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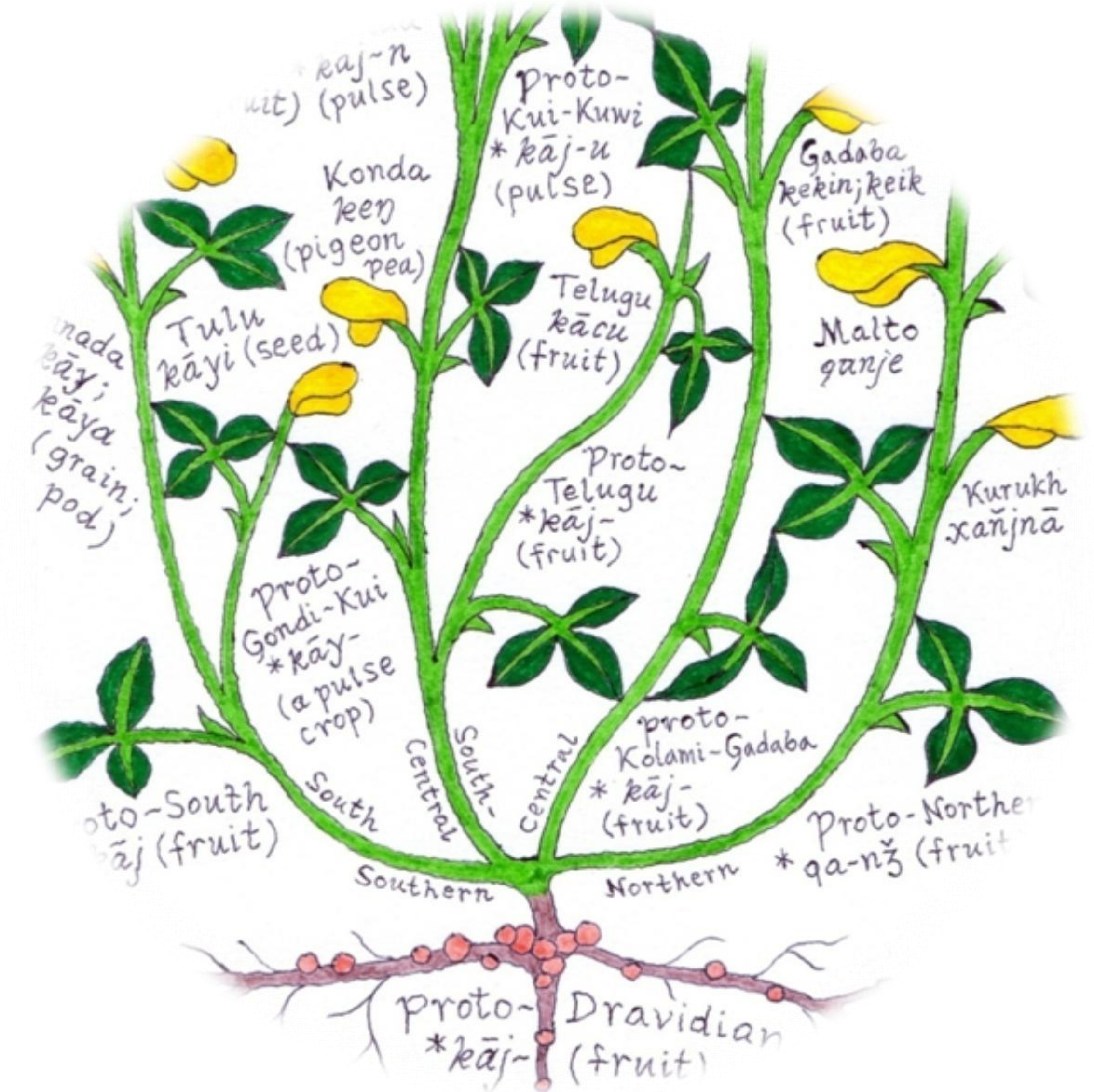

Developing a crop for the developing world

Advances in pigeonpea research

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EDITORIAL

We are pleased to present the 11th issue of Legume Perspectives devoted to pigeonpea, an important legume crop for arid and semi-arid regions of the world. The presences of diverse wild species accessions, archaeological evidences and recent studies have shown that India is the domestication centre of pigeonpea. Pigeonpea is consumed as green peas, whole grain or split peas. The seed and pod husk provides a quality feed, whereas dry branches and stems provide domestic fuel. This issue is aimed at providing information on the recent developments in pigeonpea research. This issue covered general aspects of the crop, such as origin, genomic resources, major abiotic and biotic constraints etc. We hope that the information provided here would be useful to the research community.

Thanks to all authors for their voluntary efforts and valuable contributions that have made it possible to present this 11th issue of Legume Perspectives to enrich legume society.

Rajeev K. Varshney and
Rachit K. Saxena
Managing Editors of
Legume Perspectives Issue 11

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Developing a crop for the developing world: Advances in pigeonpea research

Pigeonpea is grown in a wide range of climatic conditions with diverse maturity. It is playing a critical role in the lives of resource poor farmers in the semi-arid tropics, where it is grown for both subsistence and commercial use. However, frequent occurrence of diseases and pest outbreak and variable rainfall together with poor management practices drastically slowed down the pace of pigeonpea improvement. Pigeonpea is a unique legume crop with partial outcrossing nature. It allows implementation of promising hybrid breeding technology for breaking the yield plateau in pigeonpea. At present a number of commercial hybrids have been released with yield advantages of 30% - 50%. To strengthen the pigeonpea improvement program, plenty of modern tools and technologies such as draft genome sequence, candidate genes and improved genetic engineering methodologies etc. are now available. This is high time to move forward more vigorously with backing of new technologies to overcome the present constraints and breed new cultivars at rapid pace that will benefit poor farmers in developing world.

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Historical and phylogenetic perspectives of pigeonpea

by Mulualem T. KASSA[1], L. Jos G. VAN DER MAESEN[2], Christopher KRIEG[3, 4] and
Eric J. B. von WETTBERG[4*]

Abstract: Pigeonpea is an important staple crop across wide portions of the semi-arid tropics from Southern, Eastern and Southeast Asia, to much of Africa, and across the tropical Americas. It has a wide distribution that spans diverse environmental conditions, documented resistance to a variety of biotic and abiotic stresses, and 34 species of wild relatives within the genus. Pigeonpea could benefit greatly from molecular information to help improve yields and agronomic characteristics. Here we provide a perspective on the history, phylogeny, and domestication of pigeonpea.

Key words: crop wild relatives, domestication, pigeonpea, stress resistance, taxonomy

Introduction

Cajanus cajan (L.) Millsp. ($2n = 22$ and a genome size of 808 Mbp) or pigeonpea, is a short-lived perennial shrub that is an adaptable and globally important pulse crop with high levels of abiotic and biotic stress resistance (Fig. 1). It is grown on 4.92 million ha in primarily the semi-arid tropics and subtropics of south Asia (mainly on the Indian-subcontinent), as well as Africa, the Caribbean, Central and South America. Among these regions, 4.67 million t of pigeonpea were produced in 2013, with an average productivity of 750.97 kg ha^{-1} (2). It is a critical source of protein in the diets of many in the semi-arid tropics of Asia, Africa, and the Americas.

Pigeonpea grows in a wide range of edaphic and climatic conditions, making it well-suited to succeed in a variety of agricultural systems. Furthermore, productivity and yield can be significantly improved when molecular breeding strategies utilize genetic material in the world's existing wild and landrace populations (7). Pigeonpea belongs to the genus *Cajanus* Adans. which comprises between 32 and 34 species (16, 17). Most of these species are endemic to either Southern/South-eastern Asia or Australia (3). Among these, 16 *Cajanus* species occur in Asia (8 of which are endemic to India), 15 species in Australia (of which 13 are endemic), one species of *Cajanus* is confined to West Africa and 2 species (including *C. cajan*) are widespread throughout the tropics (Fig. 2). Taxonomic review of the subtribe Cajaninae (15) included 10 genera and about 495 species. The ten genera are *Adenodolichos* (bewteen 15 and 20 spp.), *Bolusafra* (1 sp.), *Cajanus* (34 spp.), *Carrissoa* (1 sp.), *Chrysoscias* (3 or 4 spp.), *Dunbaria* (20 spp.), *Eriosema* (150 spp.), *Flemingia* (between 30 and 35 spp.), *Paracalyx* (6 spp.) and *Rhynchosia* (230 spp.).

History of taxonomic placement

The taxonomy of *Cajanus* and related genera of the Cajaninae have been extensively studied by morphological, alpha taxonomic, and molecular approaches (9, 16). Using morphological and ecological

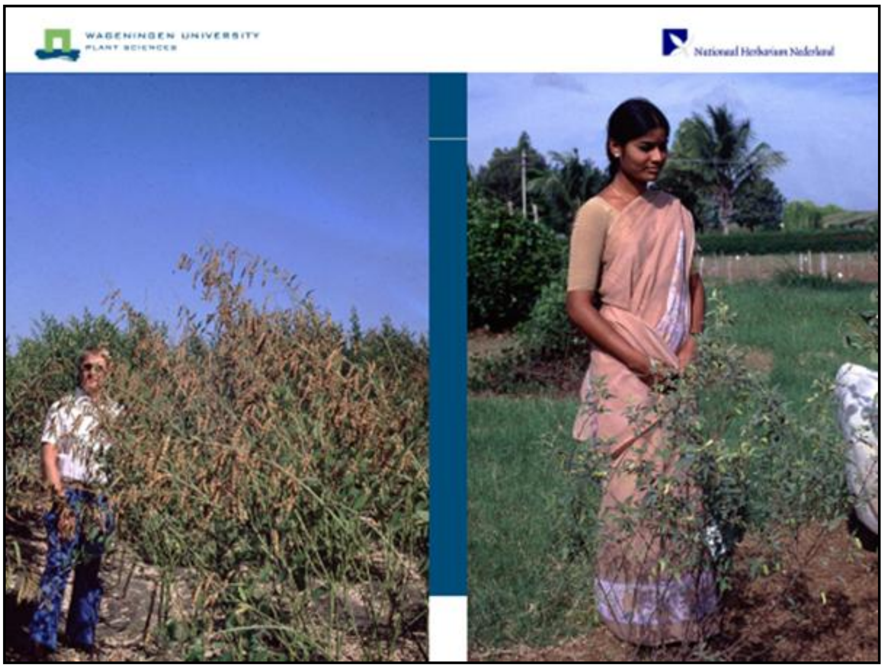

Figure 1. Growth form and habitat of cultivated pigeonpea, *Cajanus cajan* (left) and hybrid *C. cajan* × *C. trinervius* (right); used with permission from Naturalis Biodiversity Center, Botany Department, the Netherlands

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Figure 2. Images if *Cajanus lanceolatus* and *C. latisepalus*, two wild relatives of pigeonpea that vary in leaf traits and ecological distribution; used with permission from the National Herbarium of the Netherlands

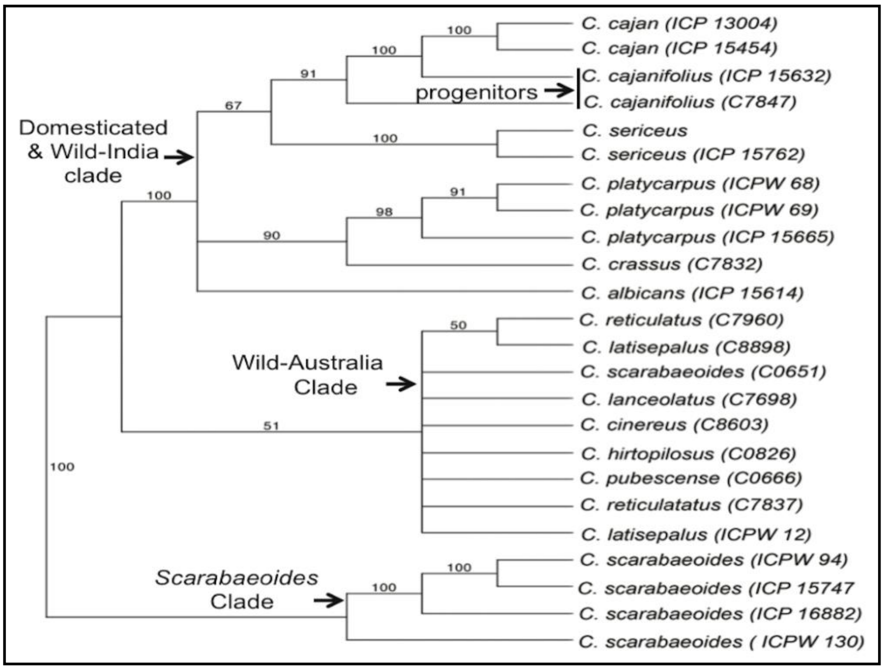

Figure 3. Phylogeny of *Cajanus* species depicted as a 50% majority rule consensus tree, reproduced with permission from (6); tree topology was inferred with maximum parsimony via heuristic searches among 1000 trees using 752 single nucleotide polymorphisms (SNPs) derived from 670 low copy orthologous genes and assayed with an Illumina Golden Gate assay; numbers above branches indicate bootstrap support (0.50%); the vertical bar indicates the putative progenitor species (two *C. cajanifolius* accessions); tree length = 2145, consistency index (CI) = 0.638, and retention index (RI) = 0.837; the Bootstrap support for the sister relationship between wild-Australia and wild-India clades (in the absence of the two *C. cajan* accessions) is 100% (data not shown)

characters such as habit, leaf structure, hairiness, pod size, strophiole characters and other traits, van der Maesen (16) grouped the genus *Cajanus* into six sections: Cajanus (2 species), Atylia Benth. (7 species), Fruticosa Maesen (9 species), Cantharospermum (Wight & Arn.) Benth. (6 species), Volubilis Maesen (6 species) and Rhynchosoides Benth. (4 species). Species in sections Cajanus, Atylia and Fruticosa have erect growth habit, Cantharospermum, and Volubilis are climbing and creeping, and Rhynchosoides contains trailing species. Three *Cajanus* species have been further subdivided into botanical varieties; *C. scarabaeoides* into var. *pedunculatus* and var. *scarabaeoides*, *C. reticulatus* into var. *grandifolius*, var. *reticulatus*, and var. *maritimus*, and *C. volubilis* into var. *burmanicus* and var. *volubilis* (16). Assessment of diversity using seed protein markers (10) reaffirmed the morphology-based groupings, such as section Cajanus (*C. cajanifolius* and *C. cajan*), while RFLP studies have been inconclusive. Recent studies using sequence data from the nuclear ribosomal Internal Transcribed Spacer (ITS) and the cpDNA (trnL-F spacer) were conducted to understand the evolutionary history and phylogenetic relationships of *Cajanus* Adans. and allied genera in the subtribe Cajaninae. The study has resolved the phylogenetic relationships of *Cajanus* and related genera in the tribe Cajaninae. In this study, *Cajanus* was not monophyletic as currently circumscribed, as species of *Dunbaria* and elements of *Rhynchosia* were nested within the *Cajanus* clade. In fact, in a taxonomic revision of *Dunbaria*, van der Maesen (14) found that some species of *Dunbaria* showed the facies of climbing *Cajanus* and suggested the possibility of placing *Dunbaria* in a secondary or tertiary genepool of cultivated pigeonpea. Future taxonomic revision and generic delimitation of *Cajanus* is warranted.

Pigeonpea is the only cultivated member of the genus, while the remaining species (all wild relatives) belong to the secondary or tertiary levels based on the gene pool concept of Harlan and De Wet (4), which is based on the genetic crossability and exchange of genetic material between the crop and the wild relatives. In pigeonpea, the allied wild *Cajanus* species belong to the secondary genepool while most Cajaninae genera belong to the tertiary genepool (15).

Pigeonpea domestication and constraints imposed by genetic bottlenecks

Recent molecular studies using several hundred genome-wide single nucleotide polymorphisms developed for Illumina's GoldenGate assay have shed new light on the domestication of pigeonpea (6, 12; Fig. 3). These studies confirm that *Cajanus cajanifolius* is the progenitor of cultivated pigeonpea, and that domestication occurred in central India. Previous taxonomic studies provided the bulk of evidence supporting of an Indian origin (1, 11, 13). This taxonomic and molecular evidence complements archaeological evidence of 4,000 year old pigeonpea remains in central India (5). Existing landrace and wild collections of both pigeonpea and *C. cajanifolius* are insufficiently numerous to accurately place domestication within India, although Andhra Pradesh, Madhya Pradesh and Maharashtra are likely candidates in the center of the Indian subcontinent (12). Further collections of both *C. cajanifolius* as well as pigeonpea landraces with more accurate passport data would continue to expand the genetic base of germplasm, and allow more in-depth analysis of the process and spatial pattern of domestication. Secondary centers of diversification for pigeonpea include East Africa, the tropical Americas, and the Philippines (6).

Conclusions and future directions

Domestication was critical for fixing traits in crops such as indehiscent seed pods and upright growth habit. In pigeonpea, the domestication is somewhat incomplete, as early dehiscent seeds remain an unwanted property. Better understanding the phenotypic consequences of the selection pressures of domestication could improve breeding efforts, and guide efforts to use wild germplasm effectively (18). In particular, we see the enormous eco-geographical range covered by *Cajanus* species in the tertiary gene pool from Australia as an untapped reserve of adaptive potential. With a better understanding of evolutionary relationships in *Cajanus* and new wild relative collections, strategies can be developed to utilize the adaptive value of that variation in breeding programs (18).

Acknowledgements

We thank Rachit Saxena and Rajeev Varshney for encouraging work on domestication and wild relative diversity. The domestication work of C. K. and E. v. W. is supported by US NSF-PGRP 13-39346.

