



جامعة نizwa
University of Nizwa

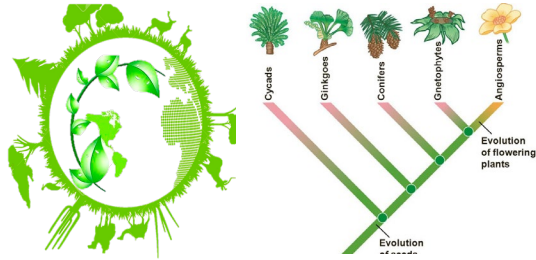


Academic Projects pertaining to **Agriculture**

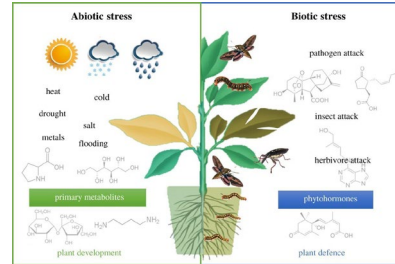


Biotechnology & OMICs Lab

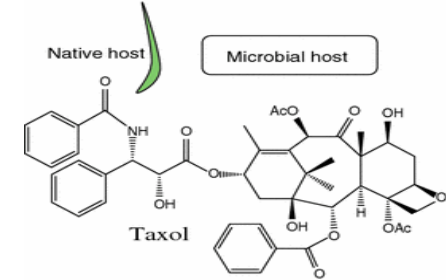
Ecology & Systematics



Plant Stress Physiology



Plant genetic diversity



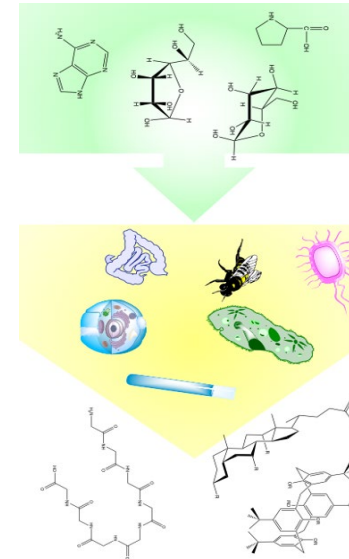
Genomics



Bioremediation



Plant genetic diversity



Tissue Culture



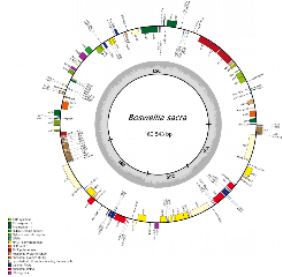


OMICs Lab

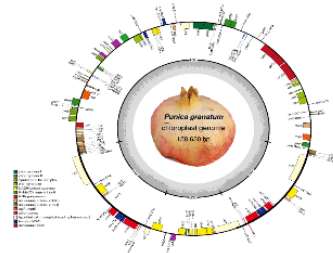
Chloroplast genomics



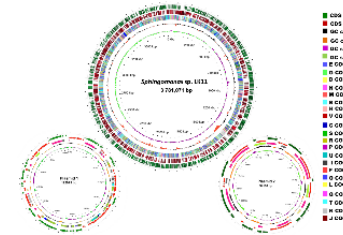
Boswellia sacra
Habitat and Tree



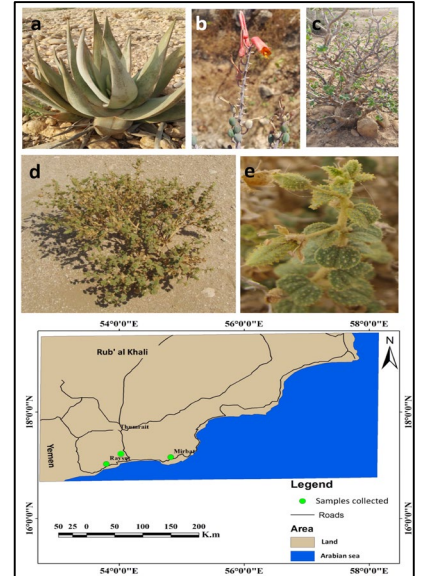
Mitochondrial genomics



Whole genomics



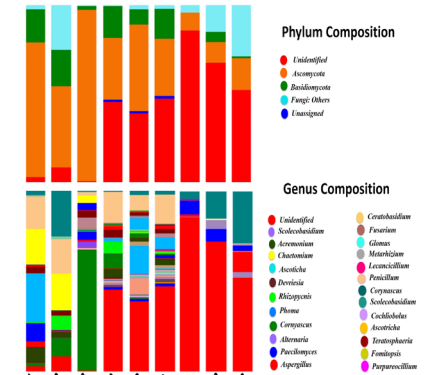
Metagenomics



Transcriptomics

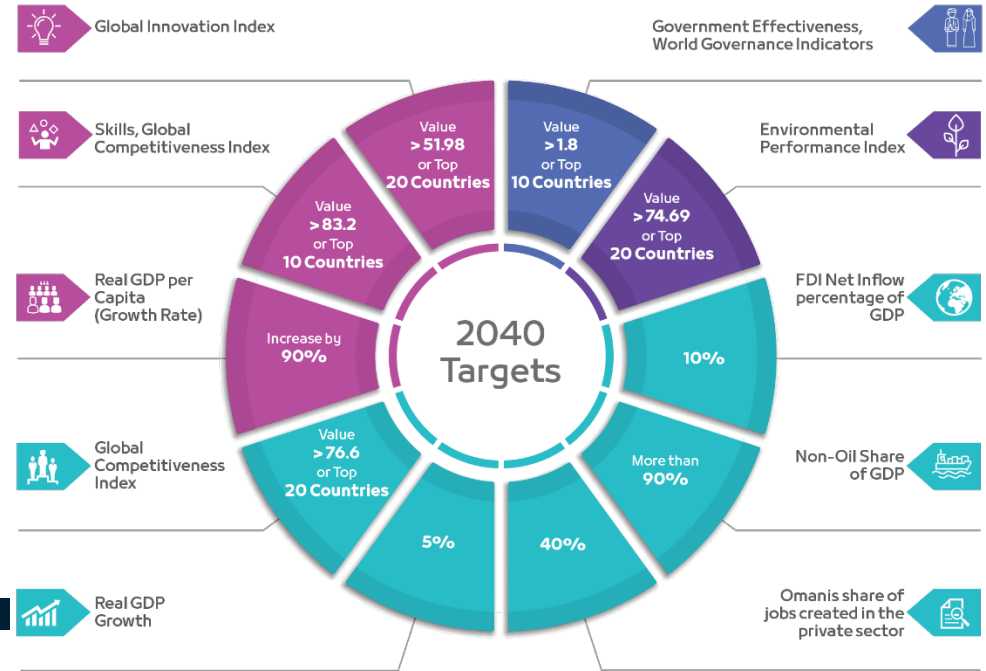
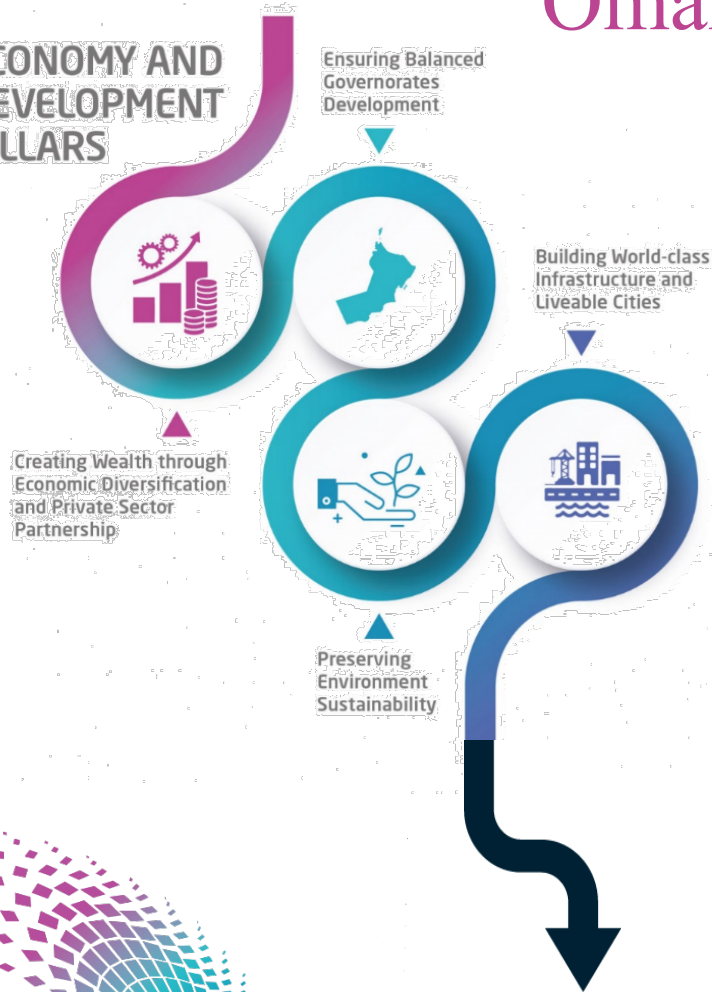


Bioinformatics



Oman Vision-2040

ECONOMY AND DEVELOPMENT PILLARS



Efficient utilization of Oman's genetic natural resources will contribute to non-oil share of **GDP**. Young Omanis development will stand out on top priorities of the envisaged projects.

Scientific research and innovation is a national priority in **Oman Vision 2040**.

Diversification of economical resources to solicit alternatives for oil and gas stands on top of research priorities.



NMSRC Strategic Projects



With the Ministry of Agriculture and Fisheries

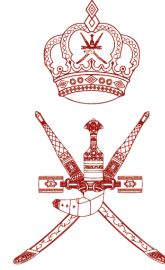
- ✓ Transcriptomic of Dubas Bug
- ✓ Genomics of Date Palm Trees
- ✓ Genomics & Metabolomics of Mango Trees
- ✓ Genomics & Metabolomics of Bananas



Ministry of Health
Sultanate of Oman

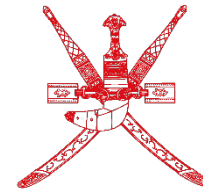
With the Ministry of Health

- ✓ Molecular Epidemiology and Sequencing of SARS-CoV-2 Virus
- ✓ Epidemiology of SARS-CoV-2 infection among health workers
- ✓ Bacterial Antibiotic Resistance



With the Diwan of Royal Court

- ✓ Office for Conservation of Environment
- ✓ Oman Botanic Garden



Ministry of Higher Education,
Research & Innovation

With the Ministry of Higher Education, Research and Innovation

- ✓ Gene Bank of Oman
- ✓ High Throughput Screening of Oman
- ✓ Genetic Natural Resources





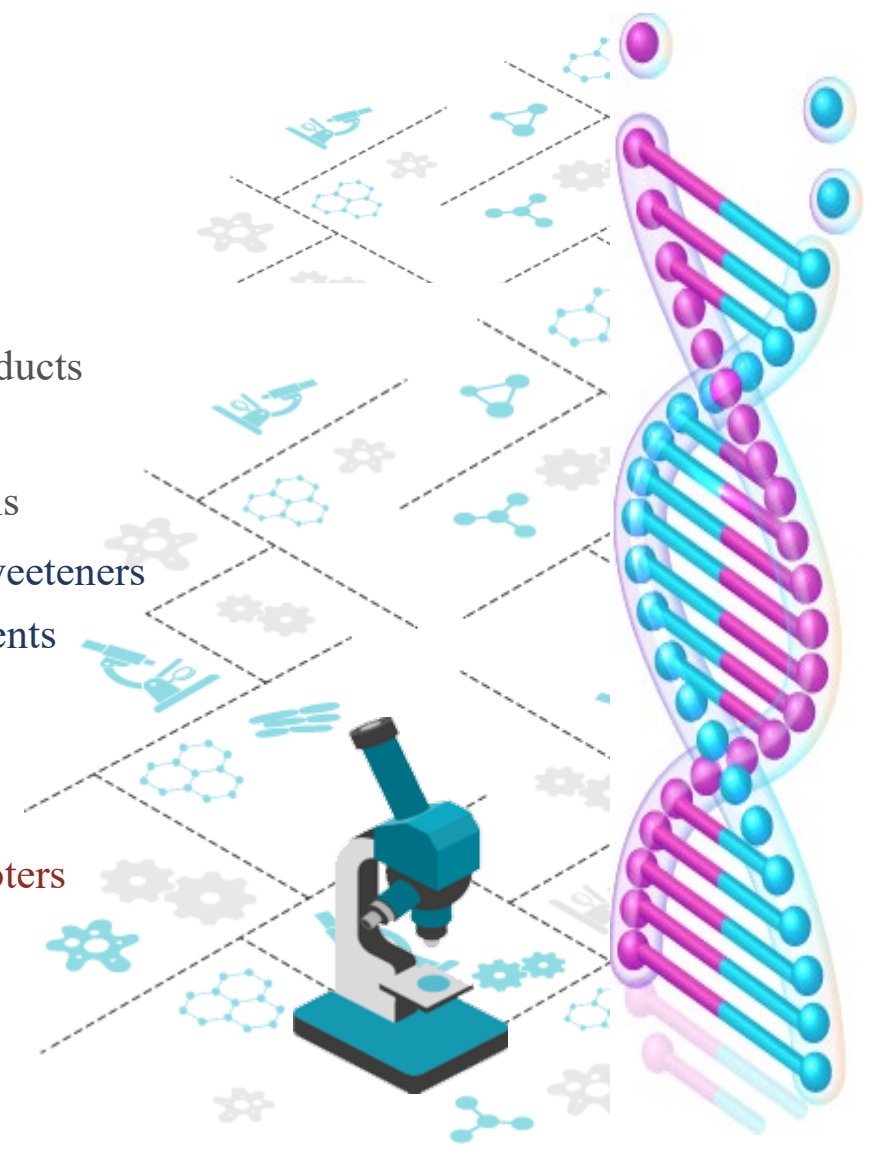
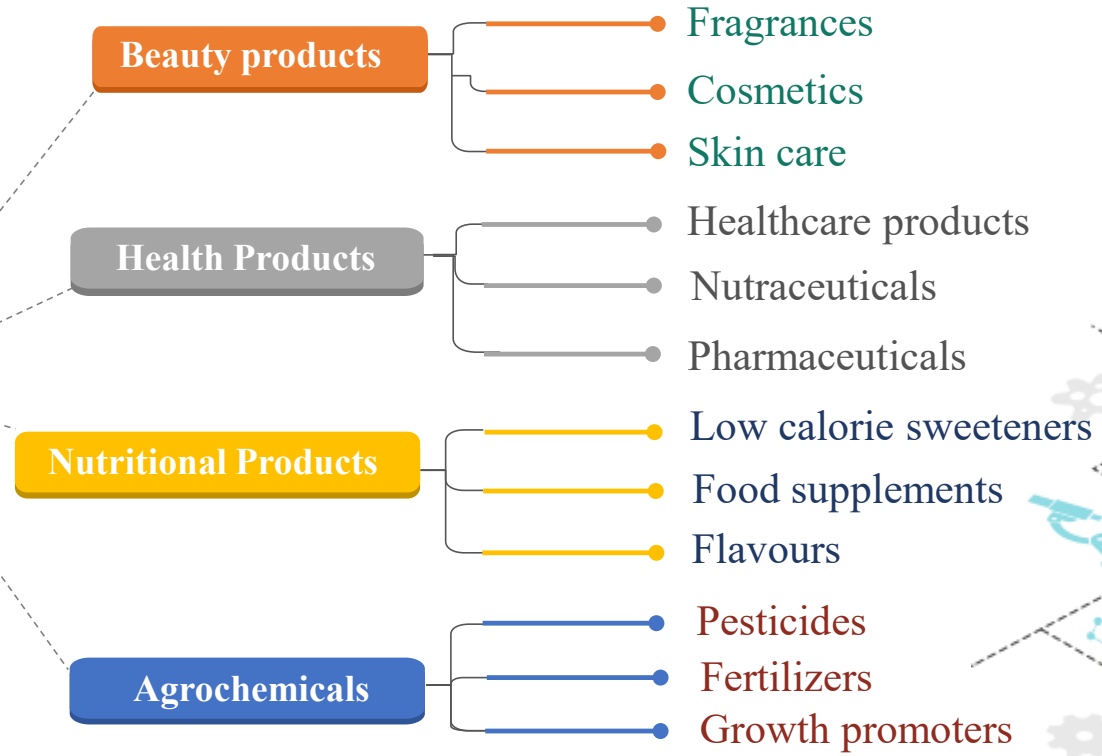
Value addition to our genetic resources

Documentation
Gene bank



Oman
Genetic Natural
Resources

Establish a solid Ground for
pharmaceutical, cosmeceutical and
agrochemical industries





Innovation. How simple it can be!

Hook-and-loop fasteners - \$100 million a year

- ✓ George de Mastral produced a prototype and named it **velcro**, a combination of the words 'velvet' and 'crochet'.
- It was patented in **1955**.
- NASA picked up the brand and began using it for astronaut equipment.
- Puma picked up on the brand for kids' shoes.
- A worldwide success, bringing in **\$100 million** (£78.6m) revenue every year.



