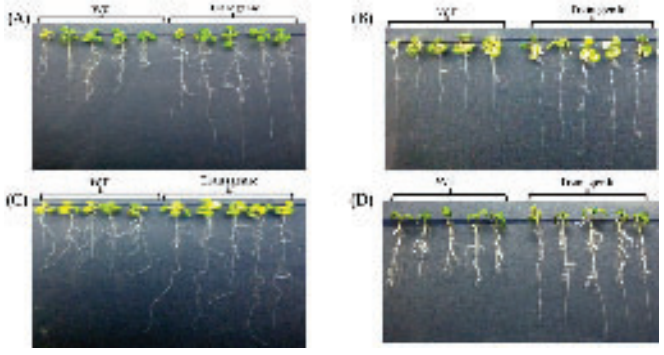

Fig. 3: Root length, morphology and metal tolerance in *Arabidopsis* in plantlets over-expressing CaGrx with control (Col-0) respectively in (A) AsIII-25µM, (B) AsV-250µM, (C) Cd-500µM and (D) Cr(VI)-300µM

significant up-regulation of the *CaGrx* gene during qRT-PCR analysis as well as longer roots, higher seed germination, and survival efficiency during each metal stress. The levels of stress markers, TBARS, $H_2O_2$, and electrolyte leakage were found to be less in transgenic lines as compared to WT revealing tolerance in transgenic plants. The total accumulation of AsIII, AsV, Cr(VI) except Cd was significantly reduced in all the transgenic lines., The Cd levels were slightly reduced in transgenic lines. The physiological parameters such as net photosynthetic rate (PN), stomatal conductance (gs), transpiration (E), water use efficiency (WUE), photochemical quenching (qP), and electron transport rate (ETR), were maintained in transgenic lines during metal stress. Various antioxidant enzymes such as glutaredoxin (GRX), glutathione reductase (GR), glutathione peroxidase (GPX), glutathione-S-transferase (GST), ascorbate peroxidase (APX), superoxide dismutase (SOD), catalase (CAT), dehydroascorbate reductase (DHAR), monodehydroascorbate reductase (MDHAR), antioxidant molecules (ascorbate, GSH) and stress-responsive amino acids (proline and cysteine) levels were significantly increased in transgenic lines which provide metal tolerance. The outcome of this study indicates that the *CaGrx* gene participates in the moderation of metal stress in *Arabidopsis*, which can be utilized in biotechnological interventions to overcome heavy metal stress conditions in different crops of agricultural importance (Fig. 3).

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**Genomics of plant insect interaction**

The Group is working on development of transgenic cotton and tomato plants for various traits. We investigate the interactions between insects and plants and search for novel targets for insect pest control. We have developed transgenic cotton plants with novel insecticidal proteins, lectins and SiRNA gene constructs which show very good toxicity against various chewing type and sap sucking pests. We have identified a *pectin methyl esterase* gene from *Withania somnifera* for enhanced methanol production as a strategy to target multiple insect pests. Other research area includes Trait improvement in cotton (fiber, male sterility and drought tolerance) and in Tomato for fruit shelf life using CRISPR/Cas technology.

## *In vivo* gene specific silencing in *Phenacoccus solenopsis* by *in planta* expression of a double-stranded RNA

Cotton a cash crop, is majorly attacked by many hemipteran pests. Amongst them, cotton mealybug, *Phenacoccus solenopsis* is devastating and causes tremendous yield loss in cotton production. Many studies have proven that the RNAi technology can effectively control agricultural pests. In the present study, 25 potential RNAi targets were selected based on previously available databases of potential target genes. To assess the effectiveness of the selected target genes, three methods were utilized for the delivery of dsRNA. Different concentrations of dsRNA molecules were fed to insects and mortality was recorded for each target gene. Based on mortality data results, three target genes were further used for expression studies. Amongst the three selected genes for expression studies, the expression of *Krüppel*-1 Homologue gene showed significant reduction at two different time-points (8 and 14 days) by 73% and 84%. Further, plant binary expression cassette was designed for *Krüppel*-1 Homologue under the control of double enhancer CaMV35S promoter. Significant down regulation by 65.1% and 75% in gene expression at two different time-points (8 and 14 days) was found for *Krüppel*-1 Homologue through transient gene silencing methods. This silencing data was found to be correlated with mortality data, in which it showed significant down regulation of gene expression in comparison to control. The results obtained from the above study are evidently showing that RNAi technology can play a potential and promising role in controlling the cotton mealybug, *P. solenopsis*. The observations also supported that hemipteran insects are highly sensitivite to RNAi using both ingestion and oral delivery of dsRNA methods. (Fig. 1)

## WsPME29, an insect inducible pectin methylesterase of *Withania somnifera*, imparts broad-spectrum resistance to chewing and sucking insects.

Pectin methylesterases (PMEs) belong to large multigene family and demethylesterify the cell-wall pectins, which lead to the methanol emission. There are two types of PMEs: Type-I and Type-II PMEs. Type-I PMEs comprises a PRO region, which share similarities with the PME-inhibitor domain and keeps PME inactivated, and it is cleaved by Subtilase (subtilisin like serine protease). Interestingly, reports have shown that *Withania somnifera* emits more methanol even in control conditions as compared to other Solanaceae species. However, an increase in methanol-emission has been reported due to cell

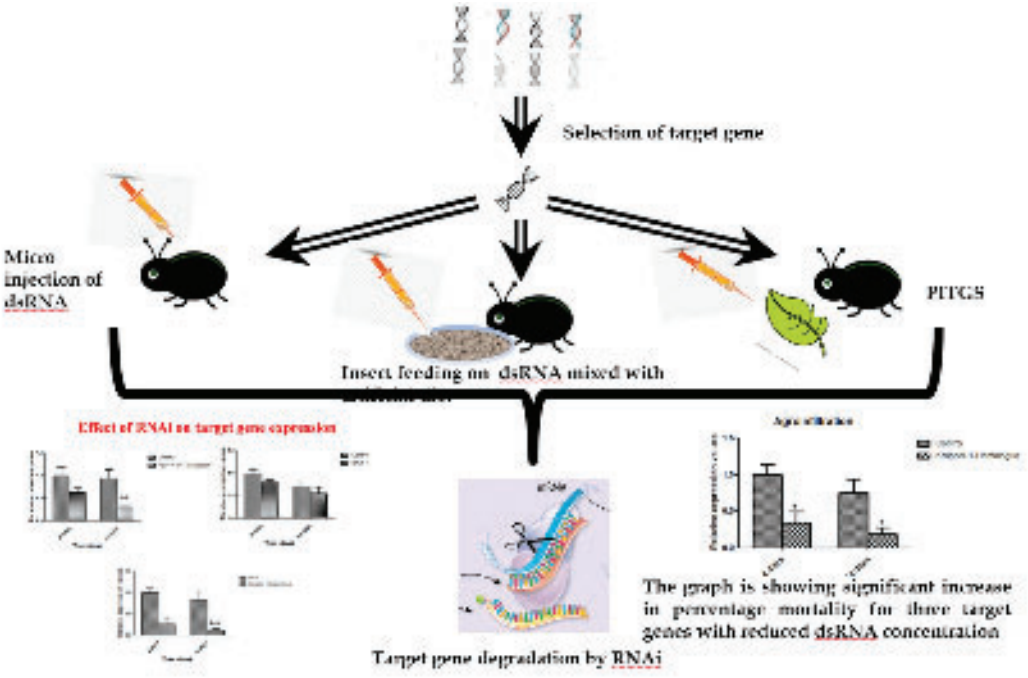


Fig. 1: *In-vivo* gene specific silencing in *Phenacoccus solenopsis* by *in planta* expression of a dsRNA

wall damage in biotic stress conditions. Therefore, *W. somnifera* was selected as a source to find the most bioactive and early-inducible *PME* for inducing broad-spectrum insect resistance. Using available transcriptomic data, 70 *PMEs* and 64 Subtilase genes were identified in *W. somnifera*. For the selection of early-inducible and highly bioactive *PME* and Subtilase, total RNA was isolated from *Spodoptera litura* infested *W. somnifera* leaf at different time of interval i.e., 0 min, 30 min, 2h, 6h and 12hr. Quantitative expression analysis suggested that *WsPME29*, Type-I PME member, and *WsSBT3* were found to be the most potential putative active *PME* and Subtilase during *S. litura* infestation, respectively (Fig. 2). We have cloned the putative *WsPME29* under the control of constitutive and inducible promoter and transformed *Nicotiana*

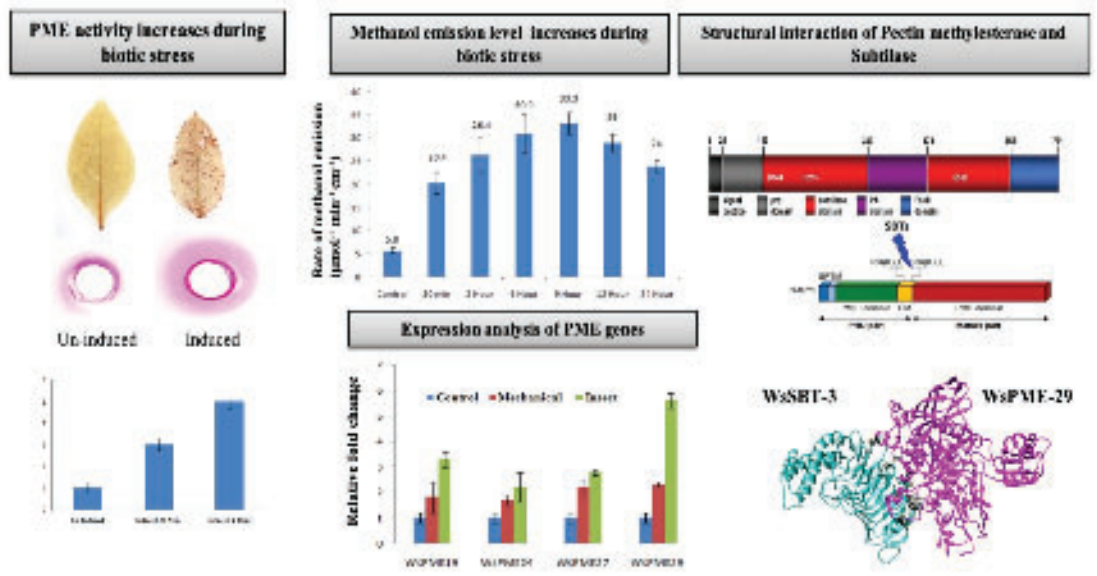


Fig. 2: Insect inducible pectin methylesterase of *Withania somnifera*

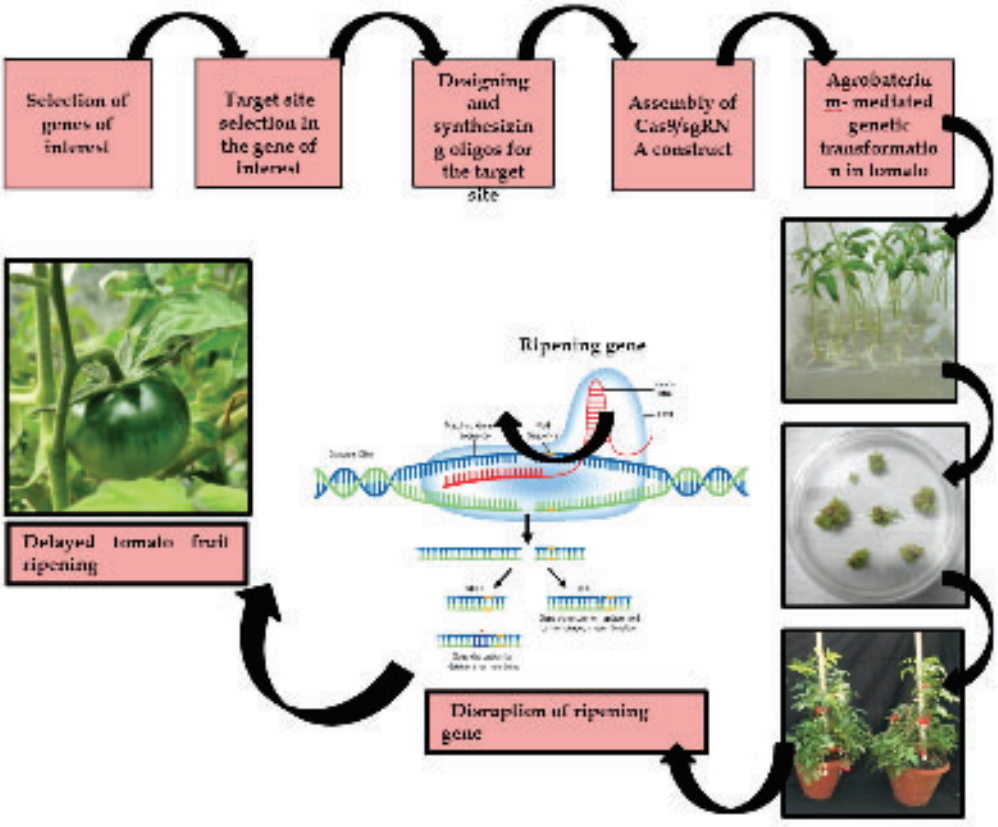


Fig. 3: CRISPR/Cas9 mediated genome editing in tomato for manipulating fruit shelf-life.

*tabacum* plants. Transgenic plant comprising constitutive and inducible *WsPME29* expression system have shown 75-85% mortality against both the chewing (*Spodoptera litura & Helicoverpa armigera*) and sap sucking (Aphid and Whitefly) insect pests on the 4$^{th}$ day and 6$^{th}$ day, respectively. The structural interaction of WsSBT3 with WsPME29 showed that WsSBT3 cleaved the processing motif and activate the mature PME (Fig. 2). We suggest that biotic stress induced WsPME29 and WsSBT3 and their interaction promotes chewing and sucking insect resistance through enhanced methanol emission.

## CRISPR/Cas9 mediated genome editing in tomato for manipulating fruit shelf-life

Tomato is a major crop that is ranked first among all vegetables in terms of its nutritional value. Although tomato production has been increasing, a large fraction is lost to post-harvest due to poor shelf life and rapid deterioration following ripening. Reducing these losses is essential and has been attempted by breeding and transgenic means to varying success. Here, in this study, we are targeting various ripening-related genes with the aid of the latest genome editing technology CRISPR/Cas9 (Fig. 3). The genes being targeted encode N-glycoprotein modifying enzymes, α-mannosidase (α-Man) and β-D-N-acetylhexosaminidase (β-Hex) and genes involved in post translational processes. The corresponding constructs have been prepared and the transgenic plants are being developed for the same. The putative genome edited plants are now being analysed for indels through sequencing of the target sites. The fruits of the genome edited plants would be expected to show delayed fruit ripening.

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**Arsenic, abiotic stress, functional genomics, transgenic, rice**

Our study described the principal understanding on the molecular basis of heavy metal toxicity and accumulation in plant parts. The study covered the transgenic and bioremediation approaches to minimize arsenic accumulation in rice which further reduces food chain contamination. We described the measures to decrease As accumulation in rice.

## Exogenous application of methyl jasmonate alleviates arsenic toxicity by modulating its uptake and translocation in rice (*Oryza sativa* L.)

Methyl jasmonate (Me-JA) is a plant growth regulator known for modulating plant responses to various abiotic and biotic stresses. The unavoidable arsenic (As) contamination in rice (*Oryza sativa*) results in reduced crop yield and greater carcinogenic risk to humans. The present work examines the significance of Me-JA induced molecular signaling and tolerance towards arsenic toxicity in rice. The arsenite (AsIII; 25µM) stress hampered the overall growth and development of the rice seedling. However, the co-application (25µM AsIII+0.25µM Me-JA) resulted in increased biomass, chlorophyll content, enhanced antioxidant enzyme activities as compared to AsIII treated plants. The co-application also demonstrated marked decrease in malondialdehyde content, electrolyte leakage and accumulation of total AsIII content (root + shoot) as compared to AsIII treated plants. The co-application was also found to modulate the expression of genes involved in downstream JA signaling pathway (*OsCOI*,*OsJAZ3*,*OsMYC2*), AsIII uptake (*OsLsi1*, *OsLsi2*, *OsNIP1;1*, *OsNIP3;1*), translocation (*OsLsi6*, and *OsINT5*) and detoxification (*OsNRAMP1*, *OsPCS2* and *OsABCC2*) revealed the probable adaptive response of the rice plant to cope up arsenic stress. Our findings reveal that Me-JA alleviates AsIII toxicity by modulating signaling components involved in As uptake, translocation and detoxification in rice. This study augments our knowledge for the future use of Me-JA in improving tolerance against AsIII stress (Fig. 1 A-H).

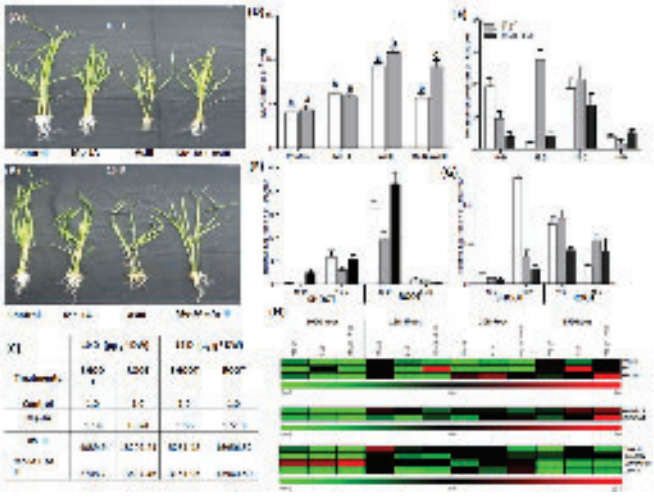

Fig. 1: Me-JA provides tolerance towards AsIII toxicity in rice by modulating molecular signalling and translocation and accumulation of AsIII in rice.(A) Effect on growth at 10 D and (B) 15 D, (C) Total arsenic accumulation using inductively coupled plasma mass spectrometer (ICP-MS) (D) MDA estimation for membrane damage, (E) Differential expression of genes CORONATINE INSENSITIVE 1;*OsCOI1*, (F) JASMONATE ZIM DOMAIN; *OsJAZ3*(G) transcription factor ;*OsMYC2* involved in JA signalling (The expression levels of genes are presented using fold-change values transformed to $Log_2$ format compared with control. All values are means of three replicates (n=3, ±SD) and repeated twice) and (H) Heat map analysis of the As transporter and detoxification related genes (Red and green color showed up and down-regulation of genes respectively)in 0.25 µM Me-JA, 25 µM AsIII and 0.25 µM Me-JA + 25 µM AsIII treated plants.

## Auxin-salicylic acid cross-talk ameliorates OsMYB–R1 mediated defense towards heavy metal, drought and fungal stress

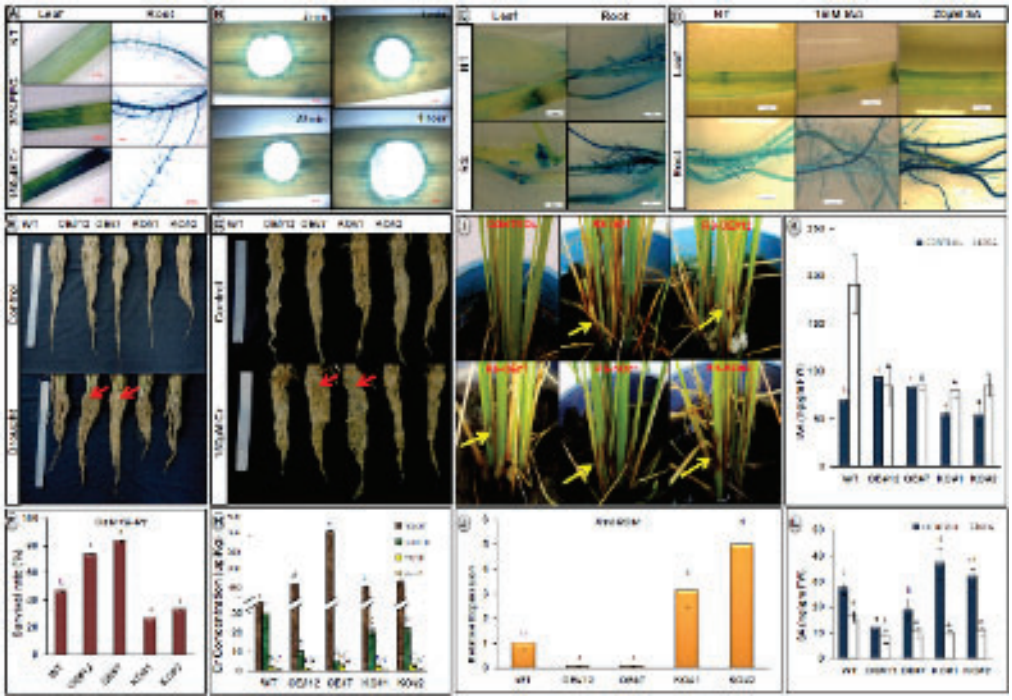

Fig. 2: *OsMYB-R1* harboring over-expression line over-come drought, chromium and *Rhizoctonia solani* stress. GUS staining of *OsMYB-R1* promoter harboring rice transgenic plants under (A) nontreatment (NT), 20% PEG and 150µM Cr (VI) stress (B) time-dependent wounding (C) *R. solani* (RS) (D) 1mM IAA and 20µM Salicylic acid (SA) (E) Change in root morphology of WT, *OsMYB-R1* over-expressing (OE#12 and OE#7) and knockdown (KO#1 and KO#2) lines after survival from drought stress in the earthen pot. (F) The survival rate of WT and *OsMYB-R1* over-expressing and knockdown lines after revival for seven days in a simulated pot experiment. (G) Phenotypic variability in roots of WT and transgenic rice after Cr (VI) treatment in a simulated pot experiment. (H) Cr (VI) estimation in roots, shoot, husk and seed of WT and transgenic lines after stress in the pot. (I) Pictorial depiction of shoots of wild-type, *OsMYB-R1* over-expressing and knockdown lines after *R. solani* treatment. (J) Relative abundance or load of fungal on each line after infection. (K, L) IAA and SA content of the wild-type and transgenic lines in non-treated and PEG-treated roots for 48 h were measured using HPLC. The bar shows the mean of triplicate values and error represents the SD. All the values are means of triplicate ± SD. Different letters indicate significantly different values applying Duncan's test p≤0.05.

The MYB TF family is an immensely large and functionally diverse class of proteins involved in the regulation of cell cycle, cell morphogenesis to stress signaling mechanism. The present study deciphered the hormonal crosstalk of wound inducible and stress-responsive OsMYB-R1 transcription factor in combating abiotic [Cr(VI) and drought/PEG] as well as biotic (*Rhizoctonia solani*) stress. OsMYB-R1 over-expressing rice transgenics exhibit a significant increase in lateral roots, which may be associated with increased tolerance under Cr(VI) and drought exposure. In contrast, its suppresssion reduces stress tolerance. Higher auxin accumulation in the OsMYB-R1 over-expressed lines further strengthens the protective role of lateral roots under stress conditions. RNA-seq data reveals over-representation of salicylic acid signaling genes and calcium-dependent protein kinases, which probably activate the stress-responsive downstream genes (Peroxidases, Glutathione S-transferases, Osmotins, Heat Shock Proteins, Pathogenesis Related-Proteins). Higher catalase, guaiacol peroxidase and superoxide dismutase activities in transgenic lines confirm that OsMYB-R1 mediates robust antioxidant system. Our results suggest that OsMYB-R1 is part of a complex network of transcription factors controlling the cross-talk of auxin and salicylic acid signaling and other genes in response to multiple stresses by modifying molecular signaling, internal cellular homeostasis and root morphology (Fig. 2 A-L).

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The group has mainly been involved in the gene expression analysis during plant development and stresses with special emphasis on fruit ripening and secondary metabolite production.

## Divergence of the MADS box gene family in *Musa*

In plants, the MADS box TFs play an important role in floral organ identity and different aspects of plant growth and development. Origin of seed, flowers, and fruit and the increasing number of MADS-box genes in the higher plants as compared to lower plants suggest that this regulatory gene family plays an important role in the evolution of plants. The role of MADS-box genes has been identified in the fruit development and ripening process in several plants such as tomato, apple, strawberry, etc.

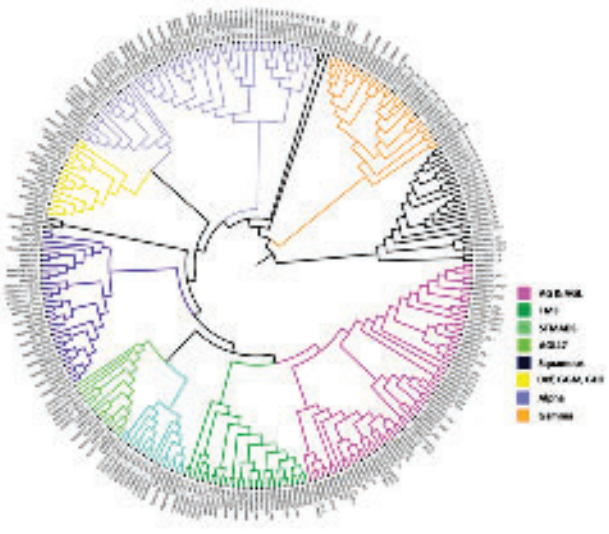

Fig. 1: Phylogenetic analysis of the Type II MADS box genes of *Arabidopsis thaliana*, *Musa acuminata* and *M. balbisiana*.

Banana belongs to the family Musaceae, and is an economically and nutritionally important fruit crop. Apart from the dessert variety that is globally consumed, a different variety of banana is also consumed as a vegetable and is economically important as well. An interesting observation is that both the species *Musa acuminata* and *Musa balbisiana* differ in their floral pattern as well as ripening of fruits. The *Musa acuminata* fruits are climacteric that show ethylene dependent ripening while fruits of *Musa balbisiana* do not ripen even on exposure to ethylene. Since the MADS box genes play an important role in floral development as well as ripening, the evolutionary divergence of MADS box genes was studied in *Musa acuminata* and *Musa balbisiana*.

Due to multiple rounds of whole genome duplication in *Musa* spp., many duplications of the MADS box genes were found in both the species. The expression analysis of the genes showed neofunctionalisation in some of the duplicated gene pairs in *Musa acuminata*. The expression of the 35 duplicated MADS box genes in *M. acuminata* was analysed using RNA-Seq data available in the Banana genome hub (Fig 1). The duplicated gene pair Ma02_g12050 and Ma04_g36630, Ma04_g20900 and Ma02_g12050, Ma06_g07660 and Ma09_g2990 0, showed a significant differential expression during fruit development and ripening as well as under ethylene treatment. Similarly, Ma11_g19830 and Ma05_g22700 showed difference in expression during fungal infection.

Earlier studies have shown the involvement of MADS-RIN gene during ripening. In banana the suppression of the MADS-RIN genes resulted in delay in ripening. In this study we identified the orthologs

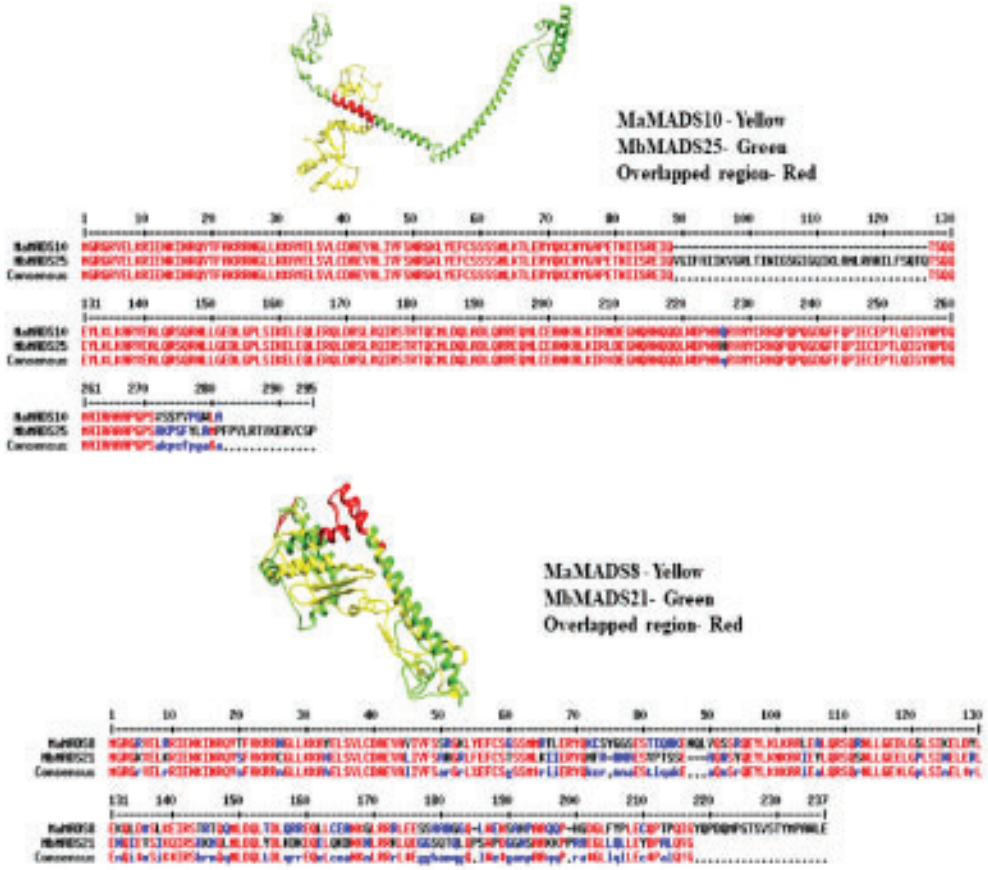


Fig.2: Structural divergence of the MADS-RIN genes in *Musa acuminata* and *M. balbisiana*.

of *Musa acuminata* and *Musa balbisiana* MADS-RIN genes. *Musa acuminata* has 10 MADS-RIN like genes and *Musa balbisiana* has only 2. The structural analysis of the closest RIN orthologs of *Musa acuminata* and (MaMADS10- MbMADS21and MaMADS8-MbMADS25) showed significant differences in structure (Fig 2). The divergent structural changes could result in divergent functional changes in these genes resulting in differential ripening behaviour.

## Evolution of the HPT gene in plants

In continuation with the previous work on the TCS (Two component system) gene family in *Musa*, we focussed on the evolution of the HPT gene family in plants. HPTs are Histidine containing Phosphotransmitter and are involved in the transfer of a phosphate group from the receiver (Rec) domain of HK (Histidine Kinase) to the Rec domain of the response regulator. It contains a highly conserved motif xHQxKGSSxS. The HPTs are present throughout

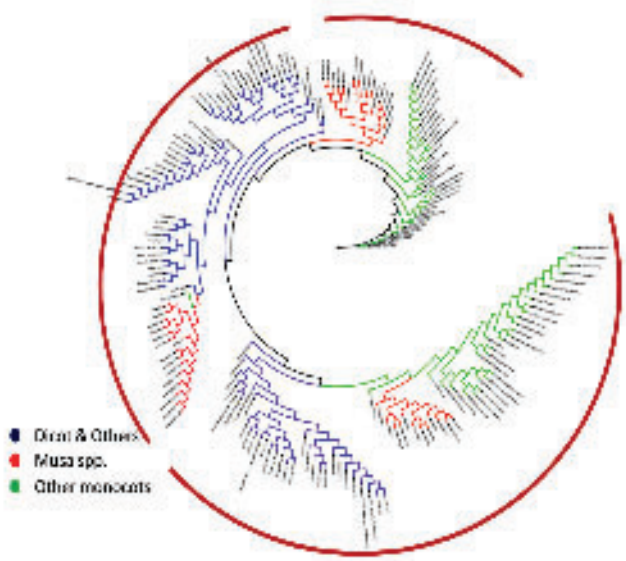


Fig. 3: Phylogenetic analysis of the HPT gene family. Clear difference in monocots and dicot HPTs were observed. Within the monocots specific increase in the Musa sp was observed.