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Pigeonpea - A unique jewel in rainfed cropping systems

by Chanda V. SAMEER KUMAR[1]*, Indra P. SINGH[2], Ravikoti VIJAYKUMAR[1], Suyash B. PATIL[1], Revathi TATHINENI[1], Myer G. MULA[1], Rachit K. Saxena[1], Anupama J. HINGANE[1], Abhisek RATHORE[1], Ch. Ravinder REDDY[1], Mallela NAGESH KUMAR[3], Chourat SUDHAKAR[3] and Rajeev K. VARSHNEY[1]

Abstract: Pigeonpea is a crop for rainfed environments endowed with several features to thrive harsh climate. It adapts well in sole crop and inter cropped conditions (with cereals, millets, oils seeds and pulses) by enhancing the system productivity and net income to the small and marginal farmers across the globe. The range of maturity duration in the crop allows it to grow in diversified cropping systems and patterns in varied ecoregions of the world. Development of cytoplasmic male sterility based hybrids provided an opportunity for enhancing the yields under marginal environments. With recent interventions in addressing the photo sensitivity and maturity have led to evolving super early varieties with less than 100 days duration, provided a scope for horizontal expansion of the crop in different agro ecological systems.

Key words: cropping systems, pigeonpea, rainfed

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is an important legume crop of the semi-arid tropics of Asia and eastern and southern Africa. Due to its high protein (21% - 25%) (5), it complements cereals for a balanced diet. Pigeonpea has multiple uses, its dry split pea used as dhal, green seeds and pods can be consumed as vegetable. This is ideal crop for sustainable agriculture as it fixes atmospheric nitrogen and releases bound phosphorous in the soil to available form. Because of its deep (3 m - 4 m) root system can thrive low moisture conditions and also helps to improve soil structural and physical properties. It also plays a greater role in control of soil erosion (1).

Crop duration

Pigeonpea landraces and cultivars have wide range for maturity duration from 90 days to 300 days. The crop can be classified in to eleven district maturity groups (Table 1) based on days to attain flowering and maturity (7). Temperature, photo and thermo period sensitivity greatly influence the specificity of adaptation of pigeonpea cultivars in different ecoregions of the globe. This has given scope for the cultivation of the crop in early, medium and late maturing groups across the world. Agro ecological cropping patterns decide the sole crop/ inter cropped situations in pigeonpea. Majority of the area of the crop falls under medium duration (from 160 days to 180 days) and limited area under early (between 120 and 140 days) and long duration (> 210 days).

Cropping systems

Owing to variable climate (vagaries in rainfall pattern and distribution) in rain-fed situations (6), pigeonpea has become a crop of minimum assurance to the small holder farmers of subsistence agriculture. It is an integral component of various rainfed cropping situations and the system productivity under inter-cropping provides assured income to the farmers. The unique cropping systems of pigeonpea are briefly presented in the next paragraphs.

Table 1. Major pigeonpea maturity groups, ICRISAT, Patancheru, Telangana, India

Maturity group	Maturity classification	Days to 50% flowering	Reference cultivars
00	Super-early	< 50	MN5
0	Extra-short	51-60	ICPL 88039
I	Extra-short	61-70	Prabhat
II	Short	71-80	UPAS 120 and ICPL 87
III	Short	81-90	Pusa Ageti and T 21
IV	Short	91-100	ICP 6
V	Short-medium	101-110	BDN 1 and Maruti
VI	Medium	111-130	Asha
VII	Medium	131-140	ICP 7035
VIII	Medium-long	141-160	ICP 7065 and Bahar
IX	Long	> 160	NP (WR) 15 and MAL 13

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Figure 1. Pigeonpea + soybean followed by wheat (after harvesting soybean rows)

Figure 2. Cotton + pigeonpea intercropping system (10:1 ratio)

Figure 3. Super early pigeonpea

1) *Sole crop*. About 20% of farmers prefer sole crop of pigeonpea particularly in sandy loams and medium to heavy clay soils. Under intensive cultivation with better adoption of integrated crop management technologies farmers are realizing 2 t ha^{-1} to 2.5 t ha^{-1}. This system also created avenues for innovative interventions like transplanting (with drip irrigation) by which the full exploitation of genetic yield potential (up to 4 t ha^{-1}) of the varieties and hybrids was achieved.

2) *Intercropping*. Majority of the area of pigeonpea falls under this category where in sorghum (*Sorghum bicolor* (L.) Moench), maize (*Zea mays* L.), cotton (*Gossypium hirsutum* L.), soybean (*Glycine max* (L.) Merr.), sunflower (*Helianthus annuus* L.), castor (*Ricinus communis* L.) and other cultivated species are intercropped (Fig. 1 and Fig. 2). In rainfed areas of semi-arid tropics pigeonpea as integral component of the cropping systems provides farmers additional income from the unit land and it also serves as insurance by providing some income under vagaries of monsoon particularly drought. Pigeonpea synergizes well with majority of the crops by enhancing system productivity and cost benefit ratio in small and marginal farming situations.

3) *Pigeonpea-wheat rotation*. Development of early duration varieties which mature in 120 days (ICPL 88039) has given scope for pigeonpea followed by wheat cropping system in north western areas of India. It has led to replacement of cereal-cereal cropping system which is not environmentally sustainable in long run (4).

4) *Rice-fallows*. Development of super early varieties which mature in less than 100 days, has addressed the issue of photo and thermo period sensitivity and specificity of adaptation in the crop (Fig. 3). These super early varieties are day neutral and photo insensitive and can be grown in any part of the year. There is tremendous potential to explore the non-traditional areas and new niches like proceeding rice fallow situations for cultivation of pigeonpea. Efforts are in progress to develop suitable agronomic package under zero tillage conditions. Presently rice fallow areas are increasingly occupied by maize and sorghum crops. This is not long term soil sustainable system owing to nutrient mining from the cereal-cereal cropping.

5) *High-altitudes*. This is an opportunity for extending pigeonpea cultivation to new niches. Photo insensitive cultivars have shown adaptation to latitudes ranging from the equator (Kenya) to 46°N(Prosser, USA) and 45°S in New Zealand. Pigeonpea cultivars ICPLs 85010, 85030 and 83105 produced 1.5 t ha^{-1} - 2.5 t ha^{-1} grain yield at Prosser (3). In china also the medium-duration varieties like ICP 7035 and ICPL 87119 were exhibited better performance in slopes of the hills.

6) *Post-rainy pigeonpea*. The post-rainy season pigeonpea is more beneficial than is rainy season crop in the coastal areas of South India (2). The variety ICPL 85063 has been released for cultivation post-rainy season and this variety produced up to 3500 kg ha^{-1} yield and farmers can intercrop with black gram (*Vigna mungo* (L.) Hepper), soybean or groundnut (*Arachis hypogaea* L.). Due to agronomic dwarfing post rainy season crop facilitates easy control of pests particularly *Helicoverpa armigera* Hübner. Under supplemental irrigation and modified package of practices post rainy yields are economical in the crop.

Summary

Pigeonpea crop is poor man's crop. Its versatility in adaption, multiple uses ensures some income to farmer under harsh climate. The economics in inter-cropping with varieties/hybrids is risk free to farmers because income earned on pigeonpea is a bonus many times and in the event of failure of main crop this income is lifesaving to farmers.

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Intercropping pigeonpea (*Cajanus cajan*) with other warm season annual legumes for forage production

by Aleksandar MIKIĆ[1]*, Vesna PERIĆ[2], Vuk ĐORĐEVIĆ[1], Mirjana SREBRIĆ[2], Marina TOMIČIĆ[1], Svetlana VUJIĆ[3], Vojislav MIHAILOVIĆ[1], Branko ĆUPINA[3] and Dušica DELIĆ[4]

Abstract: Little is known on intercropping annual legume with each other. Our team has developed a complex scheme according to the components' growth habit, growing season and way of use. In a series of trials during several seasons and on two locations in Serbia, roughly at a latitude of 45° N, pigeon pea, having good standing ability, was intercropped with several other lodging-susceptible warm season annual legumes for forage production. All mixtures proved to be economically reliable, especially with hyacinth bean and cowpea, as well as beneficial for both components, since weeds were suppressed and the photosynthetically active leaves were preserved to a much higher extent than in sole crops.

Key words: forage dry matter yield, intercropping, land equivalent ratio, pigeon pea, warm season annual legumes

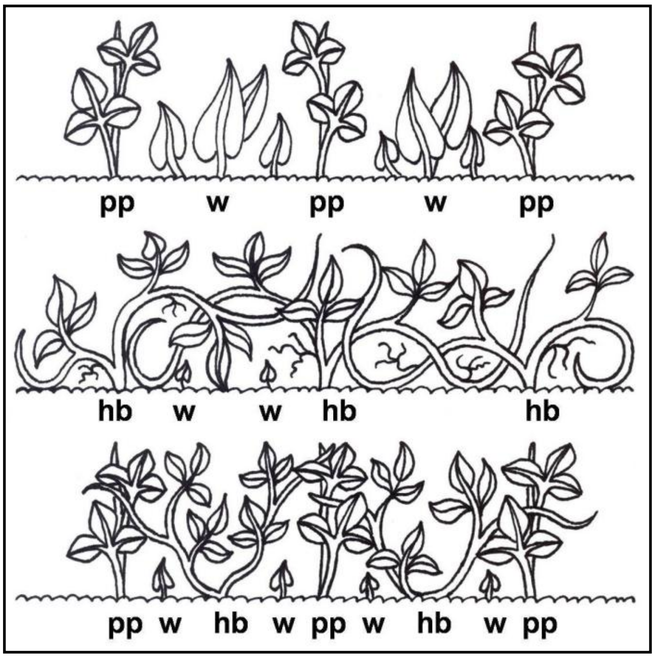

Figure 1. Some aspects of intercropping warm-season annual legumes with each other: (top row) pigeonpea (pp) has an excellent standing ability, but is easily infested by weeds (w); (middle row) hyacinth bean (hb) efficiently fights weeds, but heavily lodges and loses a great amount of leaves; (bottom row) intercropping pigeonpea with hyacinth bean is beneficial for both, since weeds are suppressed and photosynthetically active leaves are preserved (6)

Introduction

Intercropping annual legumes with each other for forage and grain production is a relatively novel agricultural practice and with rather scarce available literature (5). One of the main goals of establishing such practice is the idea of producing forage with preserved high crude protein proportion, unlike more traditional and much better studied mixtures with cereals (1) or brassicas (2), where the latter, despite numerous advantages, usually have much better competing ability and decrease both forage and grain quality of the mixtures.

Designing schemes

During the past decade, the Institute of Field and Vegetable Crops and the Faculty of Agriculture of the University of Novi Sad have recently developed specific schemes for intercropping legumes with each other, based upon four main principles (3):

1) The same time of sowing;

2) The similar growing habit;

3) The similar time of maturing for cutting (for forage production) or harvest (for grain production);

4) One component has good standing ability (supporting crop) and another is susceptible to lodging (supported crop).

According to these, intercropping annual legumes with each other was assessed in a series of field trials within three main groups: (5)

1) Autumn- and spring-sown 'tall' cool season annual legume crops;

2) Autumn- and spring-sown 'short' cool season annual legume crops;

3) Early and late maturing warm-season annual legume crops (Fig. 1).

The proportion of each components in all examined intercrops was 50% : 50%, with the regular sowing rate of each component reduced by half, in order to avoid unnecessarily excessive and economically unjustified sowing, as well as to promote this practice among the farmers worldwide as reliable and feasible (4).

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Figure 2. Intercropping pigeonpea with hyacinth bean for forage production, Zemun Polje, northern Serbia, late July 2009

Table 1. Fresh forage yield ($t\ ha^{-1}$) in the intercrops of pigeonpea and several other warm season annual legumes; average for two locations in northern Serbia, Rimski Šančevi and Zemun Polje, from 2009 to 2012

Supporting crop	Supported crop	Supporting crop forage dry matter yield	Supported crop forage dry matter yield	Total forage dry matter yield	LER
Pigeonpea	-	31.6	0.0	31.6	
-	Adzuki bean	0.0	29.0	29.0	
-	Black gram	0.0	30.2	30.2	
-	Cowpea	0.0	35.7	35.7	
-	Hyacinth bean	0.0	34.2	34.2	
-	Mung bean	0.0	32.1	32.1	
Pigeonpea	Adzuki bean	17.7	13.7	31.4	1.03
Pigeonpea	Black gram	16.8	15.6	32.4	1.05
Pigeonpea	Cowpea	18.3	19.5	37.8	1.13
Pigeonpea	Hyacinth bean	18.2	19.2	37.4	1.14
Pigeonpea	Mung bean	17.3	16.8	34.1	1.07
$LSD_{0.05}$			1.9		0.05

In terms of yield and quality, numerous advantages of mutually inter-cropping faba bean (*Vicia faba* L.) and vetches (*Vicia* spp.) or the pea (*Pisum sativum* L.) genotypes with various types of leaf in comparison to sole crops were demonstrated (7).

In the third group, pigeon pea (Cajanus cajan (L.) Huth) and soya bean (*Glycine max* (L.) Merr.) are designed as supporting crops, while hyacinth bean (*Lablab purpureus* (L.) Sweet), adzuki bean (*Vigna angularis* (Willd.) Ohwi & H. Ohashi), black gram (*V. mungo* (L.) Hepper), mung bean (*V. radiata* (L.) R. Wilczek) and cowpea (*V. unguiculata* (L.) Walp.) act as supported crops (Fig. 2).

Since 2009, a series of field trials have been carried out at Rimski Šančevi and Zemun Polje aimed at assessing the potential of various intercrops of pigeon pea and other warm season annual legumes. In most cases, the designed scheme and the postulated hypothesis proved correct, since the intercrops of pigeon pea with lodging-susceptible companion crops had higher total forage dry matter yields and economic reliability, as witnessed by the land equivalent ratio values higher than 1 (Table 1). Although not presented here, the weed proportion in the intercrops was significantly reduced than in the pigeon pea sole crop.

Future steps

It is needed to carry out the field trials in other environments than Serbia, following the same methodology. The future research should also bring more light on forage and grain yield quality. The presented models of mutual legume intercropping firmly propose reducing the sowing rates of all the components, thus providing farmers with ordinary sowing expenses, and significantly reducing or completely eliminating the use of pesticides.

Acknowledgements

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Enhancing the value of genetic resources for use in pigeonpea improvement

by Hari D. UPADHYAYA*, K. Narsimha REDDY, Shivali SHARMA, Sangam L. DWIVEDI and Senthil RAMACHANDRAN

Abstract: The ICRISAT genebank conserves over 13,700 accessions of pigeonpea from 74 countries. The collection serves as insurance against genetic erosion and provides rich source of diversity for crop improvement. Pigeonpea is often cross pollinated crop, therefore regenerated under insect proof cages, and characterized for morpho-agronomic traits, with most of the traits showing abundant genetic variation. Core and mini core collections representing diversity of the entire collection were developed to discover new sources of variation for use in pigeonpea improvement.

Key words: collection, genetic resources, germplasm, mini core collection

Plant genetic resources are the key to the success of crop improvement programs. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, has global responsibility to collect, conserve, maintain, characterize, evaluate, and document the wealth of genetic variation for use in improving pigeonpea (*Cajanus cajan* (L.) Millsp.). Major pigeonpea germplasm holdings are at ICRISAT, India (13,771 accessions), National Bureau of Plant Genetic Resources (NBPGR), India (7,488 accessions) and National Plant Genetic Resources Laboratory (NPGRL), Philippines (433 accessions) (2).

Germplasm assembly

Genebank at ICRISAT holds 13,771 accessions, including 555 accessions of wild relatives belonging to 66 species of six genera, from 74 countries (Table 1). The collection includes 9,888 accessions introduced from various organizations located in 68 countries and 3,883 accessions collected by ICRISAT through 100 collection missions in 33 countries.

Conserving the collection

At ICRISAT, pigeonpea germplasm seeds are conserved as active and base collections. About 400 g seeds in aluminum cans are preserved as active collection at 4°C and 30% RH to maintain the seed viability above 85% for 15-20 years. About 120 g seeds are vacuum sealed in aluminium foil packets to preserve at -20°C as base collection for about 50 years (10). To meet the germplasm needs for research in African countries, ICRISAT conserves 8,869 accessions at its regional genebank at Nairobi, Kenya. As a safety backup, samples of 80% accessions were deposited in Svalbard Global Seed Vault, Norway.

Regeneration

Continuous supply of germplasm for research and loss of seed viability during storage necessitates monitoring of seed viability and quantity at regular intervals. Accessions are regenerated when the seed viability is below 85% and/or seed quantity is critical (< 1/4 of total quantity) in medium-term (active collection) store, using a cost effective method of growing under insect proof cages (10).

Value addition

Pigeonpea accessions were characterized for 34 morpho-agronomic traits (3), with ~90% of the collection already characterized and additional data on abiotic (drought, salinity, and water logging) and biotic (alternaria blight, nematode, phytophthora blight, pod borer and sterility mosaic) stresses were added to enhance the value of pigeonpea genetic resources. Promising sources were identified in the collection for wilt (108 accessions), sterility mosaic disease (410), phytophthora blight (152), stem canker (26), alternaria blight (25), pod borer (27), pod fly (21), nematodes (19), drought (7), water logging (62) and salinity (56).

Diversity in the collection

Analysis of characterization data revealed abundant genetic variation for agronomic and seed traits (Table 2 and Fig. 1). Range variation for quantitative traits was maximum in the collection from primary center of diversity for pigeonpea and minimum in collection from Europe and Oceania. Shannon-Weaver diversity index (H`) (7) indicated that the accessions from South-East Asian countries such as India, Indonesia, Philippines and Thailand had the highest pooled H` for qualitative traits (0.349 ± 0.059) and accessions from Africa for quantitative traits (0.613 ± 0.006) (11).