The top down squeeze bottle - \$14 million a year

- ✓ Paul Brown, the owner of a small precision-moulding shop, spent his days coming up with and rethinking the design of the bottle. He said: "I would pretend I was silicone and, if I was injected into a mould, what I would do." His work paid off in 1991, when he came up with the idea for a bottle that would open when squeezed but remain closed if no pressure was applied. .





Innovation. How simple it can be!

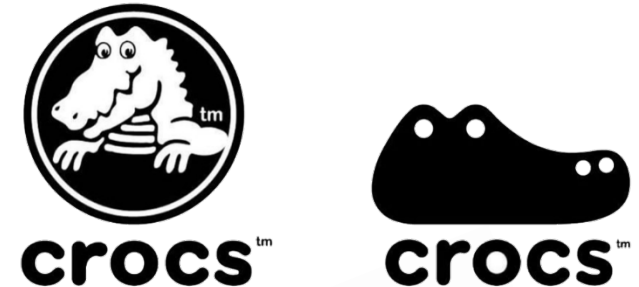
Fidget spinners - \$5 billion a year

- ✓ Originally invented as a therapeutic tool for kids with **ADHD** and **autism**, this simple spinning toy has sold to kids and adults alike since 2017.



Crocs - \$1 billion a year

- ✓ Despite not winning any fashion contests, annual sales of **Crocs** have regularly exceeded **\$1 billion** (£787m) a year. Launched in the early 2002 by three friends, Crocs were advertised to be made from a trademarked material which was “comfortable, lightweight, non-marking and odor resistant”.



Snap Wraps - \$8 million a year

- ✓ The overwhelming simplicity of **Anders' invention** pleased kids and pre-teens everywhere. The **bracelet** worked by simply slapping a straight piece of steel covered in colorful fabric to the wrist, which it instantly clasped itself around.





Value addition from our lab. How simple!



Frankincense



Frankincense crystals



Dark date syrup



White date syrup



Animal feeding



Phytohormones-rich oil



Animal feeding

One step
waste



Phytohormones-rich oil

One step

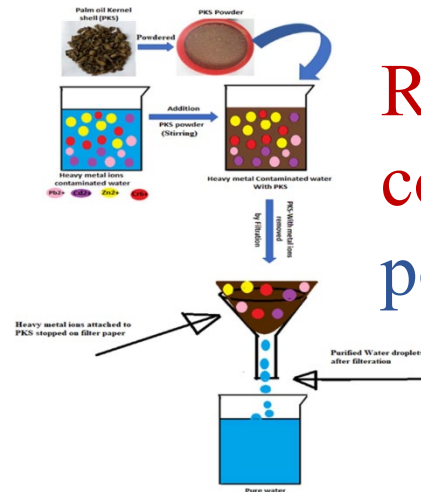


Use of date palm kernel oil for phytohormones rich **anti-wrinkle** cream

waste



One step



Renewable and **cost-effective** fillers for polymeric materials

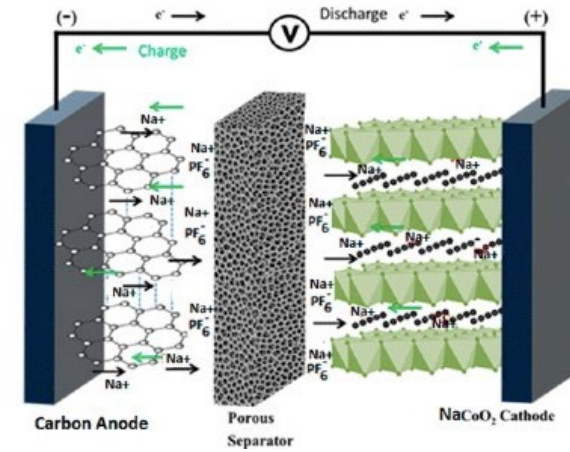
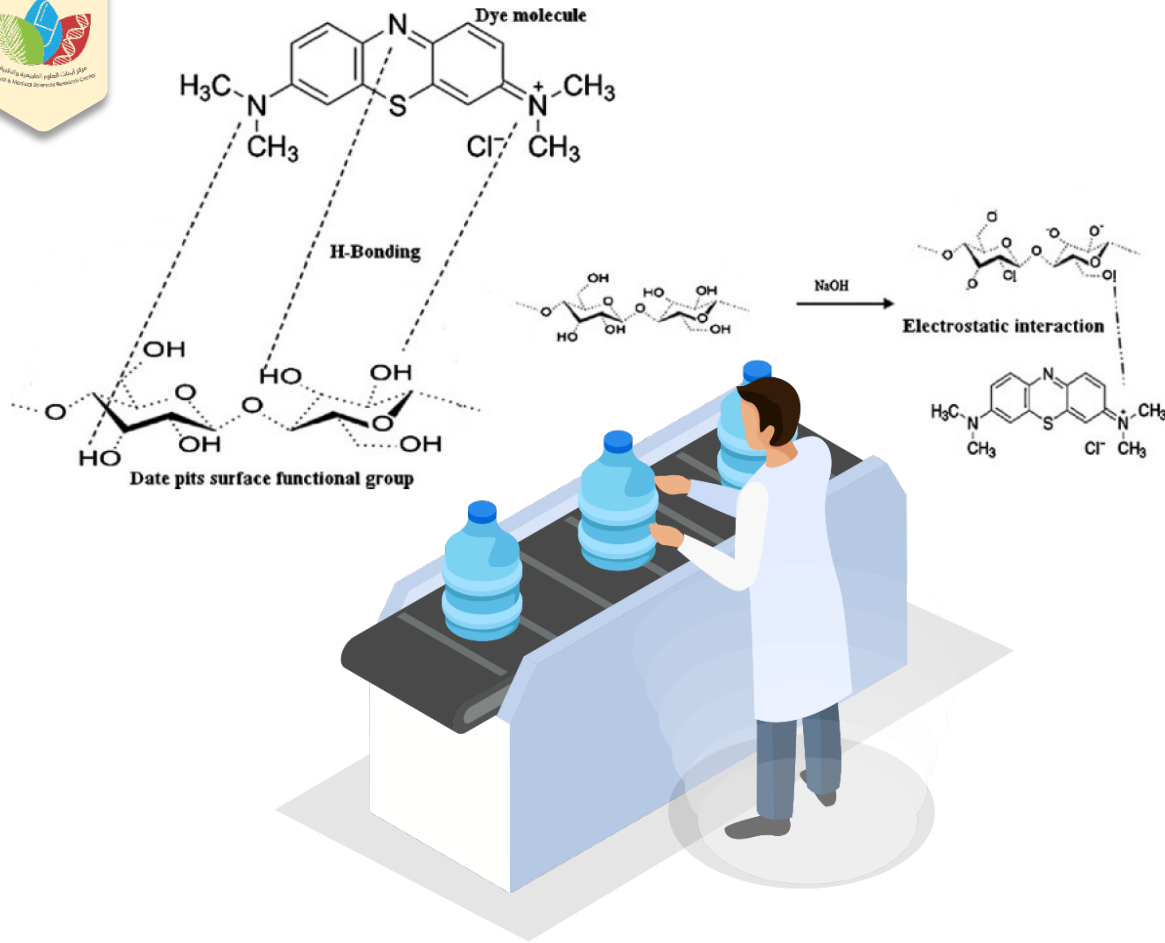


Wasted pollen

One step



Use of palm pollen for treatment of **skin conditions** and **anti-aging** treatment.



The use of date palm as a potential adsorbent for wastewater treatment to replace activated carbon

Hard carbons issued from date palm as efficient anode materials for sodium-ion batteries



Beneficial Outcomes



Paper and constructions

- ✓ Handicrafts
- ✓ Wood
- ✓ Construction materials
- ✓ Paper industry

Agriculture

- ✓ Compost
- ✓ Fertilizers
- ✓ Animal feeds- cows, goats, fish

Biofuels

- ✓ Methane
- ✓ Hydrogen production
- ✓ Ethanol
- ✓ Butanol

Biosurfactant

- ✓ Carbon capsules for treatment of stomach gases
 - ✓ Healing of wounds and burns
 - ✓ Making soap- rich of fatty acids
 - ✓ Roasted kernels as cacao alternative
 - ✓ Date kernels Coffee
- ✓ Date kernels are source of Furfural (30%) used in oil refineries and in pesticides industries

Health & Beauty



Beneficial Outcomes



Biopolymers

- ✓ Xanthan gum
- ✓ Poly (3-hydroxybutyrate)
- ✓ Curdlan
- ✓ Carotenoid

Organic acids

- ✓ Citric acid
- ✓ Lactic acid

Enzymes

- ✓ Pectinases
- ✓ α -Amylase

Nutraceutical

- ✓ Liquid or Tablets

Amino acids

- ✓ Glutamic acid



Beneficial Outcomes



Food

- ✓ Biscuits, pies & pastries production
- ✓ Date chocolate & Tamreya industry
 - ✓ Dates Pone, Date jam
 - ✓ Date powder, Date syrup
- ✓ Molasses production (Debs)
 - ✓ High-fructose syrup
 - ✓ Fructooligosaccharides
 - ✓ Beverages industry

Biomass

- ✓ Baker's yeast

Probiotic lactobacilli

Date-Palm Fibers

- ✓ Wastewater filter



Ongoing Research Projects pertaining to Agriculture at NMSRC



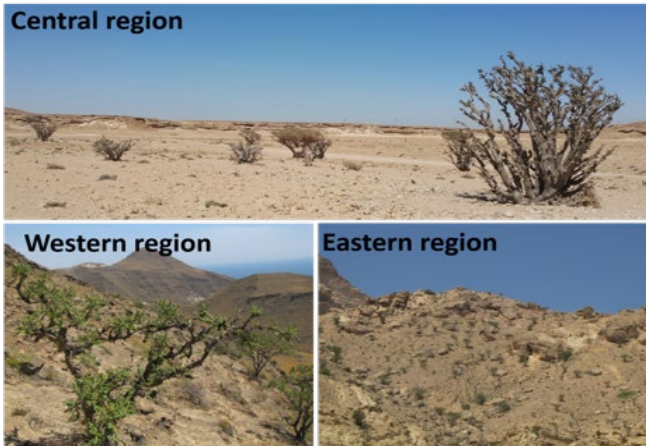


Part 1: Frankincense trees in Oman

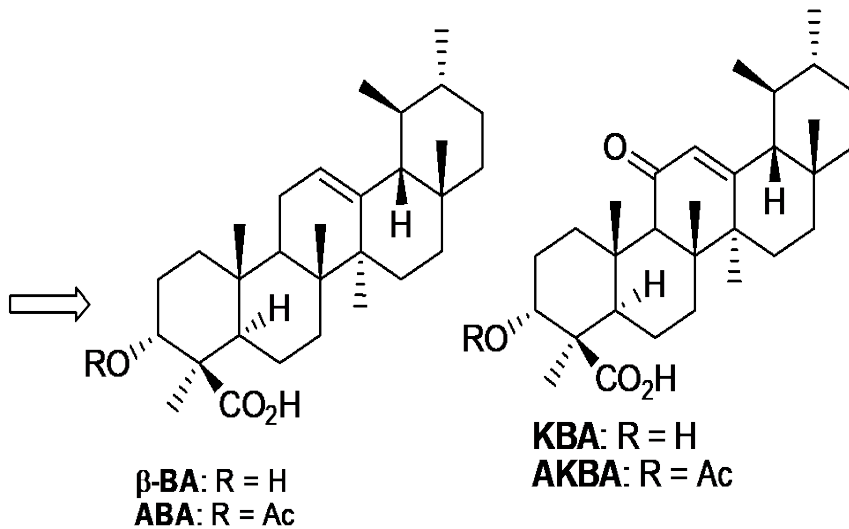




Boswellia sacra (Frankincense Tree)

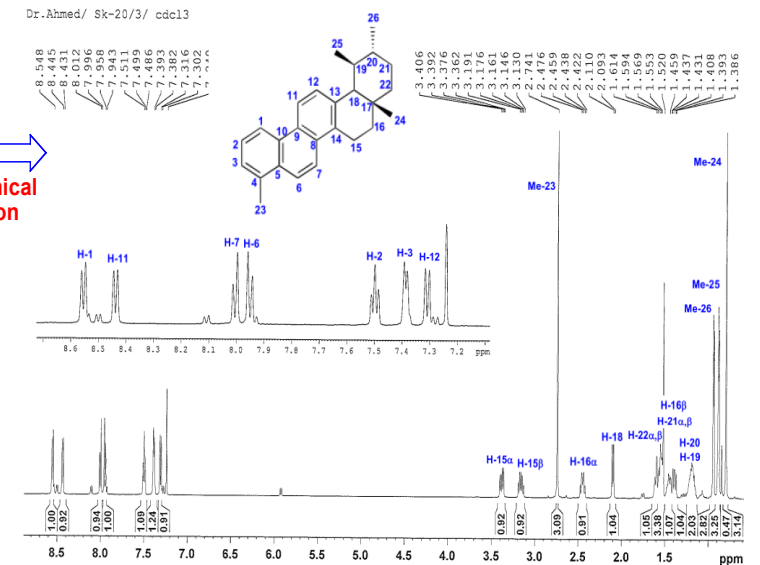


Boswellia sacra (Chemical Compounds)

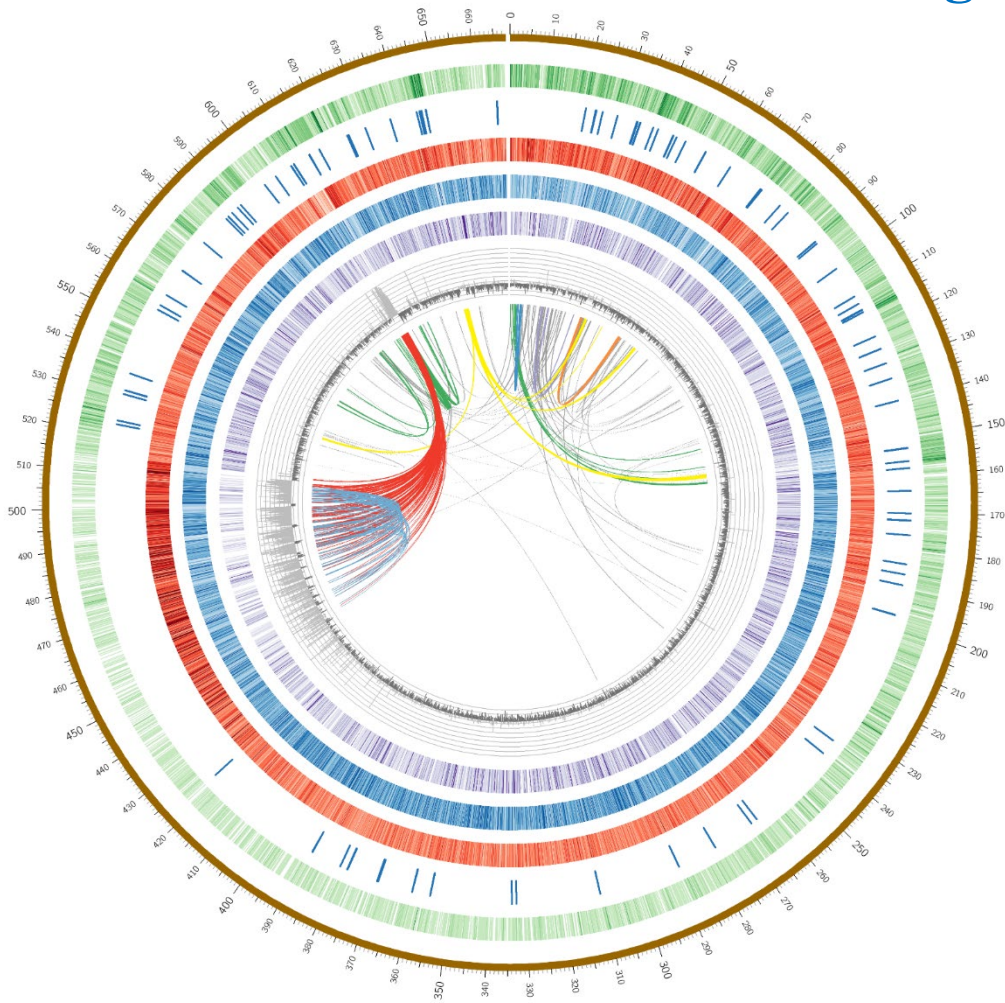


Frankincense Smoke

Phytochemical Investigation



de novo genome sequence of *B. sacra*



We report the *de novo* genome sequence of *B. sacra*, comprising 667.8 Mb DNA sequence in genome. Comparison to conserved single copy genes across the eudicot's species, the data suggests a >97% assembly of the gene space in *B. sacra* genome.