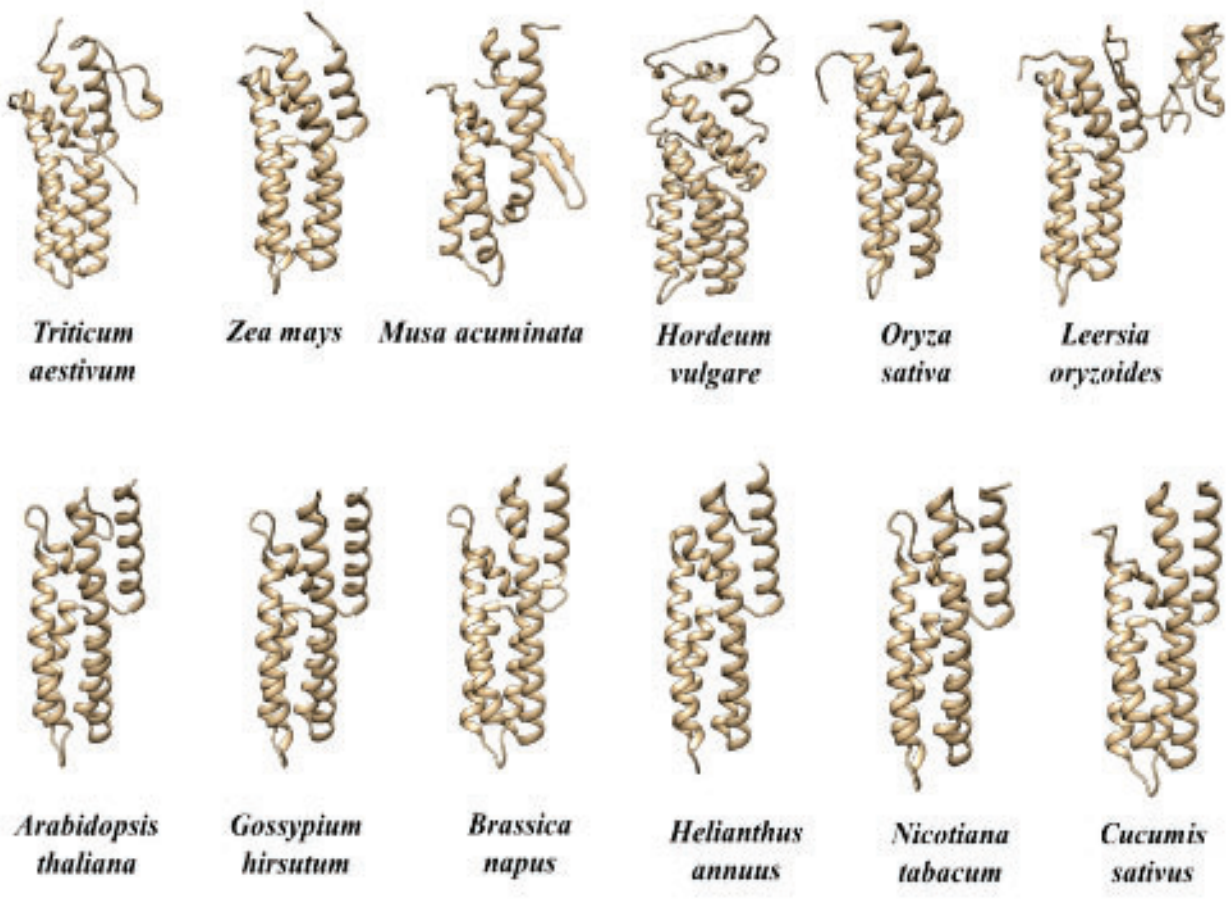


Fig. 4: Structure of various HPTs in Monocots and Dicots. The structure of the HPT genes in dicotyledonous plants are highly conserved as opposed to the monocotyledonous plants that show a high variability in structure.

the plant kingdom and are highly conserved. The plant signalling machinery has evolved much from the lower to the higher plants. Though HPT are mostly conserved their ability to interact with different types of response regulators and transduce the signal is intriguing. Subtle changes in the structure of the HPTs have vast differences in their signalling. The HPTs from the lower to the higher plants were identified and studied. Phylogenetic analysis showed that HPT proteins underwent evolving changes in their sequence as well as structure (Fig 3). They formed 3 types of proteins on the basis of sequence and 2 types on the basis of structural/functional groups. Further analysis on synteny and substitution analysis shows the presence of 2 different clusters of HPTs in plants on the basis of KA value suggesting the adaption of HPT to more specific protein. On the basis of the structural network analysis two types of HPT i.e., PHE dependent and PHE independent were observed. In other words, PHE governs the centrality of the protein in some HPTs whereas in other it could by any amino acid like LEU or GLN. This analysis also shows the change of secondary partners of centrality network in monocots and dicots (Fig 4). This could be the reason behind selecting different RRs during two-component signalling.

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## *In-silico* miRNA and their target analysis in *Cestrum nocturnum* L. (CS1) and *Cestrum diurnum* L. (CS2) in response to stress and flower-anthesis

Flower anthesis in *Cestrum nocturnum* L. (CS1) and *Cestrum diurnum* L. (CS2) takes place at night and day, respectively. It is therefore interesting to identify the miRNAs responsible for the flower-bloom in these two species. In the present investigation, Homology-search based computational analysis was employed for the identification of responsible miRNAs. A total of twenty six miRNA families in CS1 and ten miRNA families were predicted in CS2. Out of which fifteen miRNA families in CS1 and nine in CS2 were identified to regulate 1024 and 1007 target transcripts. These miRNAs showed significant function in plant circadian rhythm and several stress responses. Based on the role of these miRNAs and their corresponding gene regulation, a biological network of CS1 and CS2 was built. Gene ontology and pathway analysis indicated that miR815a, miR849, and miR172d had regulatory control over the nocturnal rhythm in CS1 by regulating majorly Phytochrome-Interacting Factor 1 (PIF1), Ubiquitin-specific protease 12 (UBP12). Similarly, miR5021, miR5658, miR5658, miR1533, miR5205a, miR1436 had regulatory control over the diurnal rhythm of majorly Flowering locus T (FT), Constitutive photomorphogenic (COP) in CS2. MiR2919, miR849, miR2673a, miR5021, miR815a, miR172 and miR1089 had a regulatory role over leucine-rich repeat (LRR), heat shock protein 70 kDa (Hsp70) in CS1 and miR5021, miR5303, miR5205a, miR1436 had the regulatory role over LRR, HSP70,

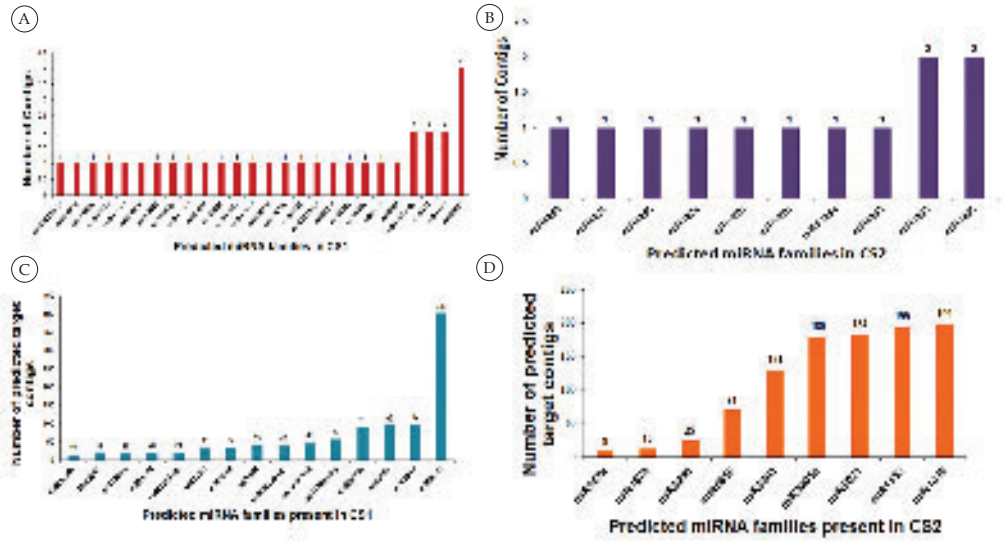


Fig. 1: Identified miRNA families with their number of predicted sequences in (A) CS1 (B) CS2 and Predicted number of target sequences for each miRNA families in (C) CS1 and (D) CS2

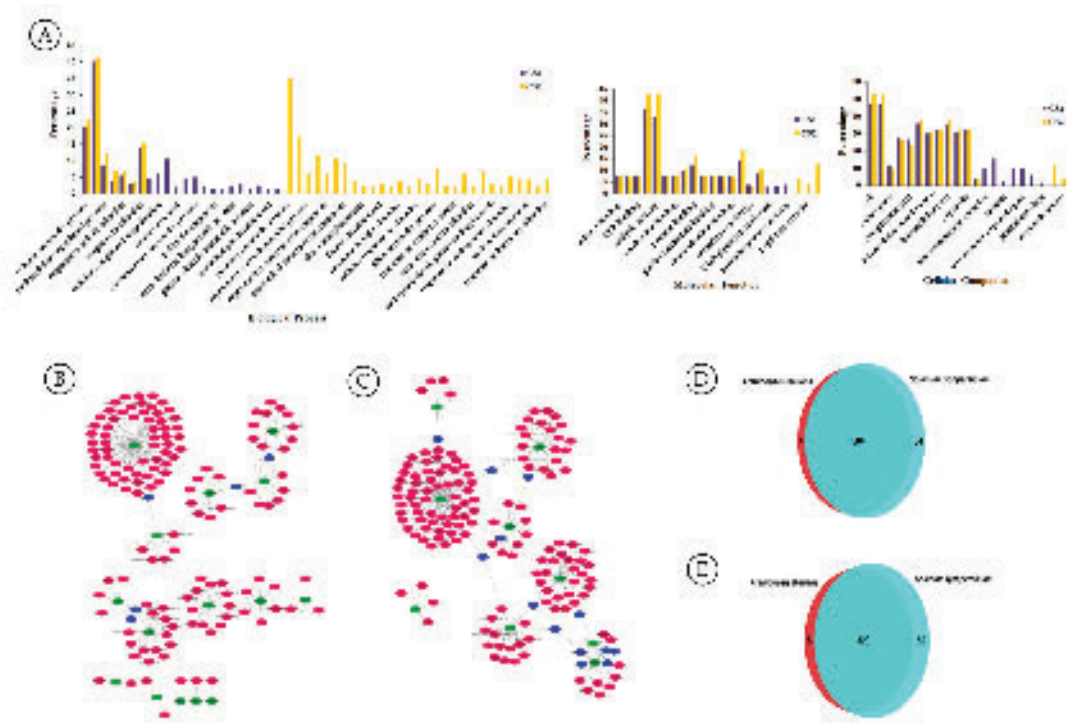

Fig. 2 : (A) Function of target transcripts controlled through predicted miRNAs. miRNA mediated gene regulatory network in B) CS1 and C) CS2 (Green colour eclipse demonstrate the identified miRNA candidates, pink colour eclipse depict predicted target, blue colour eclipse shows the common target and edges displayed MFE value between miRNA and their predicted targets). Venn diagram representing unique and shared annotations from Arabidopsis thaliana and Solanum lycopersicum in D) CS1 and E) CS2.

myb domain protein 48 (MYB48), Salt Overly Sensitive 1 (SOS1), Non-specific phospholipase C2 (NPC2) in CS2. Predicted miRNA families display maximum sequence similarity with the reported miRNAs of the same family. Majority of the predicted miRNA families were represented by only one member except (miR1023a-5p, miR172, miR172d, miR5021) in CS1 (Fig. 1A) and (miR1533 and miR1436) in CS2 (Fig. 1B). Regulation of 1024 and 1007 target transcripts was identified for 26 and 10 miRNAs families subsequently, miR5021 and miR1436 were found to have a greater number of target transcripts in CS1 and CS2 respectively (Fig. 1C and D). The target genes of CS1 and CS2 were functionally categorized in three major categories i.e. molecular function, biological process and cellular component (Fig 2A). The functional annotation of the identified miRNA targets were completed with *Arabidopsis thaliana* and *Solanum lycopersicum* (Fig. 2D and E) and the gene regulatory network was built for 15 and 9 miRNA families of CS1 and CS2 based on MFE. Their corresponding predicted target transcripts were identified accordingly (Fig. 2b and 2c).

The phylogenetic relationships among the predicted miRNAs with several other plants have been analyzed. There were 26 miRNAs predicted in CS1 and 10 miRNAs in CS2. All the identified miRNAs showed a maximum similarity with their respective miRNAs families such as *Amborella trichopoda, Acacia auriculiformis, Vigna unguiculata, Gossypium hirsutum, Glycine max, Medicago truncatula, Arabidopsis thaliana* and *Arabidopsis lyrata* in CS1 and *Glycine max, Sorghum bicolor, Populus trichocarpa, Oryza sativa, Arabidopsis thaliana, Vitis vinifera*, and *Zea mays* in CS2 (Fig. 3A-E). Hence, phylogenetic analysis was made for 2 miRNA families in CS1 and 4 miRNA families in CS2 for which substantial data were obtained. The identified miRNA families displayed higher sequence similarity with the plant miRNAs of the same family (Fig. 3J). The secondary stem-loop structures of pre-miRNA involved in circadian and stress response were studied. Fig 3F & H shows circadian rhythm related miRNA and Fig. 3G & I show stress response related miRNA in CS1 and CS2. Mature miRNAs are highlighted with cyan colour.

A comparative analysis predicted the involvement of a total of thirty six miRNA families and their corresponding target-genes in the process of flower anthesis and its corresponding stress with associated biochemical pathways in *C. nocturnum* and *C. diurnum*.

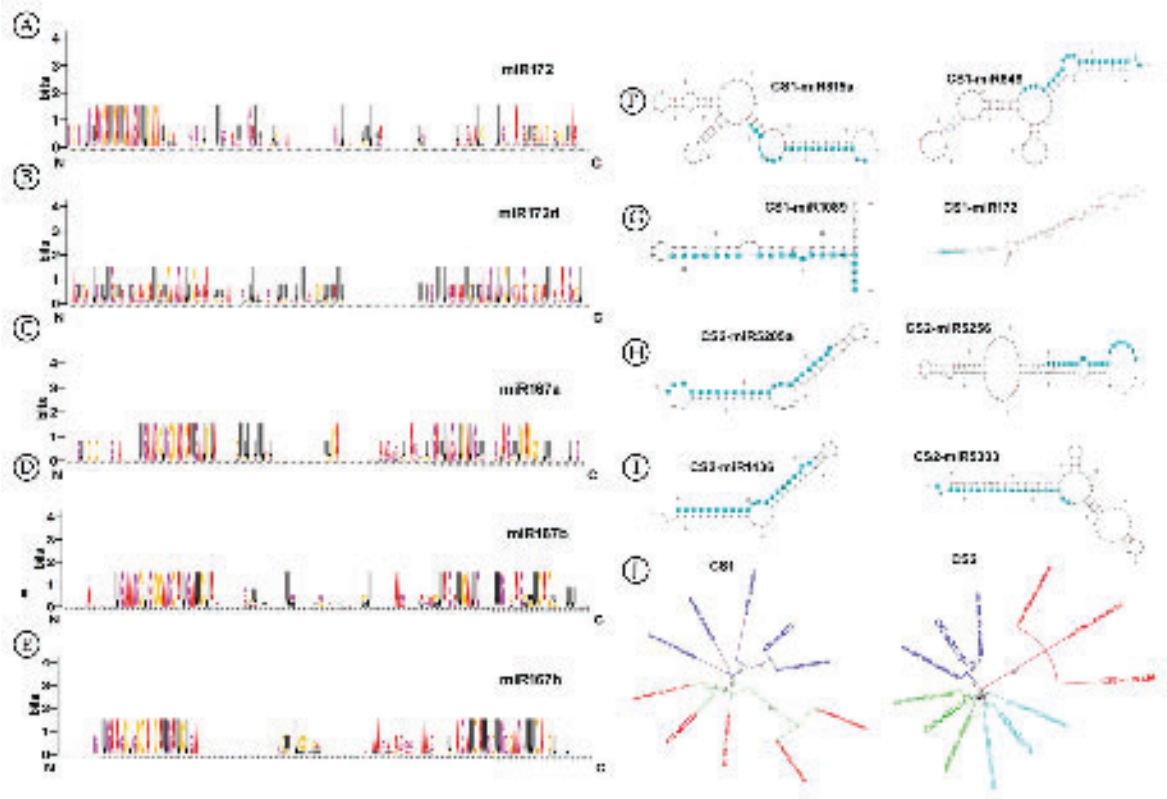

Fig. 3: The conservation study of CS1. A) miR172 with *Amborella trichopoda, Acacia auriculiformis, Vigna unguiculata* and *Gossypium hirsutum* and B) miR172d with Glycine max, *Medicago truncatula*, *Arabidopsis thaliana* and *A. lyrata*. The conservation study of CS2 C) miR167a with Glycine max, *Populus trichocarpa*, *Sorghum bicolor* and *Oryza sativa* D) miR167b with *Arabidopsis thaliana*, Glycine max, *Vitis vinifera*, and *Zea mays* E) miR167h with Glycine max, *Populus trichocarpa*, *Sorghum bicolor*, and *Oryza sa*tiva. Comparison of secondary stem-loop structures of pre-miRNA involved in circadian and stress response. (F and H) Circadian rhythm related miRNA (G and I) Stress response related miRNA in CS1 and CS2. Mature miRNAs are highlighted with cyan colour. (J) Phylogenetic analysis of predicted pre-miRNAs in CS1 and CS2. Predicted miRNAs are highlighted with bold and italic form. The bootstrap values are also shown.

MiR815a was observed to negatively regulate the chlorophyll biosynthesis and seed germination in the dark which led to the expression of a diverse set of genes which might result in night-flowering of *C. nocturnum*. Contrarily, miR1436 is found to convert the photoperiodic informations into florigen which might lead to regulate the photoperiodic flowering in plants and this might be a reason for daytime flowering in *C. diurnum*. This study also revealed the involvement of the predicted miRNAs in numerous plant stress responses such as miR2919, miR849, miR2673a, miR5021, miR815a, miR172, miR1089 was found to be involved in biotic and abiotic stresses in *C. nocturnum* and miR5021, miR5303, miR5205a, miR1436 in *C. diurnum*. Network analysis showed the regulation of 142 and 223 target transcripts through 15 and 9 distinct miRNA families respectively. The outcome of this study may furthermore enrich the understanding regarding regulation of miRNA and miRNA-mediated gene regulatory network in *C. nocturnum* and *C. diurnum*.

## Genome sequence of *Gossypium herbaceum* cultivar Wagad and identification of genomic variation to investigate the A-type cotton evolution

Cultivated cotton is an allotetraploid Cotton (AD), (n=2x=26) formed from the two diploid progenitors (A-genome and D-genome) around ~1-2 million years ago. A long term natural and artificial selection under different geo-ecological conditions generated many cotton germplasm for effective uses of natural fiber. Many studies reported cotton diversity in allotetraploid cotton through the whole genome sequencing of a large number of genotypes. Along with the allotetraploid cotton (*Gossypium hirsutum* (AD)1 and *Gossypium barbadense* (AD)2 ), A-type

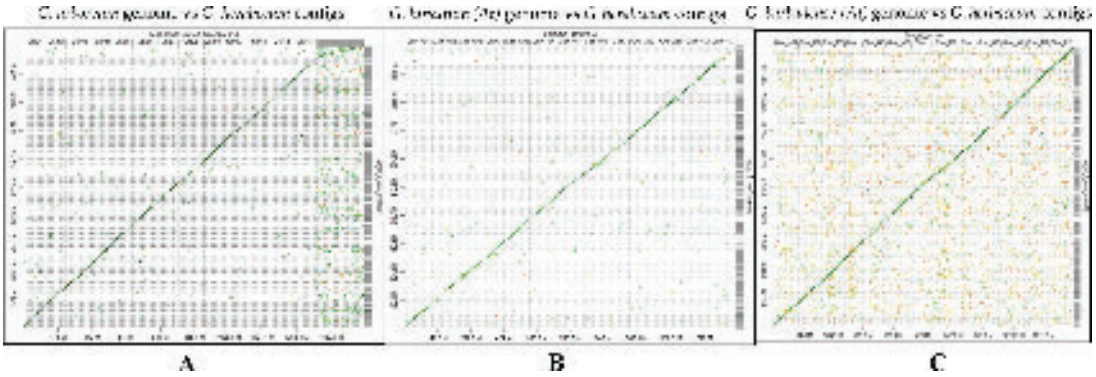


Fig. 4: Alignment of the assembled whole genome of *Gossypium herbaceum* cultivar wagad contigs to the previously reported cotton genome A) *Gossypium arboreum* B) At subgenome of the *Gossypium hirsutum* C) At subgenome *Gossypium barbadense*.

genome cotton (*Gossypium herbaceum* (A1) and *Gossypium arboreum* (A2)) are grown worldwide for quality cotton fibre.

In this context, we sequenced and assembled the *Gossypium herbaceum* cultivar Wagad (A1) for the first time through the Oxford Nanopore Sequencing Technology. We have generated 190 billion long nanopore reads with an approximate 110X genome coverage and 4356 contigs in the initial assembly process. Refining of the initial assembly has been carried out through the high-quality Illumina reads which generated 2665 contigs with 2935Kb N50 value (minimum length to cover 50% of the total length) (Table 1). To assess the completeness of the assembled genome based on single-copy orthologs, we generated the BUSCO score where 97.9% of total orthologs were present in our assembled genome (Table 2) that explain about its correctness of assembly.

**Table 1.** Data statistics by third-generation sequencing technology (Oxford Nanopore) and their assembly statistics before and after the polishing through Illumina reads.

| Data Generation | |
|---|---|
| Total read length | 190 billion |
| Total estimated coverage | ~ 110 X |
| Assembly Statistics (Initial Assembly) | |
| Number of contigs | 4356 |
| Total contigs length | 1624326245 bp |
| Assembly statistics after polishing | |
| Number of contigs | 2665 |
| Total contigs length | 1602923188 bp |
| N50 Value | 2935 Kb |

**Table 2.** Benchmarking sets Universal Single-Copy Orthologs (BUSCO) score of the assembled genome of *Gossypium herbaceum* cultivar Wagad.

| BUSCO Score | 97.9 % |
|---|---|
| Complete BUSCOs (C) | 1345 |
| Fragmented BUSCOs (F) | 3 |
| Missing BUSCOs (M) | 27 |
| Total BUSCO groups searched | 1375 |

The high quality genome of *Gossypium herbaceum* cultivar Wagad was collinear mapped on another assembled A-type genome (*Gossypium arboreum* (A2)) (Fig. 4A) and the A sub-genome of the two different allotetraploid cotton (AD1 and AD2) (Fig. 4B, 4C). In the analysis, we found a linear relation with a few misalignments which might be due to the presence of the InDels (Insertion and Deletions). We did not find any major inversion or deletion in the assembled genome (based on the previously assembled genome of other cotton species) indicating the conservation of genomic regions during the cotton evolution. In the future, we will conduct a detailed study of different InDels for the improvement of the cotton in the A-type Wagad genome.

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**Epigenetical mechanisms of plant adaptation under changing environment**

## Epigenomic response of high and low elevation populations of Indian *Arabidopsis thaliana* towards elevated $CO_2$

Understanding the plant responses towards changing environment still remains to be the goal of the plant biologists. This has become more important considering the present and expected future climate change scenario and demand to feed the growing world population. The accelerated climate change may force plants to adapt to the changing environment. Until now, only genetic factors were considered to reveal the underlying mechanisms

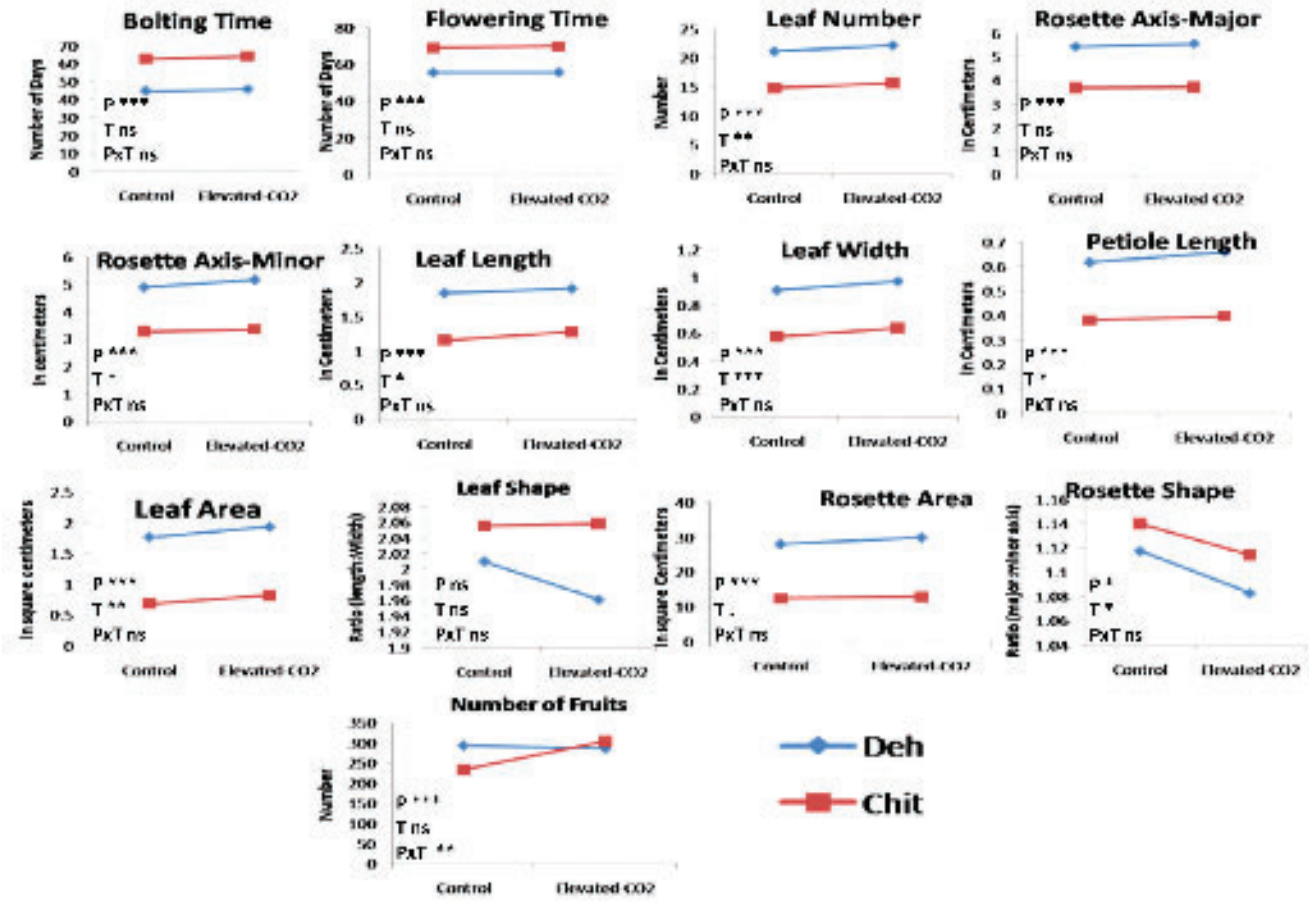


Fig 1 : Phenotypic variations in two populations of *Arabidopsis thaliana* (Deh & Chit) under elevated $CO_2$ and ambient conditions

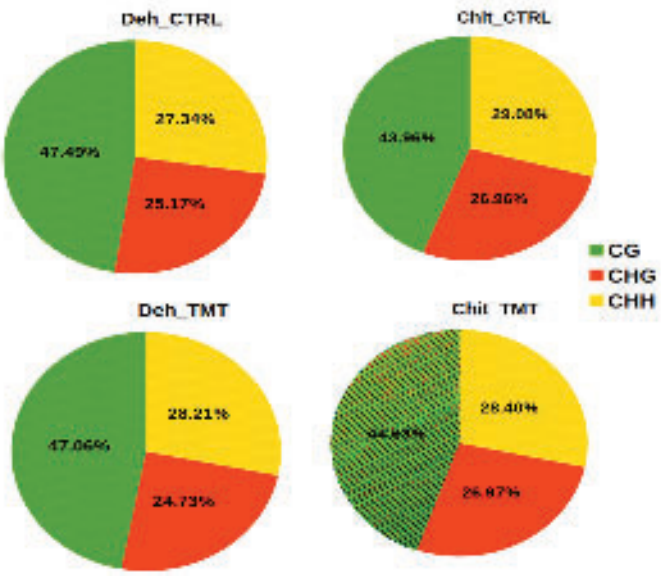


Fig. 2: Proportions of methylated cytosine in three sequence contexts, CG,CHG and CHH

involved in plant adaptation but we focus on exploring epigenetical factors by studying the natural populations of *Arabidopsis thaliana* those are growing along the steep elevation gradient ranging from 600 m (Above Mean Sea Level) to 3400 m (Above Mean Sea Level) of the Himalayas.

Fifteen accessions from each of the two populations, one originated from low elevation (DEH, 600 m amsl) and another from high elevation, (CHIT, 3500 m amsl) were planted in pots filled with Soilrite mixture. The plants were initially grown under controlled conditions for two weeks and then transferred to FACE (Free Air Concentration Enrichment) facility at CSIR-NBRI along with controls at ambient condition. The experimental design consisted of two factors: Population (P) and elevated carbon dioxide treatment (T). A total of 240 plants were used (2 treatments x 2 Populations x 15 genotypes x 4 replicates). The concentration of $CO_2$ was maintained at 410 ± 30 ppm and 550 ±30 ppm under control and elevated FACE rings, respectively. Morphological traits of the plants were measured at five weeks after germination and at the senescence phase. To determine the DNA methylation pattern of the populations, leaves from three individual genotypes corresponding to each of the two populations was collected and DNA was isolated. Twelve libraries were constructed corresponding to two populations (6 control and 6 treatment) and bisulfite sequencing were carried out.

Twenty four phenotypic traits were measured. The leaf number, length and width were increased under elevated $CO_2$ for both the populations (Fig 1). There was no variation in their life cycle under elevated $CO_2$. The productivity of high altitude population at elevated $CO_2$ was higher than the control condition. The highest proportion of methylation was in CG context (~ 45%), followed by CHH (~28%) and CHG (~25%) in both the populations under both the conditions (Fig 2). The maximum methylation in CG context lied in genic region (~70%) followed by in promoter (~18%) and inter-genic region (9%). Similarly different level of methylation was in CHG and CHH context (Fig 3). There was no significant global variation in total methyl cytosine in the two

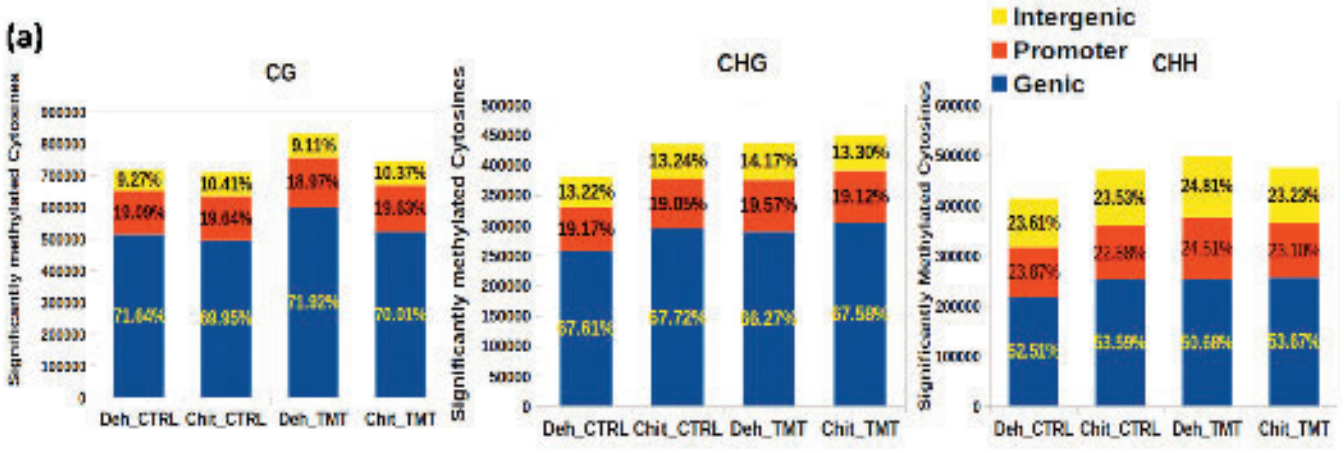


Fig. 3: Majority of the methylated cytosines lied in genic region followed by promoter and intergenic region CTRL, Control and TMT, treament

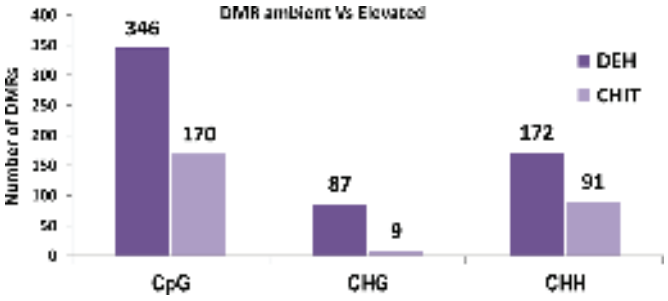


Fig. 4a: Differential DNA methylation between same population grown under elevated $CO_2$ and ambient

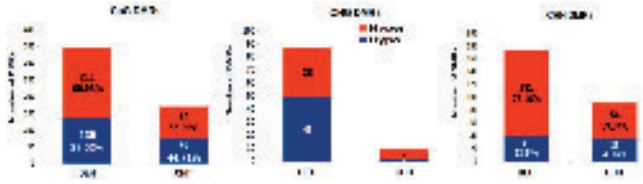

Fig. 4b: Distribution of significantly Differentially methylated regions into hyper and hypo methylated regions

populations. We identified differentially methylated regions (DMRs) between the control and elevated $CO_2$ for both the populations. The numbers of DMRs were 346 and 170 in CG context, 87 and nine in CHG context and 172 and 91 DMRs in CHH context in Deh and Chit, respectively (Fig. 4a). Most of these variations were gain-in methylations, hyper-methylated under elevated $CO_2$ in both the populations (Fig. 4b). Most of these genes were protein coding followed by the transposable elements. Only 3.3% of these genes were shared between the two populations. Significant DMRs were associated with the phenotype, trichome development, stomatal development etc. The population specific methylation patterns in response to elevated $CO_2$ were observed. There were 739, 795 and 478 DMRs between Deh and Chit in CG, CHG and CHH context, respectively under control condition (Fig 4c) and 1096, 1043 and 498 DMRs under elevated

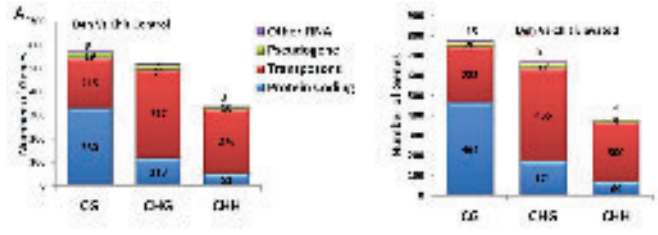

Fig. 5a: Annotation and classification of differentially methylated genes

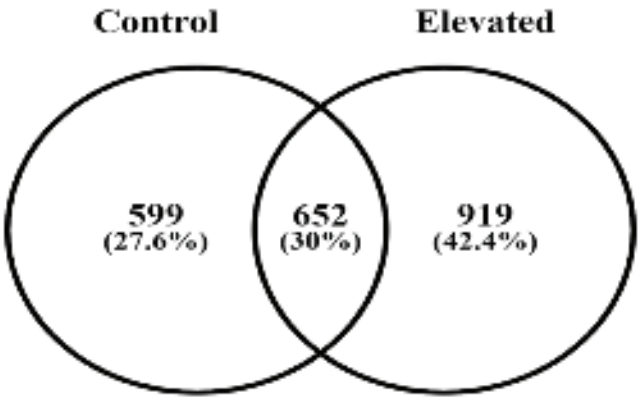


Fig. 5b: Variations in methylation between two populations under elevated $CO_2$ and ambient conditions

$CO_2$ in CG, CHG and CHH context, respectively. Most of these DMRs were hypo-methylated in CG and CHG context in Chit population under both the conditions. The CG -DMRs of control plants lied in 458 genes and 133 promoters while under elevated $CO_2$ the DMRs lied in 616 genes and 192 promoters. Similarly, DMRs in CHG and CHH context were also annotated. Majority of DMRs in CpG context were protein coding, while in CHG and CHH context, these were mostly transposable elements (Fig. 5a). Out of total differentially methylated genes between Chit control and Deh control and Chit treatment and Deh treatment, 652 genes were common between the two conditions (Fig. 5b). These commonly differential methylated genes were related to flowering time, stomatal development, trichome development etc. and these traits were differentially expressed in the two populations. The genes those were unique under control condition were related to light response, flowering, etc. The genes those were unique under elevated $CO_2$ condition were related to carbohydrate or lipid biosynthesis and metabolism. Overall, these findings suggest that the two populations responded differently towards elevated carbon dioxide.