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Table 1. Geographical distribution of pigeonpea germplasm accessions assembled at the ICRISAT, genebank, Patancheru, India

Country	Improved cultivars	Breeding materials	Landraces	Wild	Total
Angola				1	1
Antigua and Barbuda			2	4	6
Argentina			1	8	9
Australia	2	59		73	134
Bangladesh		40	35		75
Barbados			25		25
Belgium		2			2
Belize				2	2
Bolivia				8	8
Botswana				3	3
Brazil		16	2	10	28
Cape Verde		6			6
Central African Republic			2		2
China		1		1	2
Colombia		4	1	3	8
Costa Rica				1	1
Cuba				6	6
Dominican Republic		5	58		63
Ecuador				1	1
Ethiopia			14		14
Fiji				2	2
Germany		2			2
Ghana		1	1		2
Grenada			15		15
Guadeloupe		14	8		22
Guyana		7	21		28
Honduras				1	1
ICRISAT	11	1659	6		1676
India	54	2568	6378	201	9201
Indonesia		7	14	36	57
Iran		1			1
Italy		5	10		15
Jamaica		20	44		64
Kenya		26	312	5	343
Madagascar		1			1
Malawi		1	244	4	249
Maldives			1		1
Mali				4	4
Martinique			1		1
Mexico		3		59	62
Montserrat			4		4
Mozambique			31	1	32
Myanmar		60	13	8	81
Namibia				5	5
Nepal		8	112		120
Nicaragua				4	4
Nigeria		34	148		182
Oman				3	3
Pakistan		15	2	1	18
Panama				2	2
Papua New Guinea				3	3
Paraguay				5	5
Peru	1	2	2	2	7
Philippines		2	57	2	61
Puerto Rico		44	34		78
Rwanda			5		5
Saint Kitts and Nevis			6		6
Saint Lucia			17		17
Saint Vincent and the Grenadines			22		22
Senegal			10	1	11
Sierra Leone			3		3
South Africa		21	4	15	40
Sri Lanka		59	18	33	110
Taiwan		2	1		3
Tanzania		3	259	13	275
Thailand		1	40		41
Trinidad and Tobago		39	74	1	114
Uganda		1	97		98
Union of Soviet Socialist Republics			2		2
United Kingdom		5	5	1	11
United States of America		4			4
Unknown		6	3	2	11
Venezuela		75	56	3	134
Zaire			13		13
Zambia			86	7	93
Zimbabwe				10	10
Total	68	4,829	8,319	555	13,771

Wealth from the wild

Promising sources for agronomic and nutritional traits and for higher levels of resistance to various biotic and abiotic stresses were identified in wild species. Important sources include, *C. scarabaeoides* (L.) Thouars for wilt, water logging tolerance and high pod setting (9); *C. albicans* (Wight & Arn.) Maesen, *C. scarabaeoides* and *C. sericeus* (Benth. ex Baker) Maesen for sterility mosaic disease; *C. platycarpus* (Benth.) Maesen, *C. scarabaeoides and C. sericeus* for phytophthora blight; *C. albicans, C. platycarpus, C. scarabaeoides* and *C. sericeus* for alternaria blight; *C. acutifolius* (F. Muell.) Maesen, *C. albicans, C. lineatus* (Wight & Arn.) Maesen and *C. sericeus* for drought; *C. platycarpus* and *C. scarabaeoides* for early flowering (from 35 to 50 days) (5); *C. albicans, C. scarabaeoides, C. sericeus, C. reticulatus* (Aiton) F. Muell. and *Rhynchosia bracteata* Baker for pod borer, pod fly and pod wasp (6); *C. acutifolius, C. albicans, C. cajanifolius* (Haines) Maesen, *C. platycarpus, C. scarabaeoides, C. sericeus* and *D. ferruginea* Wight & Arn. for salinity (8) and *C. lineatus, C. crassus* (Prain ex King) Maesen, *C. cajanifolius*, *C. mollis* (Benth.) Maesen, *C. platycarpus*, *C. scarabaeoides* and *C. albicans* for seed protein content (31% - 34%) (4).

Documentation

Documentation of information on germplasm collections is very essential for enhanced utilization. Four types information (passport, characterization, inventory and distribution) on each accession is being maintained at ICRISAT genebank using Genebank Information Management System (GIMS). The passport information of the pigeonpea collection can be browsed through www.genesys-pgr.org or http://www.icrisat.org/crop-pigeonpea-genebank.htm.

Core and mini core collections

Non-availability of reliable information on traits of economic importance in germplasm collections of large size is the major reason for poor utilization of genetic resources in crop breeding. Representative subsets of pigeonpea germplasm in the form of core (5) and mini core collections (13) and genotype-based reference set (12) were formed for enhancing the use of germplasm in pigeonpea improvement. Evaluation of mini core resulted in identification of 23 accessions tolerant to water logging, 16 to salinity, six to wilt, 24 to sterility mosaic disease, and 11 to pod borer (14). A number of accessions with early flowering (< 85 days), large seeds (>15 g 100 seeds^{-1}), and seed nutrient dense types (seed protein, > 24%, iron, > 40 ppm, and zinc, > 40 ppm) were identified (14). Twenty seven sets of mini core were provided to the NARS in six countries for evaluation and identification of promising sources for use in pigeonpea improvement.

Access to the collection

Seeds of all FAO designated accessions are available at ICRISAT genebank under Standard Material Transfer Agreement (SMTA) of International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). To date, ICRISAT genebank provided 51,348 samples to researchers in India, 22,226 samples to researchers in 112 countries and 85,881 samples to researchers in ICRISAT.

Table 2. Variation of some economically important traits of the pigeonpea germplasm assembled at ICRISAT genebank, Patancheru, India

Character	Mean	Minimum	Maximum
Number of days to 50% of flowering	133.54	52	237
Number of days to 75% of maturity	192.12	100	299
Plant height (cm)	177.89	39.0	310
Number of primary branches (plant^{-1})	13.52	1.1	107
Number of secondary branches (plant^{-1})	31.30	0.0	145.3
Number of tertiary branches (plant^{-1})	8.80	0.0	218.7
Number of racemes per plant (plant^{-1})	150.32	6.0	915
Pod length (cm)	5.71	2.5	13.1
Number of pods (plant^{-1})	287.26	9.3	1819.3
Number of seeds (pod^{-1})	3.72	1.6	7.2
100-seed weight (g)	9.28	2.7	25.8
Seed yield (g plant^{-1})	97.37	1.0	720.0
Harvest index (%)	21.00	0.6	73.9
Seed protein content (%)	21.25	13	30.8

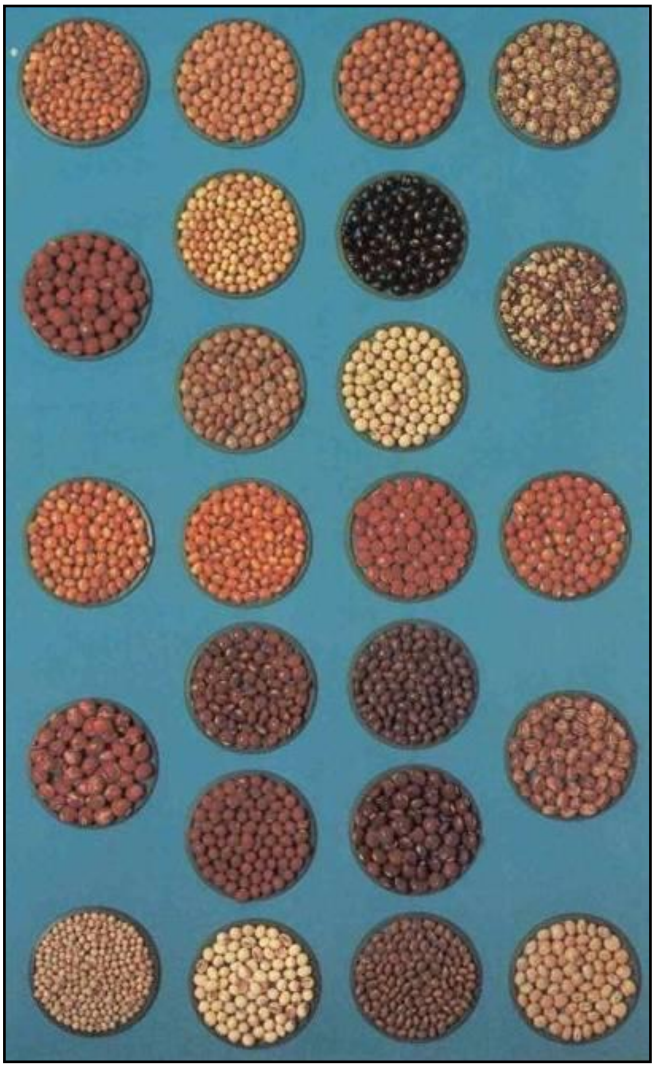

Figure 1. Diversity for seed traits in the world collection of pigeonpea at the ICRISAT genebank, Patancheru, India

Impact of conserved germplasm

The pigeonpea collection conserved in genebank provides an insurance against genetic erosion. Nine accessions were released as cultivars in seven countries. A vegetable pigeonpea landrace from India (ICP 7035) was released as cultivar in India, Fiji, Nepal, China and Philippines. Wilt resistant pigeonpea landrace ICP 8863 released as Maruti in India resulted in about US$ 62 million as net present value of benefits from collaborative fusarium wilt research representing an internal rate of return of 65% by year 1996 (1). ICP 9905, ICP 11914 and ICP 13828 released in Venezuela reportedly solved major economic problem of importing soybean worth $300 million annually. Mini core collection, an International Public Good (IPG), is serving as gateway to access entire pigeonpea collection at ICRISAT genebank.

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Pre-breeding to expand primary genepool through introgression of genes from wild *Cajanus* species for pigeonpea improvement

by Shivali SHARMA* and Hari D. UPADHYAYA

Abstract: Narrow genetic base coupled with low levels of resistance against important biotic/abiotic stresses in cultivated pigeonpea is the major constraint affecting its production and productivity globally. Wild *Cajanus* species are the reservoir of many important genes and can be utilized to improve the crop cultivars, enrich variability, and broaden the genetic base. Pre-breeding populations involving wild *Cajanus* species from the secondary and tertiary genepools as donors and pigeonpea cultivars as recipients have been developed. Considerable variability was observed in these populations for morpho-agronomic traits and for biotic stresses. Agronomically desirable and disease resistant introgression lines have been identified for use in pigeonpea improvement programs.

Key words: genepool, interspecific hybridization, pre-breeding, pigeonpea, wild *Cajanus*

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the sixth most important grain legume crop of rainfed tropics and subtropics. Though a short-lived perennial shrub, it is traditionally cultivated as an annual crop in Asia, Africa, Latin America, and the Caribbean regions. Pigeonpea has a wide adaptability to diverse climates and is cultivated in 82 countries on 6.23 million ha area with an annual production of 4.68 m t and productivity of 751 kg ha^{-1} (3). India is the major pigeonpea growing country in the world with 3.02 t of production from 4.65 million ha area (3).

In spite of large breeding efforts for pigeonpea improvement in India and elsewhere, there is a huge gap between the potential (2.5 t ha^{-1} - 3.0 t ha^{-1}) and actual yield (~0.8 t ha^{-1}). This is due to the damage caused by several biotic (wilt, sterility mosaic disease (SMD), phytophthora blight and pod borer (*Helicoverpa armigera* L.)) and abiotic (water logging, salinity and frost/cold) stresses. The use of working collection consisting mainly of a few and elite breeding lines coupled with intense selection for high yield has resulted in the recirculation of the same germplasm and hence narrow genetic base of the improved cultivars. The cultivation of a few and genetically similar cultivars has resulted in the vulnerability to pests and diseases. Therefore, efforts are immediately required towards broadening the genetic base of pigeonpea cultivars and developing improved plant types having high levels of resistance to various biotic and abiotic stresses.

Wild relatives for pigeonpea improvement

Crop wild relatives (CWR) have been used as a diverse pool of genetic resources for crop improvement, including insect and disease resistance (1, 4). Wild *Cajanus* species harbor high levels of genetic diversity to survive against various biotic/abiotic stresses, especially under changing climatic conditions and thus hold a great potential for pigeonpea improvement. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in Patancheru, India, has the global responsibility of collecting, conserving and distributing the pigeonpea germplasm comprising of landraces, obsolete varieties, breeding lines, modern cultivars, genetic stocks, mutants and wild *Cajanus* species. The ICRISAT genebank holds 13,216 accessions of cultivated pigeonpea and 555 accessions of wild species in the genus *Cajanus* from 60 countries. Based on the crossability with cultivated pigeonpea, the cultivated and wild *Cajanus* species are divided into three genepools (Fig. 1).

In wild *Cajanus* species, new and diverse sources of resistance/tolerance to various biotic stresses, such as alternaria blight (12), phyto-phthora blight (6, 8, 10), sterility mosaic disease (7), pod borer (2, 13, 18), cyst nematode (15), and abiotic stresses, such as salinity (16, 17), as well as accessions with agronomically desirable traits, such as early flowering, high seed number per pod, high seed protein content (19) and photoperiod insensitivity (9) have been identified (Table 1) for use in pigeonpea improvement.

Pre-breeding for broadening the genetic base

Although high levels of resistance is available in wild *Cajanus* species, these are not being utilized adequately in pigeonpea breeding programs. The major limitation is due to the linkage drag and different incompatibility barriers between cultivated and wild species. Under such situations, pre-breeding provides a unique opportunity to expand primary genepool by exploiting genetic variability present in wild species and cultivated germplasm, and will ensure continuous supply of new and useful genetic variability into the breeding pipelines to develop new cultivars having high levels of resistance and broad genetic base.

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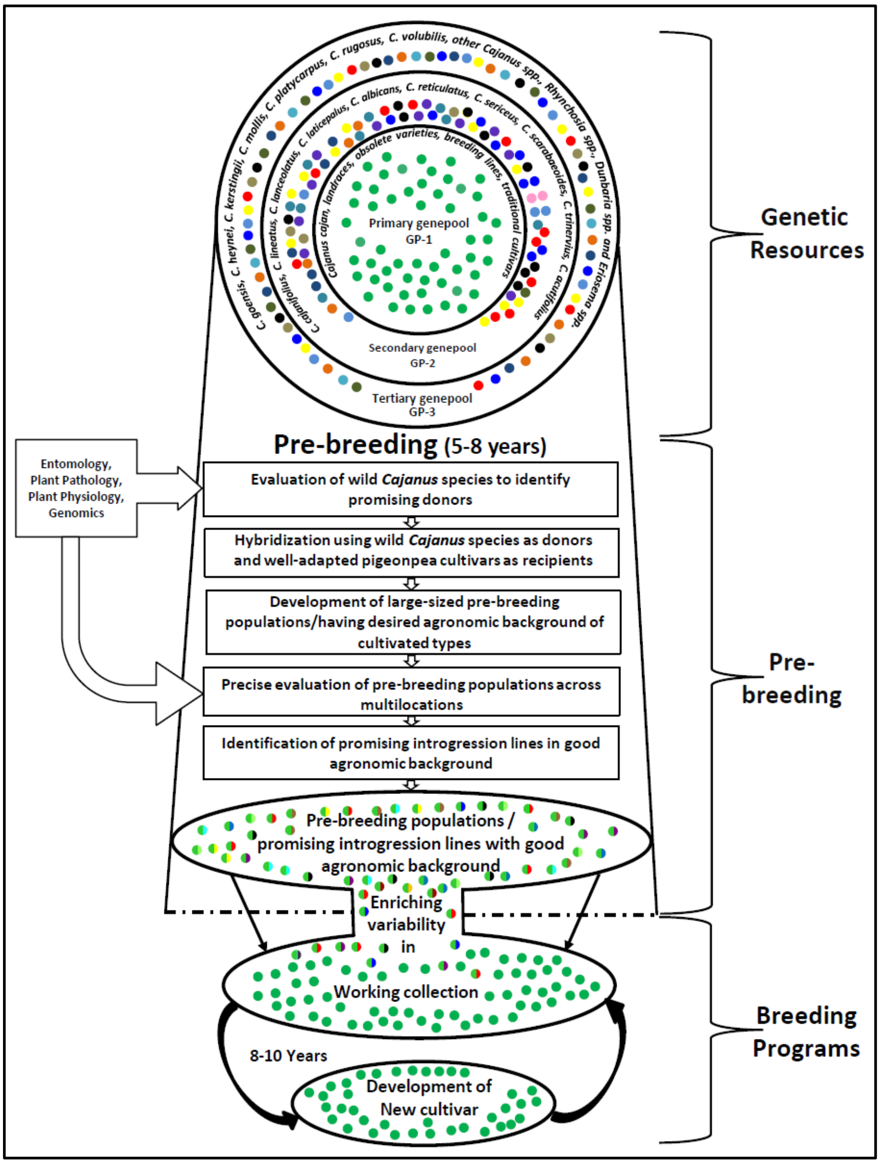

Figure 1. Pre-breeding using wild *Cajanus* species and pigeonpea cultivars for broadening the genetic base for pigeonpea improvement

Pre-breeding is comprised of three major activities: i) Identification of desirable traits and/or genes from unadapted germplasm such as exotic landraces/wild species (donors); ii) Population development following hybridization for transferring these traits into well-adapted genetic backgrounds; and iii) Evaluation of pre-breeding populations to identify desirable ILs for ready use by the breeders in breeding programs (14). Overall, pre-breeding is a time consuming and resource demanding affair (Fig. 1).

At ICRISAT, pre-breeding activities are being undertaken by utilizing the wild *Cajanus* species from secondary and tertiary genepool for pigeonepa improvement. One major achievement of using wild *Cajanus* species is the development of cytoplasmic nuclear male sterility systems (CMS). These CMS systems have been developed with cytoplasm derived from different wild *Cajanus* species (11).