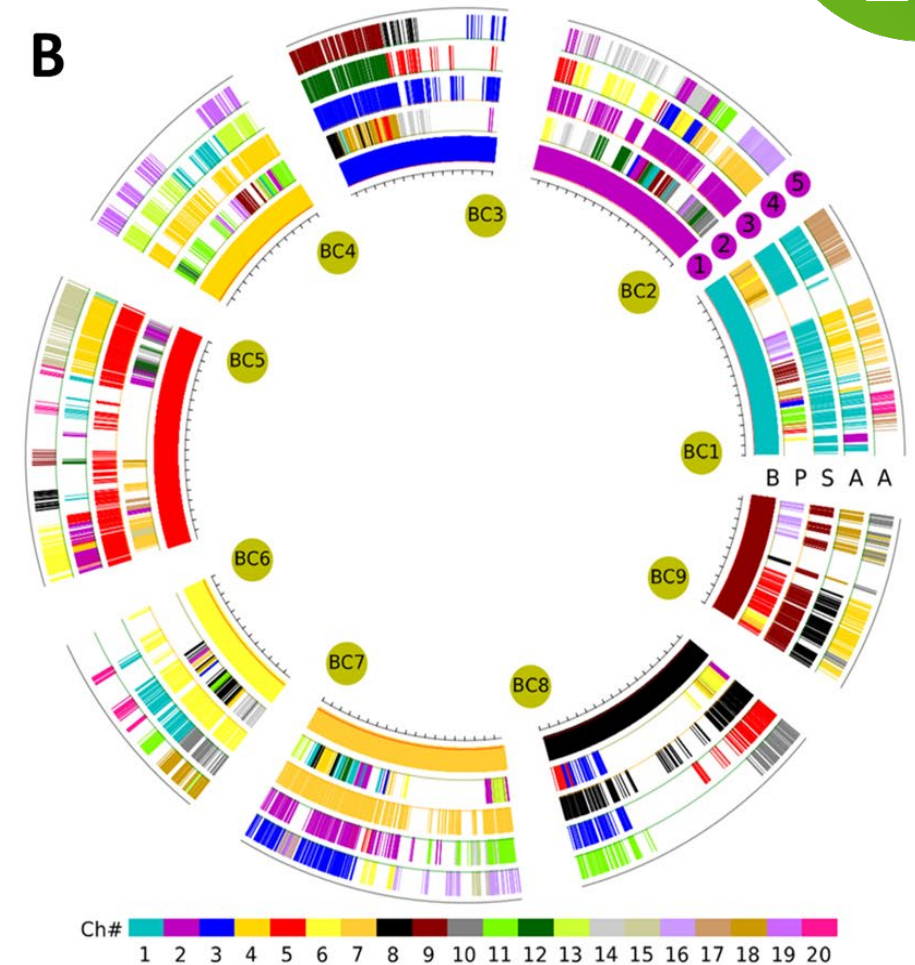
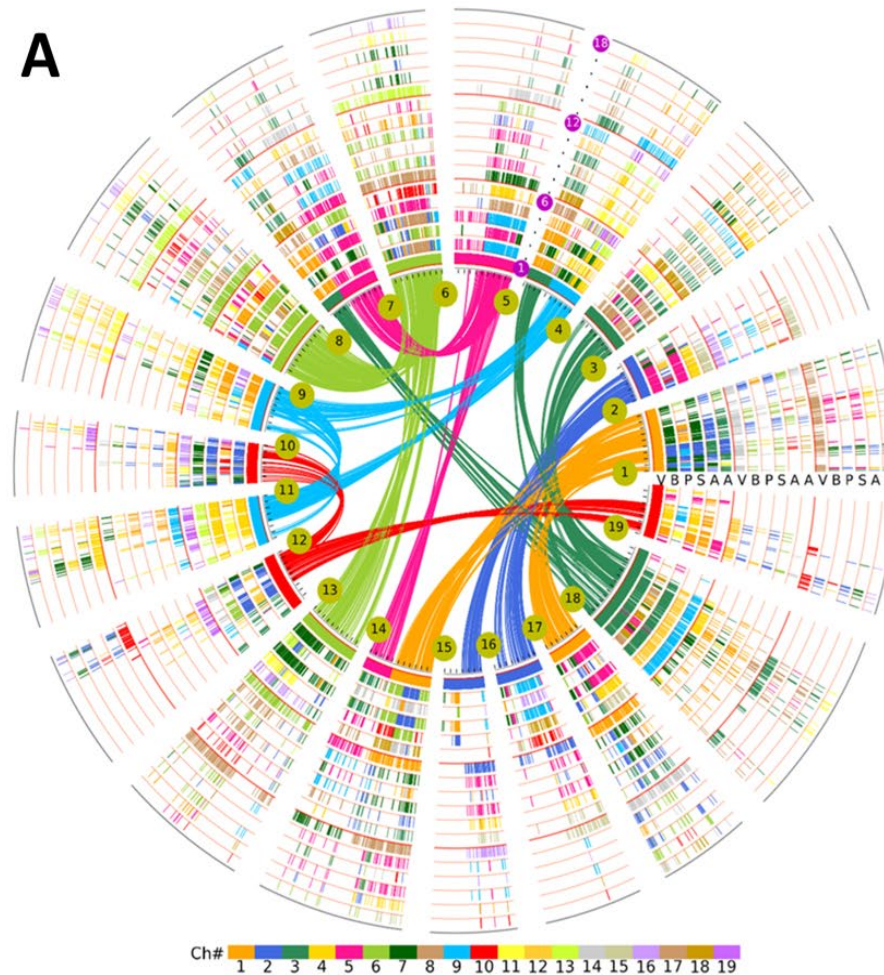
The combined length of genes was 63.6 Mb or ~9.5% of the whole genome. We found 18,564 high-confidence predictions of protein-encoding genes. The genes found in *Boswellia* have been found to play a functional role in cell-wall synthesis, arrangement, exfoliating and response to wounds. Additionally, genes related secondary metabolites (flavonoids, phenolics, terpenoids), abiotic stress tolerance, photosynthesis, metabolic and biological processes.

Circular presentation of major scaffolds (brown), gene density (green), location and presence of genes involved in terpenoid biosynthesis (dark blue), simple repeat density (red), transposable elements distribution (blue), LTR-RT density (purple), above/below mean GC% (gray) and inner circle shows the major collinear genes across different scaffolds.

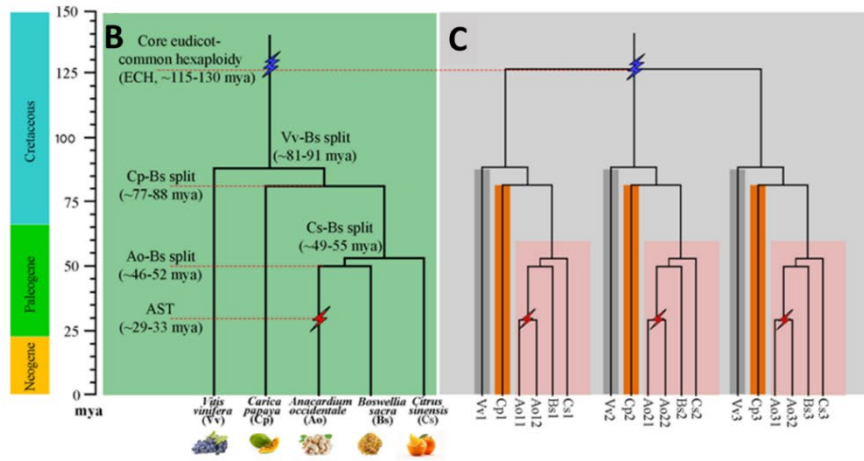
Genome multiple alignment with taxonomically related species



(A) The inner circle shows 19 chromosomes within the grape genome comprising tripled homeologs of seven assumed ancestral chromosomes, and the homoeologous genes are connected by colored lines. The 15 circles can be divided into three groups according to the major **eudicot-common hexaploidy (ECH)**, in which the first group, the inner five circles, represents the orthologs between them, and the other two groups (the intermediate and outer five circles) are paralogs comparing to the first group.



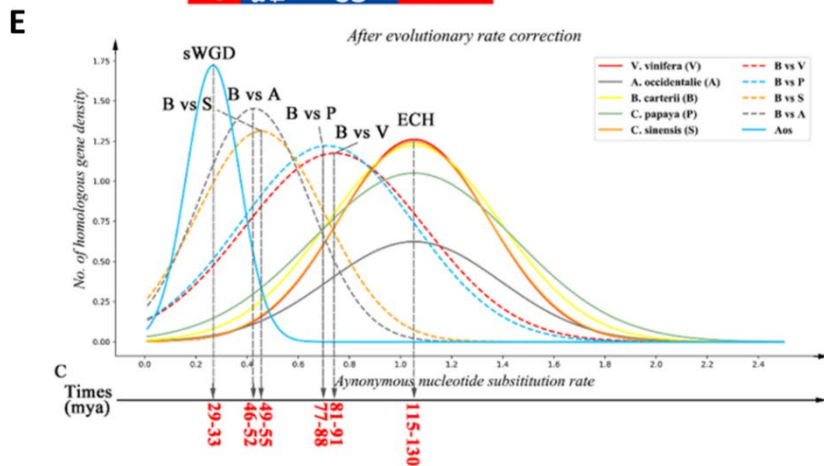
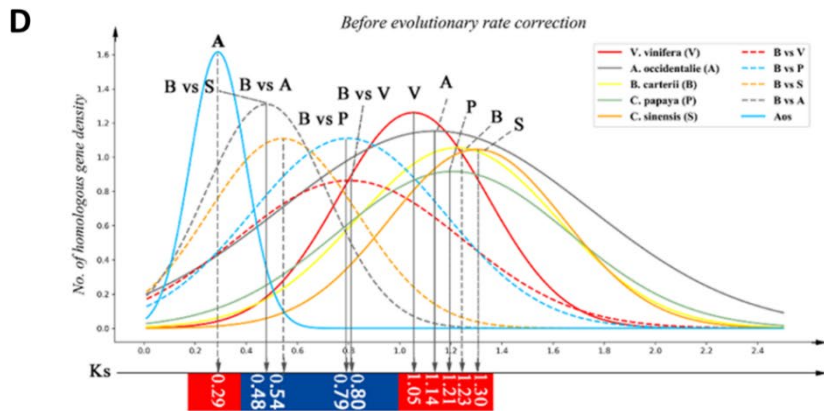
(B) Circles show the multiple alignment between the compared four genomes with *Boswellia sacra* as reference (B: *B. sacra*, P: *C. papaya*, S: *C. sinensis*, A: *A. occidentale*). The five circles show their orthologous relationship between the compared genomes, with *A. occidentale* comprising two circles to show an extra genome doubling in its genome, in contrast to the other three genomes.



(B) Phylogenetic tree of *B. sacra* (Bs), *A. occidentale* (Ao), *C. papaya* (Cp), *C. sinensis* (Cs) and *V. vinifera* (Vv). The core-eudicot common hexaploidy (ECH) is denoted by a blue flash, and the *A. occidentale* special tetraploidization (AST) is denoted by red flashes.

(C) Gene phylogeny: three paralogous genes in the Vv, Cp, Bs, Cs and Ao are denoted by Vv1, Vv2, and Vv3, and Cp1, Cp2, and Cp3, and Cs1, Cs2, and Cs3, respectively, produced by the ECH, and each has 2 orthologs and 4 out paralogs in the Ao genome (e.g., V1 has 2 orthologs, Ao11, Ao12, and 4 out paralogs, Ao21, Ao22, Ao31, Ao32 in Ao genome). The species tree was produced based on the presence of homologous genes.

Evolutionary & comparative genomics of *B. sacra* suggested that the whole genome duplication events occurred 46-52 and 49-55 million years ago from *Citrus sinensis* (orange) and *Anacardium occidentale* (cashew nut), respectively.



(D, E) Ks dating before and after evolutionary rate corrections. Anonymous nucleotide substitution rate (Ks) distribution between the selected genomes. The solid curve lines show the events of **polyploidization** that appeared in genomes, while the dash lines represent the divergent events between the two compared genomes. The x-axes represent the Ks values and the y-axes represent the density of the compared homologous genes.