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**Genetic transformation of crop plants, drought and *Fusarium* wilt stress in chickpea, insect resistance in cotton**

Our research is focused mainly on two broad areas:

1. **Drought stress tolerance in chickpea:** Drought is the most important yield-limiting factor of chickpea as most important growing areas are in the arid and semi-arid zones. Because of the heavy production losses caused by drought, it remains the foremost and biggest challenge that needs to be addressed for increasing the chickpea production.
2. **Chickpea – *Fusarium* interaction and Fusarium wilt tolerance in chickpea:** Chickpea production is mostly affected by vascular wilt disease due to fungus *Fusarium oxysporum* f. sp. *ciceris*. Fusarium can cause chickpea yield loss up to 90% worldwide. It is soil or seed-borne fungus, difficult to manage by crop rotation and fungicides application.

The group has been mainly working on the identification and characterization of chickpea genes for the development of abiotic and biotic stress tolerant transgenic chickpea plants.

### Transcriptome analysis of root samples from two drought tolerant chickpea genotypes

Transcriptome analysis of two drought-tolerant chickpea genotypes (BG-362 and P-256) subjected to

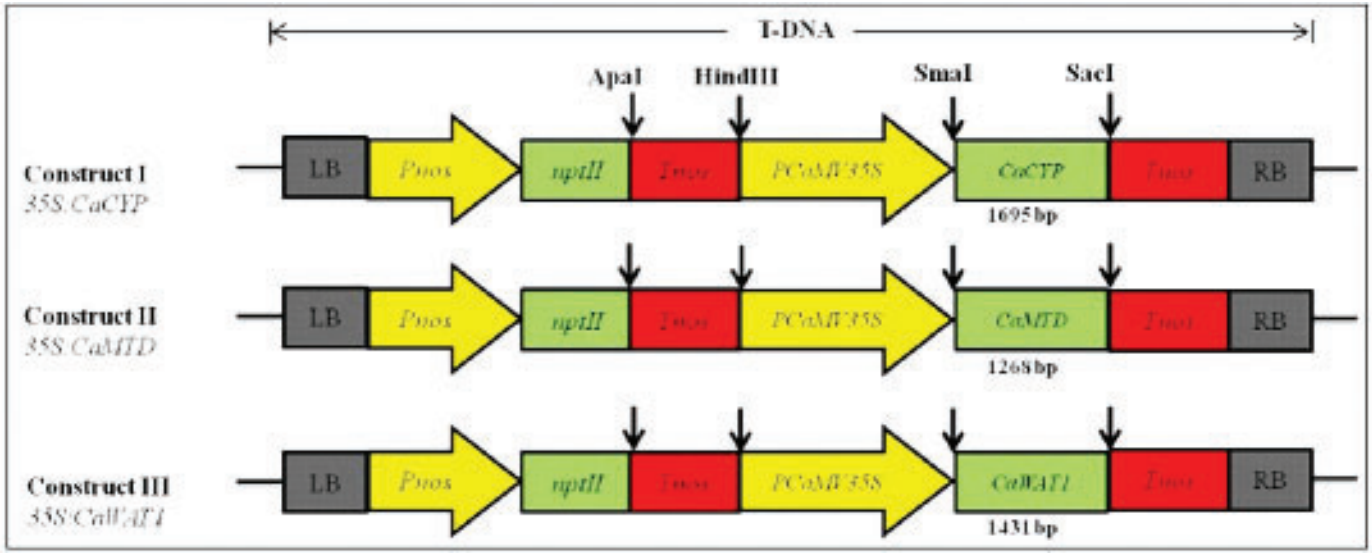


Fig. 1: Cloning of complete open reading frame of CaCYP (1695 bp), CaMTD (1268 bp), and CaWAT1 (1431 bp) genes in plant expression binary vector pBI121 using restriction sites SmaI and SacI and generation of three constructs I, II, and III, respectively.

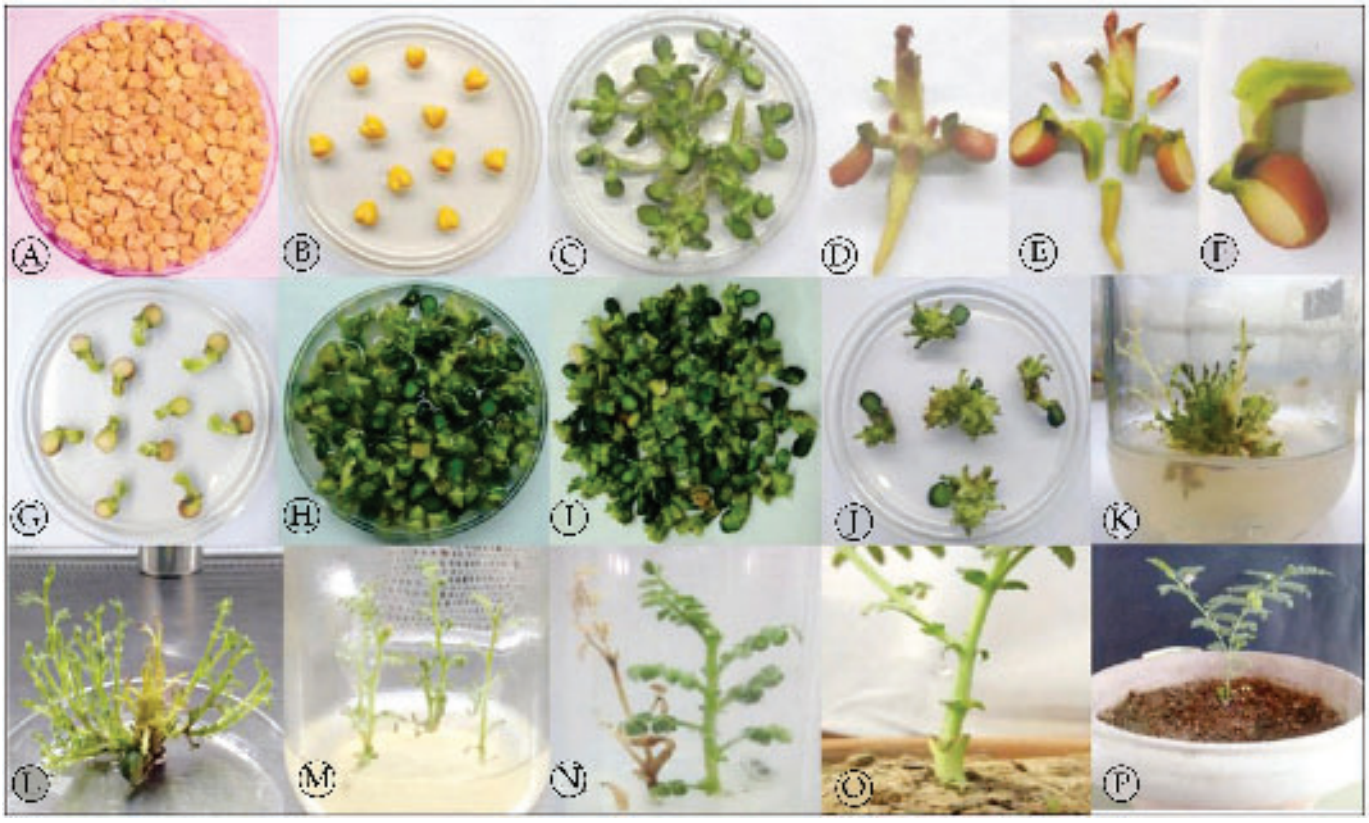

Fig. 2: Stages of chickpea transformation- A. Seeds of desi chickpea cultivar DCP92-3, B. sterilized decoated seeds inoculated on shoot induction medium, C. germinated seedlings, D., E. and F. explant preparation, G. inoculated axillary meristem explants (AMEs) in SIM, H. and I. co-cultivation of explants, J-N. co-cultivation of explants on selection media, O. grafted green shoot on root stock, P. established T0 putative transgenic chickpea plant.

PEG simulated drought conditions was performed. A total of 1,624 DEGs were identified, of which 97 were found to be common in both the genotypes. The validation of 21 randomly selected common DEGs using qRT-PCR was performed, which showed up-regulation and down-regulation of the respective genes, as observed in RNA-Seq analysis. Based on qRT-PCR results, three highly up-regulated DEGs, namely *CaCYP*, *CaMTD*, and *CaWAT1*, were cloned in the pBI121 vector (Fig. 1) and overexpressed in chickpea genotype "DCP92-3" and *Arabidopsis thaliana* (Col-0) through *Agrobacterium tumefaciens*-mediated transformation (Fig. 2). Molecular analyses of chickpea $T_2$ lines were performed using PCR, qRT-PCR, and Southern blotting. Three highly expressing $T_2$ lines of chickpea and three $T_3$ lines of *Arabidopsis* for three genes viz. *CaCYP*, *CaMTD*, and *CaWAT1* were selected for further analyses of drought-related parameters.

## LCM based Xylem specific RNA isolation from *Fusarium* infected chickpea roots and xylem-specific transcriptome analysis

Two contrasting chickpea genotypes JG-62 (wilt susceptible) and WR-315 (wilt resistant) plants were infected with a *Fusarium oxysporum* f. sp. *ciceris* race 2 strain to understand molecular interactions involved in vascular tissues specifically in xylem for blocking the fungus. To find out differential gene expression in xylem tissue, xylem parenchyma of both the chickpea genotypes was isolated using laser capture microdissection (Fig. 3). These LCM-based dissected xylem tissue cells were collected for downstream process like RNA extraction. The high quality RNA was used for transcriptome analyses aimed at deciphering xylem-specific molecular events. *Agrobacterium*-mediated transformation of Foc2 with the EGFP1 fluorescent protein marker gene was done that will useful for the study of differential colonization


**Fig. 3:** *Fusarium* infection, wilting in chickpea and pictorial representation of LCM techniques- A-B. Fixation of root samples, C-F. Block preparation of OCT media, G-K. Block fixing and cryosectioning, L. Grid of dehydration solution. M-P. Laser capturing and microdissection of xylem cells from section.

pattern of Foc2 in wilt resistant and susceptible chickpea roots. To understand the molecular basis of wilt resistance in chickpea, we investigated xylem-specific expression by transcriptome of wilt-susceptible and wilt-resistant cultivars under both Foc2 inoculated and control conditions. A total of 19,342 and 20,935 transcripts representing 16290 and 16442 genes loci were generated in JG-62 and WR-315, respectively by reference-guided assembly. This analysis revealed a total of 348 and 1,368 DEGs, among them, 131 and 233 genes were upregulated and 217 and 1,135 genes were downregulated in JG-62 and WR-315, respectively.

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- Dr. Manoj Kumar, ICMR-SRF
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# Plant Genetic Resources and Improvement

# PLANT GENETIC RESOURCES AND IMPROVEMENT

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## Research Scholars Statistics

| Sr. No. | Position Name | Numbers |
|---|---|---|
| 1. | Research Associate | 01 |
| 2. | JRF/SRF Fellow | 10 |
| 3. | Project Staff | 09 |

## Broad Areas of R&D

Genetic Improvement of Wild, Underutilized, Ornamental Crops

Selection, Genetic mapping, QTL, GWAS and Genomics-assisted breeding for crop improvement

## Major R&D Highlights

- *Cannabis* Centre was set up at Banthara Research Station, CSIR-NBRI.
- Various sets of new mapping populations of linseed were developed in cropping season by crossing different lines as parents having contrasting traits. These populations are in F2 generation which will be further progressed through SSD (single seed descend) up to F7/F8 generations for the development of recombinant inbred lines consisting genes for economically important traits of linseed. Also, the RILs i.e. RIL Pop. 1 for oil content: RKY-14 (high) x KL-213 (Low); RIL Pop. 2 for *Alternaria* blight: JRF-4 (Tol.) x Chambal (Sus.); RIL Pop. 3 for yield and its attributes: Hira (High) x Jawahar-17 (Low) and RIL Pop. 4 for flowering/maturity: Padmini (Early) x KL-213 (Late) already in F8 generations were advanced for one more generation to get a homogenous and stabilized population.
- Association mapping for major fatty acids was done from 86 accessions of linseed. The GLM approach identified 2 SNPs associated each with linoleic acid (LA) and palmitic acid (PA), 3 SNPs each with linolenic acid (LNA), steric acid (SA) and oleic acid (OA). In MLM approach, 2 SNPs with LA and 1 SNP each with LNA, SA and OA were found to be associated. The above 86 accessions were collected from 16 different states of India for evaluation of genetic diversity.
- Ninety six accessions of *Limonia acidissima* were collected from 16 different states of India for evaluation of genetic diversity using SSRs. These accessions were grouped into 3 major clusters i.e. Cluster I, Cluster II and Cluster III. Maximum number of accessions (46) were grouped into cluster II while minimum number of accessions (7) was present in cluster III. The distribution of large number of accessions in cluster II indicates their common origin.
- Ninety-five accessions of the underutilized tropical legume, winged bean [*Psophocarpus tetragonolobus* (L.) DC.] were grown and maintained in the botanic garden of CSIR-National Botanical Research Institute for further utilization. The refined seed-oils of these lines are suitable and comparable with soybean seed-oil. Safety evaluation of this refined oil on *albino* mice revealed non-significant changes in terms of body weight, organ weight, haematological and serum biochemical changes. Furthermore, the seed-cake of *P.tetragonolobus* contained proteins in the range of (34.7-35.6%), carbohydrates (21.4-23.1%), polyphenols (0.45-0.49%), *L*-DOPA (0.35-0.38%) and phytic acid (0.18-0.2%). These values are closely comparable with the soybean seed-cake.
- The genetic diversity among the ninety five accessions of *P. tetragonolobus* belonging to seven countries of African and Asiatic origin was carried out by employment of amplified fragment length polymorphism (AFLP) markers and internal transcribed spacer of nuclear ribosomal DNA (nrDNA-ITS). Associations between AFLP markers and flower, pod and seed traits like, days to 50% flowering (DFW), pod length (PDL), pod width (PDW), green pod length (GPL), number of pods per plant (PDSP), number of seeds per

pod (SDPD), 100 seed weight (SWT) and seed-oil content (SOC) were estimated. Seven AFLP markers were identified to be associated with SOC and minimum two AFLP markers were found to be associated with PDW. The population structure analysis among these accessions identified discrete sub-populations without any relationship with the geographical origin.

- A new dwarf *Chrysanthemum morifolium* variety, named 'NBRI- PUKHRAJ', was developed. The new variety is a novel dwarf, 'no-pinch no-stake', 'Anemone' type, floriferous *Chrysanthemum* variety which bears Yellow flowers that bloom during late-November to early January. It has been developed through mutation induction by gamma irradiation of parent var. 'Himanshu'. The variety was released by the Hon. UP Minister of Law & Justice Shri Brajesh Pathak.
- A new dwarf *Chrysanthemum morifolium* variety, named 'NBRI- SHEKHAR', was developed. The variety is a novel late blooming, floral-shape mutant which has been developed by gamma irradiation of its parent var. 'Su-Neel'. The new variety bears mauve flowers that start to bloom late during end-December to mid-February. The variety was released by Mrs. Sharmila Mande, wife of Hon. DG- CSIR, Dr. Shekhar C. Mande.
- The different floral gamma ray mutant lines of *Chrysanthemum* with altered trait(s) i.e. floret colour; shape; both colour as well as shape; different shades of floret colour; late-flowering were advanced to their respective next vegetative generations through rooted cuttings and suckers.
- Twenty new inter-varietal *Chrysanthemum morifolium* selections have been made on the basis of floral characteristics unique to the existing CSIR-NBRI germplasm. Further expansion of the germplasm has been made with unique combinations of ornamental traits. These selections include different recognized ornamental categories- 'Korean', 'Double-Korean', 'Anemone', 'Mini', 'Decorative', 'Semi-Quilled', 'Stellate' and 'Cineraria' types. The chrysanthemum germplasm at CSIR-NBRI is one of the most unique genetic resource of 'Garden chrysanthemum' available in the country.
- SEM studies were initiated in induced floral mutants of *Chrysanthemum morifolium* vis-à-vis their respective two somatic parents to find differences that may exist in their micro-morphological foliar characteristics i.e. stomatal size, density and trichome features which play role in withstanding various environmental stresses.
- SNP genotyping array have been developed for a number of plant species which are being employed for construction of linkage maps, tagging and introgression of QTLs for important agronomical traits, and use in marker assisted breeding programs. In cotton, QTL analysis was performed for six fibre traits such as spin length, uniformity, fiber length, bundle strength, elasticity and short fiber index by using approaches of interval mapping and composite interval mapping. A total of 34 QTLs related to different fibre traits were identified in 16 linkage group (LG). While, LG-16 has the maximum six number of fiber QTLs.
- Genome-wide association (GWAS) study was conducted in Opium poppy, resulting in identification of SNPs associated with Thebaine from both plant latex as well as one month old plant leaf samples. These key SNPs and their associated genes are being annotated to establish a linkage of these genes in thebaine development.
- The institute has taken an initaitive for development of low Tetrahydrocannabinol (THC) and high Cannabidiol (CBD) *Cannabis* lines for medicinal use and low THC and high fiber *Cannabis* lines for industrial use. HPLC protocol for determination of various cannabidiods has been standardized.

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**Genetic improvement and mainstreaming the underutilized plants through conventional and biotechnological approaches**

Sword bean (*Canavalia gladiata*), winged bean *(Psophocarpus tetragonolobus)* and tree bean *(Parkia timoriana)* are some of the legumes, which despite having tremendous nutritional value, are underutilized. Collection, maintenance, phytochemical evaluation, generation of large-scale genomic data, association of these data with specific traits, improvement of these plants through marker-assisted selection and breeding are the major objectives of the research activity.

The vegetable-oil market is expanding with low trans-fatty fat (TFA), low-cholesterol, and low-calorie products. There is an increase in the demand for edible oils mostly from developing countries. In order to fulfil the increased demand, there is a need for prospection of plants with vegetable-oil potential. So, the evaluation and characterization of fatty oils of winged bean and its further utilization was carried out.

## Collection and maintenance of winged bean

Ninety five accessions of winged bean (*Psophocarpus tetragonolobus* (L.) DC.) were procured from ICAR-National Bureau of Plant Genetic Resources (NBPGR), Akola, Maharashtra. These accessions were grown and maintained in the botanic garden of CSIR-National Botanical Research Institute, Lucknow, India for further utilization. These accessions had originated from countries: Ghana, Papua New Guinea, India, Indonesia, Philippines and Thailand. Apart from these accessions, some lines of *P. tetragonolobus* were procured from different states of northeast India, where it is extensively used for food-purposes. Collection and mainataince of 179 accessions of *P. tetragonolobus* was done at CSIR-NBRI. The detailed investigation of this plant was carried out by selecting 95 accessions from the total 179 accessions.

## Phenotypic characterization of winged bean

The collected winged bean seeds were grown in NBRI-experimental garden. Seven phenotypic traits of the 95 accessions of *P. tetragonolobus* were recorded for three consecutive cropping-seasons (Fig.1). The descriptors prepared by International Board for Plant Genetic Resources (IBPGR) were used for evaluation of the selected phenotypic traits. Observations on seven quantitative traits viz. days to 50% flowering (number of days from sowing to 50% flower opening), pod length (measured in cm as a mean of 10 dry pods), pod width (mm), days to maturity, green pod weight (g), number of pods per plant (measured as a mean of 10 dry pods), number of seeds per pod (measured as a mean seeds of 10 dry pods) and 100 seed weight (g) (Fig.1) were recorded manually as per the standard guidelines mentioned in www.biodiversityinternational.org.

## Winged bean seed-oil studies

Winged bean seeds have more than 35% of protein content which is almost equivalent to soybean. In the prevailing climatic conditions, the seed-yield of *P. tetragonolobus* varied from 2.6 to 3.8 t/ha. Being rich in proteins and lipids, it has the potential to be used in formulating nutraceutical and pharmacological products. Recently, the margarine blends prepared from winged bean seed-oil was shown to lower the atherogenic and thrombogenic indices. The consumption of this product could help in reduction of chronic heart diseases (CHD), diabetics and

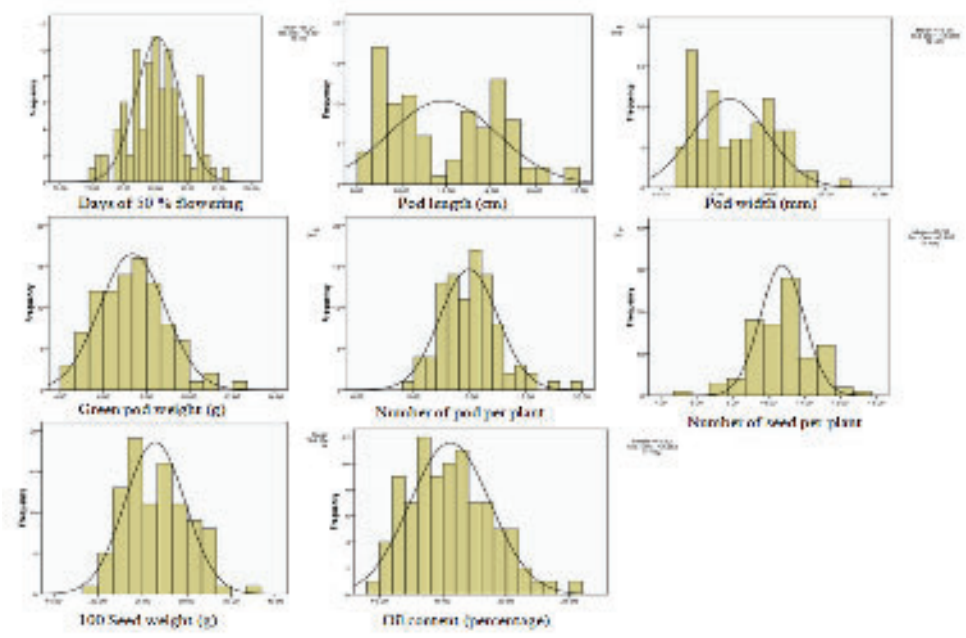


Fig.1. Frequency distribution curves on different phenotypic characters of 95 winged bean accessions from Africa and Asia

associated diseases. No oxidative derivatives and TFA were detected, when the winged bean oil was heated at 110°C for 32 h. The properties of winged bean and soybean oils appeared alike. The ratio of poly unsaturated fatty acids (PUFA) to SFA (P/S value) was greater than 1.0 for winged bean oil, it was lower as compared to soybean and peanut oils. After extraction of fatty oils, the de-oiled seed cake was used for the estimation of proteins, carbohydrates, polyphenols, *L*-DOPA and phytic acid to evaluate its potential as a balanced food supplement.

## Genetic diversity in winged bean assessed through ITS and AFLP markers sequencing

The nuclear ribosomal ITS of *P. tetragonolobus* was amplified using universal primer (TCC TCC GCT TAT TGA TAT GC) and (TCC GTA GGT GAA CCT GCG G). The ITS-PCR products were electrophoresed (0.8% agarose gel). The amplified bands were excised and purified using Nucleospin Kit. The purified DNA was quantified using nanodrop spectrophotometre and was sequenced through Applied Biosystems Automated Sequencer. The generated sequences were aligned using Clustal W programme. Further, Phylogeny was carried using MEGA6 software. The length of nr-ITS region ranged from 316 bp (NBPT70) to 698 bp (NBPT79). The ITS sequence was rich in GC content which ranged from 52.7% (NBPT8) to 51.0% (NBPT46). The nucleotide frequencies were found to be A (22.6%), C (24.3%), G (27.7%) and T (25.4%). However, the nrITS of *P. tetragonolobus* is rich in GC-content (51.8%).

## AFLP Markers trait association

A total of 181 AFLP markers were used to study the marker-trait associations for eight traits (DFW, PDL, PDW, GPL, PDSP, SDPD, SWT and SOC). Frequency distribution, including mean and standard deviation for each of the above eight traits were analyzed. The analysis was also used to calculate associations among individual markers for each of the eight traits by employing the mixed linear model (MLM) based on the kinship matrix (K-model). The kinship-matrix was generated by TASSEL ver. 3.0 (http://www.maizegenetics.net) through conversion of the distance matrix from TASSEL's cladogram to a similarity matrix, the options of EMMA were chosen for MLM. Significance of marker-trait associations was determined at $p \leq 0.05$.

Eight quantitative traits namely, DFW, PDL, PDW, GPL, PDSP, SDPD, SWT and SOC revealed significant variability among the accessions. High coefficient of variation was observed for number of pods per plant (25.97 %) followed by green pod weight (22.02%) and pod length (21.07%). From the studied accessions more desirable traits identified were- higher number of pods per plant in NBPT23, green pod weight in NBPT05, pod length in NBPT01, early flowering in NBPT23 and late flowering in NBPT03.

Altogether 35 marker trait associations (MTAs) were identified involving 26 AFLP markers. Seven AFLP markers were associated with oil content and two AFLP markers were associated with pod-width. Out of the 26 AFLP markers, 19 AFLP markers were involved in trait-specific MTAs and seven AFLP markers were involved in multi-trait MTAs and were found associated with up to three traits.

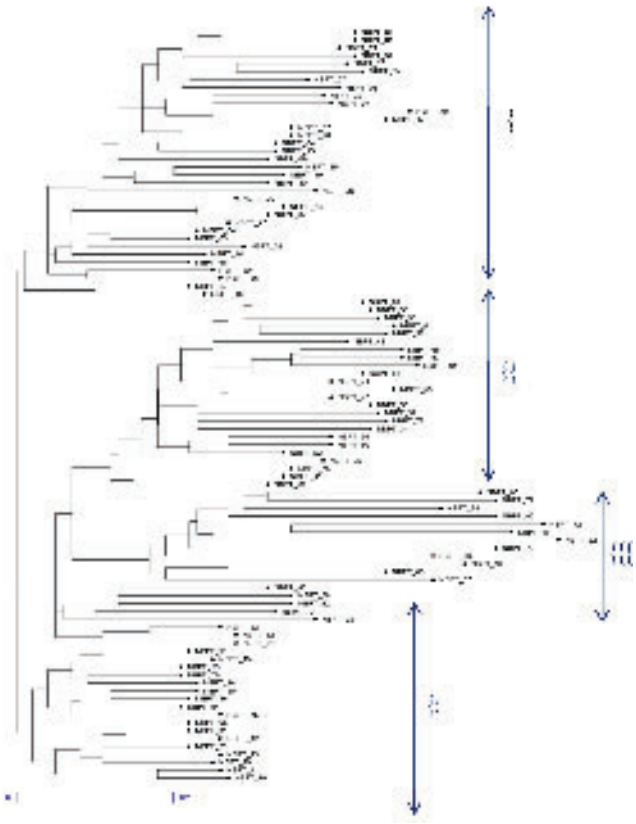

Fig. 2. UPGMA-dendrogram of 95 cultivars of winged bean based on Jaccard's coefficient

Among the 64 sets of combinations of *Eco*RI-*Mse*I primers with three nucleotides extension, four most polymorphic combinations were selected for analyzing 95 accessions of *P. tetragonolobus* (25 accessions from India, 42 from Thailand, 21 from Papua New Guinea, 4 from Ghana, 2 from Indonesia and 1 each from the Philippines and Nigeria). Each primer set generated (9-87) polymorphic fragments. A total of 181 polymorphic fragments among 205 readable bands were detected by four primer sets. The minimum and maximum percentages of polymorphisms were detected by the primer combinations *Eco*RI-ACT/*Mse*I-ACC and *Eco*RI-ACA/*Mse*I-CAA respectively. Pair-wise comparison of genetic similarity among these accessions estimated ranged from 0.17 to 0.99. Maximum genetic similarity was reported between the Indian accessions NBPT11 and NBPT10 and the minimum genetic similarity was reported between Papua New Guinea accessions NBPT32, NBPT49 with Indian accessions NBPT04, NBPT11 and NBPT17. Maximum genetic similarity was noticed between accessions NBPT54 (Thailand) with NBPT53 (Philippines) and NBPT55 (Thailand). Accessions from Papua New Guinea had the maximum genetic similarity with NBPT57, NBPT65 and NBPT66, NBPT60 accessions of Thailand.

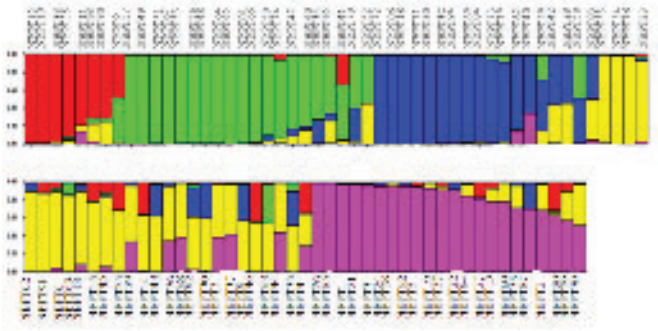

Fig. 3. Genetic relatedness of 95 cultivars of winged bean as analyzed by STRUCTURE program

**Cluster analysis**

Cluster analysis of 95 *P. tertragonolobus* accessions provided distinct groupings. The analysis based on Jaccard's genetic distance had grouped the 95 accessions into four clusters with three relatively big clusters (I, II and IV) (Fig.2). Cluster III is the smallest one accommodating only 12 accessions and majority of the accessions were from Thailand. Only one accession from India (NBPT16) is accommodated in this cluster. Two of the Indonesian accessions grouped together in cluster II. Majority of Indian accessions were grouped in cluster I and IV.

**Analysis of population structure**

The model-based population structure analysis by using STRUCTURE program grouped all the 95 accessions into five clusters/sub-populations (Fig. 3). The five clusters formed in the analysis also genetically paired with different countries. Group I consisted 8 accessions majorly from India and Thailand. Group II and V represented accessions from Indonesia along with accessions from Ghana, India, Philippines and Thailand. Group III included maximum number of accessions from India, Papua New Guinea, Thailand, Philippines except Indonesia.

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# Mutation breeding and development of trait-specific novel mutants in ornamental plants

Floriculture industry thrives on constant improvement and novelty of ornamental traits. Primary traits that are in demand for various ornamentals, either alone or in combination, include change in petal pigments/subtle hues, corolla shapes, flower size and number, extended blooming, dwarf varieties, and better vase-life. Designing ornamental crops, at will, has been a major challenge. CSIR-NBRI has been involved in floricultural research & development of novel floricultural varieties for more than 50 years, and is known for its diverse germplasm collections of many ornamentals especially Chrysanthemums, which is one of the most sought-after winter ornamental flowering crops.

Mutation breeding has been a useful tool in creating desired phenotypic, biochemical and yield traits, alone or in combinations, which are otherwise difficult to get or may take many years through conventional breeding. Specific ornamental mutants differing in one or two traits without any reversion to parental state even after successive generation cycles presents an excellent research opportunity for reverse genetics and trait-dissection at molecular genetic level.

## New ornamental inter-varietal selections in *Chrysanthemum morifolium*

Twenty new inter-varietal *C. morifolium* selections have been made on the basis of floral characteristics unique to our existing germplasm. This is in addition to 15 selections made last year. With these selections, we have further expanded our germplasm with unique combinations of ornamental traits. These selections include its different recognized ornamental categories- 'Korean', 'Double-Korean', 'Anemone', 'Mini', 'Decorative', 'Semi-Quilled', 'Stellate' and 'Cineraria' types. The *Chrysanthemum* germplasm at CSIR-NBRI is one of the most unique genetic resource of 'Garden *Chrysanthemum*' available in the country (Fig. 1).

Fig. 1. Some of the new *Chrysanthemum morifolium* selections under different ornamental categories

## Micro-morphological (SEM) studies of leaf-surface in mutant lines of *Chrysanthemum morifolium*

SEM studies were initiated in induced floral mutants of *Chrysanthemum morifolium* vis-à-vis their respective two somatic parents to find out any differences that may exist in their micro-morphological foliar characteristics which play role in withstanding various environmental stresses (Fig 2). The preliminary investigations revealed that there were significant differences in the stomatal size, stomatal density and trichome density between different parental varieties. While individual parent variety and its derived mutants were compared, no variation was observed

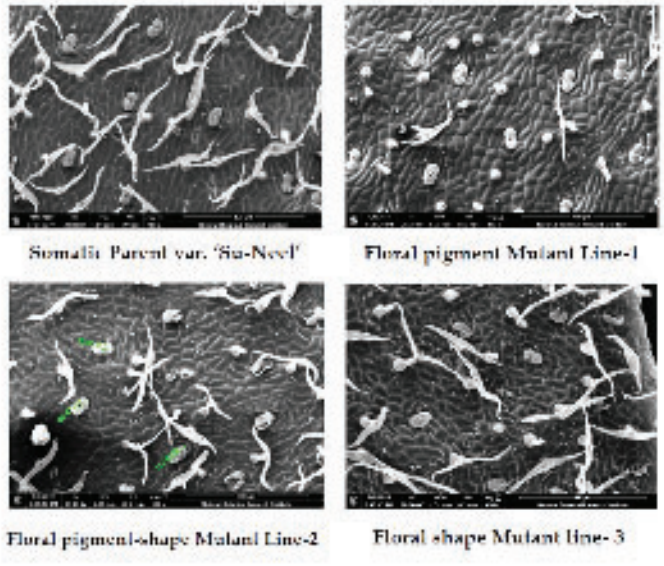


Fig. 2: Micromorphological (SEM) studies of leaf-surface in *Chrysanthemum morifolium* var. 'Su-Neel' and derived floral mutants

w.r.t. stomatal size and stomatal density, however, significant differences were observed in trichome characteristics in case of the mutants derived from parent var.-'Su-Neel', where, derived floral mutants showed reduced trichome density (by 16% - 42%) as well as reduced degree of trichome differentiation (by 78% - 14%). The study shall be further expanded to include more parental varieties and their derived ornamental mutants.