Besides this, pre-breeding activities involving wild *Cajanus* accessions as donors and popular pigeonpea varieties as recipients are in progress to develop new genepools with high frequency of useful genes, wider adaptability, and a broad genetic base for resistance/tolerance to important biotic and abiotic stresses, as well as for agronomic and nutrition-related traits. Further, to minimize the linkage drag associated with utilizing wild species in crop improvement programs, we are focusing on the development of advanced backcross populations. Using secondary genepool species, *C. cajanifolius* (Haines) Maesen (ICPW 29), *C. acutifolius* (F. Muell.) Maesen (ICPW 12 and ICPW 004), *C. scarabaeoides* (L.) Thouars (ICPW 281) and tertiary genepool species, *C. platycarpus* (Benth.) Maesen (ICPW 68) having useful traits such as tolerance to salinity and pod borer resistance (5, 16, 18), and two pigeonpea cultivars (ICPL 87119 and ICPL 85010), advanced backcross populations have been generated from five interspecific crosses, ICPL 87119 × ICPW 29, ICPL 87119 × ICPW 12, ICPL 87119 × ICPW 281, ICPL 85010 × ICPW 004 and ICPW 68 × ICPL 85010, at ICRISAT, Patancheru, India. ICPL 87119 (Asha) is a medium-duration variety and ICPL 85010 is an early-duration pigeonpea variety, both cultivated in India. Evaluating these populations for agronomic traits revealed considerable variability for days to flowering, growth habit as well as for pod and seed traits. Promising introgression lines (ILs) having high numbers of pods per plant and seeds per pod and 100-seed weight (> 20.0 g) have been identified from the population derived from a ICPL 85010 × ICPW 004 cross (Fig. 2). Evaluation of two populations derived from ICPL 85010 × ICPW 004 and ICPW 68 × ICPL 85010 crosses for sterility mosaic disease and wilt identified 15 ILs derived from *C. acutifolius* and two ILs from *C. platycarpus* having combined resistance against SMD and wilt. Besides this, one population derived from ICPL 87119 × ICPW 12 was also screened against phytophthora blight under controlled environmental conditions and the resistant ILs have been selected for confirming the resistance. Overall, pre-breeding activities have led to the development and identification of agronomically desirable and disease resistant ILs for further use in pigeonpea improvement programs.

Recently, the efforts have been initiated to introgress pod borer resistance from wild *Cajanus* species into pigeonpea cultivars. The evaluation of wild *Cajanus* species has

Table 1. Wild *Cajanus* species identified as promising donors for important biotic/abiotic stresses and agronomic traits

Species	Traits
	Secondary genepool
C. acutifolius	Pod borer
C. albicans	Alternaria blight, sterility mosaic disease, pod borer, salinity, high seed number per pod (> 6) and high seed protein (> 30%)
C. cajanifolius	Alternaria blight, and high seed protein (> 30%)
C. lineatus	Alternaria blight
C. reticulatus	Pod borer
C. scarabaeoides	Alternaria blight, streility mosaic disease, pod borer, cyst nematode, salinity, early flowering (between 51 and 118 days) and high seed protein
C. sericeus	Alternaria blight, phytophthora blight, pod borer, and salinity
	Tertiary genepool
C. cinereus	High seed number per pod (> 6)
C. crassus	High seed protein (> 30%)
C. mollis	High seed number per pod (> 6) and high seed protein (> 30%)
C. platycarpus	Alternaria blight, phytophthora blight, salinity, photoperiod insensitivity, super-early flowering (between 34 - 40 days) and high seed protein (> 30%)
C. volubilis	Alternaria blight
Flemingia spp.	Cyst nematode
Rhynchosia aurea	Pod borer and cyst nematode
R. bracteata	Pod borer
R. rothii	Cyst nematode
R. densiflora	Cyst nematode

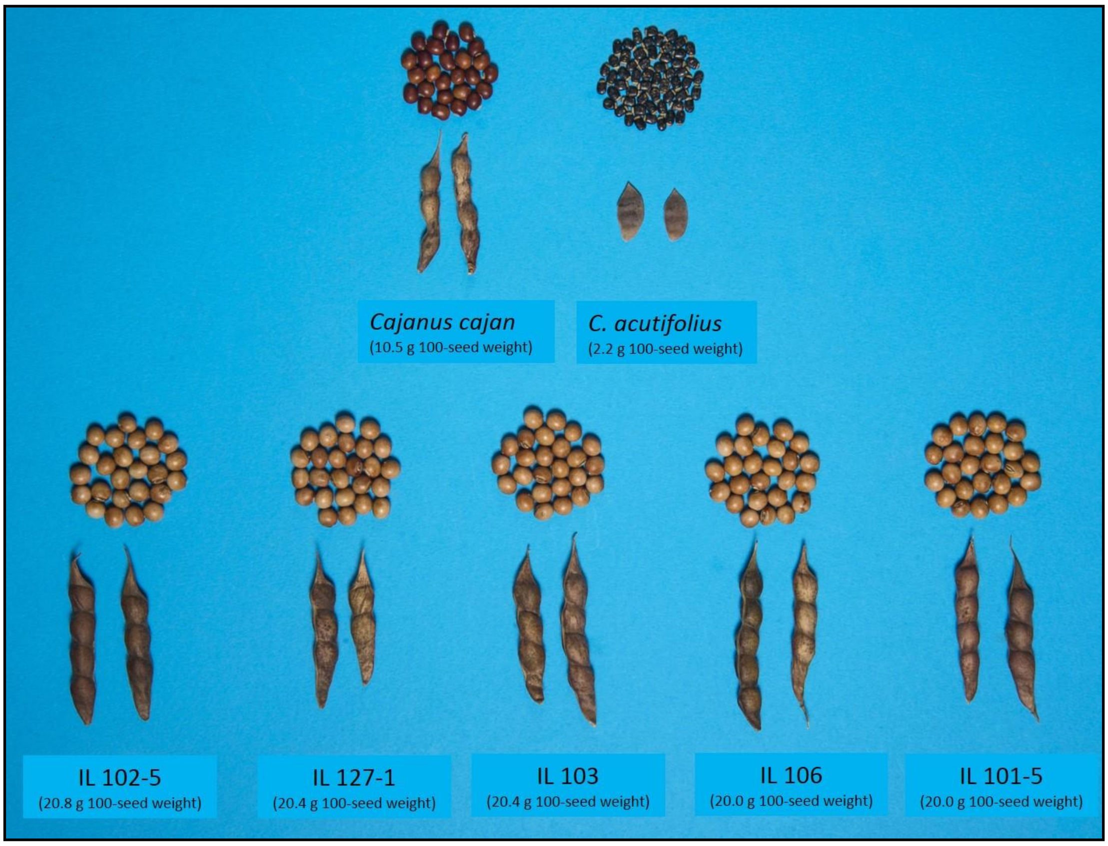

Figure 2. Introgression lines (ILs) derived from *Cajanus acutifolius* having variations for pod traits and high 100-seed weight

identified accessions/species with a diverse combination of morphological and biochemical components associated with expression of resistance to pod borer. Wild *Cajanus* accessions having high levels of antixenosis for oviposition (*C. acutifolius*, and *C. sericeus*), high expressions of antibiosis (*C. acutifolius* (Benth. ex Baker) Maesen) high density of type 'C' and 'D' trichomes (*C. scarabaeoides*, and *C. sericeus*) and low amounts of sugars and high amounts of tannins and polyphenols (13) were used in the crossing program with an objective to combine these components into common genetic background. Using four wild species, *C. acutifolius*, *C. sericeus*, *C. scarabaeoides*, and *C. albicans* (Wight & Arn.) Maesen and two pigeonpea cultivars, ICPL 87119, and ICP 8863, eight interspecific F_1 crosses were generated. Four F_1 crosses generated using a common cultivar were further crossed amongst themselves to generate two 4-way F_1 crosses in order to combine different components of pod borer resistance from different species into a common genetic background. These crosses are being advanced further to develop ILs with high levels of resistance against pod borer.

Conclusion

Wild species harbor many useful genes and can be utilized effectively to create enormous genetic variability following wide hybridization. At ICRISAT, utilization of wild *Cajanus* species has contributed significantly through the development of CMS systems for pigeonpea improvement. Further, development of pre-breeding populations using pigeonpea cultivars as recipients and wild *Cajanus* species as donors has resulted in enriching the variability for different traits in the primary genepool. Introgression lines (ILs) having good agronomic performance and high levels of resistance against important biotic stresses have been identified, which can be utilized in breeding programs to develop new cultivars with a broad genetic base. Efforts are underway to combine different components of pod borer resistance from different species into common genetic background following complex interspecific crosses and would pave a way to develop ILs having high levels of pod borer resistance. Overall, these pre-breeding activities have led to the genetic enhancement by increasing the extent of useful diversity in the primary genepool for further use by the breeders.

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An update on the host plant resistance to pigeonpea diseases

by Mamta SHARMA* and Raju GHOSH

Abstract: The production and productivity of pigeonpea is severely constrained by diseases such as Fusarium wilt, sterility mosaic disease and Phytophthora blight. These diseases can be serious alone or as component of complex. Estimates of yield loss as caused by these diseases are not precise. This paper summarises the current knowledge of pigeonpea diseases with special reference to emerging diseases in the light of climate change. Recent developments in host plant resistance including the screening techniques and sources of resistance identified over the last few years have been highlighted in this paper.

Key words: emerging diseases, host plant resistance, inheritance, pigeonpea, resistance sources

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is attacked by many soil borne and foliar diseases which results in severe economic losses globally. Among these, fungi and viruses are the largest and most important groups affecting pigeonpea (Table 1). Fusarium wilt (FW), sterility mosaic disease (SMD), and Phytophthora blight (PB) are economically important diseases of pigeonpea. Frequent occurrence of PB has been reported in major pigeonpea growing areas especially under the changed climatic scenario (7). New records of emerging diseases such as Alternaria blight, sudden death and root rots have been reported recently in pigeonpea (12, 14, 15).

Of the available management approaches, host plant resistance is the most reliable, economical and effective method for managing the diseases. In the absence of high yielding and well adopted resistant cultivars, use of certified seeds, sanitation and cropping practices to reduce inoculum, choice of sowing type and time and use of fungicide or bio-control agents would be of help for the management of these diseases. Considerable progress has been made in the past in developing the disease resistance screening techniques, identifying sources of resistance and transferring resistance genes into high yielding, improved and agronomically superior genetic background in pigeonpea. Biotechnological tools such as marker-assisted selection, genetic engineering and wide hybridization to develop crop cultivars with resistance to diseases will play a key role in future disease management programs in pigeonpea (19). In this paper, we have attempted to document the recent progress made towards host plant resistance for economically important diseases of pigeonpea along with future challenges.

Genetic resistance to pigeonpea diseases

Fusarium wilt (*Fusarium udum* Butler) is the most important disease in Indian subcontinent and Eastern Africa. Occurrence of wilting during flowering to pod filling stage causes yield losses up to 50% - 70%. Another disease severely affecting the pigeonpea yield is sterility mosaic disease (SMD) caused by pigeonpea sterility mosaic virus (PPSMV), a species of the genus *Emaravirus* causing losses up to 95% - 100% with infection occurring early at < 45 days old plants (3). Apart from wilt and mosaic, Phytophthora blight is another important disease that got the status of economic concern (7, 11, 16). The disease is caused by fungus *Phytophthora cajani* K. S. Amin, Baldev & F. J. Williams (16).

FW and SMD incidence differs from place to place due to variability in pathogen. So far 5 variants (I, II, III, IV and V) of *Fusarium udum* have been identified and documented (18) using as many as 15 differentials. We have also observed considerable variability using 73 isolates and 11 differentials collected from seven states in India (Sharma et al unpublished). Three distinct strains (Bangalore, Patancheru and Coimbatore) have been characterized for PPSMV in India (4). So far, no confirmed information regarding pathogen variability is available for *Phytophthora cajani*.

Reliable greenhouse and field screening techniques are available for FW and SMD to identify resistance sources (8). Recent advances in FW and SMD research have facilitated the selection of high-yielding varieties with durable resistance to FW and SMD. Lines derived from crosses with *C. acutifolius* (F. Muell.) Maesen and *C. platycarpus* (Benth.) Maesen have shown resistance to the Patancheru isolate of PPSMV under field conditions (5). Recently new sources of resistance to Fusarium wilt and SMD were identified in a mini-core collection of pigeonpea germplasm at ICRISAT (13). A high level of resistance was found in 24 accessions and combined resistance to FW and SMD was found in five accessions (ICPs 6739, 8860, 11015, 13304, and 14819). Recently, through multi-environment field testing, four genotypes (ICPLs 20094, 20106, 20098 and 20115) have been identified as the most stable and resistant to SMD (17). Three genotypes (ICPLs 20096, 20107, 20110) showed moderately stable performance against SMD. All these lines have medium duration of maturity and could be valuable sources of resistance for a pigeonpea breeding programs to FW and SMD. Four vegetable type genotypes (ICPs 7991, 12059, 13257 and 14291) originated from different countries were found highly resistant with no incidence of FW and SMD (10).

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Table 1. Distribution and symptoms of important and emerging diseases of pigeonpea

Diseases	Causal organism	Distribution	Symptoms
Fusarium wilt	*Fusarium udum* Butler	Bangladesh, Ghana, Grenada, India, Indonesia, Kenya, Malawi, Mauritius, Myanmar, Nepal, Nevis, Tanzania, Thailand, Trinidad and Tobago, Uganda, Venezuela	
Sterility mosaic	Pigeonpea sterility mosaic virus	India, Bangladesh, Nepal, Sri Lanka, Myanmar	
Phytophthora blight	*Phytophthora cajani* K. S. Amin, Baldev & F .J. Williams	Asia, Africa, Americas, Australia, Dominican Republic, Kenya, Panama, Puerto Rico	
Alternaria blight	*Alternaria alternata* (Fr.) Keissl. and *Alternaria tenuissima* (Kunze) Wiltshire	India, Kenya, Puerto Rico	
Sudden death	*Fusarium acuminatum* Ell. &. Ev.	India	
Dry root rot	*Macrophomina phaseolina* (Tassi) Goid	India, Jamaica, Myanmar, Nepal, Sri Lanka, Trinidad and Tobago	

In previous studies, although several screening techniques and sources of resistance to PB have been reported (7), however, no reliable and repeatable screening technique is available. Recently, Sharma et al (16) first time developed a successful method for obtaining high concentrations of zoospores followed by a reliable screening technique in pigeonpea for PB. Using this new bioassay, over 800 pigeonpea genotypes including released cultivars, earlier reported PB resistant lines, breeding lines and water logging tolerant lines have been screened. Repeated screening of promising genotypes has so far identified four genotypes with a moderate resistance to PB (ICPLs 99004, 99008, 99009 and 99048), which will be used in the further study.

Inheritance of resistance to pigeonpea diseases

Wilt resistance has been reported to be a monogenic recessive trait (6) and dominant trait (2). Saxena et al (9) have also reported dominant suppressive epistatic effect of a dominant gene over the recessive one for wilt resistance in a cross of a FW susceptible cytoplasmic male-sterility line with four FW resistant fertility restorers. Studies have been done on the inheritance of resistance to SMD and there are major differences in the interpretations made on the nature of resistance. Recently the nature of inheritance of SMD was studied in the segregating population of two crosses, Gullyal white (susceptible) × BSMR 736 (resistant) and BSMR 736 (resistant) × ICP 8863 (susceptible) (1). The above studies showed that the resistant trait was governed by two independent non-allelic genes, designated *SV1* and *SV2*, with inhibitory gene interaction (1). The limited reports available on genetics of PB resistance in pigeonpea suggest that a few major genes may control resistance in the host to PB.

Future challenges

Considerable progress has been made during the last decade in characterizing the pathogenic variability in *F. udum* and PPSMV, identifying the resistant sources and resistance mechanisms. However, there are still several gaps such as lack of precise knowledge on the existence of pathogen race/strains in *F. udum* and PPSMV, which is essential to develop durable resistant cultivars for different regions. Further, due to the variability in climatic conditions and their unpredictable occurrence, frequent outbreaks of new diseases such as PB, Alternaria blight, sudden death, root rots have become more common in pigeonpea. There is a need to address these diseases, study their biology and epidemiology to develop reliable screening techniques to identify the genetic resistance and resistance mechanism. Marker assisted breeding may be strategically useful to avoid combined effect of environmental interactions and in identification of race-specific resistant genes and their pyramiding.

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Host plant resistance to insect pests in pigeonpea: Potential and limitations

by Hari C. SHARMA

Abstract: Host plant resistance to insects is one of the components of pest management in pigeonpea. Considerable progress has been made in developing techniques to screen for resistance to *Helicoverpa armigera*. However, some of these techniques cannot be used to evaluate material for resistance to spotted pod borer, *Maruca virtrata*, pod fly, *Melanagromyza obtusa*, pod wasp, *Tanaostigmodes cajaninae* and the pod bugs, *Clavigralla* spp. Genotypes with resistance to *H. armigera*, *M. vitrata*, *M. obtusa*, and *C. chinensis* have been identified, but the levels of resistance are low to moderate in the cultivated germplasm. However, high levels of resistance have been identified against *H. amigera* in wild relatives of pigeonpea. Considerable information has been generated on mechanisms of resistance to *H. armigera* and *M. vitrata*, but there is limited information on inheritance of resistance, and the molecular markers associated with resistance to insects. The progress in transferring insect resistance into the improved varieties has been limited, and there is a need to introgress resistance genes from the wild relatives into the culigen and/or develop pigeonpea cultivars expressing *Bt* genes to confer resistance to pod borers. Cultivars with moderate levels of resistance in combination with other components of pest management will play a major role in increasing the productivity of pigeonpea.

Key words: insect pests, pigeonpea, plant resistance

Insect pest problems in pigeonpea

Over 150 insect species damage pigeonpea, of which the legume pod borer, *Helicoverpa armigera* Hübner, spotted pod borer, *Maruca vitrata* Geyer, pod fly, *Melanagrmyza obtusa* Malloch, pod wasp, *Tanaostigmodes cajaninae* La Sale, spiny pod borer, *Etiella zinckenella* Triet and pod sucking bug, *Clavigralla gibbosa* Spin. are the major pests. Black bean aphid, *Aphis craccivora* Koch, Leafhoppers, *Empoasca* spp. and green bugs, *Nezara viridula* L. are the occasional pests (32, 39). The bruchids, *Collasobruchus chinensis* L. cause extensive losses in storage. Insect pests in India cause an average of 30% loss in pulses valued at 815 million USD. The pod borer, *H. armigera* - the single largest yield reducing factor in pigeonpea, causes an estimated loss of 317 million USD in the semi-arid tropics. Globally, it causes an estimated loss of over 2 billion USD annually, despite over 1 billion USD worth of insecticides used to control this pest (1).