Boswellia socatrna



B. ovalifoliolata



B. frereana



B. carterii



B. elongata



B. serrata



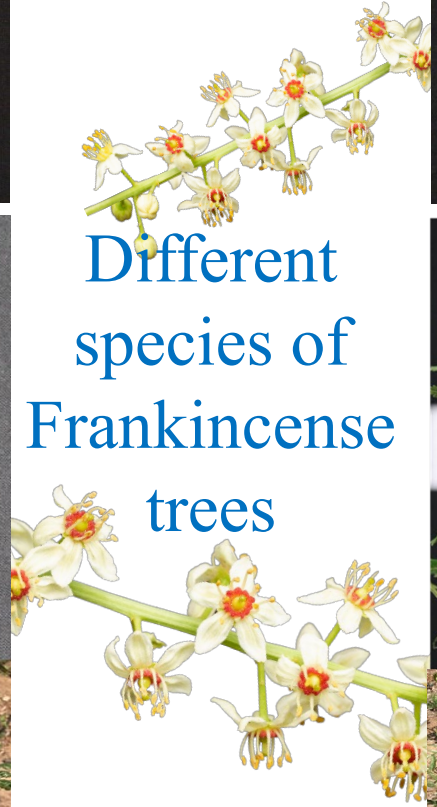
B. rivae



B. neglecta



B. bullata



Different species of Frankincense trees

B. dalzielii



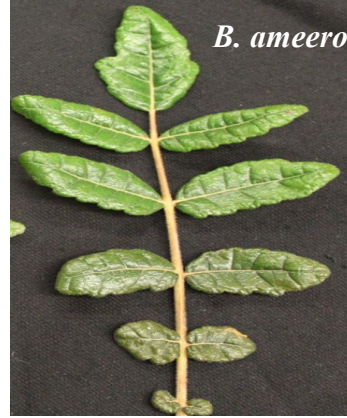
B. sacra



B. popviana



B. ameero

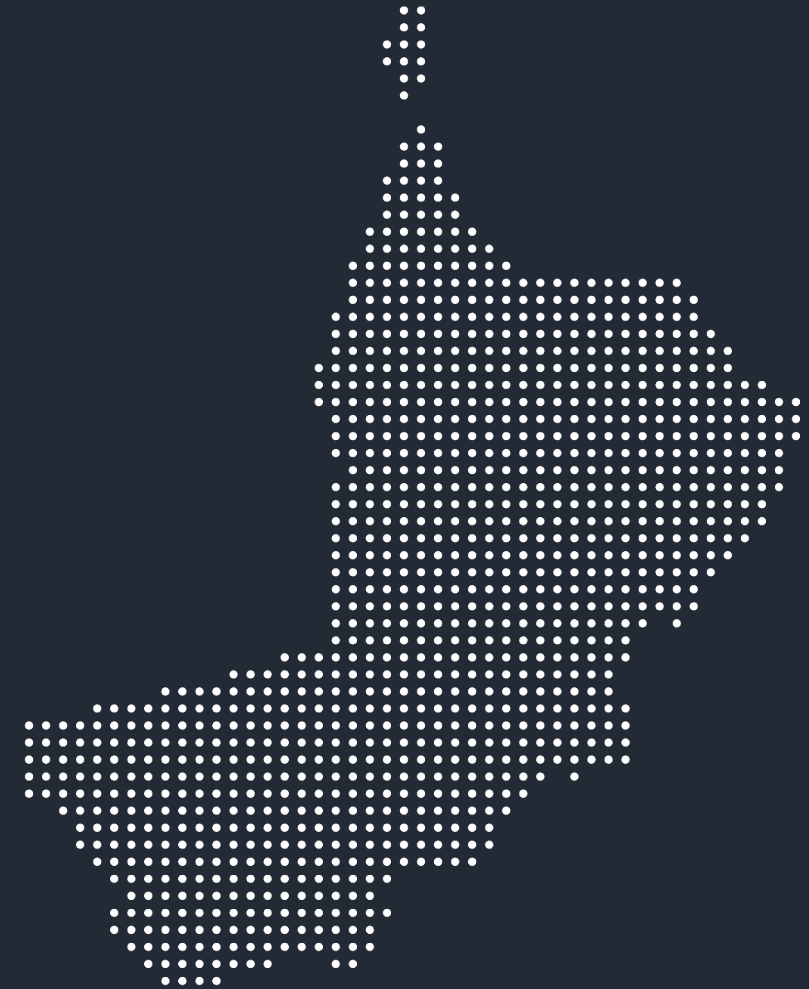


B. dioscoridis



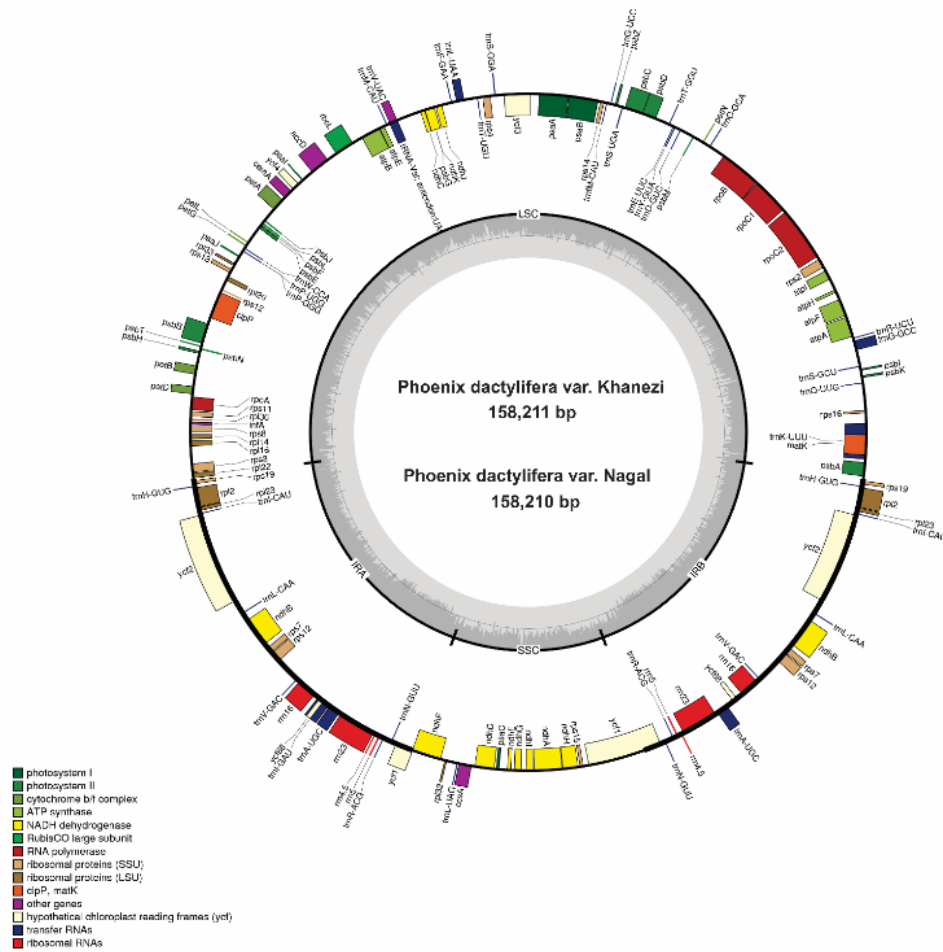


Part 2: Date palm trees in Oman



Date palm genomics

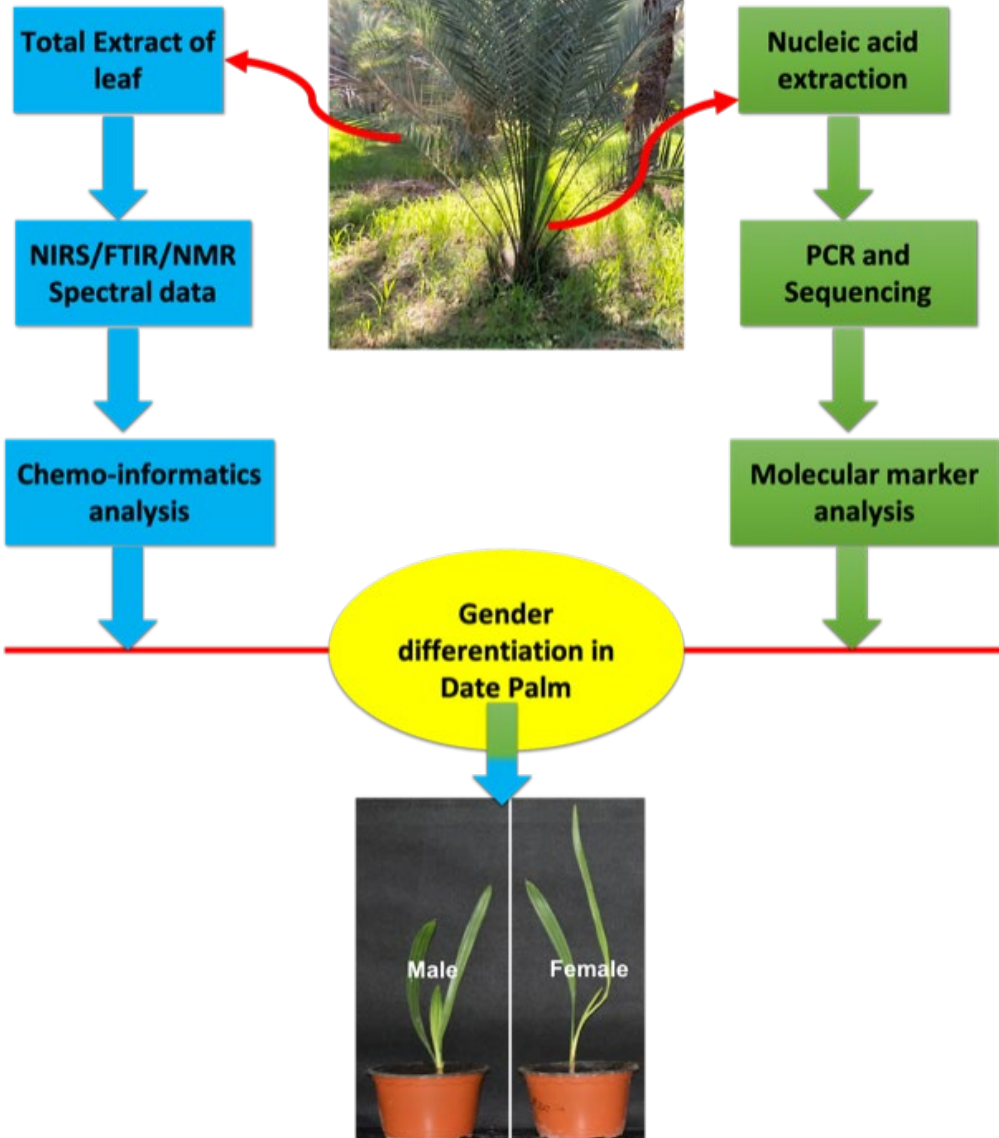
- ✓ Draft
- ✓ Chloroplast
- ✓ Mitochondrial



Region	<i>P. dactylifera</i> var Khanezi	<i>P. dactylifera</i> var Naghal	<i>P. dactylifera</i> var Khalas	<i>P. dactylifera</i> var Aseel
LSC				
Length (bp)	86090	86092	86197	86194
GC(%)	35.3	35.3	35.3	35.3
Length (%)	54.41	54.41	54.39	54.39
SSC				
Length (bp)	17575	17574	17712	17711
GC(%)	31	31	30.8	30.8
Length (%)	11.10	11.10	11.17	11.17
IR				
Length (bp)	27273	27272	27277	27276
GC(%)	42.4	42.4	42.4	42.4
Length (%)	17.23	17.23	17.21	17.21
Total				
GC(%)	37.3	37.3	37.2	37.2
Length (%)	158211	158210	158462	158458

- ✓ First chloroplast genome dataset for **Naghal** and **Khanizi** report
- ✓ Compared at genome and gene levels with **Khalas** and **Aseel**
- ✓ Phylogenetic analysis based on the whole genomes and 68 shared genes showed identical phylogenetic trees of **Khanezi** and **Naghal** forming clades with **Khalas** and **Aseel** cultivars, respectively

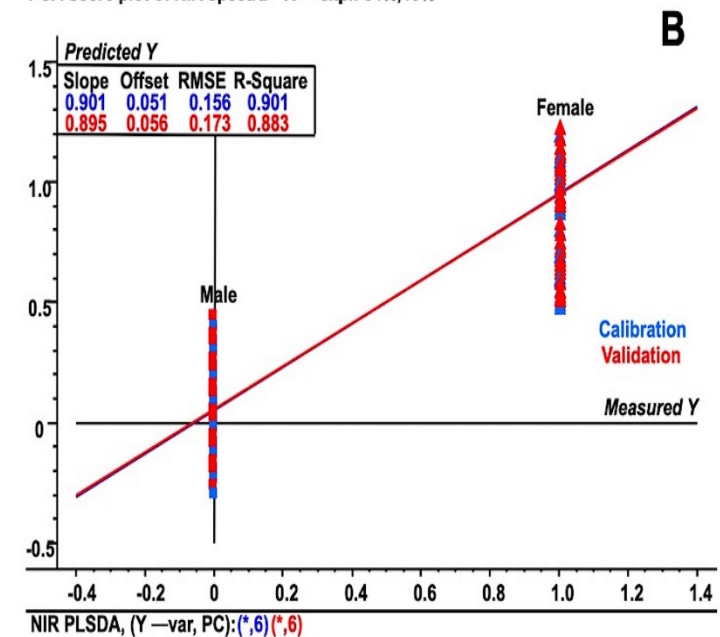
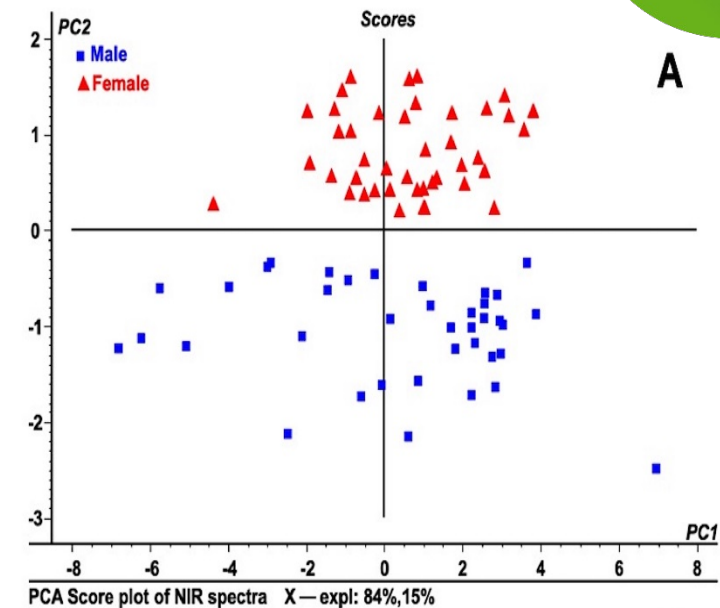
Gender differentiation in immature date palm leaf with the help of Spectroscopic and Molecular methods



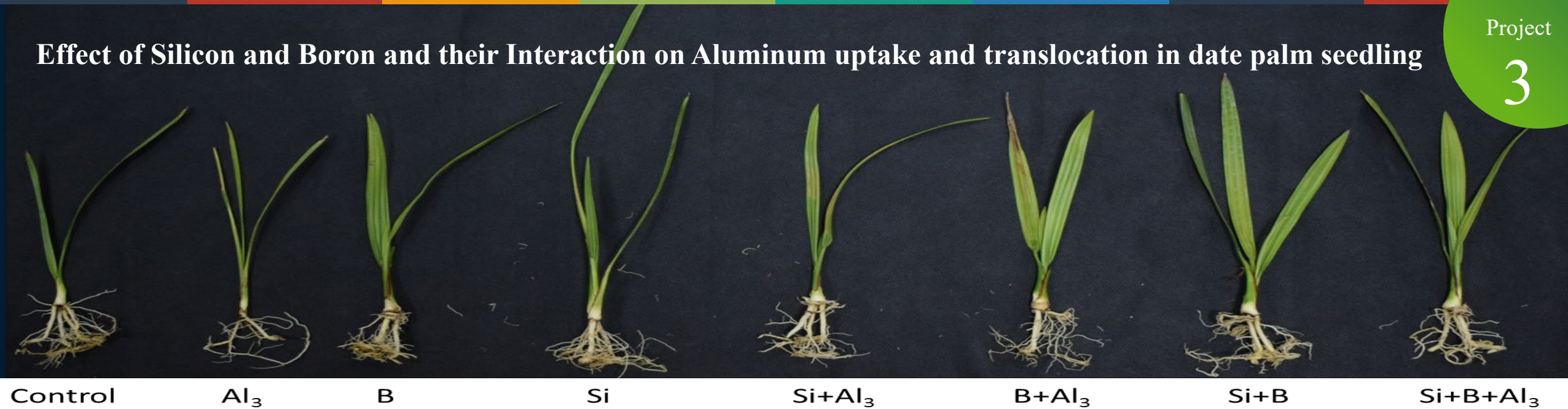
✓ Robust infrared (near-infrared reflectance spectroscopy (NIRS) and Fourier transform infrared attenuated total reflectance (FTIR/ATR)) and nuclear magnetic resonance (NMR) spectroscopy methods coupled with extensive chemometric analysis were used to identify the sex differentiation in immature date palm leaves

✓ NIRS/FTIR reflectance and $^1\text{H-NMR}$ profiling suggested that the signals of monosaccharides (glucose and fructose) and/or disaccharides (maltose and sucrose) play key roles in sex differentiation.

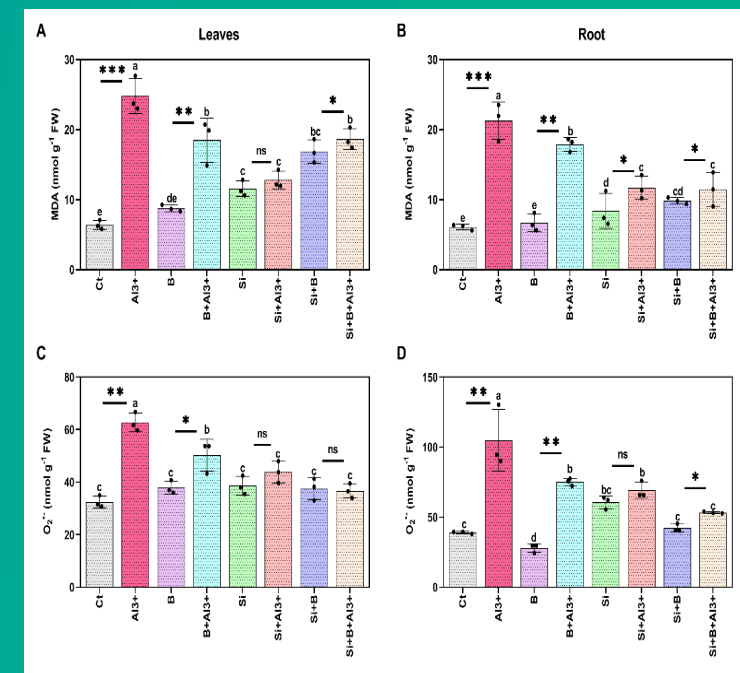
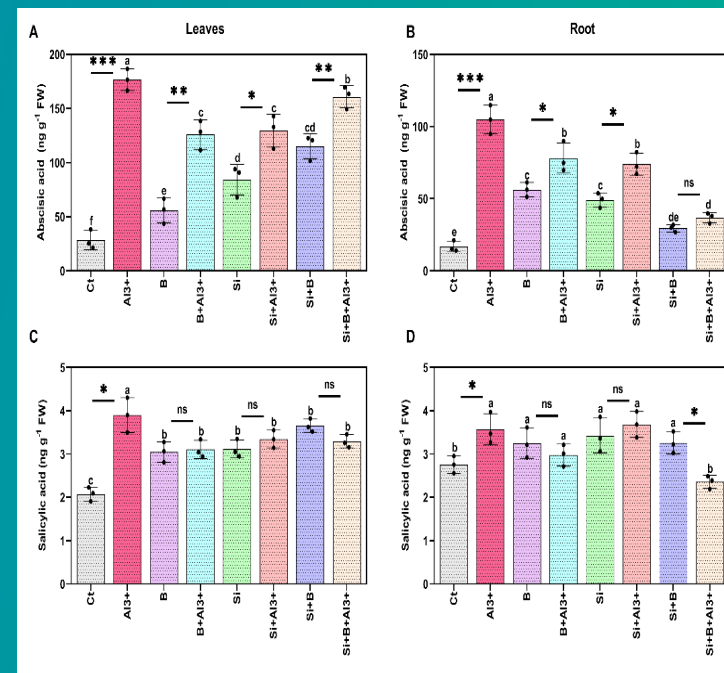
✓ Sex-specific genes and molecular markers obtained from the lower halves of LG12 chromosomes showed enhanced transcript accumulation of *mPdIRD52*, *mPdIRD50*, and *PDK101* in females compared with in males