Total six novel ornamental mutant varieties have been developed in *Chrysanthemum morifolium* during the last 8 yrs (2012-20) and two more chimera-free mutant lines from var. 'Puja' are in advanced generations.

The different floral gamma ray mutant lines of chrysanthemum with altered trait(s) i.e. floret colour; shape; both colour as well as shape; different shades of floret colour; late-flowering were advanced to their respective next vegetative generations through rooted cuttings and suckers. i.e. VgM11 generation in case of var. 'Himanshu' derived varieties, VgM16 generation in case of var. 'Suneel' derived varieties as well as of var. 'Puja' derived mutants. The altered ornamental characters of above mutants were found to be completely non-reverting to their respective somatic parents from which these were derived.

Specific ornamental mutants differing in one or a few characters derived from randomly mutated parent variety after successive cycles of isolation and selection with no reversion to parental state presents an excellent research material for trait-dissection at molecular level. Besides, contrasting germplasm resources present an ideal experimental material to identify common genomic signatures or functional elements associated with early/late/extended flowering.

## New Varieties Developed

Two new ornamental varieties of *Chrysanthemum morifolium viz.* 'NBRI-Pukhraj' and 'NBRI-Shekhar' were developed and released during the reporting period. Both the varieties have been developed through gamma irradiation.

### *Chrysanthemum morifolium* var. 'NBRI-Pukhraj'

The new variety 'NBRI-Pukhraj' is a novel dwarf floral colour mutant, developed by gamma irradiation of its parent var. 'Himanshu' (Fig. 3). The variety 'NBRI-Pukhraj' is a 'no-pinch-no stake', floriferous chrysanthemum variety that bears bright lemon yellow ray-florets (RHS Fan-1; Yellow Group 2C) that are completely ligulate (flat strap-shaped) unlike the parent variety and bears darker yellow central anemone-type disc. It flowers during late November to December.

The plant attains height up to ~30 cms; the whole plant spreads evenly like a small dome with numerous sprays bearing flowers (capitula) and buds radiating out. The maximum capitulum size (diameter across) is up to ~9.0 cm. The ray florets are ligulate with flat strap shaped lamina. It takes ~100 days to raise the variety from rooted cutting stage to full bloom stage.

Being a novel dwarf variety of a contrasting floral colour (lemon-Yellow) than its somatic parent (mllky white), it can be also used to create colourful patterns in landscape gardening.

The variety was released during Annual Chrysanthemum & Coleus Show- 2019' by Mr. Brajesh Pathak, Minister of Law and Justice, UP Government.

### *Chrysanthemum morifolium* var. 'NBRI-Shekhar'

The variety 'NBRI- Shekhar' is a novel late-blooming floral-shape mutant which has been developed by gamma irradiation of its parent var (Fig. 4). 'Su-Neel'.


Fig. 3: *Chrysanthemum morifolium* var. 'NBRI-Pukhraj' a new variety developed. A. close-up view of the flower, B. Mr. Brajesh Pathak, Minister of Law and Justice, UP Government releasing the variety at the Chrysanthemum and Coleus Show-2019


Fig. 4: *Chrysanthemum morifolium* var. 'NBRI-Shekhar' a new variety developed. A. close-up view of the flower, B. Dr. (Mrs.) Sharmila Mande, wife of Dr. Shekhar C. Mande, DG, CSIR, New Delhi releasing the variety at the Rose and Gladiolus Show-2020.

The maximum capitulum size (diameter across) is up to 9.0 – 9.5 cm. The capitula lack central disc (Type-'Decorative'). Numerous mauve ray florets, semi-quilled shaped, spread out radially giving the capitulum (inflorescence) its unique dome-shaped crown-like appearance. The variety bears mauve colour (RHS Fan-2; Red Purple Group 72A). The plant attains height up to ~60 cms. It takes 120 - 130 days to raise this proposed mutant variety from 'rooted cutting stage' to 'full bloom stage'. The rooted cuttings are planted around late-August and it starts to bloom during end-December to mid-February. This new variety is ideally suited for potted plants, and as cut-flower spray. The variety was released during 'Annual Rose & Gladiolus Show- 2020' by Dr. (Mrs.) Sharmila Mande.

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**Molecular markers, creation of genetic resources, linkage analysis, genomics assisted breeding in industrially important crops**

### Genetic and genomics resources in linseed for varietal development

Linseed is a multipurpose crop commercially grown for its oil and fibre. The linseed oil is a rich source of Omega-3 (Alpha Linolenic Acid) which provides beneficial effects in numerous clinical conditions such as, cardiovascular disease, inflammatory disorders, immune function and cancer. The flax fibre is also a widely used and valuable raw material in several industries such as textiles, paper and packaging. However, despite such excellent profile for industrial and nutritional utility, linseed has remained unexplored and neglected in India. An effort was made for development and deployment of genetic and genomic resources for linseed improvement. Various sets of new mapping populations were developed by crossing different lines as parents having contrasting traits. These populations are in $F_2$ generation which will be further progressed through SSD (single seed descend) up to $F_7/F_8$ generations for the development of recombinant inbred lines consisting genes for economically important traits of linseed. The RILs, RIL Pop. 1 for oil content: RKY-14 (high) x KL-213 (Low); RIL Pop. 2 for *Alternaria* blight: JRF-4 (Tol.) x Chambal (Sus.); RIL Pop. 3 for yield and its attributes: Hira (High) x Jawahar-17 (Low) and RIL Pop. 4 for flowering/maturity: Padmini (Early) x KL-213 (Late) already in F8 generations were advanced for one more generation to get a homogenous and stabilized population. These homogenous RILs will be further utilized for fine QTL mapping for important quantitative traits. Furthermore, 86 accessions of linseed from germplasm set were used to identify SNPs through Genotyping *By* Sequencing (GBS) for association mapping for major fatty acids. After stringent filtrations, a set of 10,057 SNPs were

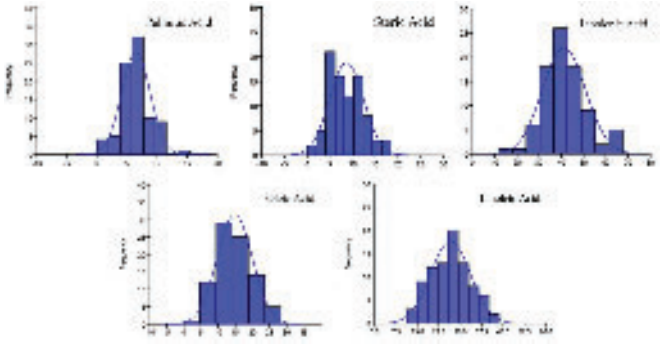

Fig. 1: Frequency distribution of different fatty acids (%) in 86 genotypes of linseed

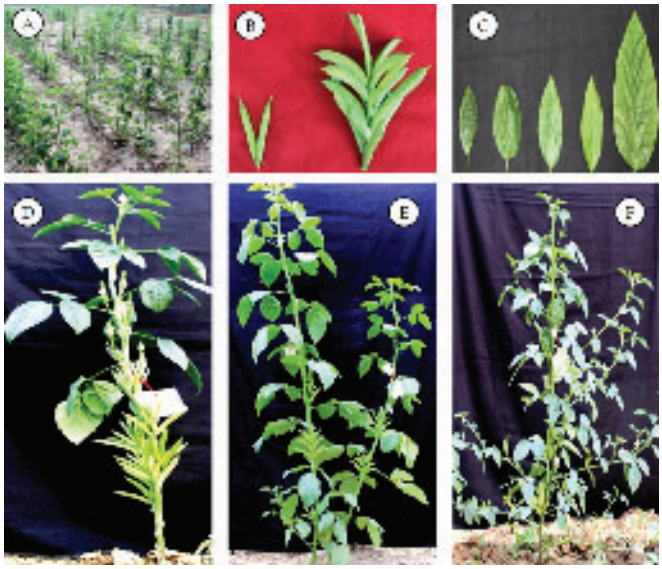

Fig. 2: Morphological variations among guar genotypes for different quantitative traits. A. Field view of guar germplasm, B. Variations in number of pods per cluster, C. Variations in leaf morphology, D-F. Variations in branching and clustering pattern in guar.

**Table 1: Marker-trait associations among 86 accessions of linseed for fatty acids with GLM and MLM approaches**

| | | GLM | | MLM | |
|---|---|---|---|---|---|
| **Trait** | **SNP** | **P value** | **Corr. P value** | **P value** | **Corr. P value** |
| **LA** | Lu7153 | 1.46E-06 | 0.01 | 4.48E-06 | 0.02 |
| **LA** | Lu11039 | 1.70E-06 | 0.01 | 3.25E-06 | 0.03 |
| **LNA** | Lu1924 | 6.10E-07 | 0.01 | 3.55E-06 | 0.04 |
| **LNA** | Lu12639 | 4.13E-06 | 0.02 | - | - |
| **LNA** | Lu15479 | 7.71E-06 | 0.03 | - | - |
| **PA** | Lu20402 | 2.36E-06 | 0.02 | - | - |
| **PA** | Lu7650 | 8.55E-06 | 0.04 | - | - |
| **SA** | Lu14807 | 4.50E-06 | 0.05 | - | - |
| **SA** | Lu20706 | 6.07E-06 | 0.03 | 1.66E-06 | 0.02 |
| **SA** | Lu15458 | 1.80E-05 | *0.06* | - | - |
| **OA** | Lu186 | 3.90E-06 | 0.013 | 1.7E-06 | 0.04 |
| **OA** | Lu2708 | 3.49E-07 | 0.004 | - | - |
| **OA** | Lu2214 | 1.57E-05 | 0.039 | - | - |

identified across 86 accessions. A large number of marker-trait associations were observed through GLM approach which reduced after FDR corrections for multiple testing. The GLM approach identified 2 SNPs associated each with Linoleic acid (LA) and palmitic acid (PA), 3 SNPs each with Linolenic acid (LNA), Steric acid (SA) and Oleic acid (OA) (Fig. 1).

In addition to the GLM approach, the MLM approach also detected several markers to be associated with various fatty acids (Table 1). In MLM approach, 2 SNPs with LA and 1 SNP each with LNA, SA and OA were found to be associated consistently. In addition to available germplasm, for creation of more genetic variations 3000 $M_2$ plants derived from EMS treated $M_{1s}$ of "Neelum" variety of linseed were grown in field for evaluation and selection. In addition, double mutagen treatment was practised on $M_2$ plants which increased the frequency of mutants and more visible mutational changes. Detailed phenotypic data was recorded on important agronomic traits. The mutant plants showed visual mutation such as albinism, tall, dwarf, change in flower color and change in capsule size.

## Phenotypic evaluation of guar (*Cyamopsis tetragonoloba*) accessions for important agronomic traits

Cluster bean or guar (*Cyamopsis tetragonoloba* (L.) Taub.) is a widely grown crop but not commercially or on large scale. Basically, guar is a drought tolerant, deep rooted and annual legume. It is self-pollinated, multipurpose and restorative leguminous crop. The crop is known for exceptionally high adaptation towards poor and erratic rains, low inputs and less care, soil enrichment properties.

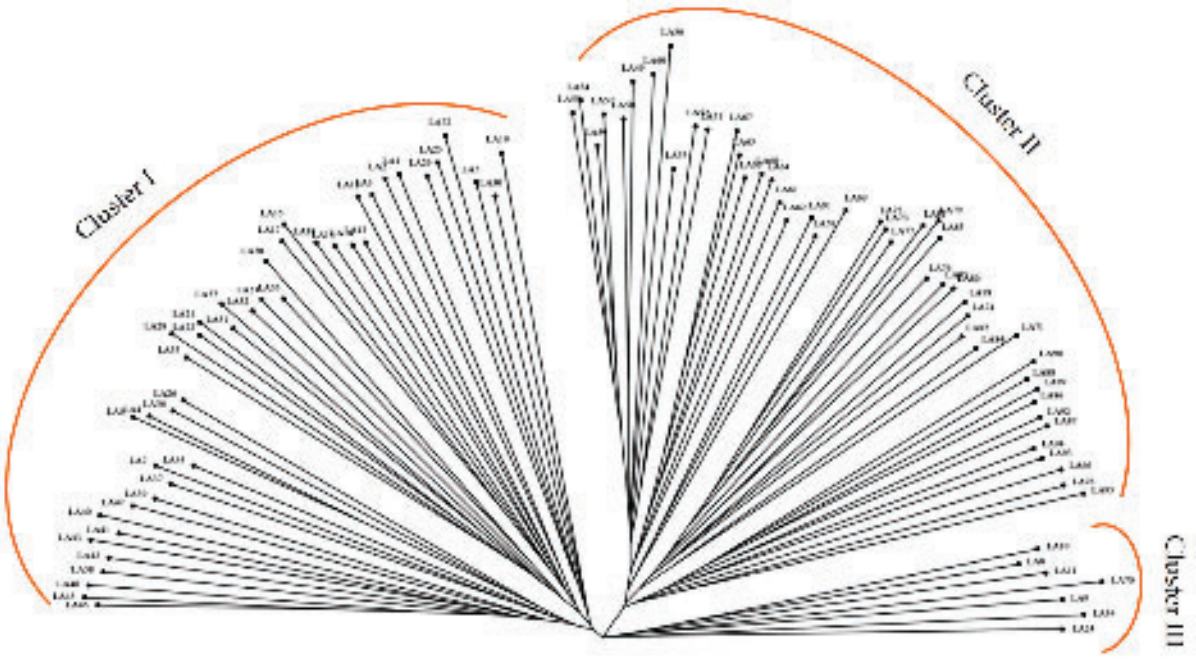


Fig. 3: Dendrogram of 96 accessions by Unweighted Pair-Group Method using Arithmetic average (UPGMA) analysis.

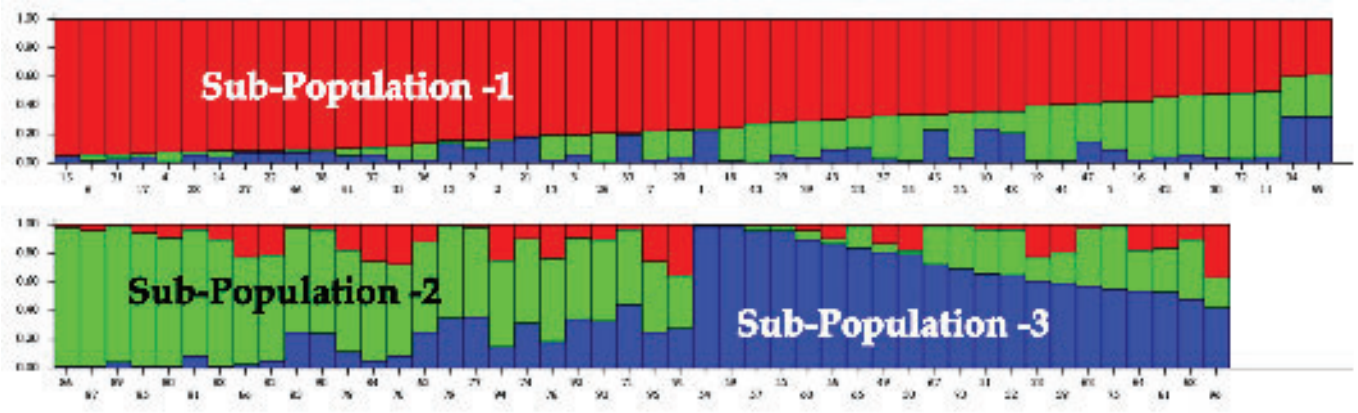


**Fig. 4:** Bar plot of 96 accessions derived from STRUCTURE analysis at K = 4

Despite several industrial importance of cluster bean, it still comes under minor crop due to unexplored knowledge of genetic diversity and unavailability of genetic resources. Keeping in view the importance of guar, its available germplasm at CSIR-NBRI was evaluated on morphological basis for genetic variability in 16 quantitative characters. A total of 277 genotypes were screened in field conditions which showed a large phenotypic variation for different traits like plant height, branching, pod number and leaf morphology (Fig. 2). The analysis of variance (ANOVA) revealed considerable variability for all the traits and lack of environmental effects. The traits such as days of flowering (DOF), Plant height (PH), Days to maturity (DM), Number of clusters per plant and Number of pods per plant showed maximum range of variation. Also, these traits had maximum heritability along with high genetic advance (GA). Therefore, these traits would play an important role during selection for any crop improvement programme.

## SSR based genetic diversity and population structure in *Limonia acidissima*

*Limonia acidissima* L. (Rutaceae) commonly known as Wood apple has two forms, one with large, sweet fruits and the other with small, acidic fruits. It is an important indigenous tree of India known since ancient time for its medicinal properties, and prescribed as a traditional medicine for the treatment of various ailments. A subset of 96 accessions of *L. acidissima* was collected from 16 different states of India for evaluation of genetic diversity. Transcriptome sequencing of *L. acidissima* was done de novo for novel SSRs synthesis as there were no earlier reports for development of genic SSR markers in this species. Among 130 SSR primers, total 30 primers showed polymorphism among 96 *L. acidissima* accessions. The average polymorphism information content (PIC) values for SSRs ranged from 0.17 to 0.81, with an average of 0.62. Number of alleles per marker ranged from 3.00 to 9.00 (avg. 5.3). The frequency of major allele ranged from 0.20 to 0.88 (avg. 0.42). Gene diversity ranged from 0.19 to 0.83 (avg. 0.66). The pair wise genetic dissimilarity varied from 0.08 to 0.49 (avg. 0.31). An UPGMA tree based on arithmetic mean of 96 accessions was constructed. The 96 accessions were grouped into 4 major clusters i.e. Cluster I, Cluster II and Cluster III (Fig. 3). Out of 96, maximum number of accessions were grouped into cluster II while minimum number of accessions (i.e. 7) was present in cluster III. The distribution of large number of accessions in cluster II indicates their common genetic origin. Further, the model-based simulation of population structure was analysed to investigate the subpopulations among the 96 accessions varying from K = 2 to K = 10. Estimated likelihood was found to be maximum at K = 3, suggesting that the population used in this study consists of three sub-populations (Fig. 4).

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## SNP-based high density genetic linkage map for intra-*Gossypium hirsutum* mapping population and QTL analysis

SNP genotyping arrays have been developed for a number of plant species which are being employed for construction of linkage maps, tagging and introgression of QTLs for important agronomical traits, and use in marker assisted breeding programs. A total of 6,491 parental polymorphic SNPs were initially considered for linkage map construction in *G. hirsutum* . However, markers showing more than 20% heterozygosity were removed from the linkage analysis, leaving a total of 4,430 polymorphic markers for linkage group (LG) analysis. We have constructed 26 LGs for the intra-*G. hirsutum* RIL mapping population with a coverage of 29577.25 cM distance and an average of 6.67 cM inter-marker distance. QTL analysis was performed for six fibre traits such as spin length (SL), uniformity (UR), fiber length (F), bundle strength (BS), elasticity (El) and short fiber index (SFI) by using approaches of interval mapping (IM) and composite interval mapping (CIM). A total of 34 QTLs related to different fibre traits were identified in 16 LGs. LG-16 has the maximum number of fiber QTLs, i.e. 6 QTLs (Fig. 1).

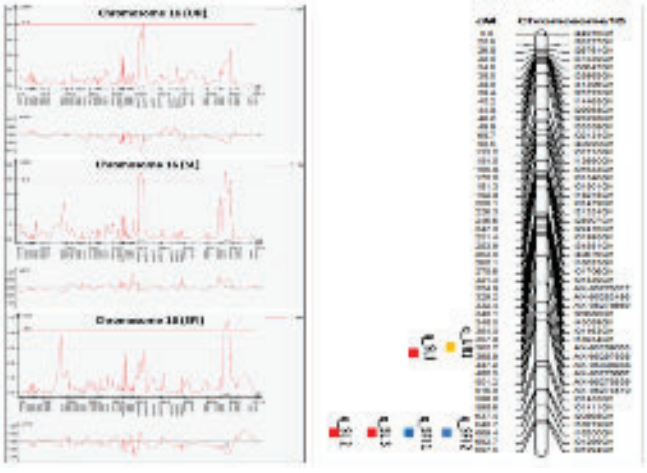

Fig. 1: Genetic linkage map of LG 16 with 6 QTLs of fiber quality traits in cotton

## Identification of superior haplotype of boll weight (BW) in Cotton

Cotton fiber yield is a very complex trait with many components. Boll weight (BW) is the key component for cotton yield. The genomics underlying BW is still unclear and under explored. A total number of 157 QTLs were assessed, out of which two QTLs associated with BW trait were identified. The identified QTL hotspot is ~2.67 Mb in size and is situated on chromosome 25 (D06). The sequence of the identified BW QTL hotspot was fetched out from the database and was annotated, which resulted in the identification of 55 genes and one transcription factor (TF) associated with boll weight. Genomics underlying BW QTL hotspots will be validated in Indian cotton core panel and in bi-parental cotton mapping population.

An India-wide 100 core panel of *G. hirsutum* with respect to boll weight has been made from 230 cotton germplasm of different sources. In addition, we are also currently making bi-parental mapping ($F_4$) population with contrasting boll weight traits of parental lines.

Statistical evaluation using phenotypic data in bi-parental mapping population was conducted. Chi square test for the $F_2$ population followed the Mendelian ratio of segregation. High mean and wide

range for different traits in mapping population indicates the presence of sufficient variability in the genetic material and traits follow absolute normal frequency distribution which indicates the scope for selection of suitable breeding material for crop improvement (Fig. 2).

## Genome-wide association (GWAS) study in Opium poppy (*Papaver somniferum* L.)

Opium Poppy (*Papaver somniferum* L.) has been widely used since ancient period due to its immense medicinal values. The latex of the opium poppy is known as opium that contains several pharmaceutically important alkaloids such as morphine, codeine, thebaine, narcotine and papaverine. Despite the ever increasing demand of thebaine, no studies have particularly focused to unravel the underlying genomics for high thebaine production, except few studies on thebaine pathways. We have developed stable high thebaine opium poppy breeding lines through inter-specific cross followed by eight successive generations of selective breeding strategy. This background of opium poppy offers scope to understand how and why the opium poppy becomes thebaine rich. Are there any allelic combinations with high Linkage Disequilibrium (LD) to make the opium poppy thebaine rich? Therefore, our study aims at combining the approaches like genotyping by sequence (GBS) and GWAS to identify the potential SNP markers associated with such variations with or without the reference genome for assembling sequencing data.

We have performed RAD sequencing of 60 core panels with 0.8t o1.5 GB/ sample. From this sequencing data, a total of 8,750 SNPs were identified by using in- house pipeline data analysis. We have also performed its metabolite profiling of these core panels for two consecutive crop years. We performed MLM model for GWAS study with admixture kinship model. This GWAS study resulted few key important SNPs associated with Thebaine from both plant latex and one month plant leaf samples (Fig. 3). We are presently annotating these key SNPs and their associated genes and trying to establish a linkage of these genes in thebaine development.

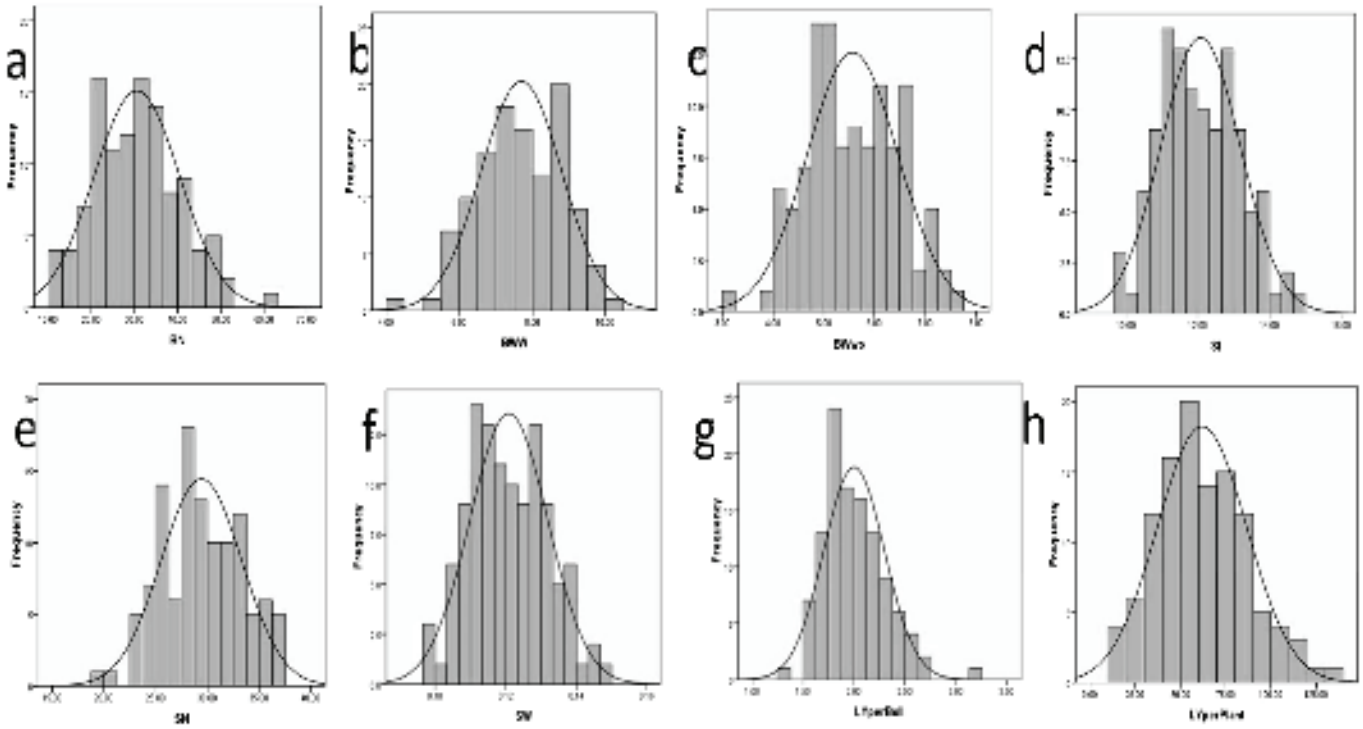


Fig. 2: Frequency distribution of F2 population in upland cotton for fiber yield traits. (a) Number of Bolls (BN); (b) Boll weight with bur (BWW); (c) Boll weight without bur (Bwwo); (d) Seed Index (SI); (e) Seed number (SN); (f) Seed weight (SW); (g) Lint Yield/ boll; (h) Lint Yield/plant

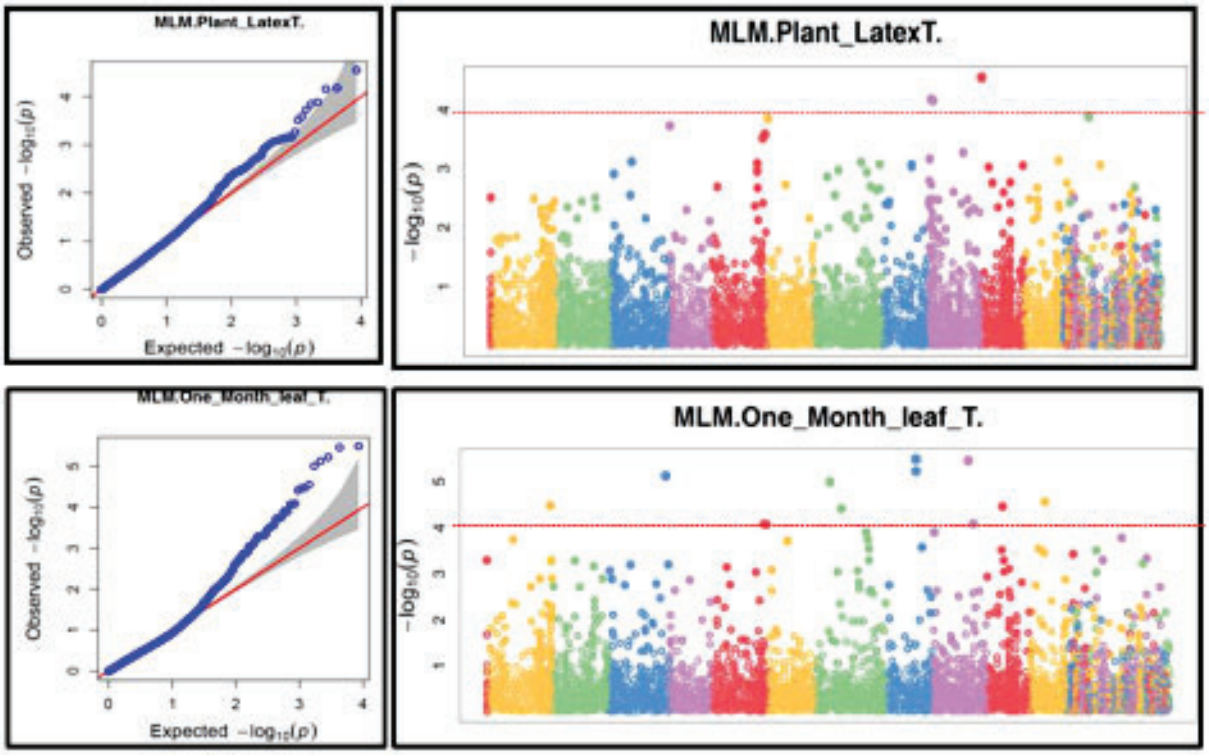


Fig. 3: GWAS analysis with Q-Q and Manhattan plot for Thebaine content from (a) Mature plant latex (b) Plant leaf of one month plant.

## Genetic improvement of Cannabis for medicinal and industrial uses

Legalization of Cannabis around the world globe is increasing day by day because of belief that its consumption would be a boom for medical uses. Researchers still do not understand the genetic root of its cannabidoids. Cannabis is a miracle and unique plant that produces fiber, edible seed, oil and a number of cannabinoids (viz. THC, CBD, CBN), which no other plants have the capacity to produce. Thus, the genes that encode the enzymes required to produce cannabinoids are unique to the cannabis genome only.

Over the past few years, large-scale DNA-sequencing efforts have been started to dissect the genes responsible for the phytochemicals produced by both drug and hemp varieties of the Cannabis that has brought the Cannabis into the modern agricultural era. The difference between hemp and marijuana is simple: The plant must contain less than 0.3% per dry weight of tetrahydrocannabinol (THC) to be hemp.

CSIR-NBRI has a wide Cannabis germplasm gene bank collection of a total 221 germplasm including 11 exotic germplasm.

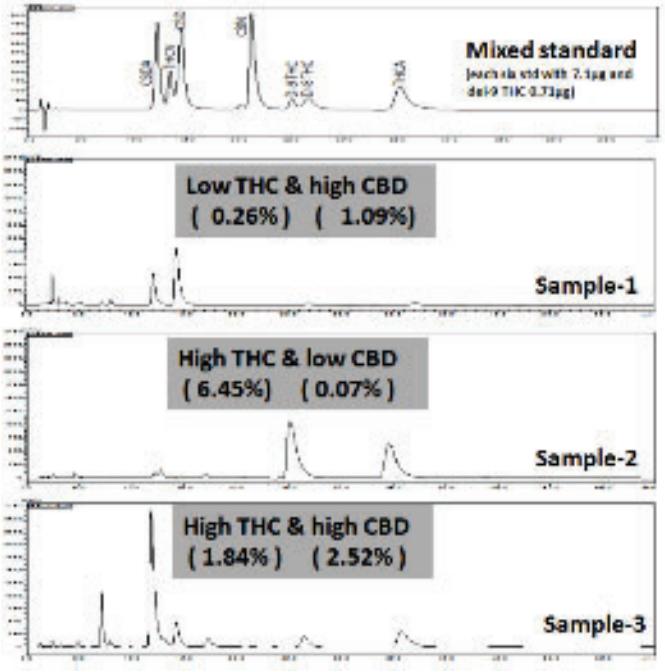


Fig. 4: Optimization HPLC profile of Cannabis germplasm with mixed standards

CSIR-NBRI has taken an initaitive for development of low THC Cannabis lines earlier and has identified four indegenous low THC lines after selection.

This has been established by THC analysis for two consecutive years. In addition, we have also taken intiative for development of low THC and high CBD Cannabis lines for medicinal use and low THC and high fiber Cannabis lines for industrial use. We have optimized the HPLC protocol for various cannabidiods (Fig. 4).

Cannabis has male, female and hermaphodite plants. Thus, for hybridization experiment, it is requsite to identify the male and female plants in early stages in the experimental plot. Sex determination will be of great importance in the breeding aspect of cannabis. The plants can be determined at the time of flowering (4-6 weeks) in the experimental field. We have developed a DNA marker system to identify male and female plants at early stgae of plant. However, we are trying to develop SCAR marker system for more specific and user friendly analysis The importance of separating male and female plants at seedling stage has immense value for stategized breeding program.