Techniques to screen for resistance to insects in pigeonpea

Screening for resistance to insects in pigeonpea under natural conditions is a long-term process because of the variations in flowering times of pigeonpea genotypes and the insect populations over space and time (Fig. 1). As a result, it is difficult to identify reliable and stable sources of resistance under natural infestation (39). Therefore, there is a need to develop techniques to screen for resistance to insects under uniform insect pressure at the most susceptible stage of the crop. The following techniques can be adopted to maximize the effectiveness of screening for resistance to insects in pigeonpea.

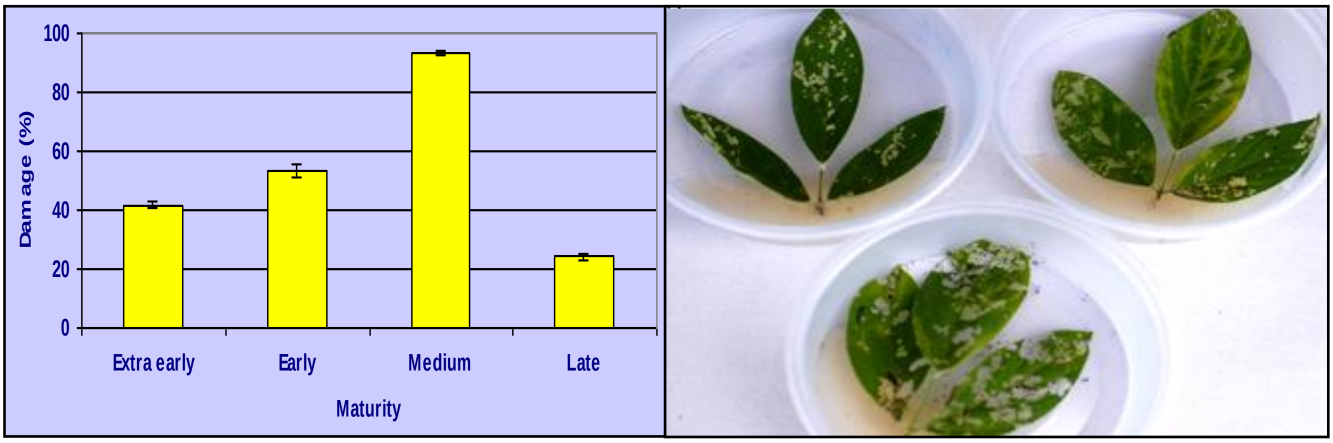

Figure 1. Pod borer damage in pigeonpea lines belonging to different maturity groups under natural infestation (left) and detached leaf assay to screen pigeonpea lines for resistance to *Helicoverpa armigera* (right)

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Planting times and use of hot-spot locations. The test material should be planted such that the most susceptible stage of the crop is exposed to optimum insect pressure. Most of the crops planted during June - July are exposed to heavy infestation by the pod borers in South central India during the rainy season, while the crops that have pods during December - January are exposed the heavy pod fly infestation (39). Hot-spots are the locations where the insects are known to occur regularly in optimum numbers across the seasons. Many locations in South Central India are hot-spots for *H. armigera* and *M. vitrata* and *M. obtusa*, which can be used to screen a large number of genotypes for resistance to insects.

Grouping the test material according to maturity and height. Because of fluctuations in insect populations over the crop-growing season, it becomes difficult to obtain uniform insect damage on genotypes flowering at different times under natural infestation (37). The early and late flowering lines escape insect damage, while those flowering in the mid-season are exposed to heavy insect pressure. To overcome this problem, it is important to group the test material according to their maturity and height. It is equally important to include resistant and susceptible checks, and/or commercial cultivars of similar maturity in each trial for proper comparisons.

Augmenting insect populations in the field. Insect density in the field can be augmented with field collected or lab reared insects to ensure optimum damage in the test material. Insect population can be augmented by placing non-destructive light, pheromone or kairomone traps. Indigenous insect populations can also be collected from the surrounding areas and released in the test plots. Kairomones present in the leaves of susceptible pigeonpea varieties are attractive to the egg-laying females of *H. armigera*, and such attractants can be used to increase insect abundance in the resistance screening nursery.

Tagging the plants/inflorescences. The test material flowering at the same time can be tagged with similar-colored labels or marked with paint. This enables the comparison of the test material flowering at the same time with the resistant and susceptible controls of similar duration. For comparisons to be meaningful, the inflorescences at flowering (between 30 cm and 45 cm long) at a particular point of time can be marked with a twine or with colored ribbons. The data on insect damage should be recorded in the tagged portion of inflorescence, and comparisons made amongst the genotypes flowering during the same period. For this purpose, 3 to 5 inflorescences may be tagged in each plot.

Artificial infestation in the field. Insects reared on artificial diet in the laboratory can be released on the test material in the field (34). Manual infestation with neonate larvae is quite effective, but it is cumbersome and time consuming. Eggs suspended in 0.2% agar-agar solution can also be spread on plants in controlled amounts through hypodermic syringes or pressure applicators. Field infestation should be carried out at the most susceptible stage of the crop. However, this technique cannot be used effectively in pigeonpea as there in no distinct plant whorl where the larvae can be released (32).

Caging the plants with insects in the field. Caging the test plants or inflorescences with insects in the field is another method of screening for resistance to insects (37). This prevents the insects from migrating away from the test plants. The cages/nylon bags (60 mesh) can be designed to cover 25 cm - 30 cm portion of the inflorescences. For valid conclusions, resistant and susceptible checks of appropriate maturity should also be included, and infested at the same time as the test genotypes. Because of large size of pigeonpea plants and the propensity of insects to lay eggs on the nylon net, it is not very effective for screening pigeonpa for resistance to pod borers.

Detached leaf assay. Detached leaf assay can be used quite successfully to screen pigeonpea plants for resistance to insects (38). The first fully expanded terminal trifoliate leaf with petiole can be placed into agar-agar (3%) in a small plastic cup or a glass jar (250 ml capacity). Ten to 20 neonate larvae are released on the test material, and data are recorded on larval survival and larval weights at 4 to 5 days after infestation, when there are maximum differences between the resistant and susceptible genotypes (Fig. 1). This test is easy and quick, and can be carried out with different parts of the same plant at different growth stages. However, results of detached leaf assay may not correspond to genotypic resistance to pod damage by the insects because of differences on physico-chemical characteristics between the leaves and the flowers/pods, as most of the pests of economic importance in pigeonpea feed on flowers and pods.

Diet incorporation assay. Incorporation of lyophilized leaves or flowers/ pods into the artificial diet can be used to assess antibiosis component of resistance to insects in pigeonpea (17, 39). Antibiosis can be assessed in terms of larval mortality, larval and pupal weights, adult emergence, and duration of development. Incorporation of 10 g of lyophilized leaf or pod powder into the artificial diet (300 ml) of diet results in maximum differences in survival and development of *H. armigera* larvae between the resistant (ICPL 332) and susceptible (ICPL 87) genotypes (29). However, there are subtle differences in larval weight and mortality between the insects reared on fresh leaves and pods and those fed on diets with lyophilized leaf or pod powder possibly because of effect of nutrients in the artificial diet on the biological activity of secondary metabolites in pigeonpea.

Measurement of resistance

Percentage damage to pods is the most common criterion for evaluating genotypic susceptibility to pod borers, *H. armigera* and *M. vitrata*. However, this criterion often leads to unreliable results due to variations in insect population over space and time, damage to flowers, dropping of the reproductive parts as a result of early infestation, and the genotypic ability to produce a second flush in case the first flush is lost due to pod borer damage. The second flush at times may escape insect damage, resulting in erroneous results. To overcome these problems, the test material can be evaluated on a 1 to 9 damage rating scale, taking into consideration the numbers of fruiting bodies retained on the plant, distribution of fruiting bodies throughout the plant canopy, and the proportion of the pods damaged by *H. armigera* and *M. vitrata* (1 = plants with little damage during the vegetative stage or showing good recovery from damage, large numbers of fruiting bodies retained on the plant with uniform distribution throughout the plant canopy, and < 10% damage to the fruiting bodies; and 9 = plants with poor recovery from damage, fewer fruiting bodies retained on the plant, uneven distribution of the fruiting bodies, and > 80% of the fruiting bodies damaged by the larvae) (32). Pod fly, *M. obtusa* and pod wasp, *T. cajaninae* damage can be evaluated by counting the number of pods infested, and the proportion of locules /seeds damaged. Pod bug damage is difficult to assess. Counting the proportion of pods

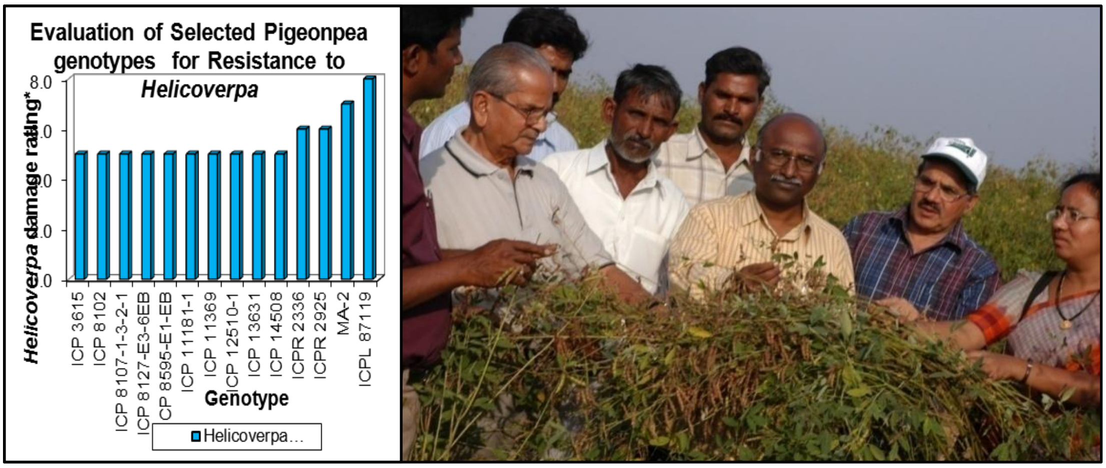


Figure 2. Relative resistance/ tolerance of pigeonpea genotypes for resistance to pod borer, *Helicoverpa armigera* (left); pod borer tolerant genotype ICPL 332WR grown on farmers fields in Telangana, India

infested, and the number of shrivelled seed can be used to assess pod bug damage. The bruchid damage can be assessed by the proportion of seeds damaged or increase in bruchid population per unit of seed weight over 30 days. The resistance/ tolerance to pod borers can also be measured in terms of loss in yield under unprotected conditions in relation to the plots maintained under protected conditions (14).

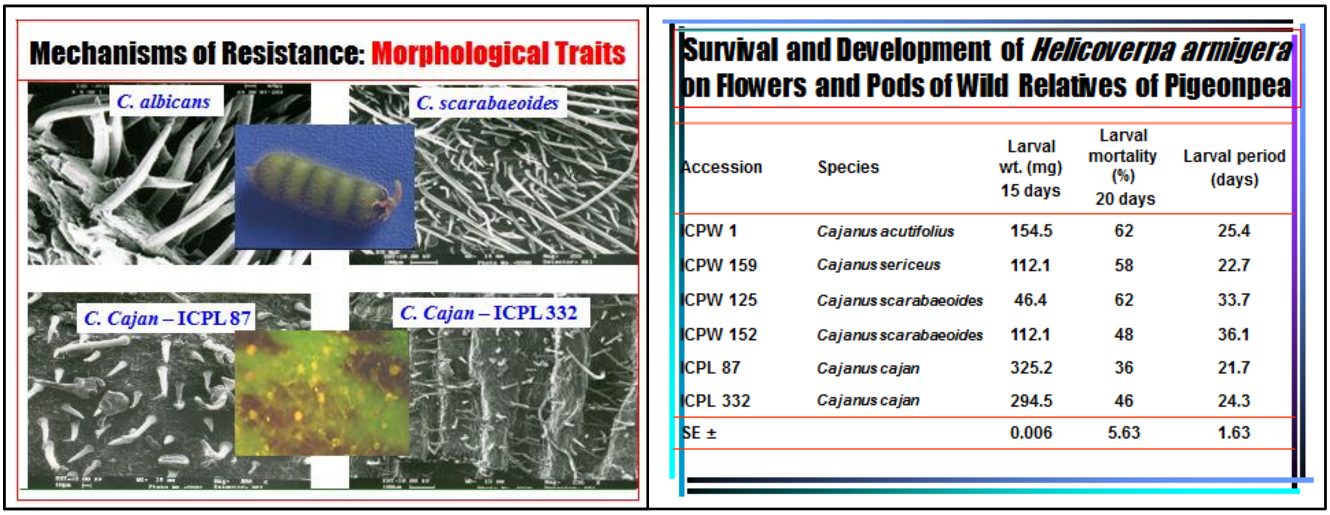
Identification and utilization of resistance

Screening of entire germplasm collections of pigeonpea (over 15,000 accessions) has led to identification of a few accessions with moderate levels of resistance to *H. armigera* (Fig. 2). However, lack of precision in evaluating thousands of accessions for resistance to the target pests probably resulted in missing many potentially good sources of resistance. In general, extra-early and determinate type genotypes are more susceptible to pod borer damage (24). P 54(b) (43); ICPL 5EB-EB (24), Phule T 1, Prabhat, T 21, Phule T 3 and 7411 (25); DL-78-1, ICPL 155, TAT 9 and TAT 10 (3); ICPL 1, H 79-6, UPAS 120, GP Nos. 17, 20, 24, 33, 30, 40, 43 and 45 (18); Bahar, ICPL 94, ICPL 154 and ICPL 85059 (10), ICPL 332, PPE 45-2 (ICP 1964), MA 2 and ICPL 84060 (28); ICPL 6, PPE 45-2, ICP 1903, MA 1, ICPL 187-1, ICPL 288, T 21, ICP 909, ICPL 86040, MAZ, ICPL 2, TA 10, ICPL 1, Pant A1, ICP 7345-1-5, BDN 7, DA 2, ICP 4070, ICP 3615, BSMR 1, ICP 10531, ICPL 201, ICP 109BB, (AUT 82-1), ICPX 77303, ICPL 87089, Bahar, ICPL 87088, ICP 7946-E and ICP 9889 (30); ICPL 7035, GAUT 85, ICPL 87075 and ICPL 151 (2); HPA 92 (13), Bori (27) and T 21 (23), PDA 88-2E and PDA 92-1E (5), PDA-92-3E, PDA-89-2E and SL-21-9-2 (4), GAUT 85035 and BDN 2 (12) and ICPL 4 (44) have been reported to be relatively resistant to *H. armigera.*

Short-duration genotypes ICP 7, ICP 13011, ICPB 2089, ICPL 187-1, ENT 11 and ICPL 98008 have moderate levels of resistance to pod borer damage (scores 6.0 to 8.0 compared to 9.0 in ICPL 151). In the medium duration, the genotypes ICP 995, ICP 1071, ICP 3046, ICP 6128, ICP 8793, ICP 9414, ICP 10397, ICP 13633, ICP 16264, ICPR 3461, ICPR 3472, ICPR 3491, ICPL 96058, ICPR 2913, ICPL 20097, ICPL 20099 and ICPL 332 WR suffered low pod damage and yielded > 1,500 kg ha^{-1}. In the long duration group, the genotypes ICP 8266, ICP 8102, ICP 8595-E1-EB, ICP 12510-1, ICP 12759, ICPL 20120, ICP 8087 and ICPL 332 WR suffered low pod damage by pod borer, *H. armigera*, and/or pod fly, and pod bug, and also exhibited high yield potential (> 1,000 kg ha^{-1}) under unprotected conditions. In the international pigeonpea *Helicoverpa* nursery, twenty-five genotypes, including the resistant and susceptible checks, were evaluated for resistance to pod borer, *H. armigera* in field trials. ICPHaRL 4985-1, ICPHaRL 4985-11, ICPHaRL 4989-7, and ICPL 332 WR showed moderate levels of resistance to pod borer damage, and exhibited yield potential of > 1,500 kg ha^{-1}.

In Tandur Region, Telangana, the yields of ICPL 332 WR ranged from 812 kg ha^{-1} to 1,250 kg ha^{-1}, and of Asha (ICPL 87119) varied from 875 kg ha^{-1} to 1,865 kg ha^{-1} and of Maruti (ICP 8863) from 780 kg ha^{-1} to 1,076 kg ha^{-1}. Most of the farmers reported a better control and lower insecticide use in ICPL 332 WR than on Asha. In Gulbarga region, Karnataka, the average grain yields were 1,127 kg ha^{-1} in ICPL 332 WR, 1,171 kg ha^{-1} in Asha and 970 kg ha^{-1} in Maruti. Among the improved varieties ICPL 84060, ICPHaRL 4985-4, ICPHaRL 4985-11, ICPL 20058 and ICPHaRL 4989-7 yielded 1,049 kg ha^{-1}, 1,050 kg ha^{-1}, 1,084 kg ha^{-1}, 1,106 kg ha^{-1} and 1,122 kg ha^{-1} respectively.

Wild relatives as sources of resistance to insects. Wild relatives of pigeonpea such as *C. scarabaeoides* (L.) Thouars, *C. sericeus* (Benth. ex Baker) Maesen, and *C. acutifolius* (F. Muell.) Maesen are highly resistant to *H. armigera* (9, 40), while ICPW 141, ICPW 278, and ICPW 280 (*C. scarabaeoides*), ICPW 214 (*Rhynchosia bracteata* Baker), ICPW 14 (*C. albicans* (Wight & Arn.) Maesen) and ICPW 202 (*Flemingia stricta* Roxb.) showed resistance to both *M. obtusa* and *T. cajaninae* (36; Fig. 3). Attempts have also been made to transfer pod borer resistance from the wild relatives into the cultigen (11, 19, 20).