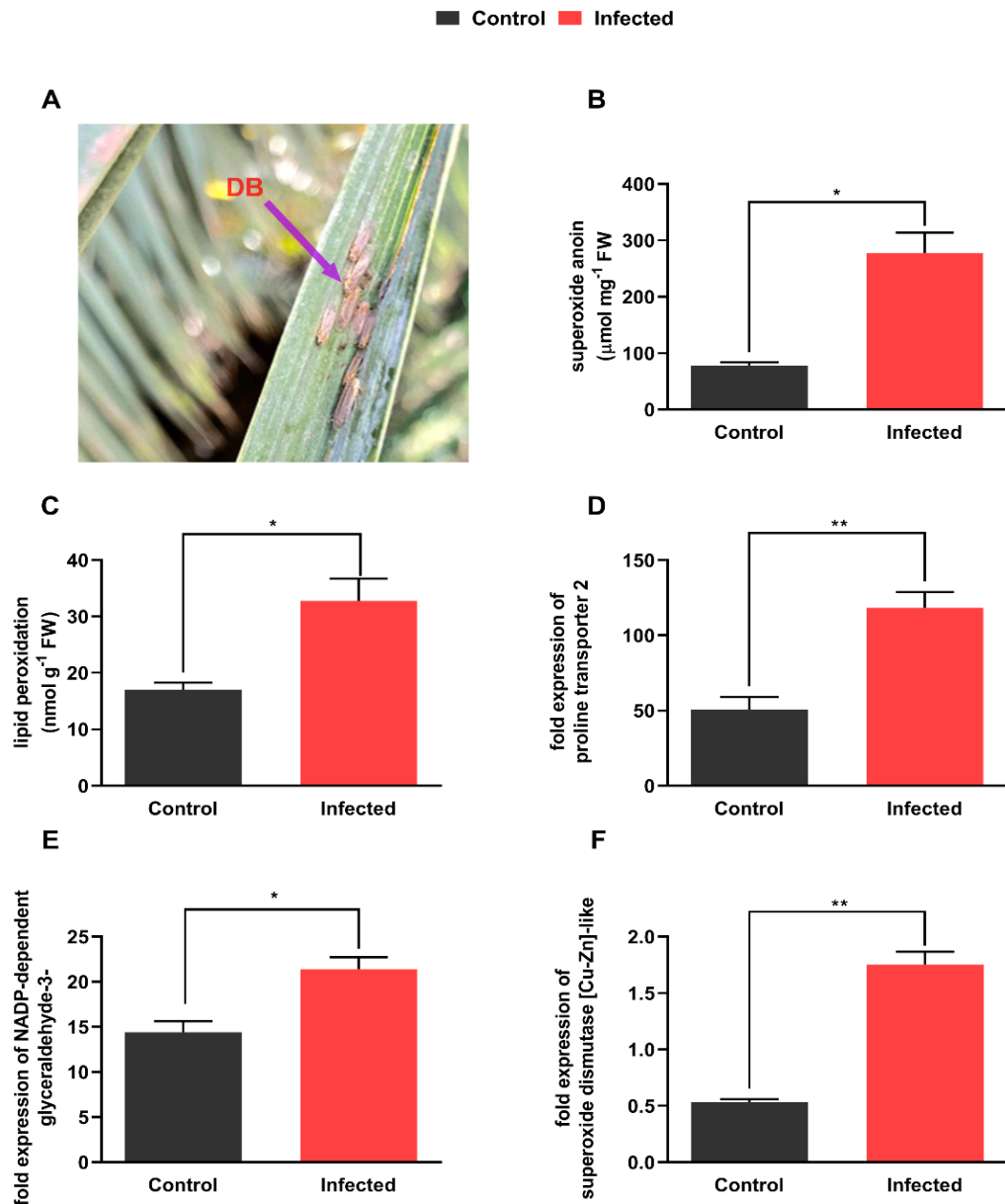
Effect of Silicon and Boron and their Interaction on Aluminum uptake and translocation in date palm seedling



- ✓ Si, B and their combination (Si+B) showed a synergistic effect against Al^{3+} induced chlorosis in date palm seedlings
- ✓ Si, B or Si+B reduced the level of MDA and $O_2^{\cdot-}$ level more significantly under Al^{3+} stress as compared to the absence of Al^{3+} stress.
- ✓ Si, B, and their combination boost Al^{3+} stress tolerance in date palm seedlings by upregulating the anti-oxidant enzymes, which help date palm seedlings to experienced less oxidative stress, under both normal and Al^{3+} stress conditions.
- ✓ Either Si, B or their combination produced less ABA and SA, which indicate that date palm seedlings experienced less stress
- ✓ Under Al^{3+} stress conditions, application of either Si, B or Si+B, downregulate ABA biosynthesis genes.



Transcriptomic analysis of Dubas bug (*Ommatissus lybicus* Bergevin) infestation to Date Palm



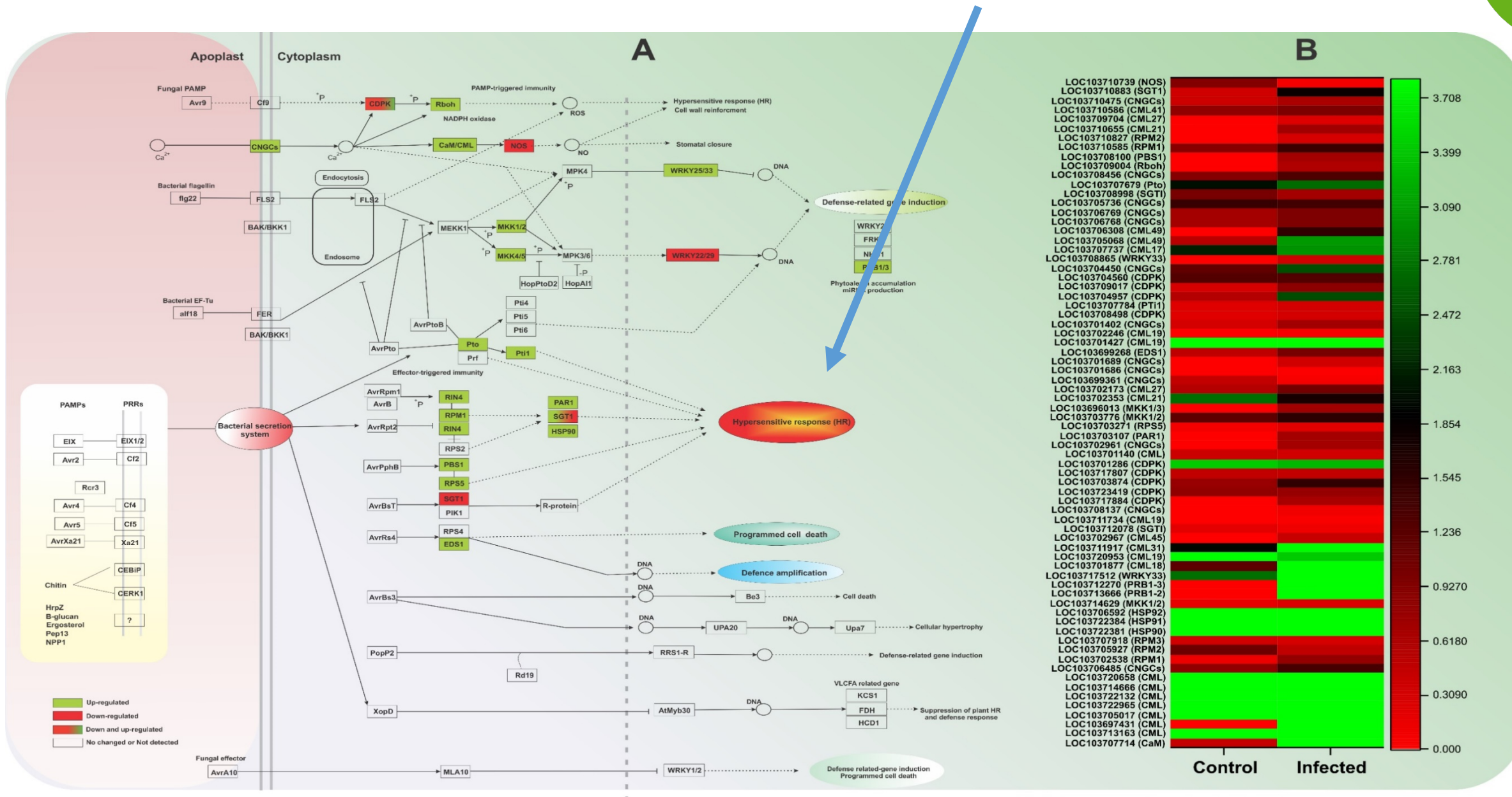
We performed **RNA-Seq** of leaf infected with or without dubas bug to understand the molecular responses of date palm seedlings. Before doing that, we noticed that dubas bug infestation significantly increase superoxide anion and malondialdehyde production to two-folds as compared to healthy control

The infection repercussions were also revealed by significantly higher contents of endogenous phytohormonal signaling of **jasmonic acid (JA)** and **salicylic acid (SA)** compared with control

Transcriptome analysis revealed upregulation of 6,919 genes and down-regulation of 2,695 genes in leaf during the infection process

In conclusion, dubas bug infection aggravated defense responses in date palm by gene networks involved in hypersensitive responses (*PAR1*, *RIN4*, *PBS1* etc.)

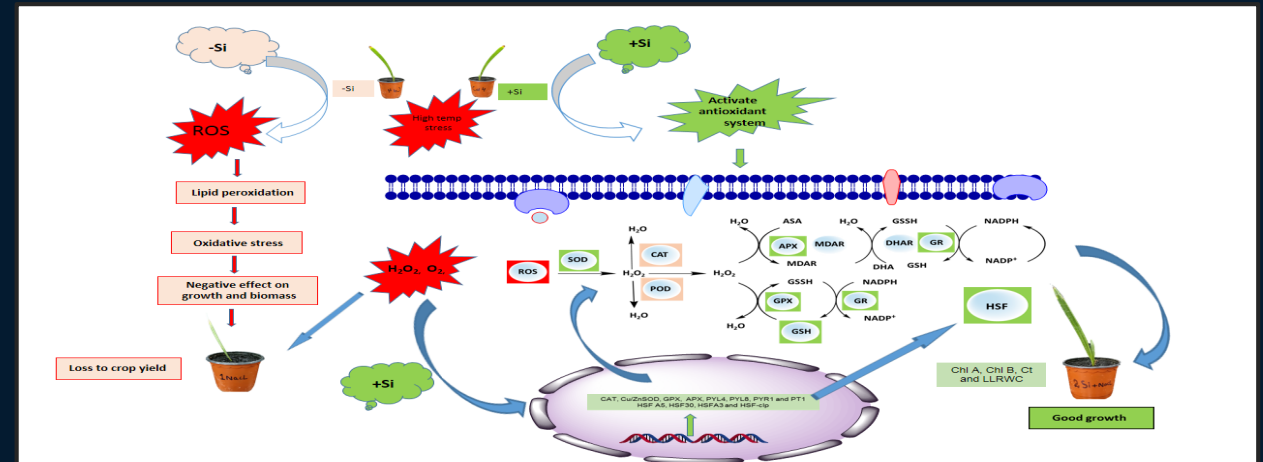
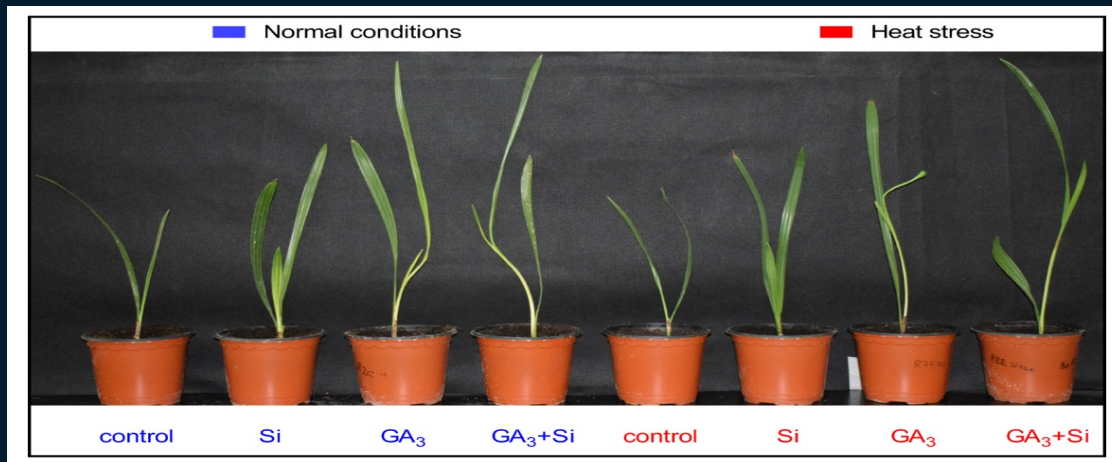
Hypersensitive responses In date palm after dubas bug infection



Investigating the integrative effects of silicon (Si) and gibberellic acid (GA₃) on date palm growth to mitigate heat stress impact:

Objectives

- ✓ Phytohormonal modulation
- ✓ Oxidative stress regulation at biochemical and molecular level
- ✓ Regulation of transcript accumulation of Heat shock Proteins (HSP) genes
- ✓ ABA related biosynthetic pathway



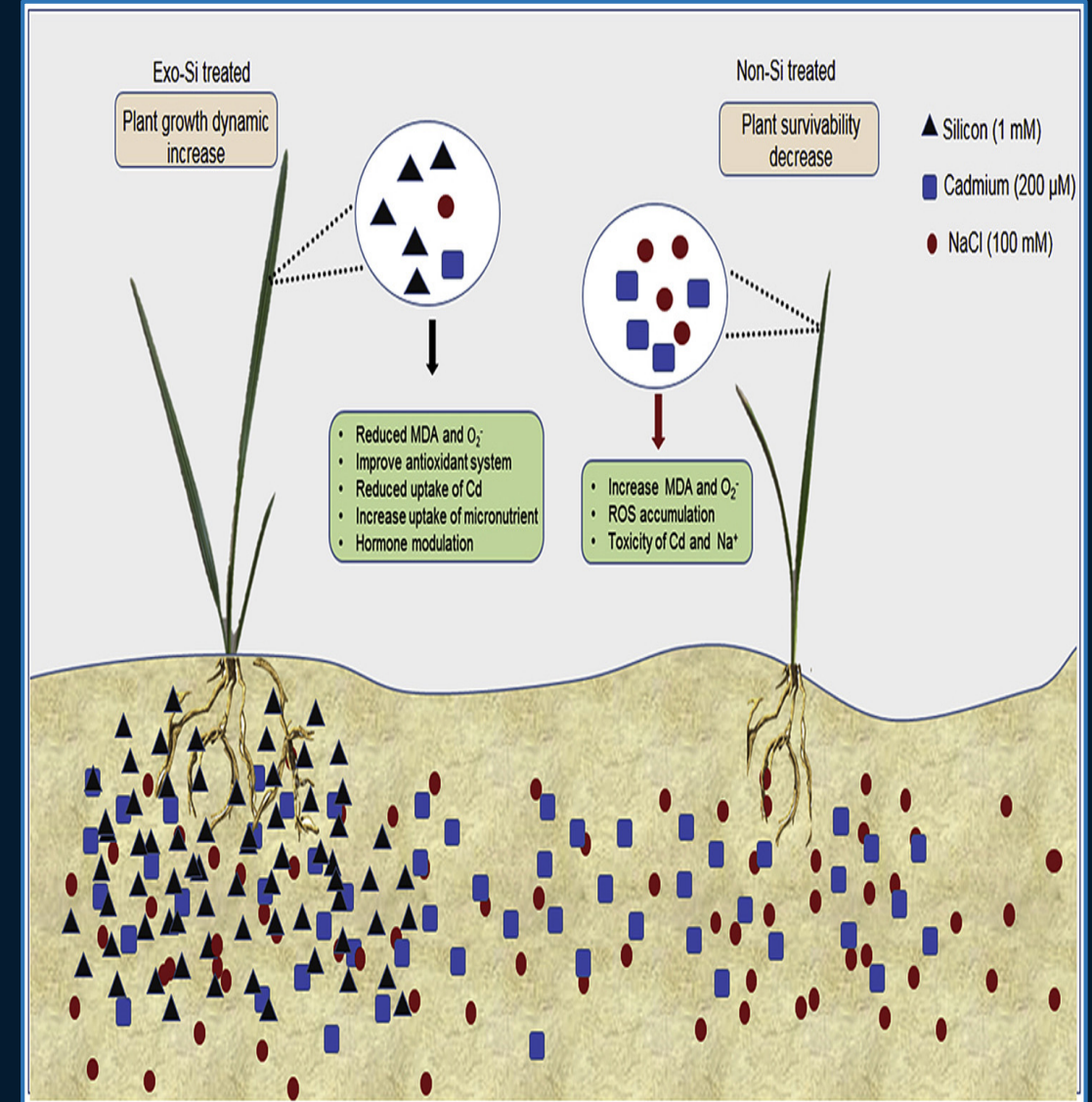
Conclusion

Exogenous GA and Si significantly activated the **heat shock transcription factors** genes, particularly *HsfA3*, and the anti-oxidative system of date palm by up-regulating the *GPX2*, *Cyt-Cu/Zn SOD*, and *CAT* transcript accumulation. interactive effects of GA and ABA influenced the hormonal cross-talk between SA and ABA by signaling-related genes (*PYL4*, *PYL8*, *PYR1*) and subsequently enhanced date palm growth and development as well as resistance to heat stress.