## FCM based genome size estimation of *Castanopsis* species (Fagaceae)

*Castanopsis*, commonly known as chinkapin, is one of the dominant genera of Fagaceae. Its raw acorns are eaten by humans and wildlife, hence have huge ecological and economic importance. Genome size determination is pre-requisite for calculation of coverage of any *de novo* sequencing. Many studies have shown that genome size is an important indicator for distinguishing different taxa. There are various techniques for assessing genome size i.e., 2C DNA content. Among all these, flow cytometry (FCM) is convenient, rapid and precise for deleting small variation in genome size among various taxa. In the present study, the leaf samples of three species of *Castanopsis* viz., *C. purpuella, C. tribuloides*and *C. armata,* were collected from Jarain, Sohrarim and Umsining areas of Meghalaya, and analyzed for their 2C DNA content with the help of flow cytometer

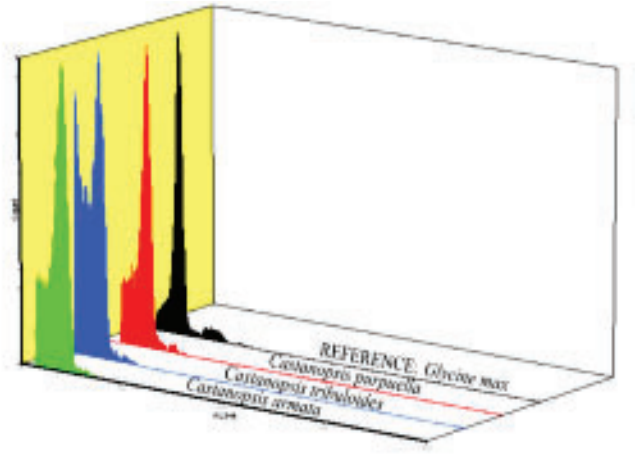


Fig. 5: Comparative G0/G1 peak position of reference standard and three *Castanopsis* species.

(Fig. 5). The results revealed that the genome size of three species of *Castanopsis* varied significantly from 2.25 to 2.55 pg/2C. The genome sizes of these *Castanopsis* species are greater than that of *Quercus* species from India, which is new for Fagaceae. The genome size also clearly segregated into the three species as evident by their different genome size in the present study. However, other parameters need to be assessed for confirming the species segregation. This indicates the successful application of flow cytometry results in segregating the elements within taxa.

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# Botanic Garden, Plant Conservation and Agro-Technology

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- Dr. Satish Yadav, Technical Officer
- Dr. Shweta Singh, Technical Assistant
- Dr. MG Prasad, Technical Assistant
- Mr. NP Yadav, Senior Technician
- Mr. Ram Karan, Senior Technician

## Research Scholars Statistics

| Sr. No. | Position Name | Numbers |
|---|---|---|
| 1. | Research Associate | 01 |
| 2. | Young Scientist | 01 |
| 3. | Project Staff | 13 |

## Aims and Objectives

- Development of new varieties of popular floricultural crops with their morphological and genetic characterization, area expansion, value addition and product development.
- Enrichment of plant diversity, specially threatened plants, their multiplication, acclimatization, assessment and documentation.
- Conservation of diverse groups of plants in specialized houses and field conservatories, their propagation and characterization, DUS testing of mandated crops.
- Capacity building by organizing trainings and skill development programmes in ornamental horticulture at various levels, extension and outreach programmes for various segments and Annual Flower Shows.

## R&D Highlights

### Botanic Garden

As part of the germplasm enrichment, some interesting plants viz., *Woodfordia fruiticosa, Ehretia canarensis, Abrus precatorius* and *Capparis zeylanica* were collected through field work in Maharashtra and Telengana. Thirteen varieties of Gladiolus (*viz.* 'Pusa Sriyan', 'Pusa Dhanwantri', 'Pusa Gunyan', 'Pusa Bindiya', 'Pusa Urvashi', 'Pusa Surya Kiran', 'Creamy Green', 'Pusa Shantiman', 'Pusa Mohni', 'Sancri', 'Australian Fair', 'Sweta', 'Pusa Kiran') were procured from IARI, New Delhi and introduced to the Botanic Garden.

### Morphological characterization of ornamentals (*Bougainvillea, Canna* and *Gladiolus*) as per DUS guidelines

Phenotypic characterization of mutant varieties along with controls for morphological traits was also done as per PPV&FRA descriptors. Morphological Characterization of 11 varieties of *Bougainvillea* ('Blondie', 'Dream', 'Elizabeth', 'Garden Glory', 'Gopal', 'Filomon', 'Mrs Alice', 'Mahara', 'Mary Palmer Special', 'Odisee' and 'Parthasarthy'), five varieties of *Canna* ('Pink Sunrise', 'King City Gold', 'Yellow Queen', 'Ambassador' and 'Cattleya') and 10 varieties of *Gladiolus* ('Aldebaran', 'Pacifica', 'Praha', 'Priscilla', 'Regency', 'Rose Supreme', 'Snow Princes', 'Tiger Flame', 'Video', 'Yellow Stone')have been completed.

## New Facilities Created

- A new plant house called '*Ficus* House' was established at the botanic garden. The house displays intersting *Ficus* species with a unique display form of Bonsai.

- A new facility for advanced propagation of plants was established at botanic garden. This unit is being used for mass propagation of plants.
- A new facility called "Navgrah Vatika" has been developed in the Botanic Garden. This comprises of garden of nine different plants, each representing the nine planets.
- A new facility for conservation of threatened plants was developed at Distant Research Centre, Gehru.
- A separate centre containing various Bamboo germplasm collection was established at distant research centre, Banthra.

## New Varieties Developed/Released

- Two gamma-ray induced mutant varieties of *Chrysanthemum morifolium viz.* 'NBRI- Pukhraj' and 'NBRI-Shekhar' were developed and released.
- An improved selection of Annato (*Bixa orellana* L.) *viz.* 'Arunima' was identified, tested for DUS characters and released.

## Plant Conservation and Agro-technology

### Tuberose (*Polianthus tuberosa* L.)

The tuberose varieties from all corners of the country were collected for evaluation in partially reclaimed sodic soil condition for their commercial cultivation and income generation for the farmers.

### Bambusetum

A Bambusetum was established during 2019-20 at DRC campus, Banthra, where a collection of diverse bamboo species, collected from different parts of the country, has been kept for display, education, conservation and related studies. So far, 61 species of bamboos have been collected and maintained in the Bambusetum.

### Amaranth germplasm bank

Collection, conservation and evaluation of 94 accessions of *Amaranthus* spp. were undertaken to evaluate the best suited for accessions cultivation on sodic soil condition. Amaranth accessions were collected from diverse locations of Uttarakhand and Uttar Pradesh, some of these included elite lines and others of wild occurrence.

### Good Agricultural Practices for cultivation of medicinal plants

- Germplasm for *Phyllanthus amarus* and *Cyperus rotundus* were collected and field trials for evaluation of their good agriculture practices were conducted.
- Agro-technology for the cultivation of *Phyllanthus amarus* and *Cyperus rotundus* has also been developed.
- *Viola pilosa*, a high demanding medicinal plant, was collected from sub temperate region of 'Kumaun' hills of Uttarakhand and successfully domesticated in dry sub humid conditions at DRC, Banthra.
- Propagation methods (seed, runner and cuttings) were also developed for successful cultivation of *Viola pilosa*. *Coptis teeta*, an endangered specieswas collected from temperate region of Mishmi hills of Arunachal Pradesh, and trials for its domestication in controlled conditions in poly house are being practiced and propagation through tissue culture and vegetatively from rhizome cuttings, is also being conducted.

### Leaf oil from Turmeric variety, 'Kesari'

We have worked on different aspects of turmeric cultivation like agro-technology and agri-economics for improved *Curcuma* variety (ies). The crop is to be popularized under the shade of orchards, multi-locational assessment for their suitability in different agro-climatic regions, agro-technology including postharvest optimization for different agro-climate zones, capacity building and training programmes on agro-techniques, distillation and value addition. Kesari variety has been developed by CSIR-NBRI, which apart from giving high rhizome yields, can also be a source of leaf essential oil. To extract the highest quantity and best quality leaf essential oil, leaves were harvested at three stages; viz. green, partially senesced and fully senesced. The leaves were hydro-distilled. Minimum amount of oil (0.88%) is obtained from green leaves whereas fully senesced leaves have 1.40% oil. The highest amount of leaf essential oil (1.70%) is obtained from partially senesced leaves. The major constituents are α-Phellandrenes (32%), terpinolene (26%), p-cymene 5.9%) and 1,8 cineole (6.5%). We have also developed agrotechnology for cultivation of turmeric for essential oil extraction from senescing leaf.

## Mass multiplication and captive cultivation of medicinal plants

Mass multiplication for quality planting material of three plant species i.e. *Tinospora cordifolia, Gymnema sylvestre* and *Commiphora wightii* was attempted at Banthra. The germplasm collected by Plant Diversity group from different locations of India have been conserved in the field gene bank.

## Conservation and propagation of dwarf cultivars of Neem

The conservation of four dwarf cultivars with high Limonoid content was done at Banthra. The morphological differences in all these cultivars were observed on the basis of shape, size and colour of leaves, flowers and barks. Efforts were made to propagate these cultivars through macro (through cuttings) and micro (tissue culture) propagation. The soil pH 8.80, electrical conductivity 0.67 $dSm^{-1}$, soil N, P and K 110, 18.5 and 276 kg $ha^{-1}$, respectively of Neem conservation site have been analysed. Total 889 cuttings of neem cultivars have been planted for clonal propagation. To enhance the rooting and survival of the cuttings we also established an experiment using two plant hormones (indole acidic acid and gibberellic acid) and one bio-fertilizer (phosphate solubilizing bacteria) along with control. Average seed weight of neem seeds varied from 71 mg/seed to 111.9 mg/seed with an average of 92.9 mg/seed. The seed oil content ranged from 38% to 43.9% in sample with an average of 40.2%. Ethanol soluble content ranged from 9.2% to 10.4% with an average of 9.7%. Azadirachtin content varied significantly among different neem seed samples.

## Effect of different sources and levels of organic matter on biomass yield and quality of Kalmegh

For standardization of the sources and levels of organic matter for the cultivation of Kalmegh (*Andrographis paniculata*), three experiments have been conducted with different doses of FYM, Pressmud and vermi-compost. Results indicated that plant height, number of branches, stem diameter, plant spread, fresh and dry biomass of the plant increased with increasing doses of FYM, Pressmud and vermi-compost. However, it was significant only up to FYM @ 15 t $ha^{-1}$, Pressmud @ 7.5 t $ha^{-1}$ and vermi-compost @ 7.5 t $ha^{-1}$. The above doses are sufficient for organic cultivation of Kalmegh.

## Out-reach/Training/Skill Development

During the reporting peroid, various programmes, training sessions, out-reach activities were organized. More than 500 persons including students, farmers, entrepreneurs, etc., were imparted training on different aspects of gardening and agro-techniques. Short term training sessions on home gardening, bonsai preparation and dehydrated flower technique were also organized at the institute as well as different villages for empowering youth, women, etc.

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**Botanic garden, plant conservation and agro-technologies, skill development and out-reach activities**

The Botanic Garden of CSIR-NBRI serves as a repository of germplasm collection of diversified groups of plants, with special reference to rare, endangered, ornamental, economic and educative significance. The major objectives are introduction, multiplication, acclimatization, assessment and documentation of important plant species and varieties from within and outside the country, especially from iso-climatic regions for enriching the germplasm collection, domestication of wild plant species of ornamental significance, development of new and novel varieties of ornamental plants for commercial purpose, and awareness and education on garden related activities.

## New plants introduced at Botanic Garden

Some interesting plants, collected through field work of our team from Maharashtra and Telengana, viz., *Woodfordia fruiticosa*, *Ehretia canarensis* and *Capparis zeylanica* are conserved and maintained at plant introduction section of the botanic garden.

Thirteen varieties of *Gladiolus* ('Pusa Sriyan', 'Pusa Dhanwantri', 'Pusa Gunyan', 'Pusa Bindiya', 'Pusa Urvashi', 'Pusa Surya Kiran', 'Creamy Green', 'Pusa Shantiman', 'Pusa Mohni', 'Sancri', 'Australian Fair', 'Sweta, Pusa Kiran') were procured from IARI, New Delhi and introduced to the Botanic garden (Fig. 1). Apart from these, two cultivars of Gladiolus ('Big Time Supreme' and 'Blue Isle') were procured from a progressive farmer from Barabanki district of Uttar Pradesh.

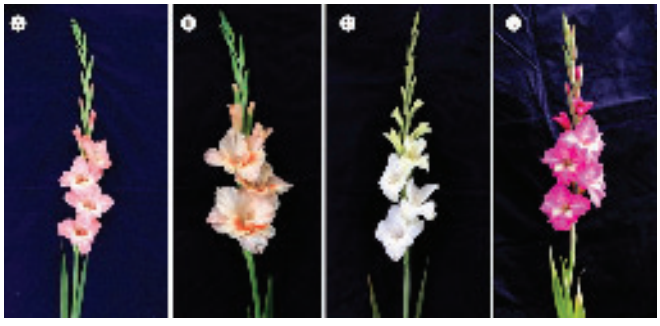

Fig. 1 (A-D): Some of the newly introduced varieties of *Gladiolus*. (A) 'Pusa Kiran', (B) 'Pusa Gunjan', (C) 'Pusa Mohini', (D) 'Pusa Srijan'

## New Facilities Created

### *Ficus* House

A new plant house, '*Ficus* House' was established at the botanic garden (Fig. 2). The house displays some intersting species of *Ficus* with a unique display form of Bonsai. Currently 30 taxa of *Ficus* are conserved in the plant house. Some of the notable species conserved in the house are *Ficus benghalensis, F. racemosa, F. religiosa, F. palmata, F. benjamina, F. glomerata* and *F. lyrata*.

Fig. 2: A view of newly developed '*Ficus* House' at Botanic Garden

### Advanced Propagation House

A new facility for the advanced propagation of plants was established at botanic garden. This unit is being used for mass propagation of plants. The facility was inaugurated by Dr. Shekhar C. Mande, Director General, CSIR, New Delhi & Secretary DSIR on 19 January, 2020 (Fig. 3).

Fig. 3: Dr. Shekhar C. Mande, DG, CSIR inaugurating newly developed Advanced Propagation House at Botanic Garden

### Navgrah Vatika

A new facility called "Navgrah Vatika" has been developed in the Botanic Garden (Fig. 4). The following nine plants representing the nine planets

Fig. 4: A view of 'Navgrah Vatika' established at Botanic Garden

are planted in a particular direction in the vatika: *Ficus recemosa, Butea monosperma, Acyranthus aspera, Ficus religiosa, Acacia catechu, Calotropis procera, Prosopis cineraria, Cynodon dactylon* and *Imperata cylindrica*.

### Threatened Plant Conservation Centre

It is estimated that there are around 400,000 angiospermic plant species in the world, and at least

Fig. 5: Plantation by Dr. Shekhar C. Mande, DG, CSIR at Field Gene Bank of Threatened Plants

25% are now threatened with extinction. Besides over-exploitation, habitat loss and degradation is the primary cause of species loss at local, regional and global scales. Institutes like CSIR-NBRI have a crucial role to play in ensuring the conservation of plant diversity for the benefits of all. For the *ex-situ* conservation of threatened plants species of India, a field gene bank is being developed at DRC, Gehru. The centre was inaugurated by Dr. Shekhar C. Mande, Director General, CSIR, New Delhi & Secretary DSIR on 19 January, 2020 (Fig. 5).

### Bambusetum

A separate centre containing various Bamboo living germplasm was established at DRC, Banthra. Currently, 61 species of Bamboo are conserved in the centre. The centre was inaugurated by Dr. Shekhar C. Mande, Director General, CSIR & Secretary DSIR on 19 January, 2020 (Fig. 6).

Fig. 6: Dr. Shekhar C. Mande, DG, CSIR inaugurating the newly developed Bambusetum at distant research centre, Banthra

## Enhancing production of agricultural systems, skill development and outreach programmes

The main purpose of the group is to develop agro-technology for sustainable development and economic utilization of sodic wastelands. This activity is important for increasing the agricultural production to ensure food security and availability of raw material for industry to meet the ever increasing demand for increasing population of our country. The group has developed improved varieties of Bixa and Turmeric. Evaluation of other medicinal and aromatic plants is in progress for identifying elite germplasm. Field experiments are also conducted for development of agro-technologies of lesser-known, but important crop plants. Efforts are also made towards popularizing CSIR-NBRI Green Technologies for economic upliftment of rural population.

## Development and promotion of Non POPs alternatives to DDT

The project aims at developing clonal propagation methods and promote cultivation of already identified four new dwarf neem (*Azactirachta indica*) cultivars with early maturity and higher limonoid yield. The *in vitro* process developed for rapid clonal multiplication of a mature tree of neem is of great practical importance, as most of the desirable characteristics appear only at maturity. These cultivars are being propagated using both tissue culture and clonal propagation techniques. The relationship between soil, nutrient contents and limonoid yield in different accessions will be established during multi-location trials.

The protocol for tissue culture based propagation of neem has been developed. Large scale macro propagation through cuttings has been standardized on the basis of age, height, thickness, season and different rooting hormones. Neem based agroforestry cropping systems by growing different medicinal and aromatic plants such as Vetiver, Asparagus, Lemongrass, Turmeric and Long Pepper have been established for assessing economical sustainability of neem cultivation. Five different geographical locations have been identified to establish multi-location trial using micro- and macro- propagated plants of neem.

## Establishment of a DUS Test Centre at CSIR-NBRI, Lucknow for *Bougainvillea*, *Gladiolus* and *Canna* crops

CSIR-NBRI is a DUS Test Centre of PPV&FRA for Bougainvillea, Canna and Gladiolus. Characterization by recording morphological characters (both vegetative and floral) of some varieties/ cultivars of Bougainvillea, Canna and Gladiolus have been done for identifying morphological variations and developing descriptors.

Detailed phenotypic characterization of mutant varieties along with controls for morphological traits was also done as per PPV&FRA descriptors for their eventual registration with the govt. authority. Morphological characterization of 11 varieties of Bougainvillea ('Blondie', 'Dream', 'Elizabeth', 'Garden Glory', 'Gopal', 'Filomon', 'Mrs Alice', 'Mahara', 'Mary Palmer Special', 'Odisee' and 'Parthasarthy'), 5 varieties of Canna ('Pink Sunrise', 'King City Gold', 'Yellow Queen', 'Ambassador' and 'Cattleya') and 10 varieties of Gladiolus ('Aldebaran', 'Pacifica', 'Praha', 'Priscilla', 'Regency', 'Rose Supreme', 'Snow Princes', 'Tiger Flame', 'Video' and 'Yellow Stone') have been completed. Besides, micro-morphological studies were initiated using Scanning Electron Microscopy (SEM) of mutant lines along with respective controls. Laminar trichome differences were observed in two mutant varieties which need further investigations.

## *Ex-situ* conservation studies of *Cycas* species in India at CSIR-NBRI Botanic Garden

The project will be carried out with objectives of conserving the Indian *Cycas* germplasm at the Botanic Garden and propagating/multiplying through cultivation of seeds and suckers. The phenology of different stages of vegetative and reproductive cycles of the species will also be taken up which will help recovery of the wild populations in case of natural or anthropogenic calamities.

## Farm based S&T interventions for socio-economic development in the aspirational district of Nabrangpur, Orissa

The extension oriented project is to improve the socio-economic conditions of Nabarangpur, Orissa---one of the most backward tribal dominated districts of India. CSIR-NBRI has undertaken popularization

of cold tolerant variety of turmeric, 'Kesari' as source of extra income from leaf essential oil. Our well tested efficient strains of bio-inoculants have also been provided to the farmers, with training and demonstration. The art of dehydrated flowers and foliages-based products has also been disseminated to the tribal women of Nabarangpur.

Three technological interventions were made for the farmers of aspirational district Nabrangpur. A total of 460 kg of 'Kesari' has been provided to the farmers alongwith package of practices. The essential oil from senesced leaves has been extracted during the harvest season of 2020. The sample of this oil has been analysed by us, and 34.16% α-Phellandrene has been reported which is the characteristic compound for the economic value of oil. The leaf oil of Kesari can be used for insecticidal and pesticidal effects, which will be taken up next year.

## Improved variety of *Bixa*

*Bixa orellana* L. is cultivated commercially to extract the Annato colour from its seeds. It contains the pigment bixin, which is a carotenoid carboxylic acid, a harmless organic dye, used as a red-orange dye for coloring not only food products such as rice, cheeses, soft drinks, butter, and soup, but also in the textile, paint, and cosmetic industries. Annatto is considered to be a potential alternative to replace tartrazine, which is banned in many countries. The seeds of improved selection contain the highest Bixin (1.54%) and ripen about 10 days early. The selection, named "Arunima", has been released by Dr. Shekhar S Mande, DG, CSIR on 02 May 2019. The saplings of variety have been provided to one NGO and one farmer for commercial cultivation.

## Out-reach Activities

Approximately 500 peoples including farmers, students, women, entrepreneurs, garden lovers were imparted training on various aspects of gardening such as dehydrated floral crafts, bonsai technique and home gardening.

## Assistance and Technical Support

Assistance and technical advice were provided to National Institute of Agricultural Research (INIAP) Ecuador for developing agro-technology of Lotus (*Nelumbo nucifera*) as an alternative crop for production in the flood-prone areas of the Ecuadorian coast. This would help develop a strategy for lotus cultivation in South America's west coast. The edaphoclimatic conditions of Ecuador and the existing cropping systems and practices were recorded. This will help in planning and executing Lotus as a crop in Ecuador.

## CSIR Integrated Skill Initiative Programme

Under CSIR Integrated Skill Initiative, CSIR-NBRI has developed employment-oriented skill development programmes in its core competency areas. Eight courses were proposed under skill initiative programme. The institute's skill development programmes are categorized in four broad groups; i.e. NSDC and its sector skill council accredited programmes, industry sponsored, programmes in institute's core strength areas and societal trainings.

As nodal officer of CSIR-Skill Development Initiative, skill development programmes were coordinated under NWP100 project. The duration of these programmes ranged from 3 days to 29 days through which 297 candidates were trained under 14 different training courses.

**Research Group**

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Germplasm conservation and evaluation of non-traditional economic plants and development of their agro-technology and outreach programmes/extension activities

The group is mainly working on the development of agro-technologies for non-traditional economically important medicinal and aromatic plants (MAPs) by introduction, domestication, nutrient management, aiming at economic utilization of partially reclaimed sodic lands. Different activities to achieve these objectives involve germplasm collection from different agro-climatic conditions, their *ex-situ* conservation, selection of elite material with good growth and yield attributes, development of their propagation for large scale multiplication and conducting field experiments for development of agro-techniques in different cropping systems, including inter-cropping with trees and other economic crops. Under outreach programmes/extension activities and rural development initiative of CSIR, the outreach efforts towards popularizing CSIR-NBRI Green Technologies for economic upliftment of rural population are being undertaken through outreach programmes.

## Aroma Mission Project

Under Aroma Mission Project, agro-technologies were developed for cultivation of turmeric for essential oil extraction from senescing leaves and increasing area under turmeric cultivation in different states. About 150 quintal rhizomes and seed materilas of the promising turmeric variety 'Kesari' were distributed among 75 farmers of Karnataka, Jharkhand, Uttar Pradesh, Bihar, Uttarakhand, Haryana, Odisha and Maharashtra. The area covered for Kesari cultivation has reached 7.55 ha. We have also developed agro-technology and agri-economics for improved Curcuma variety (ies) which would be optimized for cultivation under the shade of orchards, multi-location assessment and postharvest optimization in different agro-climatic regions, capacity building and training programmes on agro-techniques, distillation and value addition and making public aware of mission activities and achievements using appropriate interface. Organized 30 awareness cum training programmes for popularization of turmeric cultivation for essential oil extraction from senescing leaves at different locations of India. About 505 farmers were benefitted from these training programs

## Conservation of plant species

Under Phytopharmaceutical Mission Project, captive cultivation for mass multiplication of quality planting material of *Tinospora cordifolia*, *Gymnema sylvestre* and *Commiphora wightii* was undertaken. Germplasm of *Tinospora cordifolia* (62), *Gymnema sylvestre* (171) and *Commiphora wightii* (92), collected from different locations of India, are conserved in the filed gene bank at DRC, Banthra. We have developed agrotechnology for the above three medicinal plants for further plantation and distribution to the farmers for cultivation: *Tinospora cordifolia* (170 plants), *Gymnema sylvestre* (145 plants) and *Commiphora wightii* (94 plants). We have conducted three awareness trainings regarding cultivation of medicinal plants and distributed planting material to the farmers for cultivation and uplift of the farmers with balanced economic growth.

## Plant Conservation and Agro-technologies (Distant Research Centres, Banthra)

Statistical analysis of the field and laboratory data on agro-economic assessment for an intercropping model of Ashwagandha and Psyllium Husk (Isabgol) for sodic soil, integrated nutrient management for

Isabgol production in the partially sodic land, agro-technology of Turmeric, Tuberose, *Chenopodium quinoa* and other non-traditional economic plants was also made. The germplasm collection of Isabgol was enriched with collection of nine varieties.

## Development of Botanic Garden at Chandrapur, Maharashtra

Under the project establishing a "World Class Multi-purpose Botanical Garden, Chandrapur, Maharashtra", visited Chandrapur Garden Site for developing the herbal garden and laid down the plots for planting the medicinal and aromatic plants and herb garden. Prepared quality planting material of medicinal and aromatic plants for Chandrapur Botanic Garden.

## Propagation of new dwarf cultivars of Neem with early maturity and higher Limonoids yield

In the UNIDO sponsored project "Propagation of new dwarf cultivars of Neem with early maturity and higher Limonoids yield", conservation of four dwarf cultivars with high Limonoid content was done at DRC, Banthra. Five sites under different agro-climatic zones were identified, for planting micro- and macro-propagated plants of four cultivars of Neem. Land for multi location trials at Central Scientific Instruments Organization, Chandigarh, Punjab; Research Centre of Central Institute of Medicinal and Aromatic Plants, Bangalore, Karnataka; and North Eastern Hill University (NEHU), Shillong, Meghalaya, have been allotted.

## Outreach Programmes/ Extension Activities

With the objective of popularizing CSIR-NBRI green technologies, various extension/outreach activities such as six training programmes on Betelvine cultivation, 21 training programmes on cultivation of turmeric for extraction of essential oil from leaf waste and 03 field visits to DRC, Banthra were organized. In these activities, 700 farmers were trained in cultivation practices of Betelvine and turmeric. A total of 190 individuals including students and teachers from various schools and colleges visited DRC, Banthra.

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Sustainable soil fertility, drought and salt stress management through non-traditional economic plants

## Nutrients profiling of *Andrographis paniculata* under sodicity stress conditions:

### Nitrogen (N), Phosphorus (P), Potassium (K), Calcium (Ca) and Magnesium (Mg) content

Nitrogen content in roots increased with increasing salt stress condition showing the value of 4.93 g $kg^{-1}$, 6.27 g $kg^{-1}$ and 7.84 g $kg^{-1}$ with ESP level of 05.0, 18.8 and 31.3, respectively. Similar trend was also recorded in the stem and leaves of the plants. The high salt content in soil affected the plant growth. P content in root was 1.93 g $kg^{-1}$ associated with the ESP level of 18.8 and minimum 1.46 g $kg^{-1}$ in the ESP level of 05.0, respectively. Similar trend was also recorded in the stem of the plant. The potassium content in the roots of the plant significantly increased from 121.92 to 148.44 g $kg^{-1}$ by increasing ESP level from 5.0 to 18.8 but further increasing of ESP level did not increase the potassium content in the plant. This could be due to accumulation of excess amount of sodium liable to reduce potassium content in root, stem and leaves due to increasing sodium concentration in the root zone. This is the result of strong competition between potassium and sodium which affected potassium acquisition as concentration of sodium was excess than potassium that had direct effect on growth and development of the plant. The calcium content increased from 6.41 to 8.46 g $kg^{-1}$ in roots as ESP level increased from 5.0 to 18.8. Same pattern for calcium content was also recorded in stem and leaves during both the years. Similarly, magnesium content in root also increased corresponding to increasing the sodicity levels with maximum as ESP level was 18.8 (0.734 g $kg^{-1}$) and minimum in ESP level 5.0 (0.690 g $kg^{-1}$). Similar trend was also recorded in stem and leaves of the plant.

### Sodium (Na), Zinc (Zn), Iron (Fe), Copper (Copper) and Manganese (Mn)

Sodium content in roots, stem and leaves were also increased with increasing levels of the sodicity. The lowest sodium content (0.93 g $kg^{-1}$) was recorded at 5.0 ESP level (Control) and highest (4.19 g $kg^{-1}$) was with 18.8 ESP levels in roots of the plant. Similar trend was also recorded in stem and leaves of the plant. The maximum deposition of sodium was reported in roots of the plant. The availability of $Na^+$ in soil solution increases the excess sodium uptake in plant tissues. The zinc content also increased with increasing the sodicity levels in roots, stem and leaves. Iron content in roots increased with increasing levels of sodicity from 1755 to 1954 mg $kg^{-1}$ at 5.0 to 31.3 ESP level, respectively. The iron content in stem and leaves also increased with increasing order of sodicity. The iron acquisition varied from 217 mg $kg^{-1}$ ($T_1$) to 611 mg $kg^{-1}$ ($T_2$). Similar trend was recorded in leaves of the plant. The copper content in roots, stem and leaves also showed the synergistic effect corresponding to the sodicity levels. The copper content increased from 15.42 to 43.22 mg $kg^{-1}$ in roots, 4.84 to 33.76 mg $kg^{-1}$ in stem under 05.0 and 31.3 ESP levels, respectively. However in leaves, the lowest copper content (5.62 mg $kg^{-1}$) was found in control ($T_1$- ESP-05.0) and highest (25.42 mg $kg^{-1}$) at 18.8 ESP level, respectively. Manganese content also increased with increasing sodicity levels in root, stem and leaves.. The manganese content in roots ranged from 56.9 mg $kg^{-1}$ in control ($T_1$- ESP-05) to 68.2 mg $kg^{-1}$ in $T_3$- ESP-31.3, respectively. Similar trend was also recorded in stem and leaves of the plant.

**Chromium (Cr), Molybdenum (Mo), Nickel (Ni), Selenium (Se), Arsenic (As), Lead (Pb), Cobalt (Co) and Cadmium (Cd)**

Chromium content in *Andrographis paniculata* also showed the synergistic effect with sodicity as it increases with increasing sodicity levels. The chromium content in roots and stem did not show any significant effect with the given treatments. However, it significantly increased in the leaves which ranged from 9.46 mg $kg^{-1}$ to 20.82 mg $kg^{-1}$ under the ESP level of 5.0 to 31.3. Contrary to that molybdenum content did not show any trend corresponding to increasing sodicity levels. No trend was recorded for nickel content in the roots of the plant. However in stem and leaves, nickel content decreased with increasing levels of the sodicity. Similarly, no trend was recorded in selenium content in roots, leaves and stem. In case of arsenic, the increasing trend was recorded in the stem and leaves corresponding to the increasing levels of the sodicity and sodium content in the plant. The arsenic content ranged between 0.95- 1.65 mg $kg^{-1}$ in roots, 0.11-0.49 mg $kg^{-1}$ in stem and 0.47- 1.28 mg $kg^{-1}$ in leaves. The lowest content was recorded in stem, followed by leaves and roots. Lead content varied from 0.72 - 0.82 mg $kg^{-1}$ in stem, 0.82 – 1.57 mg $kg^{-1}$ in roots and 1.05 - 1.44 mg $kg^{-1}$ in leaves. Similarly, cobalt content also increased with increasing levels of sodicity and it ranged from 0.03 mg $kg^{-1}$ to 0.09 mg $kg^{-1}$ in stem, 0.52 mg $kg^{-1}$ to 0.99 mg $kg^{-1}$ in root and 0.12 mg $kg^{-1}$ to 0.18 mg $kg^{-1}$ in leaves. However, cadmium content was not detected in most of the samples either in root, stem or leaves of the plant.

The increasing trend was recorded for sodium uptake by the plants in salt affected soils with increasing levels of sodicity. The concentration of N, P, Ca, Mg, Zn, Fe, Cu, Mn, Cr, As, Pb and Co in *Andrographis paniculata* increased with increasing levels of sodicity but K, Mo, Ni, Se content decreased with increasing sodicity levels. Salt stress caused changes in macro and micro nutrients uptake, which may lead to decline in photosynthesis capacity and respiration.

**Research Group**

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Agro-technology of different medicinal and aromatic/ non-traditional economic plants, conservation and enrichment of various germplasm, ecological development of sodic waste land

The group has been involved in enhancing production of agricultural systems, skill development and outreach programme with emphasis on development of appropriate agro-technology for non-traditional economic plants, including medicinal and aromatic plants, in diverse cropping systems, aiming at economic utilization of partially reclaimed sodic lands. Different activities to achieve these objectives include germplasm collection from different agro-climatic conditions, their ex-situ conservation, selection of elite material with good growth and yield attributes, development of their propagation protocol for large scale multiplication and conducting field experiments for development of agro-techniques in different cropping systems including inter-cropping with trees and other crops.

## Plant Conservation and Agro-technology

### Bambusetum

A Bambusetum, with a collection of 61 species of Bamboo from different parts of India, was established at DRC, Banthra for display, education, conservation and related studies. This conservation effort will also help in identifying suitable bamboo species for partially reclaimed sodic land (Fig. 1)

Fig. 1: A view of Bambusetum established at Distant Research Centre, Banthra

### *Amaranthus*

Collection, conservation and evaluation of 94 accessions of three species of *Amaranthus* (*A. hypochondriacus, A. cruentus, A. caudatus*) from different parts of India were made in order to identify the best suited germplasm for successful cultivation

Fig. 2: Germplasm collection of *Amaranths* at Distant Research Centre, Banthra

on sodic soil condition. Among the accessions, some were collected from diverse locations of Uttarakhand and Uttar Pradesh and some represented elite lines procured from ICAR-NBPGR, Bhowali. The aim of the study is to explore the importance of grain amaranth as a climate resilient crop, as the yield per plant by grain amaranths is much impressive even under drought- stress, conditions of salinity, heavy metals and pests due to presence of high phenolic content which helps in tolerating the biotic and abiotic stress. It makes this crop very useful for the country,

especially in poverty-stricken and underdeveloped areas. With the above background, the work will be focusing on collection of grain amaranth germplasm across country, its maintenance and phenotypic characterization for major agronomic and quality traits. Attempts are made to collect more accessions from different locations of India (Fig. 2).