Mechanisms of Resistance: Morphological Traits

Survival and Development of *Helicoverpa armigera* on Flowers and Pods of Wild Relatives of Pigeonpea

Accession	Species	Larval wt. (mg) 15 days	Larval mortality (%) 20 days	Larval period (days)
ICPW 1	*Cajanus acutifolius*	154.5	62	25.4
ICPW 159	*Cajanus sericeus*	112.1	58	22.7
ICPW 125	*Cajanus scarabaeoides*	46.4	62	33.7
ICPW 152	*Cajanus scarabaeoides*	112.1	48	36.1
ICPL 87	*Cajanus cajan*	325.2	36	21.7
ICPL 332	*Cajanus cajan*	294.5	46	24.3
SE ±		0.006	5.63	1.63

Figure 3. Trichomes on the leaf/pod surface of pigeonpea and its wild relatives influence the genotypic resistance to *Helicoverpa armigera* (left); the wild relatives of pigeonpea affect the survival and development of pod borer (right)

Transgenic plants. While several transgenic crops with insecticidal genes have been introduced in the temperate regions, very little has been done to use this technology for improving crop productivity in the harsh environments of the tropics, where the need for increasing food production is most urgent (19). Transgenic pigeonpea plants with *cry1Ab* and soybean trypsin inhibitor (*SBTI*) genes have been developed (41), but are ineffective for controlling *H. armigera* (6).

Morphological and biochemical traits associated with insect resistance

Morphological (trichomes, cell wall lignification, branching and podding habit, and podwall hairs and trichomes) and biochemical factors associated with insect resistance can also be used as selection criteria. This permits the rapid determination of potentially resistant plant material. This also removes the variation associated with insect density, and the effect of environmental factors on the expression of resistance to insects.

Phenological traits. Pigeonpea genotypes with determinate growth habit, clustered pods, and dense plant canopy are more susceptible to pod borers, *H. armigera* and *M. vitrata* than those with non-clustered pods (33, 35, 39), while the genotypes with smaller pods, pod wall tightly fitting to the seeds, and a deep constriction between the seeds are less susceptible to *H. armigera* (23). Plant growth types and maturity also influence genotypic susceptibility to pod fly, *M. obtusa*. Podwall thickness, trichome density, and crude fiber content are associated with resistance to this insect in pigeonpea.

Leaf hairs and trichomes. Leaf hairs (that do not produce glandular secretions) play an important role in host plant resistance to insects. Wild relatives of pigeonpea such as *C. scarabaeoides* and *C. acutifolius* with non-glandular trichomes are not preferred by *H. armigera* females for egg laying (42), while glandular trichomes in pigeonpea are linked to susceptibility to *H. armigera*.

Secondary metabolites. Secondary metabolites influence host finding, oviposition, feeding, and survival and development of insects, and play an important role in host plant resistance to insects in grain legumes. Quercetin, quercetrin, and guercetin-3-methyl ether in the pod surface exudates of pigeonpea, play an important role in food selection behavior of *H. armigera* larvae in pigeonpea (7, 8). Total phenols and tannins in the podwall of pigeonpea are negatively associated with pod fly damage. Stilbene - a phytoalexin occurs at high concentrations in pigeonpea cultivars with resistance to *H. armigera* (8).

Nutritional factors. Nutritional factors such as sugars, proteins, fats, sterols, and essential amino acids, and vitamins also influence host plant suitability to insect pests. Total soluble sugars in pigeonpea podwall influence pod damage by *H. armigera*. Protein content of the podwall is associated with susceptibility, while total sugars are associated with resistance to *M. obtusa* in pigeonpea. Amylase and protease inhibitors in pigeonpea and its wild relatives have been shown to have an adverse effect on growth and development of *H. armigera* (26).

Mechanisms and inheritance of resistance

Antixenosis, antibiosis and tolerance are the major components of resistance to *H. armigera* and pigeonpea (15, 16). Numbers of *H. armigera* larvae can be estimated by sampling at the plant site where the damage has taken place, and at the appropriate phenological plant stage and time. Shaking the plants, use of sampling nets or actual counts are used to obtain an estimate of larval abundance. Numbers of larvae should be recorded in 3 to 5 plants at random in the center of each plot at 10 to 15 days after flowering. Larval mortality and prolongation of the larval period are the main components of resistance to *H. armigera* in the wild relatives of pigeonpea (31, 42).

The levels of resistance to *H. armigera* in the germplasm accessions are low to moderate. This has necessitated the need for selecting genotypes with greater ability to tolerate or recover from the pod borer damage. Since it is almost impossible to get high levels of resistance against *H. armigea* in any legume crop, search for genotypes with recovery resistance through their ability to have more pods and recover from initial damage would be more rewarding.

There is little information on inheritance of resistance to insects in pigeonpea. Trichomes in pigeonpea, which are associated with resistance/ susceptibility to *H. armigera* has been studied in interspecific crosses involving *C. cajan* × *C. scarabaeoides*. The trichomes in the wild parent (high density of the non-glandular trichomes C and D, and low density of glandular trichome A) were dominant over the trichome features of *C. cajan,* suggesting dominance of resistance over susceptibility in wild relatives, and a single gene governed this character (1).

Potential and limitations of HPR in pest management in pigeonpea

Host-plant resistance can be used as a principal component of pest control, as an adjunct to cultural, biological and chemical control and as a check against the release of susceptible cultivars. High levels of plant resistance are available against a few insect species only. However, very high levels of resistance are not a pre-requisite for use of HPR in integrated pest management. Varieties with low to moderate levels of resistance or those which can avoid the pest damage can be deployed for pest management in combination with other components of pest management. Deployment of *Helicoverpa*-resistant cultivars in pigeonpea should be aimed at conservation of the natural enemies and minimizing the number of pesticide applications. Use of the pigeonpea cultivars resistant to *Helicoverpa* will also improve the efficiency of other pest management practices, including the synthetic insecticides.

Utilization of plant resistance as a control strategy has enormous practical relevance and additional emotional appeal. It is in this context that host-plant resistance assumes a central role in our efforts to increase the production and productivity of crops. Plant resistance to insects is the backbone of any pest management system because: i) it is specific to the target pest or a group of pests, and generally has no adverse effects on the non-target organisms in the environment, ii) effects of plant resistance on insect population density are cumulative over successive generations of the target pest because of reduced survival, delayed development, and reduced fecundity, iii) most of the insect-resistant varieties express moderate to high levels of resistance to the *Helicoverpa* throughout the crop-growing season. In contrast, the pesticides have to be applied repeatedly to achieve satisfactory control of the pest populations, iv) HPR is compatible with other methods of pest control, and also improves the efficiency of other methods of pest management, and v) it does not involve any costs to the farmers.

However, plant resistance is not a panacea for solving all the pest problems. Development of plant varieties resistant to insect pests takes a long time. Some mechanisms of plant resistance may involve the diversion of some resources by the plant to extra structures or production of defence chemicals at the expense of other physiological processes including those contributing to yield (22). Although concentration of defence chemicals responsible for resistance is low in plant tissues, the total amount per hectare may be high, e.g. production cost of 34 kg of gossypol (which imparts resistance to *Helicoverpa/Heliothis* in cotton) in terms of glucose equivalent in cotton will be 70.7 kg of glucose ha^{-1} (21).

Chemical basis of plant resistance to insects at times can modify the toxicity of insecticides to insects, e.g., 2-tridecanone in wild tomato reduces the toxicity of carboryl to *Heliothis* (22). Some plant defence chemicals also affect the food quality. Most of the pigeonpea and chickpea (*Cicer arietinum* L.) genotypes with resistance to *H. armigera* are susceptible to *Fusarium* wilt (32), There is a need to break the linkage between the factors conferring resistance to the target insects and the low yield potential or arrive at threshold levels for the resistant traits (secondary metabolites) that results in reduced pest susceptibility, and at the same time do not have an adverse effect on the quality of the product.

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Hybrid pigeonpea: Accomplishments and challenges for the next decade

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Abstract: Release of the world's first commercial pigeonpea hybrid is considered a milestone in the history of legume breeding. At present three commercial hybrids with yield advantages of 30 -50% are available. This has been possible due to success breeding of (i) a stable CMS system, (ii) quality fertility restorers, and (iii) standardized seed production technology. To sustain the achievements of this breakthrough, it is essential that superior hybrids are bred at regular intervals. In this communication an attempt has been made to highlight the achievements of hybrid breeding and consolidate strategies to develop new high yielding hybrids and their seed technology using the latest breeding and genomics tools.

Key words: hybrid, male sterility, new approaches, pigeonpea, seed production

Introduction

Although the green revolution saved millions from hunger but it is also considered responsible for pushing pulses in the corner as far as their research and development is concerned, resulting in the stagnation of production and productivity. Pigeonpea (*Cajanus cajan* (L.) Millsp.) also suffered during this phase and its decade-old productivity stagnation has now become a serious concern. Releasing the first ever commercial pigeonpea hybrid represents a breakthrough towards genetic enhancement of yield. This note briefly discusses the major accomplishments achieved in breeding hybrids and strategies to sustain this momentum in the next decade.

Accomplishments

Hybrid technology. Development of hybrid technology started at ICRISAT in 1974 from scratch and it involved breeding of three major components - a cytoplasmic-nuclear male sterile (CMS) line, its maintainer, and fertility restorers. Besides this, information on seed production, genetic diversity, and quantum of hybrid vigor was also generated. The CMS system was developed by integrating nuclear genome of cultivated type into the cytoplasm of a wild species (4). The fertility restorers were identified from germplasm (7). Large scale hybrid seed production studies revealed that it is easy but needs insect pollinators. The on-farm validation at 94 locations, on average produced 1019 kg ha^{-1} of hybrid seed (Table 1). With the recommended seeding rate of 5 kg ha^{-1}, a healthy seed-to-seed ratio of 1 : 200 was achieved. Since in pigeonpea hybrid quality cannot be judged through grow-out tests, molecular markers (SSR) based purity tests were successfully developed and deployed (1, 5).

The first hybrid. The first commercial pigeonpea hybrid ICPH 2671, produced by crossing ICPA 2043 with ICPR 2671, was released in 2010 (6). In 21 multi-location trials it recorded 47% superiority over the check. In All India Coordinated Trials, the hybrid (2564 kg ha^{-1}) was 31% superior to the control. ICPH 2671 is highly resistant to diseases and tolerant to drought and water-logging. In the on-farm trials (Table 2) conducted in Maharashtra (782 trials), Andhra Pradesh (399 trials), Karnataka (184 trials), Madhya Pradesh (360 trials), and Jharkhand (288 trials) ICPH 2671 recorded 30% - 60% superiority over the best local cultivar. Overall, in all five states, ICPH 2671 was 46.6% better than the check in its productivity. Recently, two hybrids, ICPH 3762 (8) and ICPH 2740 (10), have also been released in India and these have also recorded > 30% yield advantages over the control in farmers' fields. The performance data of the three hybrids have shown that high yields can be achieved and the persistent yield plateau in pigeonpea can be smashed.

Table 1. The first pigeonpea hybrid (A × R) seed yields (kg ha^{-1}) recorded for ICPH 2671 in six Indian states

State	Locations	Highest yield	Mean yield
Andhra Pradesh	34	1750	998
Gujarat	4	1669	1179
Karnataka	2	1900	1138
Madhya Pradesh	9	3040	1674
Maharashtra	5	1017	603
Odisha	40	1040	523
Total / mean	94	-	1019

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Table 2. Performance of pigeonpea hybrids (yield, kg ha^{-1}) in the on-farm trials conducted in different Indian states

Hybrid	State	Farmers (no.)	Hybrid yield	Control yield	Standard heterosis (%)
ICPH 2671	Andhra Pradesh	399	1411	907	55
	Karnataka	184	1201	951	26
	Jharkhand	288	1460	864	69
	Madhya Pradesh	360	1940	1326	46
	Maharashtra	782	969	717	35
	Total/mean	2013	1396	953	46
ICPH 2740	Andhra Pradesh	47	1999	1439	39
	Gujarat	40	1633	1209	35
	Maharashtra	230	1525	975	56
	Madhya Pradesh	13	1814	1217	49
	Total/mean	330	1743	1210	44

Table 3. Demonstration of exceptionally high yields (kg ha^{-1}) of pigeonpea hybrids by some farmers under irrigation in the Indian state of Maharashtra

Locations	Area (m^2)	Hybrid yield	Control yield	Gain (%)
Kothoda	450	4667	3556	31
Nimgaon	1012	3951	2469	60
Salod	450	3956	2044	94
Tamoli	450	3889	2278	71
Mean	-	4116	2587	59

The challenges and strategies

The hybrid pigeonpea technology is now established and taking it to the doorsteps of the farmers is the biggest challenge before us. The extensive on-farm testing of hybrids in seven states has given positive signals to farmers about the potential of hybrids and their demand is on increase. Therefore, issues related to seed availability need attention from all corners. In this context, it is essential to convince both public and private companies about the financial viability of this technology. Therefore, besides interacting with them, on-farm seed production programs should be organized at strategic locations. In addition, to achieve maximum profitability suitable agronomic interventions should to be disseminated among farming community.

To meet important research challenges aimed to double the hybrid yields and improve the efficiency of production technology in the next decade, the key approaches are briefly outlined in the following passages.

Diversify hybrid parents. This is most important factor in breeding hybrids. The historical outbreak of southern corn leaf blight disease in the USA (11) gave a strong lesson to breeders about the significance of cytoplasmic diversity in hybrid breeding. In pigeonpea only two cytoplasm sources have been used and it necessitates breeding of more CMS lines with greater cytoplasmic diversity. For new male parents the primary gene pool of pigeonpea should be exploited. High frequency of fertility restoring genes in the germplasm (7) will benefit the program. Besides this, crossable wild relatives should also be used to generate diverse fertility restorers.

Establish heterotic groups. Grouping of germplasm into diversity-based heterotic groups is of immense value. So far in pigeonpea only seven heterotic groups based on hybrid performance have been reported by Saxena and Sawargaonkar (3) and they suggested crossing between diverse groups for achieving greater heterotic effects for seed yield. To avoid G × E effects in establishing heterotic groups, it is proposed that in future the potential germplasm should be classified on the basis of diversity information generated through both traditional as well as genomic approaches.

Explore temperature sensitive male sterility (TGMS). The ‘two parent hybrid technology’ has various advantages over the ‘three line’. This include elimination of fertility restorers and B-lines, utilization of greater variability, and production of more number of hybrids in a short time. In pigeonpea TGMS is of recent origin (2); and for the adoption of this technology in India, suitable seed production environments can be found easily (9). Efforts should also start to transfer this trait into diverse genetic backgrounds.

Use of genomics. The genomics tools that are simple, rapid, and cost effective can now be used to judge the genetic purity of hybrids and their parents. Besides this, genomics should be used to identify fertility restoring genotypes among germplasm and segregating breeding populations. The genomics should also be used to establish heterotic groups for breeding high yielding hybrids. This technology once fully developed should be made available to NARS partners and seed industry.

Breed hybrids for specific adaptation. In India many farmers take agriculture as a challenging business and invest resources to reap more profits. During extensive on-farm testing, it was observed that in certain regions/areas the farmers harvested exceptionally high yields from hybrids. Our records showed that in the Maharashtra state some farmers harvested about 4000 kg ha^{-1} from ICPH 2740 (Table 3) with > 50% superiority over the control. Therefore, to reap the genetic potential of the hybrids, it is important to develop locally adapted cultural recommendations for different cropping systems.

Improve seed technology. It is vital that quality hybrid seed is produced in greater quantities economically and with ease. To achieve this, seed production hot spots need to be identified. In addition, agronomical and ecological factors responsible for enhancing seed set should be investigated.

Summary

A breakthrough in pigeonpea breeding technology was achieved after 39 years of intensive research by ICRISAT and ICAR. The seed-to-seed ratio of 1:200 to 1:300 achieved in pigeonpea is high enough to make a commercial impact. This means that to replace about 20% (= 800,000 ha) of the pigeonpea area in India with hybrids, only 4000 ha of certified seed program would be required. In turn, it would add 40,000 t - 60,000 t of additional grain. At present it does not appear to be a difficult task but to achieve this, a firm commitment on the part of research institutions and seed industry is necessary. Further, to sustain the benefits of this technology, it is essential that strong R & D strategies are development and implemented at national level. The key for success, however, will be an efficient coordination among various public and private agencies.

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Genomic resources for pigeonpea

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Abstract: Pigeonpea is increasingly playing a critical role in the lives of many farmers in the semi-arid tropics, where it is grown for both subsistence and commercial use. The recent availability of genomic resources opened a new chapter in pigeonpea breeding and has led to a lot of progress in a relatively short period of time. Molecular markers have been developed and used for germplasm characterization. Both whole genome and transcriptome sequences have further improved our understanding of the genome. This review provides a summary of genomic resources available for pigeonpea breeding and also briefly discusses the way forward for pigeonpea improvement.

Key words: DArT, EST, NGS, QTL, whole genome sequence

Introduction

Advanced tools for the breeding and manipulation of pigeonpea [*Cajanus cajan* (L.) Millsp.] have been limited in the past but are developing quite rapidly. From just a few microsatellite markers in 2001, pigeonpea currently has a draft genome sequence (8), transcriptome assemblies, several on-going whole genome re-sequencing (WGRS) efforts to catalogue maximum possible variations and genomics-assisted breeding activities. To some extent, the research investment in advanced tools has also been matched with the development of relevant populations that have facilitated the identification of genomic regions contributing to traits of interest. The current major interest in hybrid pigeonpea production has further benefited from better characterization of male sterility through the sequencing of mitochondrial genomes.

Molecular marker availability and utilization

Simple sequence repeat markers (SSRs) have been the most widely utilized molecular markers in pigeonpea. More than 3,000 SSRs have been reported and Diversity arrays technology (DArT) markers have also been developed. These markers have been used in characterization of germplasm, development of low density linkage maps, quantitative trait loci (QTL) studies and hybrid purity testing. Additionally, single nucleotide polymorphism (SNP) markers have been recently developed, converted into competitive allele-specific polymerase chain reaction (KASPar) (6) and BeadXpress (Illumina, San Diego, CA) (5) assays (Table 1). The SNP markers have been integrated into a consensus pigeonpea map. The availability of a draft reference genome further makes WGRS and genotyping-by-sequencing (GBS) feasible for routine genotyping in pigeonpea.