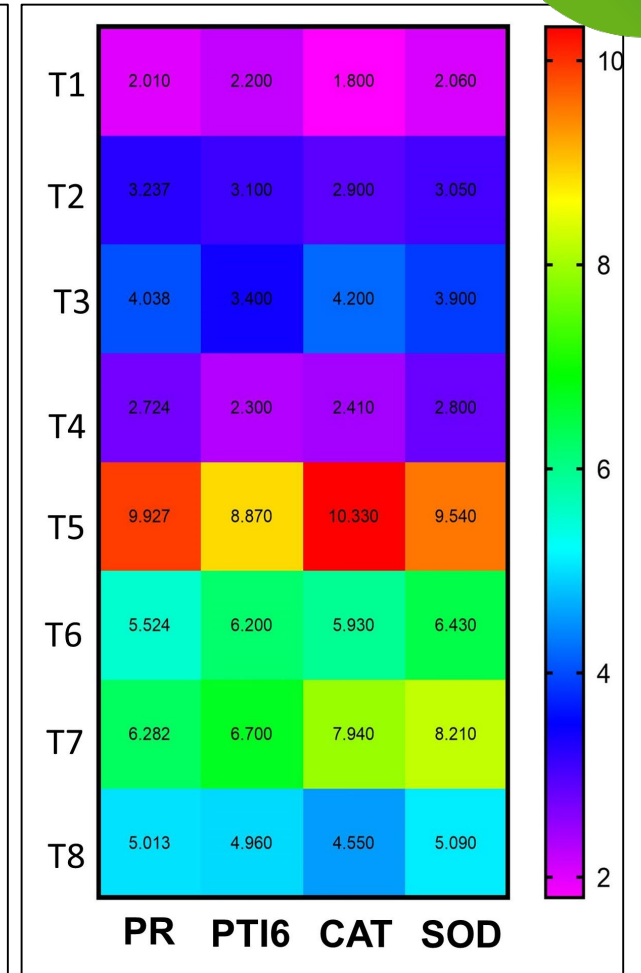
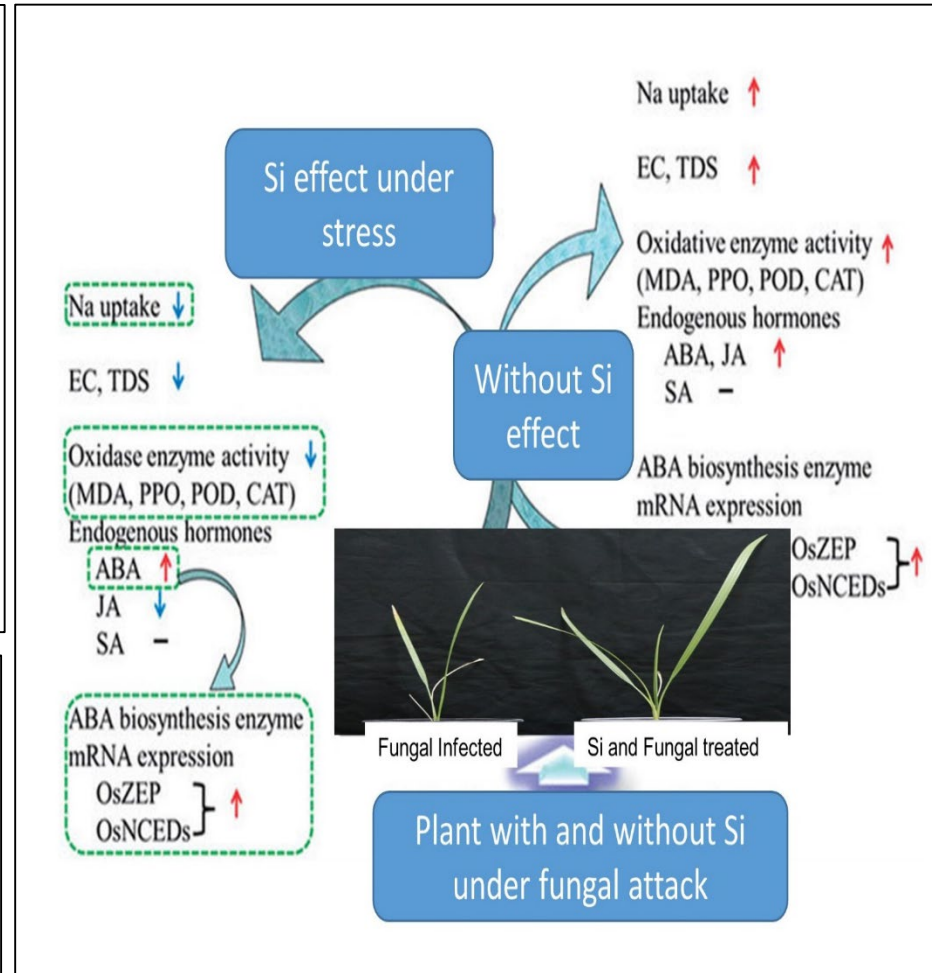
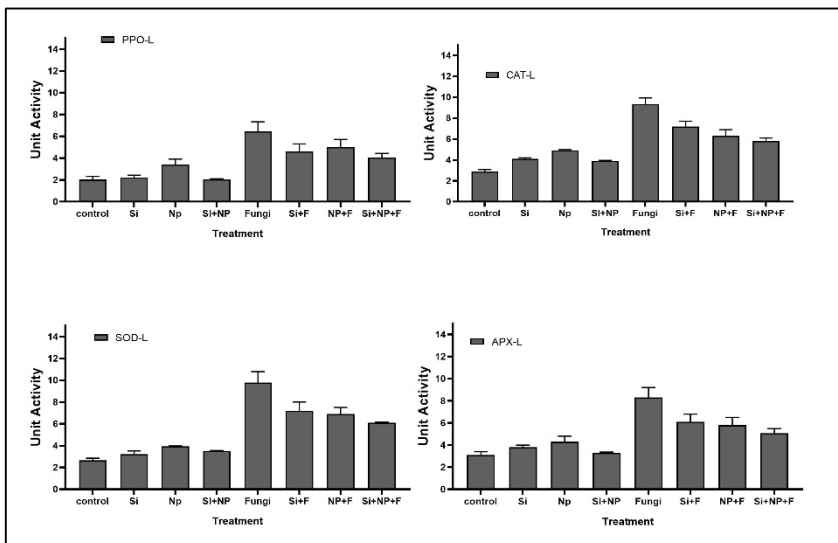
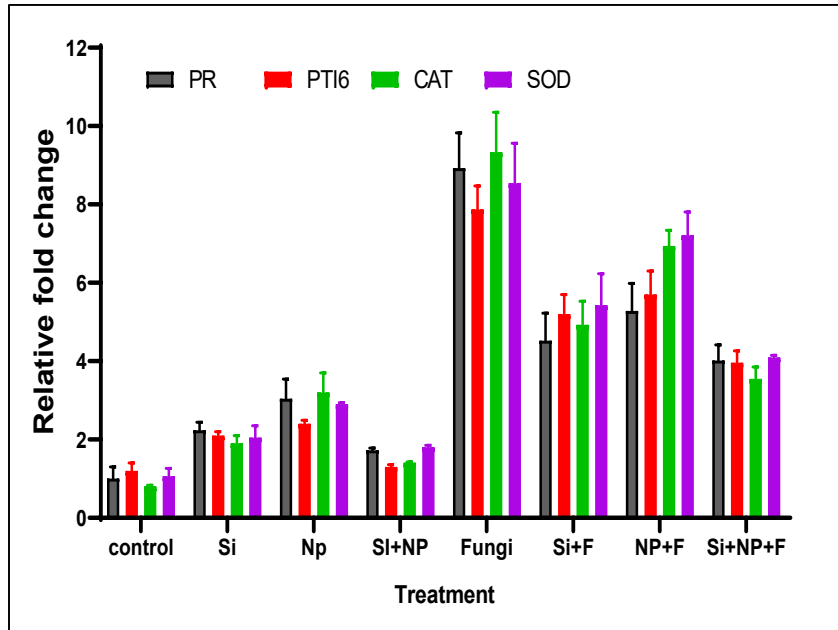
Physio-molecular effects of separate and combined cadmium and salinity stress on date palm under silicon applications

Conclusion

- ✓ Application of Si significantly enhanced macronutrient uptake
- ✓ Reduced accumulation of Cd toxicity
- ✓ Alleviated the stress-induced oxidative burst
- ✓ Down regulation of stress-related endogenous hormones (ABA, JA, SA)
- ✓ Differentially modulated stress-responsive genes (*GAPDH*, *Proline transporter 2*, *cyt Cu/Zn SOD* and *Abscisic acid receptor PYL4-like*).
- ✓ Consequently such physiological and biochemical modulation by Si under combined stresses proved to be effective strategy for enhancing date palm growth and development under metals and salinity contaminated soil



Si-mediated resistance in date palm to *Fusarium oxysporum* attack



Si treatment significantly enhanced date palm resistance to *F. Oxysporum* by modulating antioxidant defense system and stress relevant hormonal signaling.

Devising Comparative & Complementary Metabolite Annotation Strategies of Unknown Metabolite Annotation on LC-MS/MS based Metabolomics Data of Date Palm



Introduction

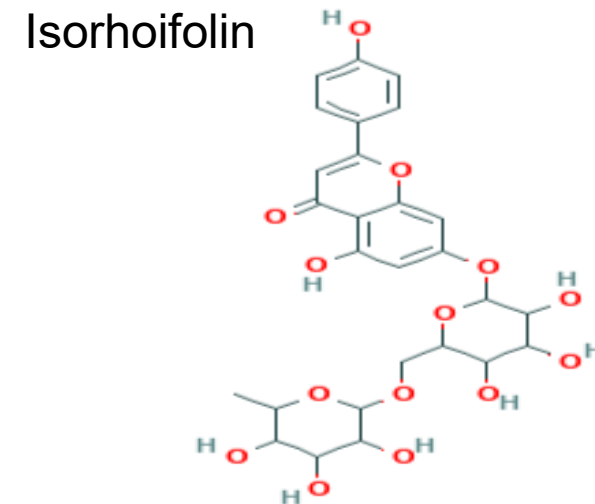
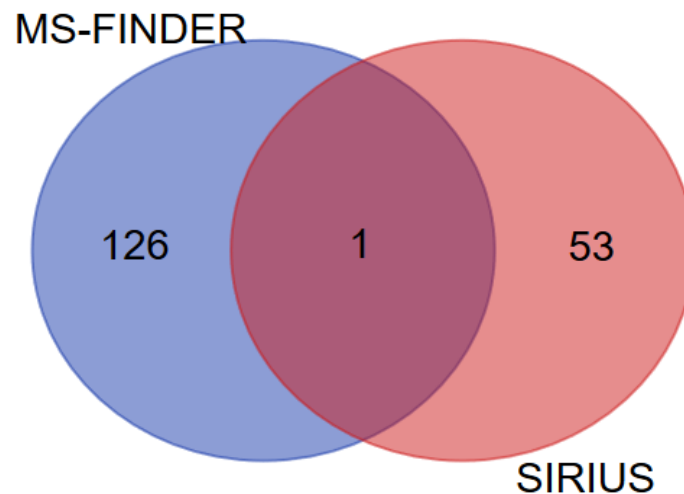
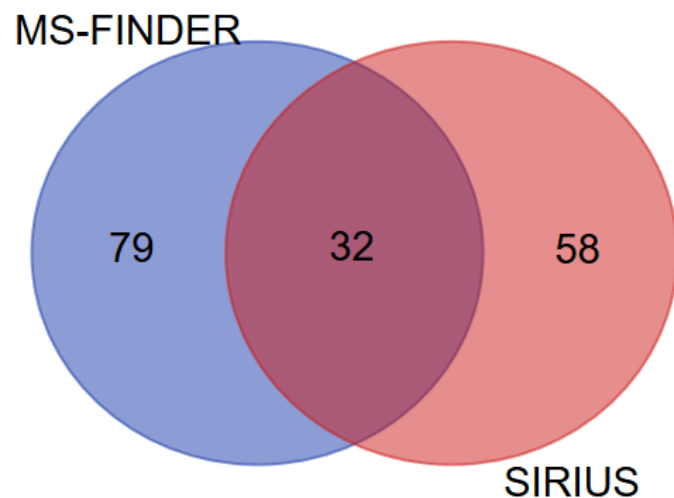
- ✓ Untargeted metabolomics datasets generated using high resolution (LC MS/MS yields only hundreds of annotations, and thousands of unknown features (i.e., defined as a unique set of m/z, intensity, and a retention time) of which only a few hundred are identifiable with accurate masses.
- ✓ Currently many unknown feature annotation strategies have evolved and offer a consortia of tools that can aid in confident identification of metabolites
- ✓ Using an example of data palm leaf Methanolic extract, we demonstrate the use of two such tools as a strategy for unknown annotation

Methodology

- ✓ Untargeted HR LC MS/MS data was acquired from date palm leaf extracts(n=3) and features were pooled for a unique set of features for this study.
- ✓ Using an Agilent 6530 LC-Q-ToF platform using a C-18 reverse phase column on an Agilent 1260 HPLC system run with flow rate of 200 μ L/min and data were acquired on positive mode only.
- ✓ Data acquisition parameters were as follows: scan range of 30-1500, scan rate of 2 spectra/sec, and collision energy for MS/MS was 10-40eV.
- ✓ The data were interrogated using open source tool MS-DIAL for spectral library matching with available open source spectra from MoNA, MassBank,GNPS.
- ✓ Compared two different tools for Unknown Feature annotation (a) **MS-FINDER** and (b) **SIRIUS** for compound identification.

Results

We observed that, out of 238 unknown features, MS-FINDER and SIRIUS aided formulae assignment of 111 and 90 features (belonging to 79 chemical ontologies), respectively, of which 32 were common to both. At the metabolite identification, MS-FINDER and SIRIUS aided annotation of 127 and 53 features, respectively, of which only a single metabolite (isorhoifolin, a 5-o-methylated flavonoid) was common to both strategies.



At the level of annotated metabolites, the single overlap was for Isorhoifolin

Conclusion

Using this comparative analysis, we demonstrated that both the in silico approaches are very complementary in unknown feature annotation, and would benefit from both tools being used for their different algorithms, databases and scoring/ filtering strategies.

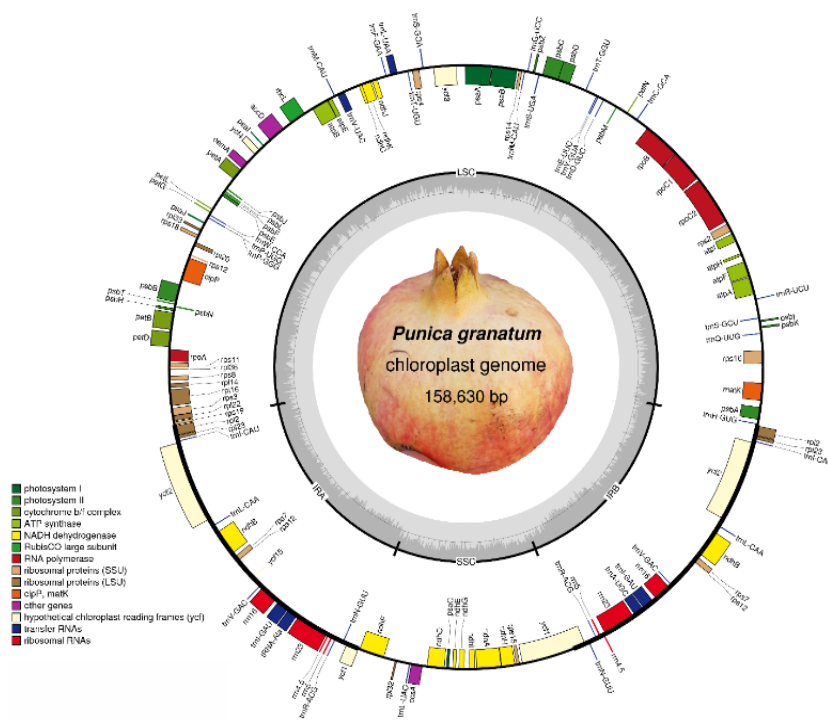


Part 3: Pomegranates trees in Oman



Pomegranate genomics

- ✓ Draft
- ✓ Chloroplast
- ✓ Mitochondrial



	P. granatum (Helow)	P. granatum	L. fauriei	L. floribun da	L. guilines s	L. indica	L. interme dia	L. speciosa	L. subcosta ta
Size (bp)	158630	158633	15244 0	152240	152193	152205	152330	152476	152049
Overall GC contents	36.9	36.9	37.6	37.6	37.6	38.5	37.6	37.6	37.6
LSC size in bp	89015	89017	83923	83967	83817	84046	83987	84051	83890
SSC size in bp	18686	18687	16933	16875	16790	16915	16873	16979	16909
IR size in bp	25466	25465	25792	25699	25793	25622	25736	25723	25625
Protein coding regions size in bp	78159	78816	81327	81045	81333	75204	81300	81309	79644
tRNA size in bp	2816	2790	2809	2742	2741	2787	2810	2742	2824
rRNA size in bp	9050	9050	9050	9044	9044	9050	9050	9046	9042
Number of genes	131	129	130	129	129	134	130	129	129
Number of protein coding genes	86	84	85	85	85	86	85	85	84
Number of rRNA	8	8	8	8	8	8	8	8	8
Number of tRNA	37	37	37	36	36	37	37	36	37
Genes with introns	11	11	11	12	13	12	13	13	13