**Tuberose**

Collection, conservation and evaluation of 29 varieties of tuberose (*Polianthes tuberosa* L.), including single type and double type flower, from IARI, New Delhi and IIHR, Bangalore were perfomed. Among these varieties, screening of the suitable one for production of long lasting flower spikes for sustainable utilization in sodic waste land is in progress. (Fig. 3).

Fig. 3: A view of Tuberose field at Distant Research Centre, Banthra

## Evaluation of Chickpea genotypes for drought tolerance

Chickpea (*Cicer arietinum* L.) is one of the major legume crops cultivated in the rainfed areas of the country, where water stress is one of the serious threats to its productivity. For defining the appropriate selection criteria for screening drought tolerant chickpea genotypes, a study was conducted, in which 40 distinct chickpea germplasm were collected from different National institutes and Universities of India and evaluated for drought tolerance at germination and early seedling stages. Furthermore, at late vegetative growth stages, physiochemical traits and multi-environment yield performance were also tested.

## Evaluation of Linseed (*Linum usitatissimum*) accessions on partially reclaimed sodic land at Banthra for screening of salt tolerance and high oil content

Linseed is an important crop produced for natural textile fibre (linen) or oil for industrial as well as culinary purpose. Study was undertaken on 120 distinct germplasm of linseed for screening the promising germplasm that can be successfully grown in partially sodic waste land and those having high oil content.

## Aroma mission

Off campus training programmes were conducted for cultivation and processing of aromatic crops in different states such as Uttar Pradesh, Bihar Uttarakhand, Haryana, Orissa and Maharashtra etc. Multi-locational trials were conducted for the CSIR-NBRI developed Kesari Variety across the country.

## Development and promotion of non-POPs alternatives to DDT

Hormonal response for seedling preparation of Neem through vegetative propagation (cutting) was investigated. Multi Location Trials sites were identified for neem plantation.

**Research Group**

- Mr. Shubhendra Singh, SRF

# R & D Outputs

# PUBLICATIONS

## Publications in SCI Journals

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7. Kumar N., Paul S., Mallick S. 2020. Climate change-induced heavy metal (or Metalloid) stress in crop plants and possible mitigation strategies. *In: Sustainable Agriculture in the Era of Climate Change*. (Eds. R. Roychowdhury, S. Choudhury, M. Hasanuzzaman, S. Srivastava). Springer, Cham: 293-326.
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12. Singh VJ, Gupta D, Sahu V, Asthana AK. 2020. *In-vitro* growth pattern of moss *Drummondia stricta*

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# PATENTS FILED/GRANTED

**Patents Granted (International)**

| Title | Inventors | Application No. | Country | Grant Date | Patent No. |
|---|---|---|---|---|---|
| A wound inducible expression construct and a method of its preparation | Sane AP, Pandey SP, Singh AP | 15/538954 | USA | May 14, 2019 | 10287597 |

**Patents Granted (India)**

| Title | Inventors | Application No. | Grant Date | Patent No. |
|---|---|---|---|---|
| A bio-inoculant composition comprising *Trichoderma* protoplast fusant useful for enhancing nutritional value and growth of plants | Mishra A, Nautiyal CS | 0010DEL2012 | December 06, 2019 | 326937 |

# HUMAN RESOURCE DEVELOPMENT

## CSIR-NBRI Participation in Trainings/Exhibition/Flower Shows/Seminars

| Sr. No. | Event Details | Venue | Date | Participating Division |
|---|---|---|---|---|
| 1. | Technology Outreach Programme for Inclusive and Sustainable Development-Tech for Seva | IIT- Delhi | August 10-12, 2019 | TTBD |
| 2. | 8th Bhopal Vigyan Mela 2019 | Bhopal | September 13-17, 2019 | TTBD |
| 3. | IISF Outreach Programme | CSIR-IITR, Lucknow | October 15-16, 2019 | TTBD |
| 4. | IISF-2019 | Kolkata | November 5-8, 2019 | TTBD |
| 5. | 'MONDEI' a Cultural Festival of Nabarangpur celebration | Nabarangpur, Odisha | December 13-17, 2019 | TTBD & Botanic Garden |
| 6. | CIMAP-Kisan Mela-2020 | CSIR-CIMAP, Lucknow | January 31, 2020 | TTBD |
| 7. | Swadeshi Mela | Swadeshi Jagran Manch, Ballia/Satish Chandra College, Ballia | January 24-February 04, 2020 | TTBD |
| 8. | CISH-Kisan Mela-2020 | ICAR-Central Institute for Subtropical Horticulture, Lucknow | February 26, 2020 | TTBD, Botanic Garden & Microbial Technology Group |
| 9. | Fruits, Vegetable and Flowers Exhibition | Raj Bhawan, Governor's House, Lucknow | February 22-23, 2020 | TTBD & Botanic Garden |

## Trainings Received by Individual

| Sr. No. | Name of Person (s) | Subject of Training Course | Organizer/ Place | Date/ Period |
|---|---|---|---|---|
| 1. | Dr. BN Singh | New paradigm in technology transfer and commercialization | CSIR-HRDG, Ghaziabad | July 8-10, 2019 |
| 2. | Dr. Vijay V. Wagh, Mr. Imtiyaz Hurrah, Mr. Amit Gupta and Ms. Aparna Shukla | Workshop on Botanical Nomenclature | Botanical Survey of India, Shillong | January 27-31, 2020 |
| 3. | Dr. Alok Lehri, Dr. Mahesh Pal and Dr. Subha Rastogi | General requirements for the competence of reference material producers as per ISO 17034:2016 | National Accreditation Board for testing and Calibration Laboratories, Gurugram/ Lucknow | October 10-12, 2019 |
| 4. | Dr. Vivek Pandey and Dr. Soumit Behera | Artificial intelligence and machine learning in Earth, Ecology, Environment, ocean and water (E3OW) theme | CSIR-HRDG, Ghaziabad | January 23-25, 2020 |

## Trainings Imparted to Groups

| Sr. No. | Name of the organization/Group | Subject of Training | No. of Participants | Place | Date/Period |
|---|---|---|---|---|---|
| 1. | CSIR-NBRI and Jeevaniya Society | Training to farmers regarding uses and application of *Trichoderma* | 50 | Shilendra Ji Farm, village Udanapur, block Hargaon, district Sitapur | May 24, 2019 |
| 2. | General Public | Dehydrated Floral Crafts | 08 | CSIR-NBRI, Lucknow | June 09, 2019 |
| | | | 167 | DRI, Chitrakoot | June 15-16, 2019 |
| | | | 02 | CSIR-NBRI, Lucknow | October 10-11, 2019 |
| | | | 127 | Nabrangpur and Umerkot, Odisha | February 10-11, 2020 |
| | | | 17 | CSIR-NBRI, Lucknow | February 25-27, 2020 |
| | | | 16 | | March 03-05, 2020 |
| 3. | CSIR-National Botanical Research Institute, Lucknow, Lichenological Society (ILS) and TERI School of Advanced Studies (TERI SAS), New Delhi | Conservation assessment of lichen species preferred in trade as per IUCN guidelines, India | 10 | TERI School of Advanced Studies (TERI SAS), New Delhi | July 11, 2019 |
| 4. | Lichenological Society (ILS); CSIR-National Botanical Research Institute, Lucknow, and Bharathiar University, Coimbatore | Identification, bioprospecting and conservation of lichens | 100 | Bharathiar University, Coimbatore | September 12-13, 2019 |
| 5. | Indian Lichenological Society (ILS) & CSIR-National Botanical Research Institute, Lucknow | Field based hands-on training on lichens systematics | 19 | Strabo Pixel Club, Sattal, Uttarakhand | September 28-October 05, 2019 |

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|---|---|---|---|---|---|
| 6. | Students, Research Scholars & Entrepreneurs | Hands on Training for Arsenic Estimation Arsenic Field Kit and Inductively Coupled Plasma Mass Spectrophotometer (ICP- MS) | 12 | CSIR-NBRI, Lucknow | October 31, 2019 |
| 7. | CSIR-NBRI under the project entitled "Farm based S&T intervention for socio-economic development in the aspirational district of Nabrangpur, Odisha" | Training cum workshops for popularization of Bio-fertilizer usage | 164 | Nabrangpur, Odisha | November 8-9, 2019 |
| 8. | Rural/tribal people particularly Gond, chero, bhutiya, bhind and baiga) of Sonebhaddra district | Outreach Training/ awareness program for usage of locally available gums, resins and dissipation of lead technologies for their urge and techno-acceptability evaluation | 100 | CSIR-NBRI | November 12-19, 2019 |

### 1.1 Skill Development Programmes Organized:

| Sr. No. | Name of the Programme | Date/period | Number of candidates | Title |
|---|---|---|---|---|
| 1. | Bio-inoculant Producer for Agricultural Application | November 01, 2019 | 11 | Govt. Sponsored Skill Development Programme |
| 2. | Soil Physico-Chemical and Soil Microbiology Analysis | December 11-13, 2019 | 01 | Industry Sponsored Skill Development Programme |
| 3. | Bio-inoculant Producer for Agricultural Application | June 18 - Jul 16, 2019 | 03 | Semi Sponsored Skill Training Programmes |
| 4. | Plant Tissue Culture Technician | July 16-August 22, 2019 | 02 | NSDC (Skill Councils) Aligned Programme |
| 5. | Carrier in Bioinformatics, Molecular Biology and Biotechnology | January 27-28, 2020 | 48 | Other Skill Training Programme |

# HONORS/AWARDS/DISTINCTIONS

## Honours/Awards/Recognitions Received by Individual

### Dr. Prabodh Kumar Trivedi awarded INSA Fellowship 2019

Dr. Prabodh Kumar Trivedi, Senior Principal Scientist and Area Coordinator, Molecular Biology and Biotechnology Division, CSIR-National Botanical Research Institute has been elected for the Indian National Science Academy (INSA) Fellowship (FNA) 2019. The Indian National Science Academy plays important role in promoting science in India, harnessing scientific knowledge for the cause of humanity as well as recognising and rewarding excellence in scientific research. The INSA has appreciated the 'outstanding' contributions of Dr. Trivedi for his major achievements in basic science applications to crop improvement especially in the area of pathway engineering of secondary metabolites in plants and in environmental biotechnology. Dr. Trivedi has been working in the area of engineering of pathways involved in biosynthesis of medicinally important plant molecules and Environmental Biotechnology. Apart from pathway engineering, he has worked extensively for the elucidation of biosynthetic pathways in important medicinal plants including *Withania* and opium poppy. He was also elected as Fellow of National Academy of Agriculture Sciences, India (FNAAS) and National Academy of Sciences, India (FNASc) for his contribution in plant science. He is also a receipient of Tata Innovation Fellowship of the Department of Biotechnology, Ministry of Science and Technology, Government of India.


Award of FNA Fellowship to Dr. PK Trivedi at General Body Meeting of Indian National Science Academy at CSIR-NIO, Goa

### Other Awardees

| Sr. No. | Name of the Person/s | Award (s) |
|---|---|---|
| 1. | Mr. Anand Prakash | Birbal Sahni Award-2018<br>(For the book 'Adivasi Aushadhiya va Arthik vanaspati Baudhik Sampada' by Uttar Pradesh Hindi Sansthan, Uttar Pradesh) |
| 2. | Dr. Aradhana Mishra | Women Scientist Award-2019 by The Biotech Research Society, India. |
| 3. | Dr. Sanjeeva Nayaka | Fellow of International Society for Environmental Botanists |
| 4. | Ms. Shikha Verma, Mr. PK Verma and Dr. Debasis Chakrabarty | Gandhian Young Technological Innovation Award-2019 for development of low grain arsenic rice by the fungal arsenic methyl transferase via bio-volatilization |

**Member, Editor, Referee, Expert, Reviewer, Judge etc. (selected, recognized, enrolled, empaneled, nominated)**

| Sr. No. | Name of the person | Details |
|---|---|---|
| 1. | Dr. Alok Lehri | • Life Member of Oil Technologist Association of India<br>• Life Member of Essential Oil Association of India<br>• Life Member of Plant Pathologists of India, Lucknow<br>• Life Member of UPAS, Lucknow<br>• Life Member of the Society of the Centre of Minor Forest Products for Rural Development & Environmental Conservation, Dehradun |
| 2. | Dr. Aradhana Mishra | • Editorial Member of *Plos One* |
| 3. | Dr. BN Singh | • Editor of Journals *Annals of Pediatrics & Adolescent Medicine, Current Analysis on Biotechnology, Cell & Cellular Life Sciences Journal, Journal of Biomedical Engineering Research, The Open Bioactive Compounds Journal* |
| 4. | Dr. ChV Rao | • Expert Member of Bureau of Indan Standards (BIS), New Delhi and Basic Science, ICMR, New Delhi<br>• CPCSEA Nominee by Ministry of Environment and Forest, New Delhi<br>• Management Committee Member of IASTAM-Indian Association for the Study of Traditional Asian Medicine<br>• Member of Board of Studies of Jamia Hamdard, Delhi |
| 5. | Dr. Devendra Singh | • Judge in Pradeshik Phal Shakbhaji evam Pushp Pradarsani Samiti, Raj Bhawan, Lucknow, Uttar Pradesh, 2020 |
| 6. | Dr. LB Chaudhary | • Managing Editor of the Journal 'Ethnobotany'<br>• Reviewer of *Biodiversity Conservation, Rheedea, Journal of Threatened Taxa, Nordic Journal of Botany, Indian Journal of Traditional Knowledge, Journal of Economic and Taxonomic Botany, Acta Botanica Croatica, Annales Botanici Fennici, Phytokeys* |
| 7. | Dr. PK Trivedi | • Editorial Board Member of *Scientific Reports, PLoS One, Physiology and Molecular Biology of Plants (Springer), International Journal of Plant and Environment*<br>• Member of Advisory Committee for Biotechnology, CST, UP<br>• Member, Board of Studies, Academy of Scientific and Innovative Research (AcSIR) |
| 8. | Dr Poonam C Singh | • London Journals Press Awarded 'Quarterly Franklin Membership (Membership ID#HI61207)' for the publication Effect of *Trichoderma koningiopsis* on Chickpea Rhizosphere Activities under Different Fertilization Regimes<br>• Associate Editor of *BMC Microbiology*<br>• Member of Editorial Board of *Global Journal of Microbiology and Biotechnology* |

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| 9. | Dr. PS Chauhan | • Academic Editor of *Plos One* |
| 10. | Dr. Sayyada Khatoon | • Editor-in-Chief of *Asian Journal of Plant Sciences*<br>• Member - Editorial Board of *Pharmacognosy Journal, Journal of Developmental biology & Tissue Engineering*.<br>• Reviewer of *Journal of Ethnopharmacology, JPC-Planar Chromatography, International Research Journal of Plant Science, Indian Journal of Traditional Knowledge, Pharmacognoy Research, Ethnobotany*<br>• Member of Experts Panel, Unani Directorate, UP |
| 11. | Dr. SK Ojha | • Shree Dhanvantari Samman in OJUS Utsav 2019 at India International Centre, New Delhi by M/s Nirog Street, New Delhi<br>• Member, Editorial Board -Multidisciplinary Journal *Eastern Scientist*.<br>• Judge in the DST - Inspire Science Projects Exhibition and Competition |
| 12. | Dr. SK Tewari | • Executive Editor, Medicinal Plants<br>• Member, Academic Council of Fragrance & Flavour Development Centre (FFDC), Kannauj<br>• Councilor, International Society of Environmental Botanists<br>• सदस्य, विज्ञान प्रगति सलाहकार समिति |
| 13. | Dr. Vidhu A Sane | • Associate Editor, *Plant Molecular Biology Reporter* |

# Ph.Ds SUBMITTED AND AWARDED

## Ph.D Theses Awarded

| Sr. No | Name of the Student | Title of Thesis | Guides | University |
|---|---|---|---|---|
| 1. | Ms. Akanksha Singh | Phenotypic diversity and transgenerational DNA methylation patterns of Indian *Arabidopsis thaliana* populations originated from the altitudinal gradient | Dr. Sribash Roy, Senior Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 2. | Mr. Arun K Kushwaha | Floristic Diversity of Sonbhadra District, Uttar Pradesh, India | Dr. LB Chaudhary & Prof LM Tiwari | Kumaun University, Nainital, Uttarakhand |
| 3. | Ms. Ashmita Tandon | Prospecting organic amendments for sodic soil reclamation | Dr. Poonam C Singh, Senior Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 4. | Ms. Babita | Exploring the role of allelic epigenetic modifications and physical interactions responsible for heterosis in *Arabidopsis thaliana* | Dr. Samir V Sawant, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 5. | Ms. Garima Pathak | Identification and characterization of aroma related genes in *Mangifera indica* L. (Mango) | Dr. Vidhu A Sane, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 6. | Ms. Hardeep Kaur | Comparative evaluation of different irrigation solutions on micro-hardness of root canal dentin-an in-vitro study | Dr. BN Singh, Senior Scientist & Dr. Praveen S Samant | Dr. RML Awadh University, Ayodhya, U.P. |
| 7. | Ms. Ila Shukla | Phytopharmacological evaluation of selected lichens in alcohol liver disease | Dr. ChV Rao, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 8. | Mr. Komal K Ingle | Morphotaxonomic and ecological studies on mangrove lichens of Gujarat state, India | Dr. Sanjeeva Nayaka, Senior Principal Scientist and Prof. Suman Trivedi | Barkatullah University, Bhopal |
| 9. | Mr. Manoj Kumar | Gene mining and application for development of drought tolerant transgenic chickpea (*Cicer arietinum* L.) Lines | Dr. Manoj Kumar, Scientist & Prof. Mohd. Aslam Yusuf | Integral University |

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|---|---|---|---|---|
| 10. | Ms. Maria Kidwai | Expression and functional characterization of arsenic responsive genes from rice (*Oryza sativa L.*) | Dr. Debasis Chakrabarty, Principal Scientist & Prof. IZ Ahmad | Integral University, Lucknow |
| 11. | Ms. Nitanshi Jauhari | Bacteria-Mediated degradation of petroleum hydrocarbons in *in-vitro* conditions | Dr. DK Upreti, Ex-Chief Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 12. | Ms. Parneeta Mishra | Studies on the role of microRNA775 in growth and development of *Arabidopsis thaliana* | Dr. Sribash Roy, Senior Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 13. | Ms. Poonam Tiwari | Molecular and functional characterization of abiotic stress responsive gene from *Oryza sativa* L. | Dr. Debasis Chakrabarty, Principal Scientist & Dr. Veena Pande | Kumaun University, Nainital |
| 14. | Mr. Pradyumna K. Singh | Nitric oxide-mediated genome-wide transcriptional modulation in rice (*Oryza sativa* L.) during arsenic stress | Dr. Debasis Chakrabarty, Principal Scientist & Dr. R.D. Tripathi, Emeritus Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 15. | Ms. Pritt Verma | Ethno-pharmacological evaluation of Indian medicinal plants on drug inducing hepatotoxicity | Dr. ChV Rao, Senior Principal Scientist & Dr. S Srivastava | Amity University, Lucknow |
| 16. | Mr. Ram Naresh | Role of *GhNAC2* in root development | Dr. Vidhu A Sane, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 17. | Ms. Rashmi Garg | Functional characterization of SlERF36 in tomato (*Solanum lycopersicum* ) | Dr. Aniruddha P Sane, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 18. | Ms. Rashmi Raj | Characterization of potyvirus isolate/es infecting *Narcissus tazetta* and their possible management | Dr. Puneet S Chauhan, Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 19. | Mr. Sankalp Misra | Characterization of salt tolerant plant growth promoting rhizobacteria from different agro-climatic zones of Uttar Pradesh | Dr. Puneet S Chauhan, Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 20. | Mr. Shatrujeet Pandey | Molecular analysis of prickleless mutant to identify potential gene network regulating prickle development in *Solanum viarum* Dunal | Dr. Pratibha Misra, Ex-Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |

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| 21. | Mr. Surjeet K Arya | Transcriptome based screening of putative RNAi targets for mealybug (*Phenacoccus solenopsis*) and their functional validation | Dr. Praveen C Verma, Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 22. | Mr. Suresh K Sharma | Effect of integrated nutrient management in African marigold (*Tagetes erecta* L.) cultivar 'Pusa Basanti' in partially reclaimed sodic soil | Dr. SK Tewari, Chief Scientist and Dr. Krishna Pal | IFTM University, Muradabad |
| 23. | Mr. Vivek Srivastava | Quality of manageemnt education in universities of Uttar Pradesh : A study | Dr. AK Gauniyal, Chief Scientist and Prof. Alok Kumar Roy | BHU, Varanasi |

## Ph.D. Theses Submitted

| Sr. No. | Name of the Student | Title | Guides | University |
|---|---|---|---|---|
| 1. | Ms. Arpita Bhattacharya | Defence modulating strength of endophytes in inducing resistance in *Solanum lycopersicum* in wilt disease infested environment | Dr. Aradhana Mishra, Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 2. | Mr. Bhoopendra K Pandey | Exploring the role of alternative splice variants of CAMTA1 in stress physiology of *Arabidopsis thaliana* | Dr. Samir V Sawant, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 3. | Ms. Deepali Srivastava | Identification and characterization of abiotic stress-responsive genes in rice for enhanced stress tolerance | Dr. Debasis Chakrabarty, Principal Scientist | Kumaun University, Nainital |
| 4. | Ms. Meenakshi Kushwaha | Contribution of microbial diversity in Soil Organic Matter (SOM) pool in a tropical dry deciduous forest | Dr. Vivek Pandey, Senior Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 5. | Ms. Madhu Tiwari | Interaction of *Agrobacterium* VirE2 protein with host protein of Rice (*Oryza sativa* L.): Implications for the T-DNA transfer process | Dr. Debasis Chakrabarty, Principal Scientist & Prof. AK Mishra | BHU, Varanasi |

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|---|---|---|---|---|
| 6. | Ms. Prateeksha | Lichenized fungi metabolites derived nanomaterials and their biomedical application | Dr. BN Singh, Senior Scientist & Prof. Mohd. Aslam Yusuf | AKTU, Lucknow |
| 7. | Ms. Shipra Pandey | Synthesis and characterization of bio-nanomaterials for management of Early Blight disease in tomato | Dr. Aradhana Mishra, Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |
| 8. | Dr Shobhit Pratap Singh (MDS) | Antimicrobial efficacy of herbal extracts against *Enterocoxccus faecalis* and *Candida albicans* as compared to Chlorhexidine and Sodium Hypochloride: An In Vitro Study | Dr.SK Ojha, Principal Scientist | Saraswati Dental College, Lucknow (Affiliated to Dr. Ram Manohar Lohia Avadh University, Ayodhya, UP) |
| 9. | Mr. Suman B Singh | Environmental studies on arsenic bioavailability and its regulation for risk assessment and remediation of contaminated soils | Dr. Pankaj K Srivastava, Principal Scientist | Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, U.P. |

# S & T Support

# PLANNING, MONITORING AND EVALUATION DIVISION

**Anil Kumar Gauniyal**

a.k.gauniyal@nbri.res.in

**Area Coordinator, S&T Support Services and**
**Head, Planning, Monitoring and Evaluation Division**

## Highlights and Major Activities

The Planning, Monitoring and Evaluation (PME) Division of the Institute acts as a liaison between Director and various R&D groups; CSIR HQ and other organizations. The Division strives to spearhead the programmes and projects of various divisions of the institute from the stage of planning to outputs of value to diverse stakeholders. The activities of the division range from scrutiny and coordinating in the evaluation of new research proposals, assist in monitoring the progress of research projects, maintenance of repository of R&D projects in both physical documents and as well as electronic databases. During 2019-20, 17 Grant-in-Aid/ Sponsored projects were populated in the R&D module as a part of ERP solutions for quick online accessibility and usability of complete accurate information. In order to commence online operations of project activities, project details of new Contract R&D were entered in the Research and Development Portal. The associated staff in the respective projects were mapped. Foreign deputation cases of Director/ Scientists for various R&D purposes were processed to visit abroad for taking part in conferences/ workshops/technical meetings, etc.

## Projects Initiated during April 02, 2019 to March 31, 2020

| S. No. | Project Number | Project title | Funding Agency | Principal Investigator | Duration Details |
|---|---|---|---|---|---|
| 1. | SSP 2906 | Development of Shodhan protocol and preparation of standardized *Cannabis* extracts based AYUSH formulation | Hemp Street Medicare Pvt. Ltd., Gurgaon | Dr. SK Ojha | 11 Months w.e.f. February 01, 2020 |
| 2. | CNP 3047 | Consultancy for establishment of biodiversity park & krishna lila theme park in shri vrindavan chandrodaya mandir & group housing, Vrindavan | Hare Krishna Movement Vrindavan Chattikara Road, Vrindavan, Mathura | Dr. AK Gauniyal | 01 Month w.e.f. July 19, 2019 |
| 3. | GAP 3466 | Biogeography, phylogenetic studies and development of e-monograph for the *Arthoniales* (lichenized fungi) in India | DST, New Delhi | PC: Dr. TS Rana<br>PI: Dr. Siljo Joseph | 60 Months w.e.f. May 01, 2019 |

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|---|---|---|---|---|---|
| 4. | GAP 3465 | Taxonomy and phylogeny of the genus *Juniperus* L. (Cupressaceae) in India | SERB, New Delhi | Dr. Baleshwar | 36 Months w.e.f. June 01, 2019 |
| 5. | GAP 3467 | Analysis of arsenic and other multi-elements accumulation in grain of different rice cultivars | Rice Research Station, Chinsurah, Hooghly, West Bengal | Dr. Sanjay Dwivedi | 06 Months w.e.f. August 19, 2019 |
| 6. | GAP 3468 | Farm based S&T interventions for socio-economic development in the aspirational district of Nabarangpur, Odisha | Agriculture and Farmers' Empowerment Department, Govt. of Odisha through CSIR-IMMT, Bhubaneshwar | Dr. SK Tewari | 12 Months w.e.f. September 12, 2019 |
| 7. | GAP 3469 | Baselines studies for ambient air quality, water, soil, terrestrial and aquatic ecology and biodiversity in and around quarry No 4&7 of the abandoned Jaganath mine vide, Talcher, District Angul, Odisha | NTPC Ltd., Talcher Thermal Power Station, Agul, Odisha | Dr. Vivek Pandey | 04 Months w.e.f. October 31, 2019 |
| 8. | GAP 3473 | Deciphering the role of nitric oxide in root development and zinc availability in rice plants | SERB, New Delhi | PC: Dr. AP Sane<br>PI: Dr. RK Tewari | 36 Months w.e.f. November 01, 2019 |
| 9. | GAP 3471 | Monographic and phylogenetic studies in the genus *Saxifraga* L. (Saxifragaceae) from India | SERB, New Delhi | PC: Dr. Priyanka Agnihotri<br>PI: Dr. AK Srivastava | 36 Months w.e.f. November 01, 2019 |
| 10. | GAP 3472 | Reducing Pathogenic damages in *betelvine* (Piper betle) using ACC deaminase containing microbes | DST, New Delhi | PC: Dr. SK Tewari<br>PI: Dr. Nivedita Singh | 36 Months w.e.f. November 21, 2019 |
| 11. | GAP 3470 | Development of rice-grain arsenic removal technique/ method for rural population of arsenic affected areas | DST, New Delhi | Dr. Sanjay Dwivedi | 36 Months w.e.f. November 27, 2019 |
| 12. | GAP 3474 | Understanding transcriptional regulation of withanolide biosynthesis in *Withania somnifera* | SERB, New Delhi | PC: Dr. MH Asif<br>PI: Dr. Sucheta Singh | 24 Months w.e.f. January 08, 2020 |
| 13. | GAP 3476 | *Ex-situ* conservation studies of the *Cycas* species in India at CSIR-NBRI Botanic Garden | MoEF&CC, New Delhi | Dr. SK Tewari | 60 Months w.e.f. January 18, 2020 |

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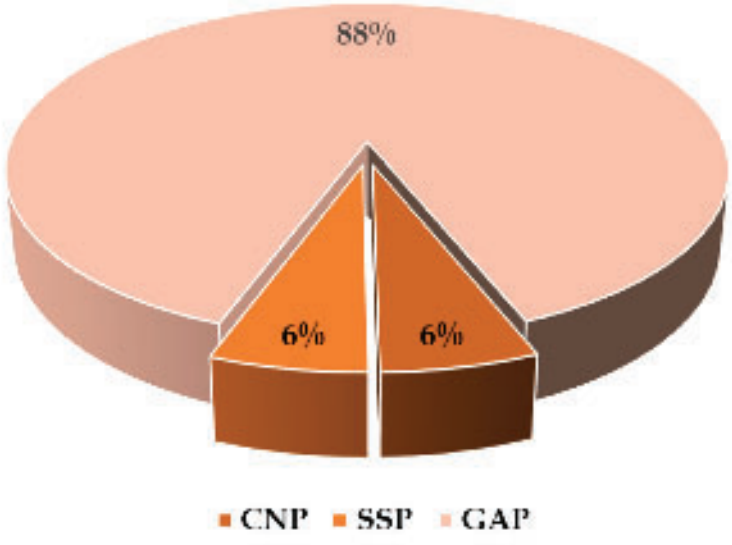
|---|---|---|---|---|---|
| 14. | GAP 3475 | Study of spatio-temporal distribution in the $F^-$ and As levels in environmental matrices of $F^-$ contaminated districts of UP (Unnao, Kanpur and Raebarelly) and its relationship with the soil chemistry | SERB, New Delhi | Dr. Shekhar Mallick | 36 Months w.e.f. February 05, 2020 |
| 15. | GAP 3477 | Taxonomy and phylogeny of the genus *Uraria* Desv., (Leguminosae) in India | SERB, New Delhi | Dr. TS Rana | 36 Months w.e.f. Febraury 10, 2020 |
| 16. | GAP 3479 | Assessment of conservation status and phylogeny of endemic hornworts (*Anthocerotophyta*) in India | SERB, New Delhi | Dr. AK Asthana | 36 Months w.e.f. February 18, 2020 |
| 17. | GAP 3478 | Leveraging genetic resources for accelerated genetic improvement of Linseed using comprehensive genomics and phenotyping approaches: Sub Project 2, Component-1: Development of reference genome and core set using molecular markers | DBT, New Delhi | Dr. HK Yadav | 60 Months w.e.f. February 29, 2020 |

**Projects Initiated During April 01, 2019 to March 31, 2020**



## Deputation of CSIR-NBRI Personnel Abroad during 2019-20

| S. No. | Name | Place of Visit | Deputation Period | Purpose of Visit |
|---|---|---|---|---|
| 1. | Dr. Priyanka Agnihotri | Beijing, China | July 08-14, 2019 | To attend a conference organized on From sea level to world roof: Uplift history and biological evolution of the Himalaya and to deliver a lecture on the Flora of Pan-Himalaya |
| 2. | Dr. PS Chauhan | Hong Kong Polytechnic University, Hung Hom, Kowloon Hong Kong, China | June 12-15, 2019 | To attend the third International conference as invited Speaker in The Hong Kong Polytechnic University, Hung Hom, Kowloon Hong Kong |
| 3. | Prof. SK Barik, and<br>Dr. SK Tewari | Ecuador, North America | November 13-15, 2019 | To attend the technical meeting to provide assistance on exploring *Nelumbo nucifera* as an alternative crop for production in the flood-prone areas of the Ecuadorian coast |
| 4. | Prof. SK Barik | Lismore, Australia | February 10-15, 2020 | To attend workshop on Governance of Global Taxonomic Lists, Charles Darvin University, Australia (February 10-12, 2020) and to undertake field visit and discussion on *Cannabis* research with Southern Cross University, Lismore, Australia (February 13-15, 2020) |

## Team

- Dr. RN Gupta, Senior Technical Officer
- Mr. Vivek Kumar Gupta, Technical Assitant
- Mrs. Sandhya Srivastava, Senior Stenographer
- Mr. Atul Srivastava, Senior Stenographer
- Mr. Shubham Tandon, Technician
- Mr. Sagar Kumar, MTS

# TECHNOLOGY TRANSFER & BUSINESS DEVELOPMENT DIVISION

**Vivek Srivastava**

vivek@nbri.res.in

**Head, Technology Transfer & Business Development Division**

## Highlights and Major Activities

Technology Transfer & Business Development (TTBD) division is interface of the institute for bridging the gap between R&D at lab and stakeholders. It identifies key inventions for intellectual property right protection. Scientists are helped for preparing patent draft, prior art search and response to office action. Division interacts with industry for information dissemination by participating in various exhibitions, putting up information on web site and interacting and exchanging information by various mode of communication. Various agreements viz., Consultancy, Secrecy, Sponsored, Technical Services, with project funding agencies, with academia for joint R&D work are also facilitated.

The division has been facilitating training programme each year for post graduate students of various universities and colleges which entail updating the skills and knowledge of the outside students and faculty in the core competences of the institute.

Division has also undertaken various activities related to CSIR-KVS Scientist Student Connect Programme - "JIGYASA". CSIR and Kendriya Vidyalaya (KV) Sansthan have signed agreement for connecting CSIR Institutes with school students to develop scientific temper in young minds under this programme.

Division has interacted with various industries for seeking funds under "corporate social responsibility" for institutes R&D.