Linkage maps and quantitative trait loci (QTLs) identified

Due to the low polymorphism levels within the cultivated species experienced in pigeonpea, earlier linkage maps were developed using F_2 mapping populations between inter-specific crosses (3, 9). With the increasing numbers of polymorphic markers, intra-specific linkage maps have been generated based on genic SSR markers (3) and also on Bacterial Artificial Chromosomes (BAC)-end SSRs (1). The linkage maps have been further used to identify QTLs for several agronomic traits (1, 3). Both QTL analysis and comparative genomics have led to the identification of *CcTFL1* (4), a likely candidate gene for determinate growth habit. High density linkage and association mapping studies are in progress, especially in combination with GBS and WGRS in order to identify novel alleles for traits of agronomic importance such as disease resistance and yield and yield related traits.

Table 1. Genomic resources in terms of molecular markers, genotyping assays and sequence reads available in public domain

Genomic resource	Number of markers/assays and reads
Simple sequence repeat (SSR) markers	3,200
Single nucleotide polymorphisms (SNPs)	10,000
GoldenGate assays	768 SNPs
KASPar assays	1,616 SNPs
Sanger expressed sequence tags	~20,000
454 /FLX reads	496,705
Tentative unique sequences (TUSs)	21,432
Illumina reads(million reads)	> 160 (14 parents)

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Genome and transcriptome sequences

The draft genome sequence for pigeonpea has recently become available (8). Scaffolds representing about 72.7% of the genome (estimated total genome size of 833 Mb) have been assembled for the genotype ICPL 87119 (popularly known as Asha) using the Illumina platform. The draft genome, which has 48,680 protein coding genes, has also provided a large resource of molecular markers, e.g. 309,052 SSRs and 28,104 SNPs. Mitochondrial genome sequence of three pigeonpea lines (ICPA 2039 - male sterile line, ICPB 2039 - the maintainer line and ICPH 2433 - a hybrid line) and a wild relative (ICPW 29) have also been sequenced in an effort to characterize the molecular mechanisms of cytoplasmic male sterility (CMS) (7). A transcriptome assembly comprising of 21,434 transcript assembly contigs (TACs) (2) has been generated, which combined a number of earlier transcriptome studies by analyzing 9,888 Sanger ESTs, 43,324 contigs from 1.696 million FLX/454 reads and 127,754 tentative unique sequences (TUSs). The genome and transcriptome data, together with their associated gene annotations are available on the Legume Information System (LIS) at http://www.legumeinfo.org. The LIS provides a community resource that integrates genetic, genomic and trait data across legume species. The raw data is available on the webpage of the International Initiative on Pigeonpea Genomics (IIPG) website at www.icrisat.org/gt-bt/iipg/Home.html.

Gaps

There is need to undertake more functional characterization of interesting genes identified from the genome and transcriptome sequencing processes in order to improve the annotation of the available reference genome. TILLING (Targeted induced local lesions in genome) can further reveal rare mutations resulting in novel phenotypes as has been done in other major crops. There are currently no known reports of genomic selection in pigeonpea. The possibility of undertaking WGRS/GBS together with precise trait phenotyping in pigeonpea makes genomic selection a very attractive process for varietal and hybrid improvement.

Conclusion and outlook

The genomic resources made available in pigeonpea have positioned pigeonpea well for advanced and facilitated breeding process. The relevant mapping populations will be useful in addressing some of the most serious breeding challenges including pests and diseases. Other than the utilization of wild species accessions in the understanding of cytoplasmic male sterility, the wild relatives present an alternative source of novel genes that can now be exploited with relative ease given the availability of genomic resources. Innovation in pigeonpea will come from translating the available advanced tools into practical solutions for the farmer, consumer and processors.

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Genetic transformation of pigeonpea: An overview

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Abstract: Biotechnology over the years has emerged as a promising tool to overcome biotic and abiotic constraints in crop species that lack the required traits for crop improvement through conventional and molecular breeding approaches. New engineering tools are now available not only for single gene traits, but also to engineer multiple genes or plant regulatory machinery for driving the expression of different stress-responsive genes. Here, we discuss the recent progress and current status of transgenic technology in pigeonpea towards developing host plant resistance to various biotic and abiotic stresses and its use in the improvement of this important pulse crop.

Key words: genetic transformation, pigeonpea, trait, transgenic, tissue culture

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is an important pulse or grain legume crop cultivated in semi-arid tropical and subtropical areas of the world that ranks third in Asia and sixth in the global pulse production after beans (*Phaseolus* spp.), pea (*Pisum sativum* L.), chickpea (*Cicer arietinum* L.), broad bean (*Vicia faba* L.) and lentil (*Lens culinaris* Medik.). Most of the differences in potential yields and the actual harvests by pigeonpea farmers have been attributed to several biotic and abiotic stress factors, besides the low productivity potential of marginal lands, where this crop is commonly grown.

Genetic improvement of pigeonpea has been restricted due to the non-availability of suitable genetic resources and strong sexual barriers between the cultivated and wild species. Recombinant DNA and genetic transformation technologies can circumvent limitations due to taxonomic barriers and limited gene pool for resistance to pathogens, insect pests and tolerance to various abiotic stresses. Further, molecular biological techniques provide capabilities to engineer host plant resistance that is effective against both the specific and to a broad spectrum of pathogens and are genetically stable. However, for effective use of genetic engineering techniques, efficient regeneration and recovery of stable transformants is essential.

Tissue culture and transformation systems

Various laboratories have reported successful regeneration of pigeonpea by direct and indirect organogenesis from a variety of explants ranging from hypocotyls, immature embryos, leaves, cotyledons, nodal halves of cotyledons, and cotyledon-derived nodular callus (Fig. 1). Amongst the various explants used, direct organogenesis from cotyledonary node and leaf explants appear to be highly reproducible and efficient for use in genetic transformation studies. The type of genotype, physiological maturity and the nature of tissues (vegetative or reproductive) appear to be important factors

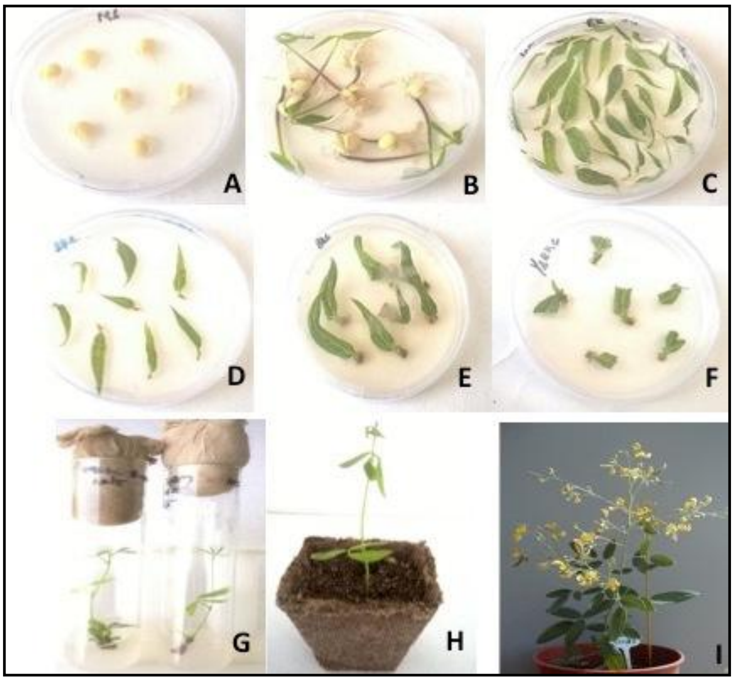

Figure 1. Regeneration of adventitious shoots and development of plants from leaf explants of *Cajanus cajan* L. (Millsp.): (C & D) leaf explants at 0 d on MS medium supplemented with 5 ⌠*M* BA and 5 ⌠*M* kinetin; (E) differentiation of shoot buds from petiolar cut end; (F) leaf explants with proliferating multiple shoots on shoot development medium with half-cut lamina; (G) individual shoot on MS medium supplemented with 0.58 ì*M* GA3 (elongation medium) after 7 d; (H) well-rooted putative transformant after hardening; (I) a well-established transgenic pigeonpea plant at flowering stage

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besides the growth regulators to bring about the expected response in pigeonpea tissue cultures. Although pigeonpea was considered to be recalcitrant for long, recent reports on its genetic transformation with convincing molecular evidence indicate a feasibility of *Agrobacterium*-mediated genetic transformation. *Agrobacterium*-mediated gene transfer using leaf discs, shoot apics and cotyledonary nodal explants in pigeonpea was obtained (1, 2, 6, 7, 8), as well as a non-tissue culture-based method of generating transgenic pigeonpea using *Agrobacterium tumefaciens*-mediated trans-formation of injured embryonal axes (5).

Status of transgenic research in pigeonpea

Several transgenic traits have been incorporated in pigeonpea such as insect resistance, protein quality, and edible vaccines. Nevertheless, resistance to *Helicoverpa armigera* Hübner (legume pod borer) in pigeonpea is an ideal seed borne solution to enhance its productivity through an integrated pest management. *H. armigera* is the most important yield constraint in pigeonpea for which there is no absolute resistance available in the cultivated germplasm. Besides the genes producing insecticidal proteins from *Bacillus thuringienses* Berliner (Bt) and proteases, insecticidal chitinase is also important in controlling the devastating pod borer by dissolution of the chitin, an insoluble structural polysaccharide that occurs in the exoskeleton and gut lining of insects. Gene pyramiding with two different insecticidal genes and tissue-specific expression to reduce the risk of developing insect resistance isanother attractive option to combat this pest for durable resistance. Expression of a chimeric *cry1AcF* (encoding *cry1Ac* and *cry1F* domains) gene in transgenic pigeonpea has been demonstrated towards resistance to *H. armigera* (4). Research activities at ICRISAT involving *Bt cry* genes have yielded promising results where a large number of transgenic events are currently being evaluated for their efficacy. These transgenics not only showed high mortality of the larva but also resisted the damage caused by the larvae.

Pigeonpea transgenics carrying *dhdps-r1* gene for the overproduction of sulfur-containing amino acids, driven by a phaseolin or an *Arabidopsis* 2S2 promoter have been developed using *Agrobacterium* transformation and particle bombardment (10). A 2- to 6-fold enhanced DHDPS activity compared to the wild type was observed in the transgenic immature seeds which reflected a 1.6 to 8.5 times enhanced free lysine content compared to the wild types. Moreover, based on the lysine degradative enzyme, lysine ketoglutarate reductase (LKR) it was revealed that at later stages of seed development, LKR activity increased in the transgenic lines, that not only increased lysine levels but also resulted in conspicuous increase in free threonine. At ICRISAT, work is ongoing to develop biofortified pigeonpea for the enhancement of β-caretone (provitamin A), is a precursor of vitamin A. Success in producing transgenic pigeonpea plants with high-levels of β-caretone will have much to contribute to the malnourished population in the drylands of the world.

Besides, there have been efforts on developing pigeonpea as potential edible vaccines for goat and sheep to rinder pest virus and peste des petits ruminants virus, using haemaglutinin gene of rinder pest virus and haemaglutinin neuraminidase gene of *peste des petits ruminants virus* (PPRV-HN) respectively (3). Similarly, a constitutively expressed P5CSF129A gene in pigeonpea transgenics showed a higher proline accumulation and a lower lipid peroxidation than their non-transformed counterparts when subjected to 200 mM NaCl (9).This manifested in an enhanced growth, more chlorophyll and relative water content under high salinity, thereby suggesting that overproduction of proline could play an important role against salt shock and cellular integrity in pigeonpea.

Conclusions

In absence of availability of traits/genes-conferring resistance to biotic and abiotic constraints in the primary/cross-compatible gene pool, application of genetic engineering technology is a viable option to address complex problems in pigeonpea cultivation. Genetic transformation of pigeonpea can be seen as a logical extension of plant breeding research that has a considerable potential to benefit the global pigeonpea production systems. Since the implications of risk assessment studies of transgenics are dependent on the social context, a participatory approach is needed to determine the balance of benefits to risks. It is critical to determine baseline data on food safety, against which the safety of these transgenics can be evaluated. While this technology is critical in overcoming severe bottlenecks associated with conventional and/or molecular breeding approaches, a challenge will be to use this technology as part of a long-term strategy to improve nutrition, preserve biodiversity, and promote more sustainable agricultural practices.

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An overview of varietal development programme of pigeonpea in India

by Indra P. SINGH*, Abhishek BOHRA and Farindra SINGH

Abstract: In India, pigeonpea varietal improvement programme was started in the beginning of 20th century. As a result large number of pure line varieties was developed. In 1967 for systematic pigeonpea breeding programme All India Coordinated Pulses Improvement Project (AICPIP) was created which was followed by establishment of All India Coordinated Research Project on Pigeonpea in 1996. These developments encouraged and supported the systematic research on resistance breeding particularly for biotic stresses including diseases like Phytophthora stem blight, wilt, sterility mosaic and Alternaria blight and insect pests like pod fly and pod borer. These efforts resulted the development, release and notification of high yielding, stable and disease resistant varieties of pigeonpea like, UPAS 120, Pusa 992, Rajeshwari, ICPL 87119, ICP 8863, BSMR 736, BSMR 853, DA 11, NDA 3, Bahar, MA 6 and IPA 203. At present most of the pigeonpea area of the country is under these varieties.

Key words: disease resistance, hybrids, pigeonpea breeding, plant type, varieties, yield

Breeding for improved varieties of pigeonpea was initiated in the country at the beginning of the 20th century particularly with the establishment of Imperial Agricultural Research Institute at Pusa in 1910. The major breeding philosophy was selection against the wild traits mostly favoured and conserved during the process of evolution in the nature such as indeterminate growth habit, non synchronous maturity, pod shattering, seed dormancy, photo-thermo sensitivity, spreading habits, seed colour and so on. As a result large number of pure line varieties was developed on the basis of their good performance at a particular location in specific climatic conditions. Creation of All India Coordinated Pulses Improvement Project (AICPIP) in 1967 is considered to be the landmark in pigeonpea breeding of the country. Later on, pigeonpea breeding got further momentum when in 1996 trifurcation of All India Coordinated Pulses Improvement Project resulted in creating the All India Coordinated Research Project on Pigeonpea, chickpea and MULLaRP crops.

Major achievements

Breeding for high and stable yield. Yield is a complex trait to breed for because of its low heritability and high genotype × environment interaction. To overcome this, efforts were made to identify high and stable genotypes by evaluating advanced breeding lines at AICRPIP locations across the country over the years. This has resulted in identification of over 100 varieties since the inception of AICRPIP in 1967. These varieties are not only high yielding under different situations but also incorporate one or the other desirable feature, making them a good agronomic base for further improvement. To increase yield potential, hybridization among diverse parents in various fashions like biparental, triple cross, double cross has been attempted followed by convergent breeding to accumulate high yielding genes and other desirable traits. Seed size, pods per plant and seed per pod have been pursued as selection criteria for improving yield indirectly. Some of the high yielding varieties with wide adaptation are UPAS 120, Pusa 992, TT 401 and Rajeshwari (Table 1), BDN 2, Maruthi, Asha, BSMR 736, BSMR 853, BDN 708, MA 3, JKM 189, Vipula and TJT 501 (Table 2) and Bahar, T 7, Sharad, Pusa 9, Narendra Arhar 1, MA6, MA 13, Narendra Arhar 2 and IPA 203 (Table 3). Singh (8) identified appropriate plant type in pigeonpea for high and stable yield in different agro-climatic conditions.

Mutation breeding has been employed to generate additional variability since mid fifties. Initial experiments were mainly aimed at observing morphological variations induced by mutagenesis. Further experiments were expanded to study effectiveness and efficiency of a wide array of physical and chemical mutagens. A wide array of economically useful mutants, both induced and spontaneous, such as resistant to key diseases, male sterility, short duration, plant type, seed size and plant height has been reported. Some of them have been either released directly as variety or used as donor for improving the traits.

Breeding for resistance to biotic stresses

Breeding for diseases. Three diseases *viz.* Fusarium wilt, sterility mosaic and Phytophthora stem blight are very important from economic loss point of view because pigeonpea production suffers a lot from the following three diseases:

1) Wilt. It is caused by *Fusarium udum* Butler. Several workers have reported the occurrence of pathogenic variability. Systematic breeding programmes were initiated at different centres to develop resistant varieties. *Viz* ICP 8863 (Marruthi), ICPL 87119 (Asha), BDN 1, BDN 2, C 11, NP (WR) 15, Narendra Arhar 1, ICPL 87 (Pragati), Jawahar (KM 7), BSMR 175, BSMR 736 etc. This was made possible due to development of screening techniques and identification of resistant donors. Crash programmes were also initiated under AICRPIP to develop varieties resistant to wilt, which resulted into the development of resistant varieties.