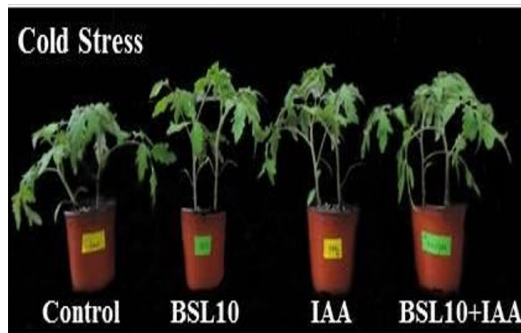
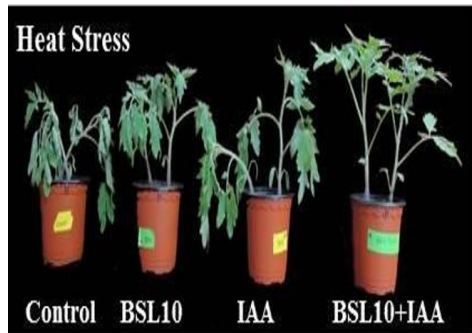
- ✓ Comparison of the *P. granatum* whole cp genome with seven Lagerstroemia species revealed an overall high degree of sequence similarity with divergence among intergenic spacers



Part 4: Tomato plant in Oman



Stress Tolerance and Plant-Microbe Interaction



Controlled environment



Drought (20% soil moisture)

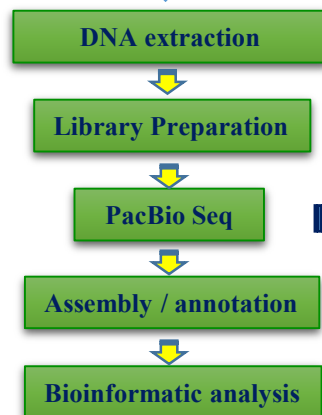
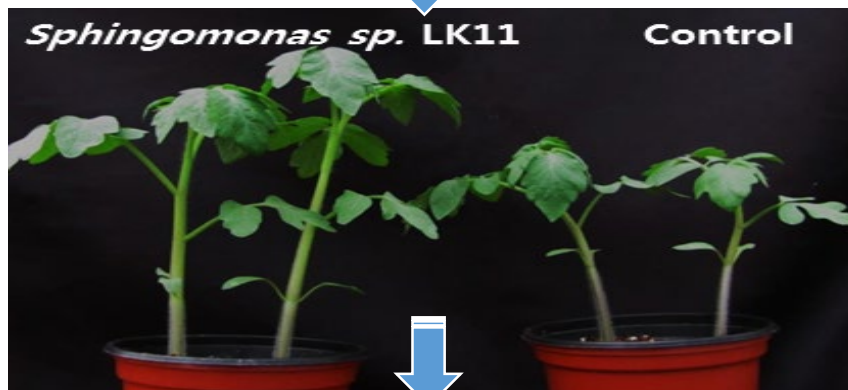
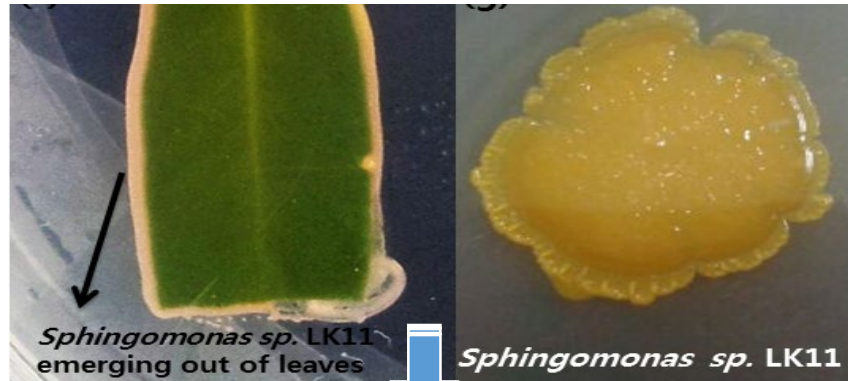
Chilling stress (5C)

Heat stress (40C)

Salinity stress (140mM)

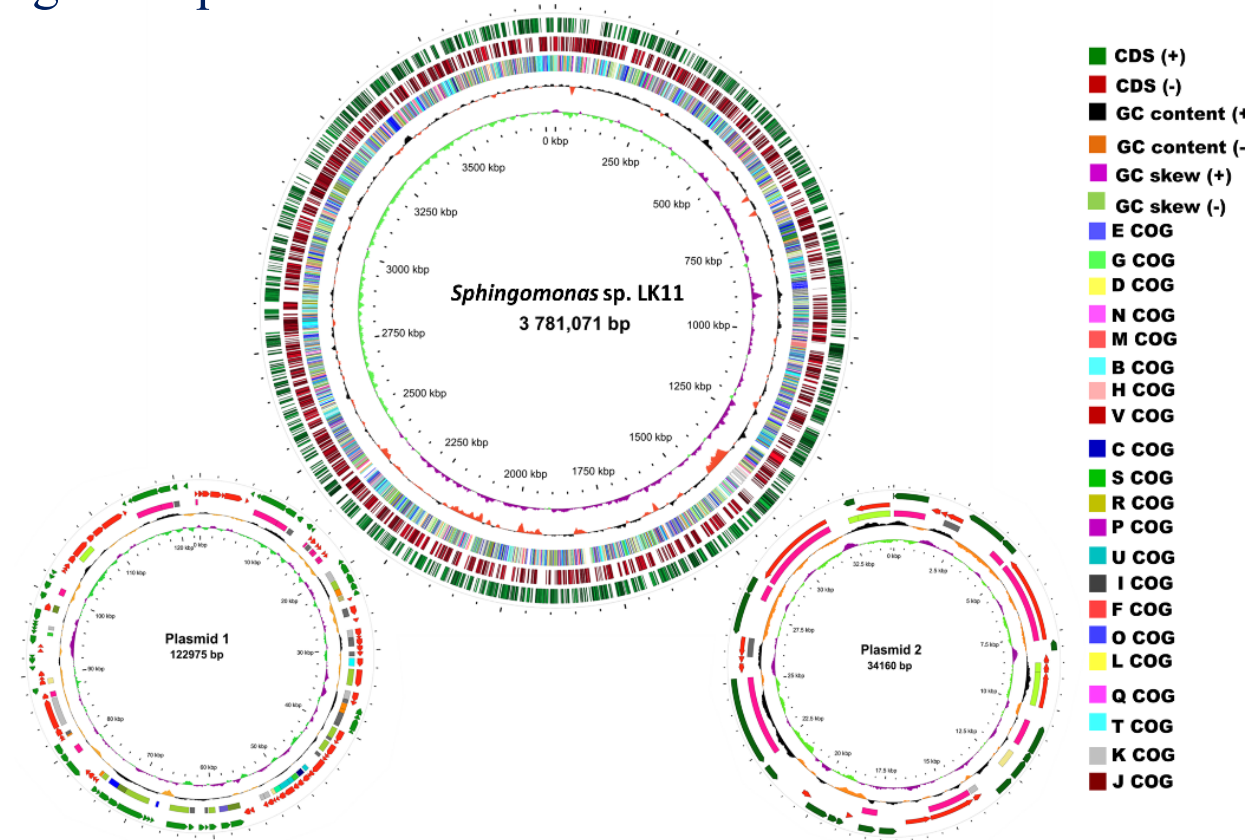
- ✓ An **endophytic fungi** isolated from *Boswellia sacra*'s leaf, showed improved tomato plant growth during heat, drought, salinity and chilling stress
- ✓ The **endophyte application** increased the activities of endogenous phytohormones SA/ABA and showed an increase in gene expression of their synthesis
- ✓ The result proved important to use this strain as plant growth promoting **fungi** at broader field trails

Bacteria from medicinal plant and effects on tomato



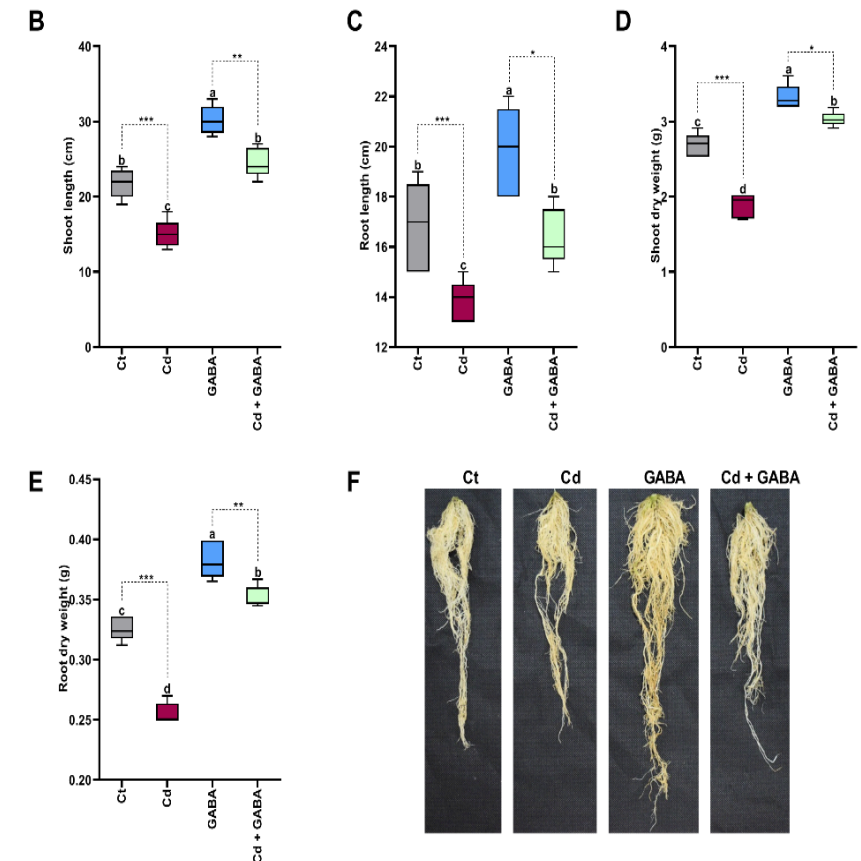
An **endophytic bacteria** isolated from arid land medicinal plant showed improved tomato plant growth during heat, drought, salinity and chilling stress

The whole **genome sequence** analysis confirmed the presence of genes related to plant growth promotion



Effect of exogenous application of GABA on uptake of Cd in tomato and increase tolerance level to heavy metal stress by regulating antioxidant enzymes and plant stress responsive hormone

- ✓ Exogenous application of GABA significantly improve tomato plant growth during cd contamination.
- ✓ The cd induced oxidative stress was significantly reduced by GABA application

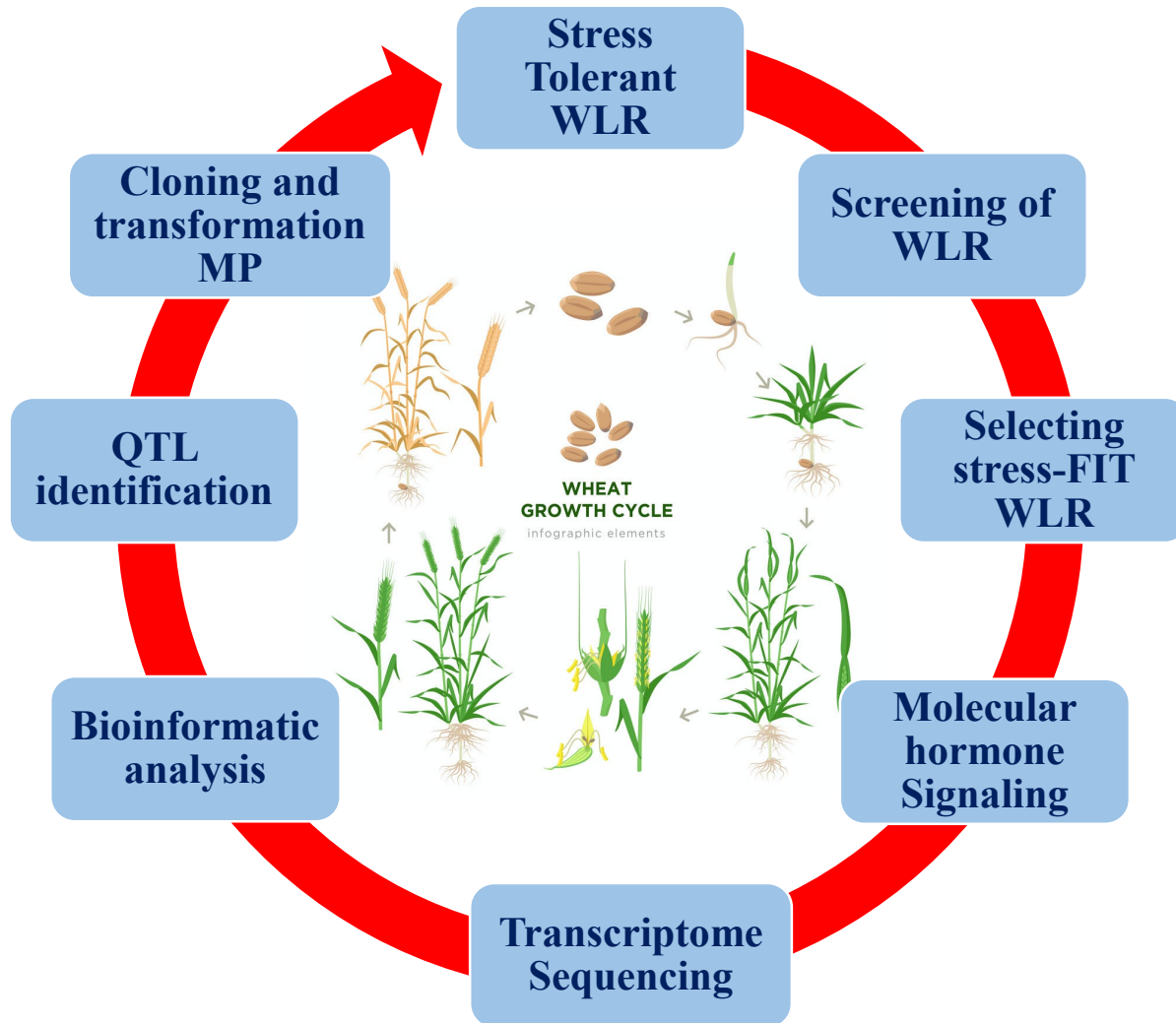




Part 5: Wheat plant in Oman

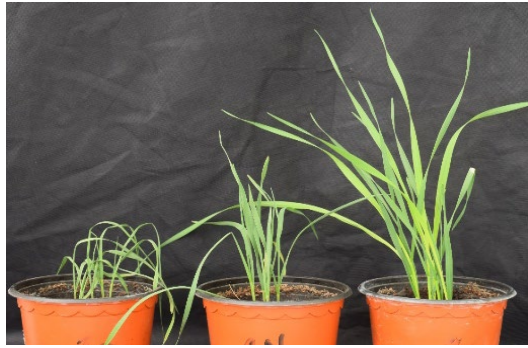


Evaluation of Omani wheat landraces against heat and drought stress tolerance through in-depth genomic approaches



- ✓ To evaluate the adaptability of selected **Omani wheat** landraces in drought and heat stress conditions and understand the physio-chemical-molecular expression patterns and their responses.
- ✓ To elucidate and understand the gene(s) responsible for enhancing drought & heat stress tolerance and performing detailed transcriptomic analysis to usher gene networks involved in **stress tolerance mechanisms**.
- ✓ To elucidate and characterize selected **QTLs** through SNP, transcriptomic analysis and characterizing the phenome for tolerant landrace using next-generation sequencing methods

Experiments In Progress...