## MoUs/MoAs/MTAs Signed

| S. No. | Details | Client | Date |
|---|---|---|---|
| **National** | | | |
| 1. | For together performing activity comparative study of bio-formulation with chemical fungicide against *Fusarium* wilt disease control | Narendra Dev University of Agriculture & Technology, Faizabad – UP | April 04, 2019 |
| 2. | Jointly with Indian Veterinary Research Institute, Bareilly for evaluation of herbal acaricides formulation | M/s. RODEC Pharmaceuticals Pvt. Ltd., Ghaziabad – 201001 | May 29, 2019 |
| 3. | For providing a project report for setting up a biodiversity park around the Vrinadavan Mandir | Hare Krishna Movement Vrindavan Chattikara Road, Varindavan | July 19, 2019 |
| 4. | For procurement of Chickpea germplasm | Indian Institute of Pulses Research (IIPR), Kanpur | August 20, 2019 |
| 5. | For project entitled 'Biotechnological interventions through RNAi approach for management of Banana Bunchy Top Virus (BBTV) in North East region of India' with DBT, New Delhi | Department of Biotechnology, New Delhi | October 09, 2019 |
| 6. | For GM cotton expressing a fern insecticidal protein 'Mscl4' | ICAR-Indian Institute of Vegetable Research, Varanasi – 221305 | December 17, 2019 |

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|---|---|---|---|
| 7. | For integrative taxonomic analysis for assessment of diversity and phylogenetic relationships of *Citrus* from Northeast region | Department of Biotechnology, New Delhi | January 10, 2020 |
| 8. | For product development and partner support for demonstration farming and value addition" with DBT, New Delhi on 10.01.2020. | | |
| 9. | For quantitative assessment and mapping of the diversity of non-flowering plants of Northeast India | | |
| 10. | For mainstreaming the lesser-known bioresources | | |
| 11. | For discovery of molecular markers and genes suitable for cotton improvement | Tierra Agrotech private limited, Hyderabad | January 17, 2020 |
| 12. | For development of Shodhan protocol and preparation of standardized cannabis extracts based AYUSH formulation | Hemp Street Medicare Pvt. Ltd., Gurgaon | January 19, 2020 |
| 13. | For procuring Linseed material for genome sequencing | ICAR-National Bureau of Plant Genetic Resources, New Delhi | March 12, 2020 |
| 14. | Access and Benefit sharing (ABS) agreements for patent applications signed between National Biodiversity Authority (NBA) and CSIR (CSIR-NBRI). | National Biodiversity Authority (NBA), Chennai | |
| **International** | | | |
| 1. | For procurement of plasmid vector (91135 Pdirect_22c) | ADDGENE, USA | August 20, 2019 |
| 2. | For procurement of plasmid vector (115488pEG302 22aa Sun Tag NtDRMcd nog) | | |
| 3. | For procurement of plasmids vectors | | January 24, 2020 |

## Technologies Transferred

| S. No. | Name | Client | Date |
|---|---|---|---|
| 1. | Herbal floor disinfectant and cleaner | Licensing Agreement signed with M/S 3D Nutrients 101, New Road, Ratlam (M.P.) – 457001 | December 06, 2019 |
| 2. | NBRI-DentoGel for Toothache | | |
| 3. | ZanthoDent (Toothpaste) | | |
| 4. | Alcohol based herbal hand sanitizer gel | Supplementary Licensing Agreement signed for with M/S Satguru Biologicals Private Limited, Barabanki – UP | March 20, 2020 |

## Training for Post Graduate Students

A total number of 83 students were imparted research trainings in different disciplines of plant science and applied subjects. The short term training/project work/dissertation for the students from various universities and colleges were coordinated by the division.

A revenue of rupees twelve lakh forty eight thousand was generated as training fee during the year 2019-20.

## School Visits Coordinated

Visits of individuals including research scholars, students from various universities, schools and colleges, farmers, general public to Institute's facilities such as herbarium, botanic garden, exposition and various laboratories are coordinated by the division. More than 5000 individuals/students visited CSIR-NBRI during April 2019-March 2020.

**Team**

- Ms. Swati Sharma, Senior Technical Officer
- Mr. BL Meena, Technical Assistant
- Mr. Yatish Tiwari, Senior Stenographer

# NBRI JIGYASA CORNER

## Mission Objective

'JIGYASA' is one of the major initiatives taken up by CSIR at national level for further widening and deepening its Scientific Social Responsibility (SSR). On the one hand, this programme would explain the culture of curiousness and scientific nature on the other.

Council of Scientific and Industrial Research has launched a student-scientist connect programme 'JIGYASA' in collaboration with Kendriya Vidyalaya Sangathan (KVS); the sole objective of which is extending the classroom leaning and focusing on a well-planned research laboratory based learning.

## Models of Engagement

- Student Residential Programmes
- Scientists as Teachers and Teachers as Scientists
- Lab specific activities / Onsite Experiments
- Visits of Scientists to Schools/Outreach Programmes
- Science Clubs
- Popular Lecture Series/ Demonstration Programme at Schools
- Student Apprenticeship Programmes
- Science Exhibitions
- Projects of National Children's Science Congress
- Teacher Workshops
- Tinkering Laboratories

## Major Activities

Under Jigyasa initiative, CSIR-NBRI organized different programmes and guided lab tours for the KV students during the year 2019-20. Different basic lab experiments covering the tissue culture, DNA isolation, and microscopy were also included in the programme. A refresher course for the KV teachers was also organized by the institute to enhance the science teaching capabilities. The guided tour to famous botanic garden of the institute provided a great opportunity to learn about the curious and novel plants. Special visit to third largest herbarium of the country is a great tool to create awareness among the science students. The details of visits of different Kendriya Vidyalaya to CSIR-NBRI are as under:

| Sr. No | Activity | Date | Name of the School | No. of students participated | No. of teachers attended |
|---|---|---|---|---|---|
| 1. | Visit to Botanic garden, Exposition, Herbarium and Lecture by scientist with an interactive session | May 08, 2019 | Kendriya Vidyalaya, Eastern Railway, Mughalsarai | 12 | 02 |
| | | May 27, 2020 | Kendriya Vidyalaya, GTC Cantt., Varanasi | 30 | 04 |
| | | July 15, 2020 | Kendriya Vidyalaya, RDSO, Lucknow | 42 | 03 |
| 2. | Scientist –students interaction programme | July 22, 2019 | Kendriya Vidyalaya, IIIT Jhalwa, Prayagraj | 50 | 04 |
| | | July 24, 2019 | Kendriya Vidyalaya, Basti | 23 | 03 |
| | | August 05, 2019 | Kendriya Vidyalaya, Gomti Nagar, Lucknow | 50 | 02 |
| | | August 26, 2019 | Kendriya Vidyalaya, Gonda | 45 | 05 |
| 3. | Awareness Programme at school on the occasion of World Ozone Day | September 16, 2019 | Kendriya Vidyalaya, Gomti Nagar, Lucknow | 120 | 06 |

| | | | | | |
|---|---|---|---|---|---|
| 4. | Jigyasa Programme on the occasion of CSIR Foundation Day 2019 | September 26, 2019 | Kendriya Vidyalaya C.R.P.F., Lucknow | 49 | 4 |
| | | | Kendriya Vidyalaya, Barabanki | 75 | 5 |
| | | | Kendriya Vidyalaya, Unnao | 40 | 5 |
| | | | Kendriya Vidyalaya Canttt, Lucknow | 36 | 3 |
| | | | Kendriya Vidyalaya, Chakeri, Kanpur | 160 | 11 |
| 5. | Scientist –Student Interaction Programme | October 04, 2019 | Kendriya Vidyalaya, Cantt, Faizabad | 30 | 03 |
| | | November 29, 2019 | Kendriya Vidyalaya, Bakshi Ka Talab, Lucknow | 16 | 02 |
| | | December 04, 2019 | Government Inter College, Nishatganj, Lucknow | 50 | 3 |
| | | December 12, 2019 | Kendriya Vidyalaya, Banaras | 35 | 07 |
| 6. | Workshop on World Soil Day | December 05, 2019 | Kendriya Vidyalaya Gomti Nagar, Lucknow | 24 | 2 |
| 7. | Scientist –students interaction programme | December 13. 2019 | Kendriya Vidyalaya, Barabanki | 100 | 8 |
| | | December 18, 2019 | Kendriya Vidyalaya, Bakshi Ka Talab, Lucknow | 130 | 6 |
| | | January 24, 2020 | Kendriya Vidyalaya, Faizabad | 150 | 5 |
| | | January 25, 2020 | Kendriya Vidyalaya, Mau | 200 | 7 |
| | | February 10, 2020 | Kendriya Vidyalaya, Sahajhanpur | 215 | 4 |
| | | February 11, 2020 | Navodaya Vidyalaya, Kotabagh Nainital | 320 | 12 |
| 8. | Workshop on Advance Laboratory Techniques | February 12-14, 2020 | Kendriya Vidyalaya Gomti Nagar, Lucknow and Kendriya Vidyalaya, Bakshi Ka Talab, Lucknow | 30 | 05 |

**Team**

**Nodal Scientist:** Dr. Vivek Srivastava

**Co-Nodal Scientist:** Dr. AK Gauniyal

**Team Members:**

Dr. Vinay Sahu, Dr. KK Rawat, Ms. Swati Sharma, Mr. BL Meena, Mr. RR Rastogi

## Glimpses of Jigyasa Programme

















# INFORMATION, PUBLICATION AND EXPOSITION DIVISION

## Highlights and Activities

Information and publication functions as one of the important S&T support systems of the Institute. It primarily handles the scientific information compilation, dissemination and publication work. The division also serve information needs of scientists, researchers, students, industrialists, planners, administrators, and people from other walks of life on various aspects of plant sciences and related research disciplines.

The main functions of IPL include collection, collation, publication and effective dissemination of the S&T information resources generated by the Institute through different communication tools, including print and electronic media.

It serves as the principal communication link between the Institute and society including stakeholder groups. The division also manages the organization of different scientific events, press meets, celebration of various national and international days designated for scientific, technological and strategic importance to nation. It also bears the public relation to the press and media for promoting and showcasing institute's achievements to the science community and the public.

Its primary function is publication of the research and development outcomes and outputs of the Institute in the form of *NBRI News Letter* (a quarterly in-house publication), *Annual Report*, and other science and popular books, bulletins and calendars on different themes of topical interests on plants, environment, biotechnology, agro-technology, ornamental horticulture, etc.

**Publications**: It is one of the major activities of the division. Following publications were brought out during 2019-2020:

ι) Educational Material (Calendar) for the year 2020 was designed and produced on the theme "India's Wild ornamentals for Commercial Horticulture".

ii) CSIR-NBRI Annual Report**:** Annual Report 2018-2019 was compiled and brought out. It was released on the occasion of Annual Day of the Institute on October 25, 2019.

iii) CSIR Annual Report**:** Progress report on important R&D projects was compiled with respect to CSIR-NBRI, which covered significant contributions of CSIR-NBRI in the areas of Science & Technology, HRD activities, Awards and Distinctions, Patents Filed & Granted and sent to CSIR HQ for inclusion in the CSIR Annual Report 2018-19.

**Sale of Publications** : ₹ **15, 260/-**

**Parliament Questions**: Forty Seven parliament questions received from CSIR HQ were answered.

## Exposition

Exposition of CSIR-NBRI serves as a unique facility which act as interface for showcasing the recent research and developments of the institute. It provides an easy platform for students and visitors to understand the scientific developments. The facility was visited by large number of school students and visitors from different community throughout the year. The exposition also has a special gallery showcasing ethnobotanical culture of the past eras.

During the reporting year, more than 3500 visitors from different institutes, society and organization visited the Exposition. The facility was open on different national and international occasions for the common public, school children, teachers, researchers etc.

Some of the important delegates like, Dr. Shekhar C Mande, DG, CSIR, New Delhi, and Dr. (Mrs.) Sharmila Mande, Dr. Rajib Gogoi, Senior Scientist, Botanical Survey of India (Sikkim Circle) visited the exposition facility during the period.

**Section In-charge: Dr. PA Shirke, Chief Scientist**

**Email ID:** info-nbri@nbri.res.in

### Team

- Dr. KN Nair, Senior Principal Scientist
- Mr. Anand Prakash, Senior Principal Scientist
- Mr. Yogendra Nath, Principal Technical Officer
- Mr. AC Little, Principal Technical Officer
- Mr. Alok Kumar, Senior Technical Officer
- Mr. Rajat Raj Rastogi, Technical Assistant
- Mrs. Satyabhama, Senior Technician

# LIBRARY-KNOWLEDGE RESOURCE CENTRE (KRC)

The KRC provides services and facilities to meet the S & T knowledge requirements of the Institute's R & D activities. It operates with the following objectives, to:

- Support the learning process of the researchers through provision of knowledge/ information.
- Meet knowledge/information needs of the scientists, researchers and students to support their research activities.
- Respond effectively, where possible, to the knowledge/ information needs of the Institute's clientele.

CSIR-NBRI KRC is an automated open access library. KRC is fully automated with LibSys automation software. It provides automated circulation services to the users throughout working hours of the institute. Bibliographic information of the KRC resources is made available to the users through an Online Public Access Catalogue (OPAC). 'Inter Library Loan (ILL)' and 'Document Delivery Service (DDS)' facilities are provided to the users of the institute, CSIR and DST laboratories/organizations. KRC enables to provide online access of Electronic Resources like e-journals, e-databases to the end users. It also conducts training programs and workshops from time to time on using e-resources for the benefit of the scientists, technical staff, researchers and students of the institute. Every year, especially on the occasion of the Hindi Pakhwada, KRC organizes an exhibition of Hindi Books.

## Library Holdings and Reprography Services

KRC currently holds a total of 31065 books and 30069 bound journals. It currently subscribes a total of 554 journals, including 62 print and 482 online journals covering diverse fields of Plant Sciences, besides four databases viz., iThenticate (Plagiarism Checker), Web of Science and TAIR (The Arabidopsis Information Resource) and JSTOR Collection on Global Plants.

KRC plays a major role in information dissemination by providing reprography services to the scientific community of the CSIR and DST labs free of cost, and to the other organizations of India and abroad on payment basis.

A Botanical Archive has been maintained in the KRC which houses rare and hand-written manuscripts in Persian and Arabic languages, illustrations of plants dating back to 18th century and other original botanical literature and files containing biographic details, signatures, and important documents of eminent botanists/ scientists and institutions/ societies.

| CSIR-NBRI KRC Collections | |
|---|---|
| Books | 31065 |
| Journals Bound Volumes | 30069 |
| Total No. of Books and Bound Journals | 61134 |
| Theses | |
| • AcSIR | 67 |
| • Other Universities | 83 |
| Annual Reports | |
| • CSIR Institutes | 44 |
| • Other Organizations | 137 |

| Additions in KRC holding during the year 2019-2020 | |
|---|---|
| Books: | |
| • Purchased | 49 |
| • Received as Complimentary copies/Gifts | 16 |
| Bound journals | 02 |
| Total number of books and bound journals added during 2019-20 | 68 |
| Current Periodicals Subscribed: | |
| • Print only | 44 |
| • Print + Online | 01 |
| • Online subscribed directly by CSIR-NBRI | 10 |
| • Online subscribed through CSIR Consortium (NKRC) on share basis | 472 |
| • Complimentary /Gifts | 27 |
| Total number of Periodicals (titles) | 554 |
| Databases subscribed: | |
| • Subscribed direct by KRC, CSIR-NBRI | 02 |
| • Subscribed through CSIR Consortium (NKRC) on share basis | 02 |

## Training Imparted and Special Demonstration Programmes Held

KRC provides one year Apprentice Training to 6 students (4 Degree & 2 Diploma holders) in Library Science every year under the Apprentice Scheme of Government of India.

### Section In-charge

**Dr. KN Nair**
Senior Principal Scientist
**Email ID:** knnair@nbri.res.in

### Team

- Mr. ML Kain, Principal Technical Officer
- Mrs. Leena Wahi Gupta, Senior Technical Officer

# CENTRAL INSTRUMENTATION FACILITY (CIF)

## Highlights and Major Activities

Central Instrumentation Facility of the institute is having high tech and sophisticated instruments to provide the analytical services to the industries/ institutes/organizations/individuals. CIF is NABL accreditated based on the requirements of ISO-IEC-17025-2017. CIF is providing analytical services for the analysis of essential oils, vegetable oils, herbal drugs, and heavy metals using sophisticated analytical instruments like GCMS, IRMS, TD-NMR, TEM, SEM, GLC, HPLC, HPTLC, Atomic Absorption Spectrometer, UV spectrophotometer and Stereomicroscope etc. The institute has expertise in quantitative and qualitative analysis of several groups of secondary metabolites viz. polyphenols, alkaloids, withanolides, andrographolides, furoco-umarins, fatty acid, aromatic chemicals etc. Complete infrastructure for analysis of medicinal and aromatic plants and contract research (in public-private mode of partnership) is available with the institute.

**New Equipment Installed:**

One new instrument Gas Chromatography –Head Space (GC-HS) was installed in CIF of the institute.

Gas Chromatography-Head Space

## Details of Analytical Testing and other Technical Services Provided

CIF has provided analytical services to industries/ organization/ entrepreneurs/individuals (External samples) and various scientist/staff of the institute (Internal samples). The details of external and internal samples analyzed are as given in the table.

| **Analytical testing services provided (1st April 2019 to 31st March 2020)** | |
|---|---|
| External Samples | |
| • No. of samples analyzed<br>• Revenue Generated | 66<br>Rs. 1,56,763.00 |
| No. of industries/organizations/ Entrepreneurs/individuals benefitted | 19 |
| Internal Samples | |
| • No. of samples analyzed<br>• Revenue Generated | 4321<br>Rs. 70,11,400.00 |
| Maintenance and repairing of instruments | |
| Total number of jobs (internal equipments repairing) completed | 150 |
| NABL/ other similar Accreditation status | |
| CSIR-NBRI has been accreditated since 2008 as per the requirements of ISO/IEC-17025/2005 from NABL (National Accreditation Board for Calibration and Testing Laboratories), Quality Council of India (QCI), Govt. of India. NABL-Gurgaon after surveillance audit in March 2020 recommended for continuation of NABL-Accreditation of the institute up to 17.10.2020 as per the requirements of ISO/IEC-17025-2017.<br>**Certificate No. : TC-7972**<br>**Area of Scope- Herbal drugs, Essential oils, Vegetable oils, Soil and water samples**<br>Participated in International and National PT/ILC programme: 03 | |

**Scientist In-charge**

**TN Khoshoo Block**
Dr. Alok Lehri, Senior Principal Scientist

**KN Kaul Block**
Dr. Vivek Pandey, Senior Principal Scientist

**Team:**

- Dr. Anil Kumar, Senior Technical Officer
- Dr. Sanjay Dwivedi, Senior Technical Officer
- Dr. Abhishek Niranjan, Senior Technical Officer
- Dr. SK Behera, Senior Technical Officer
- Dr. GG Sinam, Senior Technical Officer
- Mr. Jai Chand, Technical Officer
- Mr. Dileep Singh, Technician
- Mr. Pawan Kumar, Technician

# INFORMATION AND COMMUNICATION TECHNOLOGY DIVISION (ICT)

Information & Communication Technology Division looks after the following services in the institute:

## NBRI LAN (Local Area Network)

It is fully managed and designed as per National Knowledge Network (NKN) compliance, continuous updating and management of dynamic CSIR-NBRI website (www.nbri.res.in). CSIR-NBRI has got High Speed Internet connectivity of 100 Mbps from National Knowledge Network (NKN) since January, 2011 for R&D and administrative purposes.

## ICT Server

ICT Division is maintaining following servers for institutional requirement using Intel Xeon base 2U rack servers for HP & IBM Make:

- Microsoft Active Directory Server for user authentication and internet access.
- The institute's new website is running on XAMPP Server using PHP and is GIGW compliant.
- IIS web server for Institutional Intranet application i.e. Intranet.
- Kaspersky Endpoint Protection 12 Antivirus is running in LAN systems currently.
- LibSys server for managing Library records.

## Network & IT Security

ICT division is using KES 12 antivirus for servers and desktop PCs as per Institutional requirement.

## Application & Database Software Used

Microsoft Visual Studio 2005/2008 Professional Edition.

## Hardware, Software & Network Maintenance

Management of problems associated with hardware, software, LAN, IT Security etc. is taken care by ICT for smooth functioning of LAN, PCs, Servers etc. ICT has played a major role in installation and maintenance of BAS (Biometric Attendance System) system in the institute. Recently two Polycom videoconferencing systems were installed in the institute for day to day VC meetings.

From time to time technical support and infrastructure related to IT is being provided by ICT to the Administrative staff for conducting, 'Data Entry Operator' and similar computer based exams for various selections.

**Scientist In-charge**

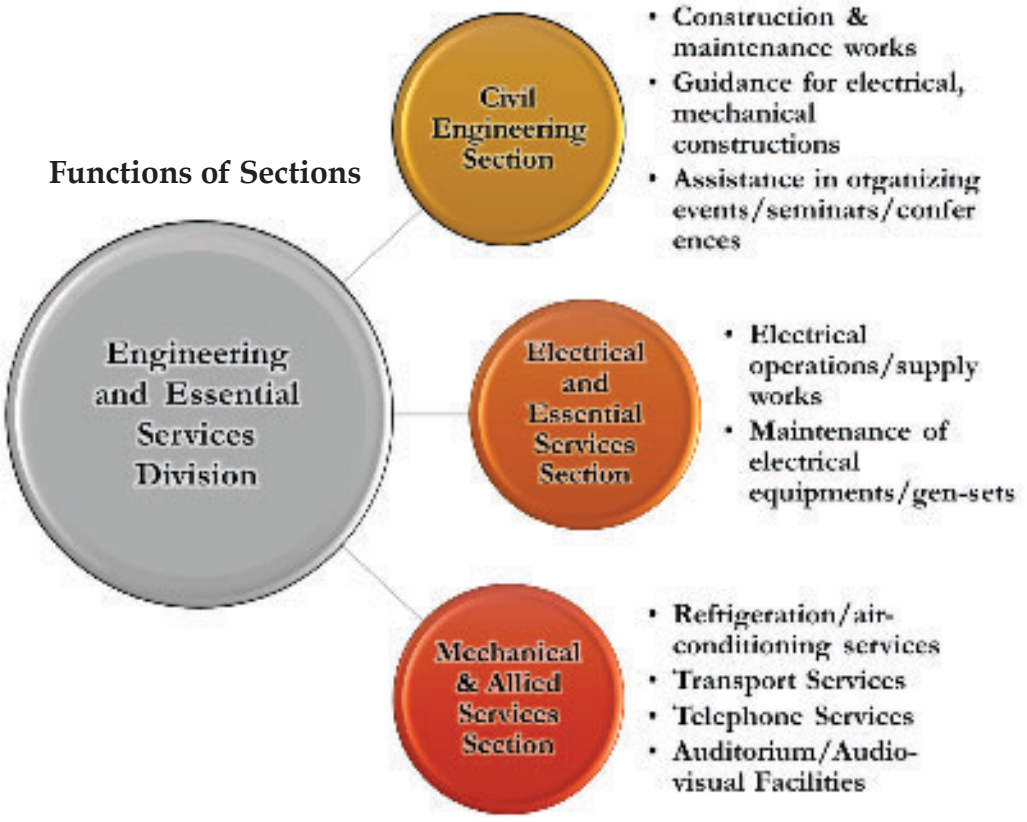
Dr. SK Bag, Principal Scientist

**Email ID**: sumit.bag@nbri.res.in

**Team**

- Mr. Surajeet Kumar, Senior Technical Officer
- Mr. Prashant Srivastava, Technical Officer
- Mr. Dev Ranjan, Technical Assistant

# ENGINEERING AND ESSENTIAL SERVICES DIVISION




The engineering & essential services division manages all the civil engineering, electrical & air conditioning requirements of the institute including installing new equipments and maintenance of various facilities in all its campuses.

## Civil Engineering Section

**Section In-charge**

Er. Lalit Kumar Srivastava, Executive Engineer (Civil)

Email ID: l.srivastav@nbri.res.in

### Team

- Mr. Moinuddin Khan, Senior Technican
- Mr. GD Nigam, Senior Technican
- Mr. Harish Chand, MTS
- Mr. Om Prakesh, MTS
- Mr. Cheda Lal, MTS
- Mr. Sajeewan, MTS
- Mr. Sapan Kumar, MTS

## Electrical and Essential Services Section

**Section In-charge**

Er. Somanath Swain, Assistant Engineer (Electrical)

**Email ID:** somanathswain@nbri.res.in

### Team

- Mr. Saral Ram, Senior Technician
- Mr. Ajay Kumar, Technician
- Mr. Rakesh Kumar, Technician

## Mechanical & Allied Services Section

**Section In-charge**

Er. Harendra Pal, Assistant Executive Engineer (Mech.)

**Email ID:** harendrapal@nbri.res.in

### Team

- Mr. Dinesh Singh, Senior Technician
- Mr. Ashish Rav, Technician
- Mr. Raj Singh, Technician
- Mr. Anoop Kumar, Technician
- Mr. Surjeet Kumar, Technician
- Mr. Pawan Kumar, Technician

# राजभाषा यूनिट

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- राजभाषा विभाग, गृह मंत्रालय, भारत सरकार द्वारा जारी दिशा निर्देशों का पालन।
- कार्यालयी कामकाज को राजभाषा हिन्दी में करने हेतु प्रयास।
- संस्थान की विभिन्न वैज्ञानिक एवं तकनीकी गतिविधियों/उपलब्धियों को जनसामान्य तक राजभाषा हिंदी में पहुंचाने हेतु प्रयास।
- संस्थान में राजभाषा विभाग, गृह मंत्रालय, भारत सरकार द्वारा जारी दिशा निर्देशों के अनुसार निर्धारित समय में राजभाषा कार्यान्वयन समिति की चार तिमाही बैठकों का आयोजन कराना।
- हिन्दी कार्यशालाओं, हिन्दी दिवस आदि का आयोजन कराना।

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वर्ष 2019–20 में आयोजित विभिन्न कार्यक्रमों, व्याख्यानों कार्यशालाओं, प्रशिक्षण कार्यक्रमों एवं अन्य विशिष्ट गतिविधियाँ –

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संस्थान में दिनांक 11–12 अप्रैल, 2019 को 'पादप अनुसंधान में नये आयाम' विषयक दो दिवसीय वैज्ञानिक हिंदी संगोष्ठी का आयोजन किया गया। दिनांक 11 अप्रैल, 2019 को संगोष्ठी के उद्घाटन सत्र में प्रो. अनिल कुमार त्रिपाठी, पूर्व निदेशक वै.औ.अ.प.–केंद्रीय औषधीय एवं सगंध पौधा संस्थान, लखनऊ, मुख्य अतिथि के रूप में आमंत्रित थे। संगोष्ठी में संस्थान की विभिन्न प्रयोगशालाओं में हो रहे शोध कार्य संबंधी 50 शोध पत्रों का हिन्दी में प्रस्तुतीकरण संबंधित वैज्ञानिक, तकनीकी अधिकारी एवं शोध छात्र/छात्राओं द्वारा किया गया।

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संस्थान की राजभाषा कार्यान्वयन समिति के तत्वाधान में दिनांक 06.09.2019 एवं दिनांक 27.12.2019 को कार्यालयी कामकाज में राजभाषा हिन्दी के प्रगामी प्रयोग में और भी वृद्धि लाने के लिए हिन्दी कार्यशाला का आयोजन किया गया। संस्थान के सूचना एवं प्रकाशन अनुभाग में कार्यरत श्री रजत राज रस्तोगी, तकनीकी सहायक एवं सदस्य राजभाषा कार्यान्वयन समिति ने 'हिन्दी इनपुट टूल्स एवं वाइस टाइपिंग' विषयक व्याख्यान प्रस्तुत किया साथ ही संस्थान के अधिकारियों/कर्मचारियों को जानकारी दी कि किस तरह टाइपिंग न जानने वाले अधिकारी/कर्मचारी भी वाइस टाइपिंग का प्रयोग करके हिन्दी में कार्य संपादित कर सकते हैं।

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संस्थान द्वारा सितम्बर माह में 02 सितम्बर से 16 सितम्बर, 2019 के मध्य हिन्दी पखवाड़े मनाया गया जिसका उद्घाटन मुख्य अतिथि डॉ. योगेश प्रवीन, प्रसिद्ध साहित्यकार, लखनऊ द्वारा किया गया। हिन्दी पखवाड़े के अंतर्गत विभिन्न कार्यक्रमों जैसे हिन्दी पुस्तक प्रदर्शनी, हिन्दी ज्ञान प्रतियोगिता, हिन्दी टिप्पण आलेखन प्रतियोगिता, हिन्दी वर्ग पहेली प्रतियोगिता, हिन्दी कवि सम्मेलन का आयोजन भी किया गया।

हिन्दी पखवाड़े का समापन हिन्दी दिवस आयोजन के साथ दिनांक सितम्बर 16, 2019 को किया गया। समापन समारोह में डा. अमिता दुबे, सम्पादक उत्तर प्रदेश, हिन्दी संस्थान, लखनऊ मुख्य अतिथि ने 'हमारी राजभाषा हिन्दी की वैज्ञानिकता' विषयक व्याख्यान प्रस्तुत किया।

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संस्थान की राजभाषा पत्रिका विज्ञानवाणी –2018 अंक 24 को नगर राजभाषा कार्यान्वनय समिति का–2 द्वारा द्वितीय सर्वश्रेष्ठ पुरस्कार से सम्मानित किया गया।

संस्थान से प्रकाशित पुस्तक ''आदिवासी औषधीय व आर्थिक वनस्पति बौद्धिक सम्पदा, उत्तर प्रदेश एवं उत्तराखण्ड'' लेखक–आनन्द प्रकाश, वरिष्ठ प्रधान वैज्ञानिक एवं सदस्य सचिव राजभाषा कार्यान्वयन समिति को उत्तर प्रदेश हिन्दी संस्थान, लखनऊ के स्थापना दिवस समारोह दिनांक

30.12.2019 को मुख्य अतिथि माननीय श्री योगी आदित्यनाथ, मुख्यमंत्री तथा माननीय श्री हृदय नारायण दीक्षित, अध्यक्ष विधान सभा, उत्तर प्रदेश की अध्यक्षता में प्रतिष्ठित बीरबल साहनी पुरस्कार–2018 प्रदान किया गया।

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| 1. | प्रो. सरोज कान्त बारिक, निदेशक | अध्यक्ष |
| 2. | डॉ. श्रीकृष्ण तिवारी,<br>वरिष्ठ प्रधान वैज्ञानिक | उपाध्यक्ष |
| 3. | श्री आनन्द प्रकाश,<br>वरिष्ठ प्रधान वैज्ञानिक | सदस्य सचिव |
| 4. | श्री मुकुंद सहाय, नियंत्रक (प्रशासन) | सदस्य |
| 5. | डॉ. संजीव कुमार ओझा,<br>प्रधान वैज्ञानिक | सदस्य |
| 6. | डॉ. के.के. रावत,<br>वरिष्ठ तकनीकी अधिकारी | सदस्य |
| 7. | श्रीमती किरन टोप्पो,<br>वरिष्ठ तकनीकी अधिकारी | सदस्य |
| 8. | श्रीमती स्वाति शर्मा,<br>वरिष्ठ तकनीकी अधिकारी | सदस्य |
| 9. | श्री संजीव शेखर,<br>वित्त एवं लेखा अधिकारी | सदस्य |
| 10. | श्री दिनेश कुमार,<br>भण्डार एवं क्रय अधिकारी | सदस्य |
| 11. | श्री बिजेन्द्र सिंह,<br>हिन्दी अधिकारी | सदस्य |
| 12. | श्रीमती सोना लमसल,<br>सहा. अनुभाग अधिकारी | सदस्य |
| 13. | श्री रजत राज रस्तोगी,<br>तकनीकी सहायक | सदस्य |

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# EVENTS

## Student Plant Science Fest 2019

A three day 'Summer Plant Science Fest-2019' was organized by CSIR-NBRI, during April 11-13, 2019. Prof. AK Tripathi, Director, Institute of Science, Banaras Hindu University (BHU), Varanasi, was the chief guest at the inaugural function of the Fest on April 11, 2019. Prof. Alok Dhawan, Director, CSIR-IITR, Lucknow and Prof. VP Kamboj, Former Director, CSIR-CDRI also graced the occasion. The event was coordinated by Dr. Vidhu A Sane.






Summer Plant Science Fest 2019: (A) Inaugural Function, (B) Dr. Purnima Sharma delivering lecture, (C) Participating students and research scholars, (D) Certificate distribution, (E) Participants with Dr. Alok Dhawan, Chief Guest of the valedictory function

The Fest included a one and a half day Hindi Seminar on "Paadap Anusandhan me Naye Aaayam" in which 40 research scholars, technical staff and scientists of CSIR-NBRI presented their research work in Hindi. A short science film and photographs related to plant science and nature photographed by the research scholars was also showcased during the event.

Dr. Purnima Sharma, Managing Director, Biotech Consortium India Limited (BCIL), New Delhi was the chief guest on April 12, 2019. She informed the participants about the financial assistance from different agencies, guided young entrepreneurs for introducing new start-ups and creating market platform for their technologies and products. Dr. Suchita Markan, Assistant General Manager, BCIL, New Delhi, briefed about BCIL and the different stages from the conceptualization of technology to its commercialization and discussed various possible bottlenecks and solutions.

The fest concluded with a valedictory function on April 13, 2019. Prof. Alok Dhawan, Director, CSIR-IITR, Lucknow, was the Chief Guest at the closing ceremony. He delivered a lecture on the 'Toxicity in Plants' with various exemplary studies and cautioned about various toxic elements found in different groups of edible plants/fruits. He also distributed certificates of appreciation to the participants.

## National Technology Day Celebration

CSIR-National Botanical Research Institute, Lucknow, celebrated the National Technology Day on May 13, 2019. Different facilities, viz., Exposition, Herbarium, Library, Botanic Garden and various R&D Laboratories of Institute were opened for students and general public during the day.

On this occasion, Prof. AK Singh, Former DDG (NRM), ICAR, New Delhi and Former VC, RVS Krishi Vishwa Vidyalaya, Gwalior, was the Chief Guest and he delivered the Technology Day Lecture on 'Addressing Sustainable Development Goals through Natural Resource Management Technologies'.

While highlighting the importance of natural resources, Prof. Singh informed that about 17.5% of total global population lives in India and 50% of which depends on agriculture for living. It is a worrisome fact that India, an agricultural based country, has now been declared as a water stressed country.

Prof. Singh mentioned that due to global warming, water demand for irrigation will be raised by 10% per centigrade increase in temperature. Thus, it is estimated that by the year 2025, with the challenge of 10% decrease in irrigation water, India will have to produce 37% more wheat and rice to feed its consistently growing population. We are also facing the challenge to increase our land productivity four times, water productivity three times, labour productivity six times and energy efficiency two times by the year 2050. Apart from this, we also have to improve our soil health, which is currently showing 50 to 80% deficiency of essential nutrients.


National Technology Day Celebration: (A) Inaugural Function and (B) Prof. AK Singh delivering National Technology Day Lecture

## World Environment Day Celebration

CSIR-NBRI, Lucknow and International Society of Environmental Botanists (ISEB) jointly celebrated the World Environment Day on June 08, 2018. Dr. Ashiho A. Mao, Director, Botanical Survey of India, Ministry of Environment, Forest and Climate Change, Government of India was the Chief Guest of the Function.

Dr. Ashiho A. Mao, in his lecture discussed the diversity and importance of Rhododendrons of North-Eastern India and Himalayan regions where they are found between 600 and 6000 meter altitudes. He informed that Rhododendrons are considered as an indicator of altitude in the Himalayas. In Sikkim, the Rhododendrons have been conserved by establishing a sanctuary. He also provided detailed information on value added products developed from Rhododendrons.

Dr. Mao further deliberated that in India, the number of trees per capita is the lowest in the world. To tackle various environmental challenges, we must ensure to plant as many tress as possible, which would provide safe and clean environment for future generations.





World Environment Day Celebration: (A) Prof. SK Barik welcoming Dr. AA Mao, Chief Guest of the Function, (B) Dr. Mao delivering lecture, (C) Dr. Mao felicitating winner of Essay Competition organized on the occasion, (D) NBRI-ENVIS center exhibition

## International Day of Yoga

To commemorate the International Day of Yoga, CSIR-NBRI, Lucknow organized a Yoga Session on June 21, 2019 where trained yoga experts from the Art of Living group, Lucknow highlighted the benefits of yoga and not only provided tips for a healthy life-style by adopting yoga in our daily lives but also demonstrated various yoga exercises (yoga asana) to scientists, students and staff of the institute, who participated in this session with great enthusiasm

Yoga Day Celebration

## Scientific Ethics Orientation Programme

CSIR-National Botanical Research Institute, Lucknow, organized a Scientific Ethics Orientation Programme at the institute on July 22, 2019. Prof. Sujit Bhattacharya, Chief Scientist, CSIR-NISTADS, New Delhi, was the chief guest and the key speaker. Prof. Bhattacharya elucidated the importance and implications of scientific integrity and ethics in research and publications. He emphasized on the need for developing institutional guidelines and mechanism to maintain high integrity and ethical behavior by all those involved in scientific research and publications.





Scientific Ethics Orientation Programme: (A) Dr. KN Nair, highlighting the genesis of the programme, (B) Prof. Sujit Bhattacharya, Chief Guest delivering the lecture, (C) participating scientists and students, (D) Prof. SK Barik, Director felicitating Prof. Bhattacharya

## Birth Anniversary Celebration of Padma Shree Dr. SR Ranganathan

The birth anniversary of Dr. SR Ranganathan, the Father of Library Science in India, was organized by CSIR-NBRI on August 13, 2019. Dr. Ranganathan was known for his outstanding contributions to Library sciences, including the drafting of five laws of library sciences, adopted as the guidelines for library and librarians worldwide, and the Colon classification scheme.

Prof. NR Satyanarayana, Former Head, Department of Library and Information Science, Lucknow University was the chief guest of the function. Prof. Satyanarayana presented detailed sketch of the personal and professional life of Dr. SR Ranganathan. He pointed out that the mission of a library professional was to provide right information to the right user in a right format at right time. "Modern technological development demands that professionals must be equipped with ethics to take right approach in our profession. On this occasion, a Workshop on 'Web of Science Portal' was also organized for the benefit of the students and scientists of the institute.





Birth Anniversary Celebration of Padmashree Dr. SR Ranganathan: (A) Lamp lighting by the dignitaries at inaugural function, (B) Prof. NR Satyanarayana, offering floral tribute to the portrait of Dr. SR Ranganthan, (C) Chief Guest & other dignitaries at the function, (D) participating scientists and students

## Awareness Programme on Nutrition for Women and Children

CSIR-NBRI, Lucknow, organized Training Programmes on "Eradication of Poverty by Popularizing the use of Local Medicinal Plants to Prevent Malnutrition" for the benefits of scheduled tribe and scheduled caste children and women at Janta Junior High School, Biruha Kasimpur Village, Gosainganj, Lucknow, on August 10, 2019 and village Pahadnagar, Tikariya, Gosaiganj, Lucknow on Novermber, 05,2019.

The participants were briefed about the main objectives of the training and informed about the medicinal & nutritional benefits of locally available plants such as drumstick (Sehjan) and green amaranthus (chaulai). Besides, the use of millets, grains and curd as food or food supplements was explained to the participants. Special kits comprising information of medicinal plants and capsules containing drumstick plant powder were distributed to 350 women and children.

Glimpses of awareness programme

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राजभाषा विभाग, गृह मंत्रालय, भारत सरकार के दिशानिर्देशानुसार, सीएसआईआर–राष्ट्रीय वनस्पति अनुसंधान संस्थान, लखनऊ द्वारा दिनांक 2–16 सितम्बर, 2019 के मध्य हिन्दी पखवाड़े का आयोजन किया गया। इसके अंतर्गत विभिन्न वैज्ञानिकों, अधिकारियों व कर्मचारियों में हिन्दी के प्रति अभिरुचि बढ़ाने, प्रचार–प्रसार तथा कामकाज में हिन्दी के प्रगामी प्रयोग को बढ़ावा देने हेतु विभिन्न कार्यक्रम आयोजित किये गये। संस्थान के अधिकारियों, कर्मचारियों के लिए विभिन्न हिंदी प्रतियोगिताओं का भी आयोजन किया गया।

हिन्दी पखवाड़े के अंतर्गत आयोजित कार्यक्रमों की श्रंखला में सीएसआईआर–राष्ट्रीय वनस्पति अनुसंधान संस्थान, लखनऊ में दिनांक 12 सितम्बर, 2019 को कवि सम्मलेन का आयोजन किया गया। इस अवसर पर प्रदेश के ख्याति प्राप्त कवियों जैसे डॉ. शिव भजन 'कमलेश', डॉ. राजेन्द्र शुक्ल 'राज', श्री भोलानाथ 'अधीर', श्री राजेंद्र पंडित,

श्री मंजुल मिश्र 'मंजर', श्री अनुज 'अब्र', श्री धीरज मिश्र द्वारा कवितापाठ किया गया। श्री प्रसून मिश्र ने कार्यक्रम का संचालन एवं कविता पाठ भी किया। पखवाड़े का समापन दिनांक 16 सितम्बर, 2019 को किया गया। समापन समारोह में मुख्य अतिथि के रूप में डॉ. अमिता दुबे, सम्पादक हिन्दी संस्थान, उत्तर प्रदेश मौजूद थीं। डॉ. अमिता दुबे ने 'हमारी राजभाषा हिन्दी की वैज्ञानिकता' विषयक व्याख्यान में बताया कि हिन्दी के प्रचार, प्रसार एवं उत्थान में भारत की विश्व में बढती ख्याति एवं आर्थिक संबंधों का भी बड़ा योगदान है। विभिन्न देशों के लोग भारत में व्यवसाय करने के लिए हिन्दी को जानने एवं समझने का प्रयास करने लगे हैं ताकि सबसे अधिक भूभाग में सबसे अधिक बोली जाने वाली हिन्दी भाषा के माध्यम से अधिक से अधिक लोगों तक पहुँच बनाई जा सके। उन्होंने बताया कि हमारी राजभाषा हिन्दी का व्याकरण संस्कृत की व्याकरण अर्थात पाणिनि सूत्र पर आधारित है जो अत्यंत व्यवहारिक एवं नियमबद्ध हैं साथ ही वैज्ञानिक भी हैं। इसलिए आज के कंप्यूटर युग की दौड़ में हमारी हिन्दी किसी भी समृद्ध भाषा से पीछे नही हैं एवं पूर्णतः कंप्यूटर के लिए उपयुक्त हैं। उन्होंने सभी से अनुरोध किया कि जब मौका मिले तब हिन्दी किताबें पढ़े और इसे एक आदत बनाएं।



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## 78th CSIR Foundation Day Celebration

CSIR-NBRI celebrated 78th Foundation Day of Council of Scientific & Industrial Research (CSIR) on September 26, 2019. Prof. Vinay Kumar Pathak, Vice Chancellor, Dr. APJ Abdul Kalam Technical University, Lucknow was the chief guest of the function. On this occasion, the institute observed an "Open Day" and various Laboratories, Botanic Garden, Herbarium and Exposition of the Institute were kept open for students and general public. Over 1500 students of 20 schools from Lucknow and neighboring districts, 500 students from various Kendriya Vidyalayas of Lucknow, researchers and general public visited the institute on this occasion. The visitors were briefed about the history, on-going R&D activities and major research achievements of the institute. Prof. Pathak, also distributed certificates and mementoes to 10 employees who had completed 25 years of CSIR service and 26 employees who had superannuated during the year. Winners of the Science Essay and Drawing competitions organized on this occasion for the children of CSIR-NBRI staff, were also felicitated.


78th CSIR Foundation Day Celebration: (A) Dignitaries lighting the lamp at inaugural function, (B) Prof. Vinay Kumar Pathak, Chief Guest felicitating winners of science essay and drawing competition, (C) Prof. Pathak felicitating retirees, (D) Student visiting the herbarium on the occasion, (E) Pollution Awareness Exhibition organized by ENVIS Centre, (F) Visit of teachers and students from different schools on the occasion.

## 66th Annual Day Celebration of CSIR-NBRI

CSIR- NBRI, Lucknow celebrated its 66th Annual Day on October 25, 2019. Dr. Ramesh V. Sonti, Director, National Institute of Plant Genome Research, New Delhi was the Chief Guest of the function. On the occasion, Prof. SK Barik, Director, CSIR-NBRI presented the annual progress for the period 2018-19 and informed about some of the major achievements made by the Institute during the reporting period viz., development of three new herbal formulations - 'Anti-toothache herbal hydrogel', 'Herbal nano-floor disinfectant and cleaner', and 'Anti-termite formulation'; a microbial consortia for on-farm degradation of rice straw, and Zinc solubilisation and Iron uptake in crops; "Tricho-straw pellet", another formulation comprising microbe colonized rice straw pellet for sodic soil reclamation; two thebaine rich varieties - 'Ayush' (NBIHT-3), 'Abha' (NBMHT-4) and a high opium and seed yielding variety - 'Madakini'.

The dignitaries released the institute's Annual Report 2018-19 and two new herbal products viz. 'Zanthodent' (an herbal toothpaste free from Flouride, Trichlosan and synthetic chemical preservatives) and "Floor Disinfectant & Cleaner" (a water soluble plant-based herbal product developed using nanotechnology). Dr. Sonti delivered the Annual Day Lecture on 'Induction and suppression of host innate immunity in plant-pathogen interactions' and elucidated how plants stay free from diseases. He explained that plants continuously face vigorous attack from different kind of pathogens and they do not have cellular immune system like animals, they all have pathogen triggered immunity. "Once a pathogen releases cell wall degrading enzyme, that degrades cell wall and plasma membrane, it triggers a cascade of reaction resulting into an innate immune response in the plant cell", he added.






66th Annual Day Celebration of CSIR-NBRI: (A) Dignitaries lighting the lamp at inaugural function, (B) Prof. SK Barik, Director, CSIR-NBRI presenting annual progress report, (C) Dignitaries releasing Annual Report 2018-19, (D) Launching of Herbal products by the dignitaries, (E) Dr. Ramesh V. Sonti, Chief Guest delivering lecture.

## Vigilance Awareness Week

CSIR-NBRI, Lucknow observed Vigilance Awareness Week during October 28-November 02, 2019. On this occasion, Dr. PA Shirke, Chief Scientist administered the pledge to the staff members.

An essay competition was also organized for the wards of CSIR-NBRI staff during the week. The week was concluded with the organization of invited lecture programme. Mr. Satya Narayan Sabat, IPS was the key speaker and he delivered the lecture on 'Integrity-a way of life'. Winners of the essay competition organised during the occasion were felicitated .

CSIR-NBRI, Lucknow also organized Vigilance Awareness Campaigns among the villagers of Aurawan and Kallipaschim village of the Lucknow district. Information on integrity and vigilance was given to the participants.


Vigilance Awareness Week: (A) Prof. SK Barik, Director welcoming the chief guest Mr. Satya Narayan Sabat, IPS, (B) Mr. Satya Narayan Sabat delivering his lecture, (C) Pledge by the staff members, (D) Awareness programme organized by CSIR-NBRI at different villages.

## Hands on Training For Arsenic Estimation by Arsenic Field Kit and Inductively Coupled Plasma Mass Spectrometer (ICP-MS)

CSIR-NBRI, Lucknow and Rashtriya Krishi Vikas Yojna through Department of Agriculture, Uttar Pradesh jointly organized a one day hands on training programme on 'Arsenic Estimation by Arsenic Field Kit and Inductively Coupled Plasma Mass Spectrometer (ICP-MS)' on November 01, 2019. A total of forty participants from 20 districts of U.P. participated in the programme. The training included subject-based lectures with experimental sessions.

Dr. Soraj Singh, Director, Department of Agriculture, Uttar Pradesh was the chief guest of the function and delibrated the role of Ayurveda and modern medicine in the health security in combating the

complex health issues. He also distributed Arsenic Field Kit to participants.

Dr. PS Chauhan, Principal Scientist presented the outline of the programme. The participants were also informed about the skill development programs being run by the institute.


Hands on Training for Arsenic Estimation: (A) Inaugural function of the training programme, (B) Training under progress, (C) Dr. Soraj Singh, Chief Guest addressing the participants, (D) Dr. Singh distributing certificates and arsenic kits to the participants.

## World Soil Day-2019

CSIR-NBRI, Lucknow celebrated 'World Soil Day' on December 05, 2019. On this occasion students and teachers from Kendriya Vidyalaya, Gomti Nagar, Lucknow visited the institute under Jigyasa programme. Students not only interacted with scientists but were also given the opportunity to perform various hands on experiments in the Soil Laboratory.

Dr. PA Shirke, Chief Scientist, highlighted the year's theme of world soil day 'Stop Soil Decay, Save the Future' and expressed concern over extensive agricultural practices and deforestation which are the main reasons for soil erosion.

Dr. SK Tewari, Chief Scientist, interacted with the students and explained about the role of plant microbe interaction in the soil.

Theme based lectures on soil science were also organized for the students. Dr. Lal Bahadur informed about the essential soil nutrients, their deficiencies and symptoms in the plant while Dr. Suchi Srivastava highlighted the plant microbe relationship and its importance in maintaining the nutrient availability in the soil.

Prof SK Barik, Director interacted with the students and discussed about their experiences and future goals. He also encouraged them to take up science as career. He also felicited the winers of the quiz organized for the participating students on the occasion.


World Soil Day Celebration: (A) Dr. SK Tewari, Chief Scientist highlighting the genesis of programme, (B) (C) and (D) Hands on training imparted by the experts to students, (E) Felicitation of winner of quiz competition, (F) Participating students with resource persons and Director Prof. SK Barik

## Annual Chrysanthemum and Coleus Show 2019

CSIR-NBRI, Lucknow organized a two-day Chrysanthemum & Coleus – 2019 show at the Central Lawn, Botanic Garden during December 07-08, 2019. The show was inaugurated on December 07, 2019. The show attracted 112 exhibitors with a total of 1072 exhibits.

The Closing Ceremony was organized on December 08, 2019. Shri Brajesh Pathak, Hon'ble Cabinet Minister of Legislative, Justice, Rural Engineering Services, Uttar Pradesh Government, was the Chief Guest of the show and distributed the prizes to the winners.









Annual Chrysanthemum and Coleus Show: (A) and (B) Judges evaluating the entries of the exhibits, (C) Winning flower entries of the show, (D) A view of the show ground (E) A view of the show ground, (F) Mr. Brijesh Pathak, Chief Guest of the valedictory function releasing the new variety of chrysanthemum, (G) Mr. Singh distributing the prizes to the winners, (H) Chief Guest with the winners of the show

## Annual Rose and Gladiolus Show 2020

A two-day annual Rose and Gladiolus Show was organized during January 18-19, 2020 at the central lawn of the Institute. The show attracted a total of 647 entries belonging to 69 exhibitors were received from various Govt., Semi-Govt. Departments, Autonomous Bodies, nurserymen, individual growers, gardeners, ladies, etc.

The Show concluded on January 19, 2020 with the prize distribution ceremony. On the occasion, Dr. Shekhar C Mande, Director General, Council of Scientific and Industrial Research, New Delhi and Secretary, Department of Scientific and Industrial Research, Government of India was the Chief Guest of the show. He along with his wife Mrs. Mande gave away the prizes to the winners.

On this occasion, Dr. (Mrs.) Sharmila Mande released a new variety of Chrysanthemum 'Shekhar' developed by CSIR-NBRI, Lucknow. This is a late blooming decorative type, floriferous chrysanthemum variety which bears mauve colored flowers that bloom during late December to mid-February.

During the event, two agreements were signed, one with M/S Hempstreet Pvt. Ltd. Delhi for cannabis based Ayush formulations and the other with M/s Tierra Agrotech Pvt. Ltd, Hyderabad for transfer of 1000 cotton genotypes to CSIR-NBRI for research activities.


Annual Rose and Gladiolus Show: (A) and (B) Judges evaluating the entries of the exhibits, (C) and (D) View of the show ground, (E) Mrs. Mande releasing a new variety of Chrysanthemum 'Shekhar', (F) Dignitaries releasing the Rajbhasha Patrika 'Vigyan Vani', (G) Prize distribution by Dr. Mande, DG, CSIR and Mrs. Mande, (H) Transfer of agreement documents on the occasion, (I) Dr. Mande, DG, CSIR and Dr. (Mrs) Mande with winners of the show.

## National Science Day

CSIR-National Botanical Research Institute, Lucknow celebrated National Science Day on 28th February 2020. The theme for the year was 'Women in Science'.

On this occasion, Dr. Leena Tripathi, Principal Scientist, International Institute of Tropical Agriculture, Kenya was the Chief Guest and delivered The National Science Day Lecture on 'Application of Modern Biotechnology for Crop Improvement: Case Study from Banana'.

In her lecture, Dr. Tripathi mentioned that climate change, fungal and bacterial diseases and other biological attacks are affecting crop yield negatively, which need to be addressed immediately. Citing the example of banana plant, she said that banana fruits are nutritious and are very popular as food. However, due to pest attacks and other diseases, not only a large amount of crop is destroyed annually but also creates a huge gap between the plant potential and actual yield. Hence, developing resistance is the best cost effective solution.

The day was observed as 'Open Day' for public and students. During the day approximately 600 students from various school, colleges visited the institute and its facilities.





National Science Day Celebration: (A) Lamp lighting by the chief guest on the occasion, (B) Dr. Leena Tripathi, Chief Guest of function delivering the science day lecture, (C) and (D) students visiting the different facilities of CSIR-NBRI on the occasion.

## 3rd Prof KN Kaul Memorial Lecture

CSIR-National Botanical Research Institute, Lucknow remembered its Founder Padma Bhushan Professor Kailash Nath Kaul by holding its 3rd Prof KN Kaul Memorial Lecture on March 02, 2020.

Prof. Kailas Nath Kaul was a great Indian botanist, naturalist, agricultural scientist, horticulturist, herbalist and plant collector, who originally conceptualized the setup of the National Botanic Gardens (NBG), currently known as CSIR-National Botanical Research Institute. (It was taken over by the CSIR in 1953).

On this occasion Prof. SR Yadav, Department of Botany, Shivaji University, Kolhapur was the Chief Guest while Prof. SK Sopory, Former VC, JNU, New Delhi was the Guest of Honour.

Professor Yadav, in his lecture titled "Changing Role of Botanic Gardens: A unique benefit for humans" informed that about one fourth of the world's known plant species have been conserved in botanic gardens.

Earlier, the programme was started with a floral tribute to the Prof. KN Kaul. While welcoming the guests, Prof. SK Barik, Director, CSIR-NBRI commemorate priceless contribution of Prof. KN Kaul in the field of science.





Prof. KN Kaul Memorial Lecture: (A) and (B) Floral tribute to Prof. KN Kaul by the dignitaries, (C) Prof. SR Yadav, Chief Guest delivering the memorial lecture, (D) other dignitaries and guests present on the occasion

# ACADEMY OF SCIENTIFIC & INNOVATIVE RESEARCH (AcSIR)

Established in 2011 as an 'Institution of National Importance' (interim operations started in June, 2010), the Academy of Scientific and Innovative Research (AcSIR) has adopted the mandate to create and train some of the best of tomorrow's Science & Technology leaders through a combination of innovative and novel curricula, pedagogy and evaluation. AcSIR's focus is on imparting instruction and providing research opportunities in such areas that are not routinely taught in regular academic universities in India.

Department of Scientific and Industrial Research (DSIR), Ministry of Science & Technology, Government of India has recognized AcSIR as a Scientific and Industrial Research Organization (SIRO).

## Mission

The mission of the Academy is to create highest quality personnel with cross- disciplinary knowledge, aiming to provide leaders in the field of science and technology. Nurture a research-propelled, technology-enabled, industry-linked, socially conscious higher education platform. Achieve a seamless integration of intellectual strengths with current market needs with a people centric focus. Develop niche capability required to bolster research efforts in futuristic science.

**Courses offered at AcSIR-NBRI during 2019 - 2020**

| S. No. | Subject | Code | Status |
|---|---|---|---|
| 1. | Computation/Bioinformatics | 1-0002 | Compulsory |
| 2. | Basic Chemistry | 1-0003 | Compulsory |
| 3. | Bio-techniques and Instrumentation | 2 3601 | Compulsory |
| 4. | Plant Microbe Interaction | 2 3604 | optional |
| 5. | Cell Signaling | 2 3606 | optional |
| 6. | Molecular Breeding of Plants | 2 3610 | optional |
| 7. | Biodiversity | 2 3611 | optional |
| 8. | Environmental Biochemistry and Biotechnology | 3 3605 | optional |
| 9. | Phylogenomics | 3 3610 | optional |
| 10. | Taxonomy and speciation | 3 3606 | optional |
| 11. | Development biology- plants | 2 3607 | optional |
| 12. | Genomics: Information flow in Biological System | 2 3603 | optional |
| 13. | Plant Environment Interaction | 2 3605 | optional |
| 14. | Epigenetics and Chromatin Organization | 2 3608 | optional |
| 15. | Climate change and Plants | 3 3603 | optional |
| 16. | Cell and Tissue Engineering | 3 3602 | optional |
| 17. | Research Methodology, Communication /ethics/safety | 1-0004 | Compulsory |
| 18. | Biostatistics | 1-0001 | Compulsory |
| 19. | Seminar course (Seminar Bio & Presentation) | 3 3601 | Compulsory |
| 20. | Cell Signaling | 2 3606 | optional |
| 21. | Biology of Inheritance | 2 3602 | optional |
| 22. | Plant Conservation & Reproductive Biology | 3 3607 | optional |
| 23. | Plant Morphogenesis & Regeneration | 2 3612 | optional |
| 24. | Bioremediation | 3 3604 | optional |

| | |
|---|---|
| **Number of students enrolled for Ph.D. until March 31, 2019** | 136 |
| **Ph.Ds. awarded during 2019-20** | 13 |
| **Ph.Ds. theses submitted during 2019-20** | 16 |

**Coordinator**

Dr. Debasis Chakraborty/Dr. Vidhu A Sane, Senior Principal Scientist

**Executive Assistant**

Ms. Harshita Nag

# Research Council (As on 31.03.2020)

| | | | |
|---|---|---|---|
| **Dr. Deepak Pental**<br>INSA Senior Scientist,<br>Centre for Genetic Manipulation Crop Plants (CGMCP), Delhi University, South Campus, New Delhi | Chairman | **Dr. RK Kohli**<br>Vice-Chancellor, central University of Punjab, Punjab | Member |
| **Prof. SR Yadav**<br>Department of Botany<br>Shivaji University, Kolhapur | Member | **Dr. Ram A. Vishwakarma**<br>Director, CSIR-Indian Institute of Integrative Medicine, Jammu | Member |
| **Shri Anand Chordia**<br>Director (Technical),<br>M/s Pravin Masalewale, Pune | Member | **Dr. KSMS Raghavarao**<br>Director<br>CSIR-Central Food Technological Research Institute, Mysore | Member |
| **Dr. Anil Prakash Joshi,**<br>Founder, Himalayan Environmental Studies and Conservation Organization (HESCO), Dehradun | Member | DG, CSIR or his nominee | Member |
| **Dr. Shree Kumar Apte,**<br>DST Emeritus Professor, Modular Labs Bhabha Atomic Research Centre, Mumbai | Member | **Prof. SK Barik,**<br>Director<br>CSIR-National Botanical Research Institute, Rana Pratap Marg, Lucknow | Member |
| **Prof. R Umashanker**<br>Department of Crop Physiology, University of Agricultural Sciences, GKVK, Bellary Road, Bengaluru | Member | **Dr. SK Tewari**<br>Chief Scientist<br>CSIR-National Botanical Research Institute<br>Rana Pratap Marg,<br>LUCKNOW | Member-Secretary |

**Institutional Complaint Committee**

- Dr. Vidhu A Sane, Senior Principal Scientist - Chairperson
- Dr. Sharad Srivastava, Senior Principal Scientist - Member
- Dr. Mehar H Asif, Principal Scientist - Member
- Mrs. Aarati Ganguli, Expert Lawyer - Member
- Mr. Rajiv K Verma, Section Officer - Member - Convenor

# Management Council (As on 31.03.2020)

| | |
|---|---|
| **Prof. SK Barik**<br>Director<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Chairman |
| **Prof. Alok Dhawan**<br>Director<br>CSIR-Indian Institute of Toxicological Research, Lucknow | Member |
| **Dr. AK Gauniyal**<br>Senior Principal Scientist<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Dr. KN Nair**<br>Senior Principal Scientist<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Dr. Samir V Sawant**<br>Senior Principal Scientist<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Dr. Suchi Srivastava**<br>Principal Scientist<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Dr. BN Singh**<br>Senior Scientist<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Dr. Abhishek Niranjan**<br>Senior Technical Officer<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Mr. Sanjeev Shekhar**<br>Finance & Accounts Officer<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member |
| **Mr. Mahendra Singh**<br>Administrative Officer<br>CSIR-National Botanical Research Institute<br>Lucknow - 226 001 | Member Secretary |

# EXPENDITURES AND EARNINGS DURING 2019-20

| I. EXPENDITURE | Figure in Lakhs of Rupees |
|---|---|
| **A. Revenue** | |
| 1. Salary & Salary Linked Allowances | 3015.612 |
| 2. Other Allowances | |
| a. Reimbursement of Medical Expenses/CGHS/Medical Charges | 69.898 |
| b. Overtime Allowance | 1.983 |
| c. Honorarium | |
| d. Leave Travel Concession | 12.295 |
| e. Travel Allowances (India) | 34.785 |
| f. Travel Allowances (Foreign) | |
| g. Professional Update Allowance | |
| h. Total Other Allowances (a to g) | 118.961 |
| **3. Total Salaries (1+2h)** | **3134.573** |
| 4. P-04 Contingencies | 690.077 |
| 5. P-05 H.R.D. | |
| 6. P-06 Lab. Maintenance | 585.942 |
| 7. P-701 Staff Qrs. Maintenance | 113.631 |
| 8. P07 Chemical/Consumables & Other Research Expenses | 311.597 |
| **9. Total Revenue (3 to 8)** | **4835.820** |
| **B. Capital** | |
| a) P-50 Land Cost | |
| b) (i) P-50 Works & Services/Electrical Installations (Lumpsum) | 120.104 |
| b) (ii) P-50 Works & Services/Electrical Installations (Other) | |
| c) P-50 App. & Equip./Computer Equipments | 135.945 |
| d) P-50 Workshop Machinery | |
| e) P-50 Office Equipments | |
| f) P-50 Furniture & Fittings | 7.800 |
| g) P-50 Library (Books/ Journals/ e-Journal) | 52.698 |
| h) P-50 Model & Exhibits | |
| i) P-50 Vehicles | |
| j) P-50 Tools & Plants | |
| k) P-50 Software development/procurement/LAN/WAN | |
| l) P-26 -ICT | |
| m) (i) P-702 Staff Quarters (Construction) (Lumpsum) | 35.651 |
| m) (ii) P-702 Staff Quarters (Construction) (Other) | |
| **Total Capital (a to m)** | **352.198** |
| **Total A+B** | **5188.018** |
| **C. Special Project FBR/NCP/FTC/FTT/RSP/HCP/HARIT/Lab Projects etc.** | |
| 1. Revenue | |
| (i) Travel Allowances (India) | 24.838 |
| (ii) Travel Allowances (Foreign) | |
| (iii) Contingencies | 16.133 |
| (iv) Maintenance | 40.828 |
| (v) Chemical, Consumables & Other Research Expenses | 543.190 |
| **Total Rev.(C1)** | **624.989** |

| | |
|---|---|
| 2. Capital | |
| (i) Work's & Services | 14.255 |
| (ii) Apparatus & Equipment | 19.291 |
| (iii) Other Capitals | |
| **Total Capital(C2)** | **33.546** |
| C. Total allocation FBR/NCP/FTC/FTT/RSP/HCP/HARIT/ Lab Projects etc. (C1+C2) | **658.535** |
| **Total National Labs. (A+B+C)** | **5846.553** |
| **D. OTHERS** | |
| P-804 Pension & Other retirement benefits | 2764.596 |
| P-801 and P-62 ISTADS | |
| P-803 PPD/TNBD | |
| P-805 HRD | |
| P-80508 RAB | |
| P-807 Publicity & Exhibition | |
| P80804 Grant to other Sci. Organisations | |
| P80805 CSIR Guest House (Science Centre) | |
| P80806 Celebrations | |
| P906- Advance | |
| (i) Conveyance/Computer Advance | |
| (ii) House Building Advance | |
| (iii) Others | |
| **Total Central Admin.** | **2764.596** |

| **II. Earnings** | |
|---|---|
| **RECEIPTS** | |
| R04 Donation | |
| R05 Contribution | |
| R06 Miscellaneous Receipts | 92.837 |
| R906 Recovery of Advances | 1.490 |
| **TOTAL R06+R906** | **94.327** |
| **R071 LAB RESERVE** | |
| a) Royalty Premia | 15.497 |
| b) Testing & Analytical Charges | 1.211 |
| c) Other Technical Service | 9.234 |
| d) Job Work | 8.399 |
| e) Rest of R 071 heads | 97.571 |
| **Total Lab Reserve(R-071)** | **131.912** |
| **R909 EXTERNAL CASH FLOW** | |
| a) Government departments/PSU's | 1203.989 |
| b) Private agencies | 193.835 |
| c) Foreign government/agencies | |
| **TOTAL ECF (a+b+c)** | **1397.824** |
| **Royalty & Premia for distribution (R907)** | **1.858** |

# PERSONNEL (As on 31.03.2020)

## Director

SK Barik

## Chief Scientists

PA Shirke
SK Tewari

## Sr. Principal Scientists

TS Rana
AK Gauniyal
KN Nair
Anand Prakash
LB Chaudhary
Vivek Pandey
Samir V Sawant
AP Sane
Vidhu A Sane
Alok Lehri
Sayyada Khatoon
PK Singh
ChV Rao
TS Rahi
Sharad K Srivastava
Sanjeeva Nayaka
Ashish K Asthana
Mahesh Pal
SK Ojha
OP Sidhu

## Principal Scientists

Vivek Srivastava
Subha Rastogi
Indraneel Sanyal
Debasis Chakrabarty
CS Mohanty
HK Yadav
Meher H Asif
Arvind Jain
PS Chauhan
Shekhar Mallick
SK Behera
SN Jena
PC Verma
SK Bag
Manjoosha Srivastava
Suchi Srivastava
AP Singh
Aradhana Mishra
Poonam C Singh
Baleshwar

## Senior Scientists

Sribash Roy
Devendra Singh
Priyanka Agnihotri
Lal Bahadur
BN Singh
VV Wagh
RC Nainwal
Manoj Kumar

## Pr. Technical Officers

Yogendra Nath
M L Kain
AC Little
D K Purshottam

## Sr. Tech. Officers (3)

R K Tripathi
Alok Kumar
Shankar Verma
Lalit K Srivastava

## Sr. Tech. Officers (2)

Anil Kumar
Daya Shanker
Sanjay Dwivedi
Abhishek Niranjan
Bhagwan Das
Atul Batra
Sushma Verma
RN Gupta
Rajeev Kumar
Girdhari Sharma
Harendra Pal

## Sr. Tech. Officers (1)

SK Behera
Vinay Sahu
MK Shukla
Kiran Toppo
MM Pandey
Surjit Kumar
Swati Sharma
Leena Wahi Gupta
SK Sharma
KN Maurya
Babita Kumari
GG Sinam
Sumit Yadav
KK Rawat

## Technical Officers

Somanath Swain
Satish Kumar
Prashant Srivastava
Jai Chand

## Technical Assistants

Shweta Singh
Rameshwar Prasad
Rekha Kannaujia
Shashank K Mishra
Komal K Ingle
Bharat Lal Meena
Vivek K Gupta
Rajat Raj Rastogi
Devranjan
Vandana Tiwari
MG Prasad

## Administration

Mahendra Singh, AO
Sanjeev Shekhar, F&AO
Dinesh Kumar, SPO
RS Chaudhary, SPO
Prasoon Misra, SO
SK Singh, SO
Sachin Mehrotra, SO
RK Verma, SO
Prabha Tirkey, SO
KK Saxena, SO
BP Pande, PS
SK Pandey, Security Officer
Bijendra Singh, Hindi Officer