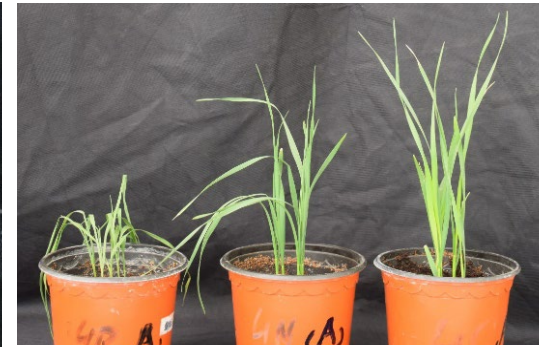
Drought

Control



Drought

Control



Drought

Control



Drought

Control



Drought

Control



Drought

Control



Drought

Control



Drought

Control



Drought

Control



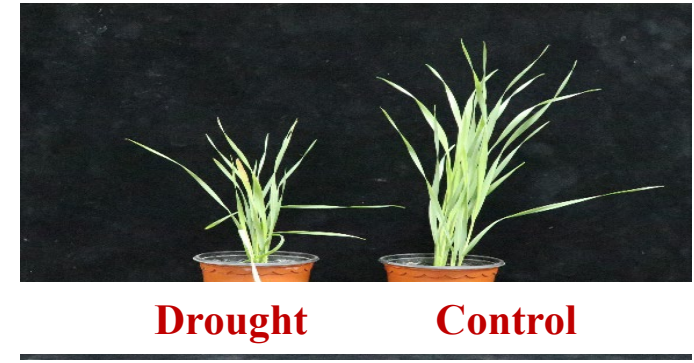
Drought

Control



Drought

Control

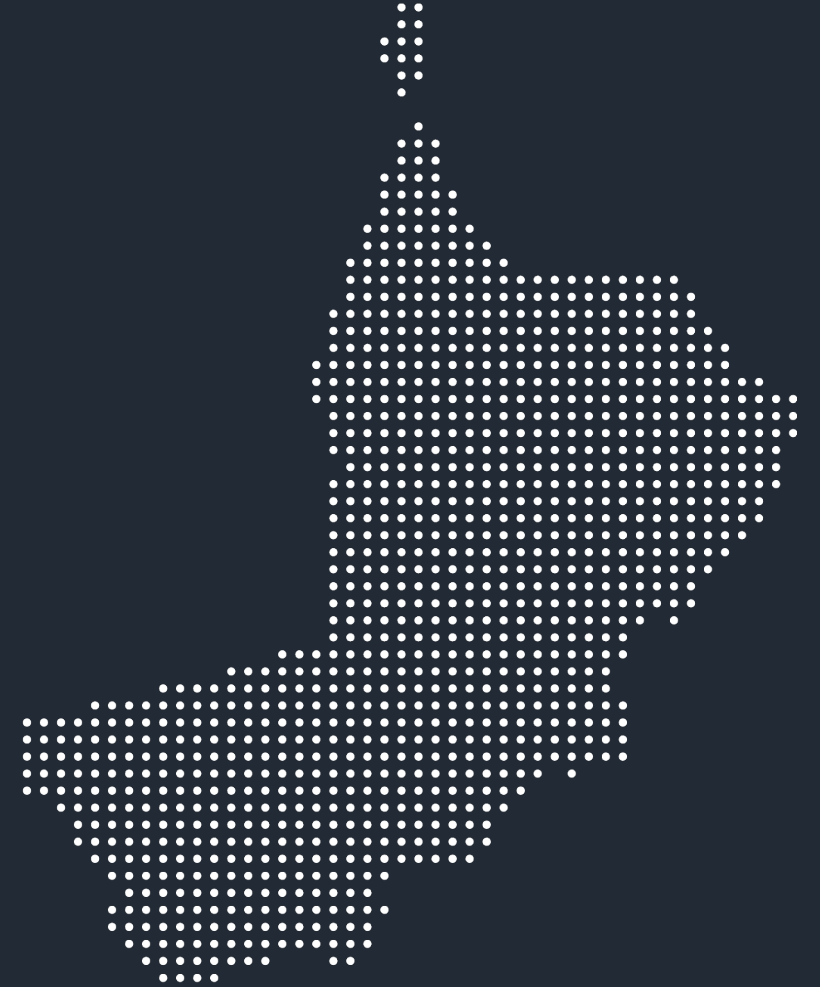


Drought

Control



Part 6: Diversity of different mangoes cultivars in Omani



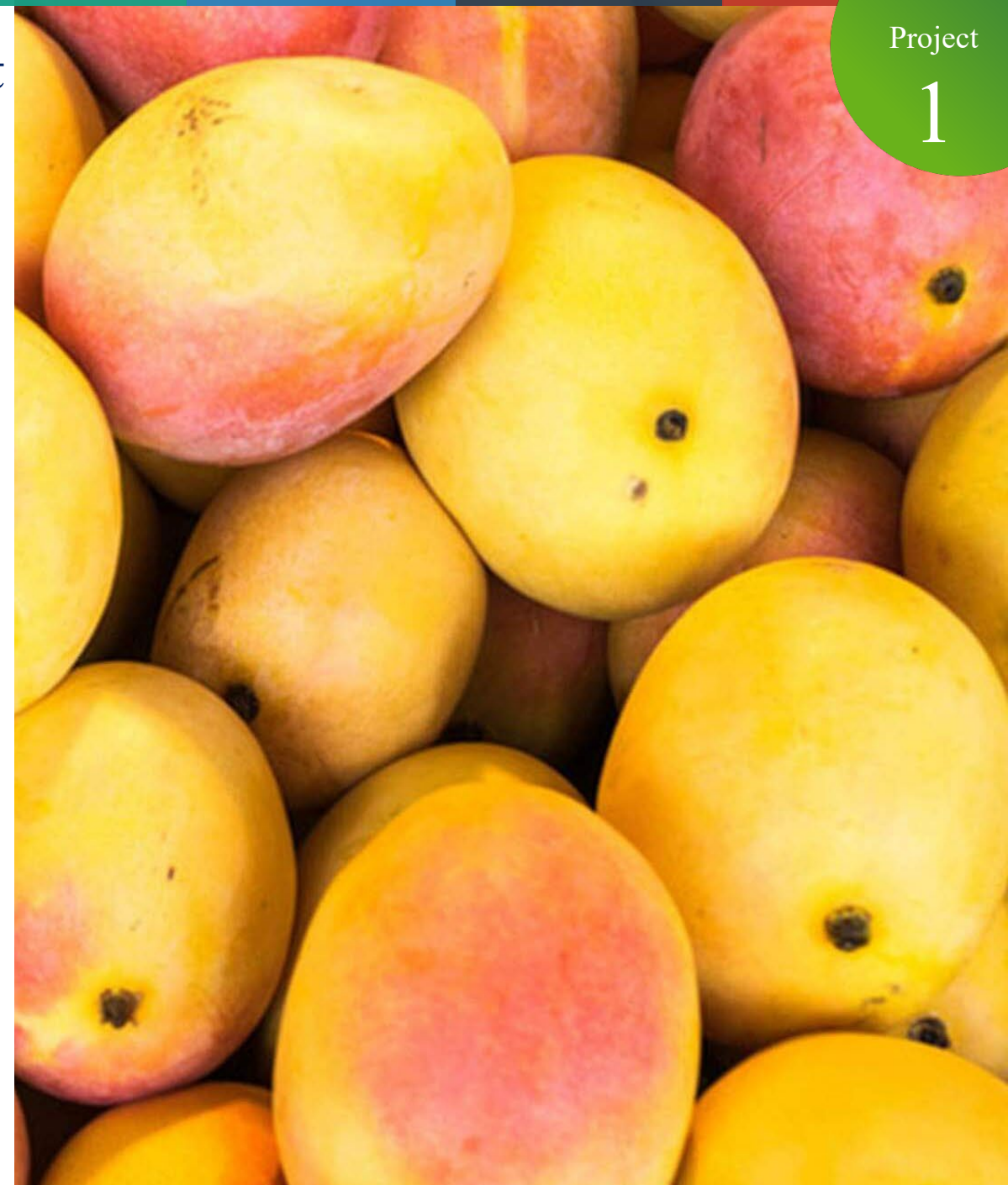
Genomic and metabolomics diversity of different Omani mangoes cultivars

Introduction

- ✓ Mango in Oman and is the third largest in production quantity after date palm and banana. The resistance to disease has led to a greater interest in studying the diversity of Omani mangoes to characterize locally grown mango. Limited Information is available on the genetic diversity or germplasm characterization of cultivated mangoes in Oman.

Objectives

- ✓ To assess variability among the Omani mangoes cultivars for different targeted and non-targeted metabolites and fruit quality traits
- ✓ To understand and map-up the metabolomic (primary and secondary) composition of all Omani cultivars of mangoes
- ✓ To establish a strategy to explore the genetic basis controlling metabolite accumulation in Omani mangoes cultivars.
- ✓ To distinguish all cultivars by mapping the essential metabolites for Sugar biosynthesis
- ✓ Characterization of significantly discriminant metabolites contributing to the spatial and phylogenetic chemodiversity.
- ✓ Genomics and Transcriptomics of various cultivars.
- ✓ Genome wide association studies among cultivars.



Sample Preparation



Tissue Harvest



Quenching
(Liquid N₂)



Extraction

Metabolomics Data Acquisition

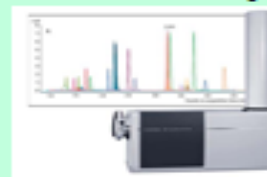
Metabolites
Extraction



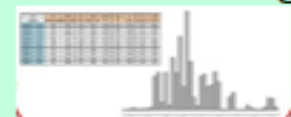
GC/LC for Metabolites
Purification



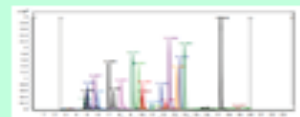
MS analysis



Data Processing



MS Data



Genomics and transcriptomics



DNA

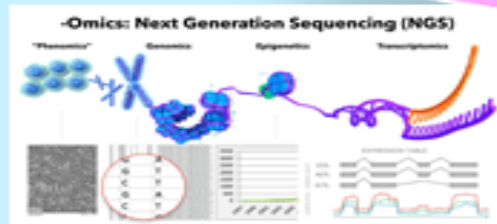
Ion S5
sequencing



Genome annotation



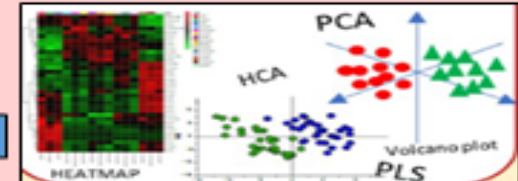
Bioinformatics



Biomarkers
Identification &
Pathway/cluster
analysis



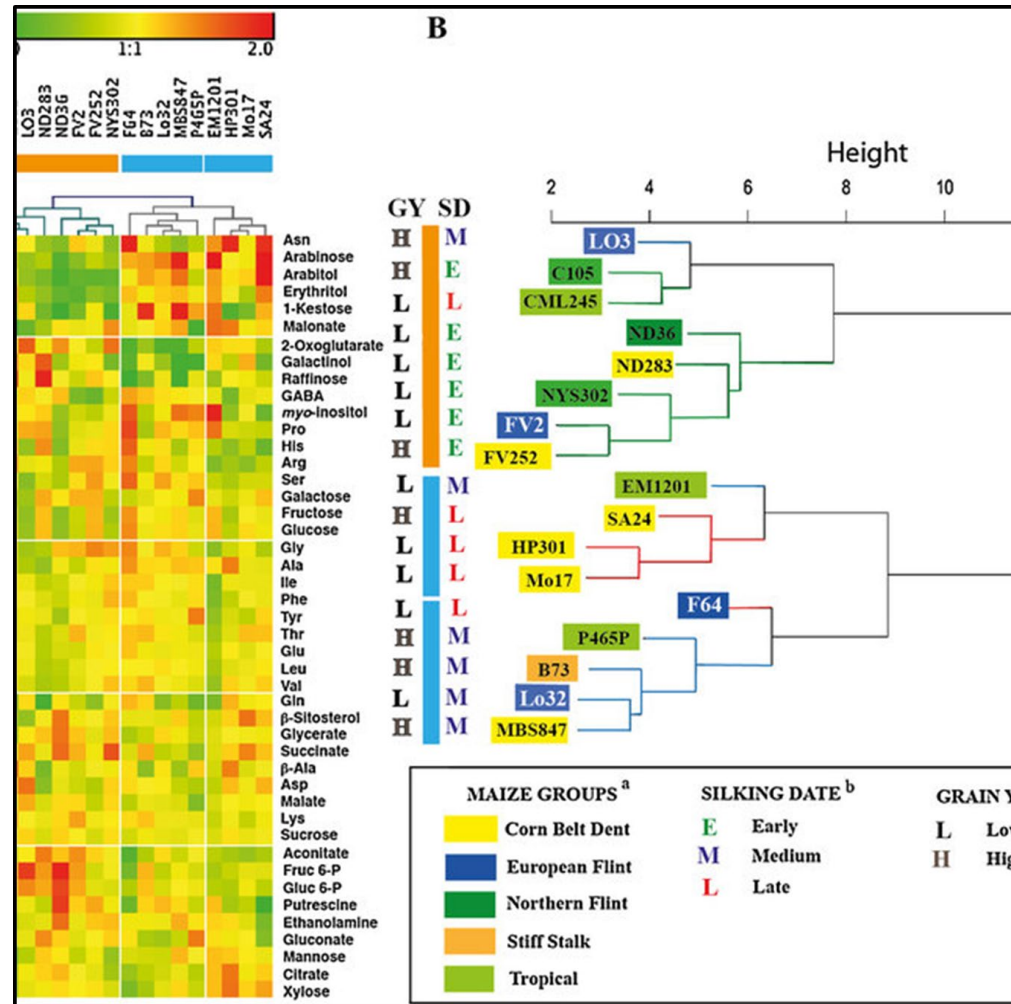
Data reduction



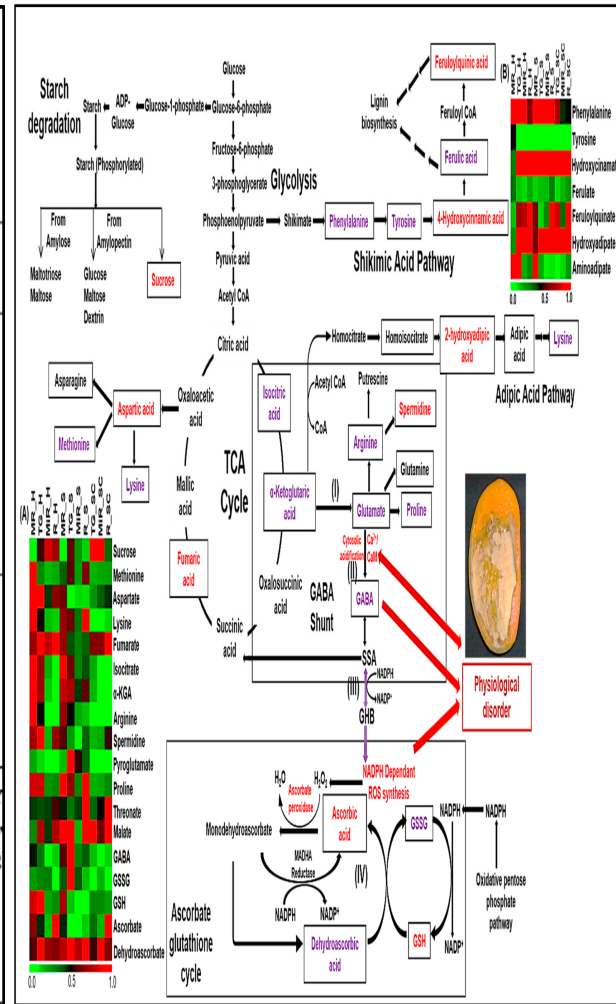
Data Analysis

Results

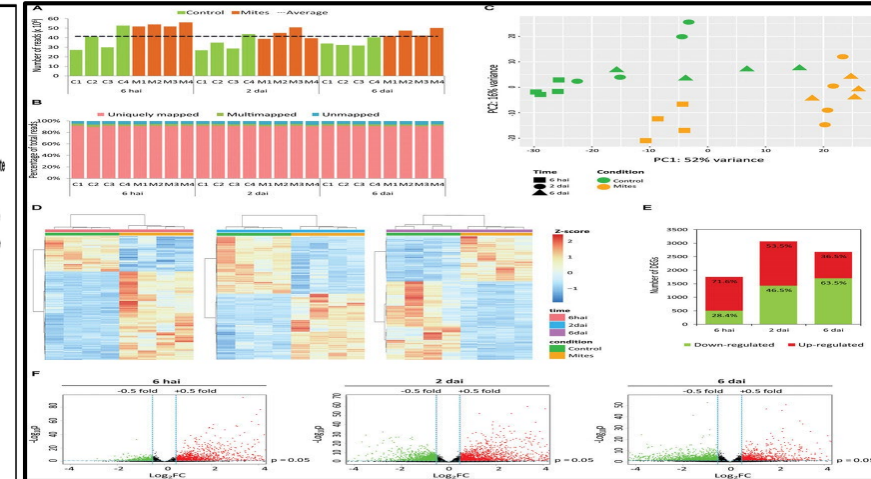
Hierarchical classification of metabolites



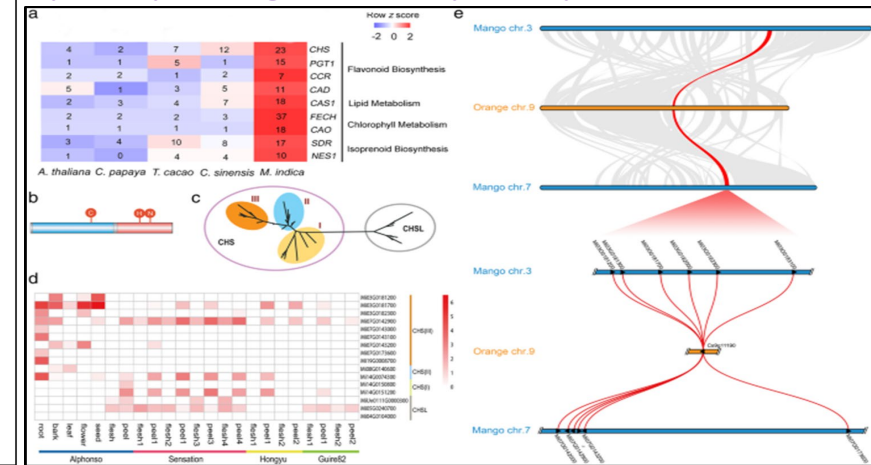
Pathway analysis



Transcriptomic analysis



Synteny and gene family analysis



**End of the
Presentation**