2) Sterility mosaic. The causal agent of the disease has been recently reported to be a virus and named as pigeonpea sterility mosaic virus (2). This virus spreads through mite vector, *Aceria cajani* ChannaBasavanna, Srinivas et al. (13) reported the monogenic recessive inheritance as well as digenic complementary gene interaction for diverse

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Table 1. Early maturing varieties of pigeonpea developed in India since independence

Variety	Pedigree	Area of adaptability	Year	Special features
Pusa Ageti	Brazil 1 x NP 69	Northern and Central India	1972	Determinate, susceptible to pod borer
T 21	Type 1 x Type 190	Northern and Central India	1973	Wider adaptability
Co 2	Selection from P 4728	Tamil Nadu	1974	Small seeded
PA 3	Selection from germplasm	North India	1975	Multiple disease resistant
Prabhat	Type 1 x Type 190	NWPZ	1975	Extra early and compact
UPAS 120	Selection from P 4768	NWPZ	1976	Wider adaptability, high yielding
Hy 5	Selection from PI 3701	A.P. and Karnataka	1980	White seeded, resistant to sterility mosaic
Pusa 84	Pusa Ageti x Type 21	Northern India	1980	Semi determinate
AL 15	Selection from P 8-9	Punjab	1981	Suitable for multiple cropping
Vishakha 1 (TT 6)	Mutant of Type 21	Maharashtra	1982	Erect and compact
Pusa 74	Khargaon 2 x Pusa Ageti	Northern India	1982	Semi determinate, medium tall
Manak	Type 21 x UPAS 120	Northern India	1983	Extra short duration
TAT 10	TT 8 x TT 2	Maharashtra	1984	Extra short duration
Co 4 (580)	Pure line selected from germplasm of Hyderabad	Tamil Nadu	1984	Medium large seed
Sagar (H 77-208)	Type 21 x UPAS 120	Haryana	1984	Semi spreading, indeterminate
TT 5	Mutant of Type 21	Northern India	1984	Semi spreading
Pusa 33 (Ramanujam)	C 11 x UPAS 120	Northern India	1985	Tolerant to wilt and sterility mosaic
ICPL 151 (Jagriti)	ICP 6997 x Prabhat	Western U P, South and Central India	1985	Determinate
ICPL 87 (Pragati)	Type 21 x JA 27	All Zones	1986	Resistant to wilt and suitable for ratooning
Pusa 85	UPAS 120 x NO. 148	Northern India	1987	Indeterminate and semi spreading
AL 201	AL 16 x QLP 200	Punjab	1993	Indeterminate
Pusa 855	Mutant of Type 21	Northern India	1993	Indeterminate, medium large seed
ICPL 84031 (Durga)	Prabhat x UPAS 120	Andhra Pradesh	1995	Extra early, determinate
AKT 8811	Selection from ICPL 6 x DA 6	Maharashtra	2000	Indeterminate, high yielding
Pusa 992	Selection from 90306	NWPZ	2002	Indeterminate, high yielding
CORG 9701	Selection from PB9825	Tamil Nadu	2003	Indeterminate, large seed
GAUT 001E	ICPL 269 x Pusa sweta	Central Zone	2004	Indeterminate, cream colour seeds
PAU 881	H 89-5 x ICPL 85024	NWPZ	2007	Indeterminate, yellowish orange seeds
TT 401	ICPL 84008 x TT 6	Central Zone	2007	Indeterminate, cream colour seeds
TJT 501	ICPL 84008 x TT 6	Central Zone	2008	Tolerant to drought, semi spreading
PA 291	UPAS 120 x KPBR 80-2-1	NWPZ	2009	Indeterminate, tolerant to *Phtophthora* stem blight
VLA 1	ICP6 x Pant 2	NHZ & NWPZ	2011	Indeterminate, early maturing and semi - spreading
Phule T 0012	ICP 332 x BSMR 736	CZ	2012	Moderately resistant to fusarium wilt, SMD and tolerant to pod borer and pod fly.

isolates and different crosses. Monogenic recessive inheritance is also reported by Singh et al. (12). A crash programme within AICRPIP to develop sterility mosaic resistant varieties of pigeonpea has resulted into the development of several resistant varieties *viz*. Hy 3c Bahar, Sharad, Asha, BSMR 175, BSMR 736, Pusa 9, Narendra Arhar 1, MA 3 etc.

3) Phytophthora stem blight. The disease is caused by fungus *Phytophthora drechsleri* f. sp. *cajani* (Pal et al.) Kannaiyan et al., which is highly variable. Singh *et al.* (11) reported the inheritance of resistance to Kanpur race in which it was found that two homozygous recessive gene (pdr_1 pdr_1 pdr_2 pdr_2) were responsible for resistance in the parents 'KPBR 80-2-1'and 'KPBR 80-2-2' and that a single recessive gene (*pdr pdr*) was responsible for resistance in the parents, 'Hy 3C' and 'BDN 1'. Resistant varieties could not be developed till date, however, some breeding lines are reported to be tolerant *viz.,* KPBR 80-2-1, KPBR 80-2-2, GAUT 82-55 and ICP 8103. Among the wild species some accessions of *Cajanus platycarpus* are reported to be resistant to Phytophthora blight. Efforts are now being made to develop varieties with multiple diseases resistance at AICRP centres.

4) Alternaria blight. This disease occurs in Bihar and Eastern U.P. in the crop sown in Pre-rabi season. This fungus is also variable and is known as *Alternaria alternata* (Fr.) Keissl. Resistance to it is governed by a recessive gene (4). Varieties/lines resistant to this disease are Sharad, Pusa 9, ICPL 366 and MA 126-1.

Breeding for insect pest resistance. Pod borer (*Helicoverpa armigera* Hübner) and pod fly (*Melanagromyza obtusa* Malloch) are the two most important pests of pigeonpea besides *Maruca testulalis* Geyer etc. Pod borer causes great loss to the pigeonpea of all maturity groups while pod fly mainly affects the yield of late duration pigeonpea.

1) Pod borer. Selecting single plants under pesticide free conditions, subsequent progeny evaluation, and continued selection and selfing have resulted in the identification of relatively stable differences among genotypes for the damage caused by *H. armigera* or compensation in yield after damage particularly in the medium duration

Table 2. Medium duration varieties of pigeonpea developed in India since independence

Variety	Pedigree	Area of adaptability	Year	Special features
Sharda (S8)	Brazil 1 x NP (WR) 15	Delhi and Karnataka	1971	Profuse branching
C 11	Sangareddy (Andhra Pradesh) Local selection	Central and South India	1975	Wilt resistant
No. 148	Local selection from Nagpur germplasm	Central India	1975	Semi spreading, profuse branching
JA 3	No. 148 x C 11	M. P.	1975	Semi spreading
BDN 1	Local selection from Bori 192-42	Maharashthra & MP	1978	Wilt resistant and white seed
BDN 2	Local sel. from Bori germplasm	Maharashthra & MP	1979	Wilt resistant and white seed
PT 221	Local selection	South zone	1979	White seed
GS 1	Selection from local germplasm	Karnataka	1979	White seed
LRG 30	Local selection of Lam	Andhra Pradesh	1980	White large seed
LRG 36	Local selection	Andhra Pradesh	1982	Profuse branching
Hy 3 A	2817-1-A	South Zone	1980	White large seed
Hy 3 C	PI 2817-2	Andhra Pradesh	1982	Semi spreading, large seed, large pods
WB 20	Prabhat x B 517	West Bengal	1983	Resistant to Alternaria blight
ICPL 8863 (Maruthi)	Selection from landrace of Maharashtra	South Zone	1985	Indeterminate, resistant to wilt, spreading, small and white seed
ICPL 332 (Abhaya)	Selection from ICP 1903 E-1-4E2	Andhra Pradesh	1989	Resistant to wilt
JA 4	No. 148 x C 11	M. P.	1991	Resistant to wilt
BSMR 175	(PA 3 x ICP 7035) x BDN 2	Maharashtra	1991	White seed, resistant to wilt & sterility mosaic
BirsaArhar1	Selection from BR 65	Bihar	1992	Resistant to wilt
ICPL 87119 (Asha)	C 11 x ICPL 6	Central Zone & South Zone	1993	Indeterminate, spreading, large brown seed, resistant to wilt and sterility mosaic
Co 6	Mutant of SA 1	Tamil Nadu	1993	Indeterminate
TS 3	ICP 87051 x PT 221	Karnataka	1995	Large white seed and resistant to sterility mosaic
BSMR 736	ICP 7217 x No. 148	Maharashtra	1996	Red seed, resistant to wilt and sterility mosaic
KM 7 (Jawahar)	ICP 8863 x LRG 30	Central Zone	1996	Resistant to wilt and Phytophthora blight
MA 3	Selection from Malviya Arhar 2	Central Zone	1999	Spreading, constricted pods
ICPL 85063 (Laxmi)	BDN-1 x (T 21 x JA 275)	Andhra Pradesh	2000	Semi spreading, suitable for pre-*rabi* planting
BSMR 853	(ICPL 7336 x BDN 1) x BDN 2	Central Zone	2001	Resistant to wilt and sterility mosaic
MA 3	MA 2 x Bahar	Madhya Pradesh	2002	Spreading
TT 401	ICPl 84008 x TT 6	Central Zone	2004	Indeterminate, large seed
BDN 708	BDN 2 x ICPL 87119	Central Zone	2004	Resistant to wilt and sterility mosaic
Vipula	ICPL 151 x Prabhat	Central Zone	2006	semi spreading, resistant to wilt
BRG 1	Hy 3C x Hosakote	South Zone	2006	indeterminate , vegetable type
JKM 189	BDN 2 x ICPL 87119	Central Zone	2006	tolerant to drought, resistant to wilt
BRG 2	Selection from Nalamangala Local	South Zone	2009	semi spreading, dual purpose type
PKV,Tara (TAT-9629)	ICPL 84008 X TT6	CZ	2011	indeterminate, semi spreading and tolerant to pod borer and pod fly
Rajeev Lochan	Sel. from ICPL 92060	Chattishgarha	2011	Resistant to wilt & SMD
WRG-65	WRG-13 X ICPL-87051	SZ	2012	Indeterminate, spreading, medium, resistant to wilt, tolerant to pod borer
BDN 711	Sel. From BPG 111	CZ	2012	Indeterminate, spreading, resistant to wilt and SMD, escape terminal drought

group. Breeders have used these sources to incorporate low susceptibility into good agronomic background using the pedigree method of breeding. ICPL 87088 and ICPL 87089, ICPL 84060 and ICPL 332 are the lines developed in this way that produced some yield, even during the heavy pod borer epidemic that devastated pigeonpea and cotton in peninsular India.

2) Pod fly. The second most damaging pest of pigeonpea in Asia is the pod fly. This small black fly lays eggs through the wall of the young pod, and its larva feeds in a seed. The fly emerges from the pod through a characteristic round hole. Singh and Lal (10) studied the inheritance of resistance to pod fly and observed that the resistance is governed by two genes with interaction between recessive and dominant alleles. Lal *et al.* (1999) has also reported that the PDA 88-2E and PDA 89-2E are good combiners for pod fly resistance. Based on 6-11 years of screening some pigeonpea lines have been identified as resistant to pod fly. These lines are PDA 88-2E, PDA 89-2E, PDA 92-2E and PDA 93-2E.

Breeding for early maturity

Breeding short duration varieties has been directed for irrigated areas, where the wheat crop can be taken after harvest of such pigeonpea varieties, which mature by the middle of November. Besides, for drought escape short duration varieties suit well. Development of early maturity pigeonpea varieties has made pigeonpea-wheat rotation a great success in northern states.

Breeding for *rabi* planting

In high rainfall areas of eastern Uttar Pradesh, Bihar and West Bengal, the pigeonpea population becomes sub-optimum when planted during the monsoon season. To ensure optimum plant stand, sowing during September-October, when

Table 3. Long duration varieties of pigeonpea developed in India since independence

Variety	Pedigree	Area of adaptability	Year	Special features
Type 7	Selection from landrace of Lucknow	NEPZ	1960	Compact tall
WB-7 (Sweta)	Pure line selection from landrace	West Bengal	1972	Semi compact
B 517 (Chuni)	Selection from N 4554	West Bengal	1972	Spreading
Type 17	Selection from landrace of Pratapagarh	UP	1978	Semi spreading
Gwalior 3	Sel. from local germplasm of Muraina	UP, MP	1980	Spreading, profuse secondary branches
Bahar (1258)	Selection from landrace of Motihari	NEPZ	1980	Resistant to sterility mosaic, suitable for pre-rabi sowing, high yielding
DA 11 (Sharad)	Bahar x NP (WR) 15	Bihar	1993	Compact, resistant to Phytophthora blight and sterility mosaic, suitable for pre-rabi sowing
Pusa 9	UPAS 120 x 3673	NEPZ	1993	Indeterminate, resistant to Phytophthora stem blight and sterility mosaic, suitable for pre-*rabi* planting
NA-1 (Narendra Arhar-1)	Selection from landrace of Faizabad	UP	1997	Resistant to sterility mosaic and tolerant to wilt and Phytophthora stem blight
KA 32-1 (Amar)	Selection From Bahar	UP	1997	Compact, resistant to sterility mosaic
K 91-25 (Azad)	Bahar x KPBR 80-1	UP, Bihar	1999	Resistant to sterility mosaic
MA 6 (L)	MA 2 x Bahar	NEPZ	2002	Indeterminate, spreading, and resistant to *SMD* and wilt
MAL 13	(MA 2 x MA 166) x Bahar	NEPZ	2004	Spreading, resistant to sterility mosaic ant tolerant to wilt, large seed size
NDA 2	Selection from NDA -1	NEPZ	2005	Compact, indeterminate, tolerant to wilt
NDA 3	ICP 8862 x ICPL 11204	NEPZ	2006	Compact, indeterminate, large seed
IPA 203	Bahar x AC314 x AC314	NEPZ	2012	Resistant to SM, tolerant to Phytophthora blight and Fusarium wilt

rainfall ends, has been found appropriate and reasonable. Pandey and Singh (5) have suggested that the number of primary branches/plant and pods/plant are the prime contributing characters to seed yield in *rabi* pigeonpea. For this situation, Bahar, WB 20 (105), AS 71-31, DA11, Pusa 9 and NDA 3 have been developed. In Bihar Alternaria leaf blight has attained serious form in *rabi* crop and the variety DA 11 (Sharad) which is resistant to this disease is recommended.

Breeding for ideal plant type

Four types of plant habits *viz.,* erect plants with crowded inflorescence, erect plants with scattered inflorescence, spreading plants with straggling branches and spreading plants with non straggling branches were distinguished by Shaw et al. (7). Chauhan and Johansen (1) proposed a plant type for short-duration pigeonpea for subtropical and tropical environments. In subtropical environments, yield-maximizing traits would include photoperiod insensitivity, annual growth habit, short height (< 150 cm), moderate biomass (13 t ha^{-1}), higher partitioning, reduced length of reproductive period and water logging tolerance. For tropical environments, a moderate photoperiod sensitivity, as well as perenniality, high rate of biomass production and tolerance to drought, cold and water logging are important characters. High yielding early-types could be produced by making crosses between determinate and indeterminate types and selecting for large seeds and longer pod-bearing length with more primary branches (8). In late types emphasis on more branches and seeds per pod may be desirable in addition to increased pod bearing length and seed size.

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Overview of pigeonpea research in Myanmar

by Khin Lay KYU[1]*, Tun SHWE[1] and Chanda V. SAMEER KUMAR[2]

Abstract: Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the third most important pulse in Myanmar. Aberrant weather and climatic abnormalities significantly reduced the crop productivity in present-day rain-fed agriculture. Adoption of location-specific short and medium duration varieties as well as hybrids are needed to improve livelihood of vulnerable small holders. Monywashwedingar is a popular variety which has been selected by using pedigree method from naturally out-crossing local landraces. In 2013, ICPH 2433 (2507 kgha^{-1}) showed 62.41% yield superiority over standard check, Yezin-3. In 2014, ICPA 2039 x Line-25 (2239 kgha^{-1}) exhibited 57% yield superiority over ICPL 88039. These findings showed the prospects in enhancing the productivity of pigeonpea in Myanmar.

Key words: hybrid pigeonpea, landraces, Myanmar

Introduction

Myanmar is predominantly an agricultural country and pulses play an important role in its economy. Myanmar is the world's second largest exporter of pulses with the exports crossing 1.45 million t mark annually. Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the third most important pulse crop and grown exclusively for export. According to Department of Agricultural Planning under the Ministry of Agriculture and Irrigation, the area of pigeonpea is 643,000 ha in 2013-2014 covering about 14% of total pulses production. It is mainly cultivated as an intercrop with cotton (*Gossipium hirsutum* L.), groundnut (*Arachis hypogaea* L.), sesame (*Sesamum indicum* L.), green gram (*Vigna radiata* (L.) R. Wilczek), and sunflower (*Helianthus annuus* L.) in Sagaing, Mandalay and Magwayregions of Central Dry Zone of Myanmar. Although the Department of Agricultural Research (DAR) had been released some improved varieties, the yield level of pigeonpea is still stagnating. To promote the productivity of pigeonpea in the country, the researchers explored various options and believe that adoption of hybrid breeding technology can provide the derived answer.

Varietal improvement programme

Myanmar has strong collaboration with ICRISAT since 1976 and more than 400 pigeonpea breeding materials have been introduced from ICRISAT and six improved varieties had been released for commercial cultivation (Table 1). Since the inheritance of yield and associated characters is confounded with the effects of phenologyin pigeonpea (Saxena, 2008) and its phenology is highly influenced by photoperiod, temperature, and their micro-climatic interactions, local landraces have wider adaptability than improved varieties. Monywashwedingar is a popular variety in the country which has been selected by using pedigree method from naturally out-crossing local landraces.

Traditionally, pigeonpea is mainly grown under rain-fed cultivation by using traditionally long-duration (> 200 days) varieties and the crop has to face most vulnerable to vagaries of weather. As a result of which partial or total crop failure has become very common leading to a significant yield reduction and great economic loss to the farmers. Thus to prevent the farming communities from economic loss due to vagaries of weather and climatic abnormalities, the plant breeders have realized the need to develop high-yielding short duration lines with wide adaptability and yield stability that can escape serious drought in June-July and terminal drought in reproductive stage to enhance the crop productivity and to diversify the legume-based cropping systems. Currently, ICRISAT short duration varieties ICPL 88039, ICPL 87, UPAS 120, ICPL 98010 and ICPL 98015 have been replaced in the drought prone area of Magway and Mandalay regions.

Table 1. Pigeonpea varieties released in Myanmar

Serial number	Genotype	Released name
1.	HPA-1	Yezin-1
2.	BR-172	Yezin-2
3.	ICPL-87	Yezin-3
4.	ICPL 93003	Yezin-4
5.	ICPL 87119	Yezin-5
6.	ICPL 96061	Yezin-6

Hybrid breeding. Hybrid breeding technology had been introduced from ICRISAT in 2007 and ICPH 2671, ICPH 2740, and ICPH 3461 had been identified as promising across over three research stations in 2008-2009 (Fig. 1). Subsequently, the hybrid ICPH 2671and ICPH 2740 were demonstrated in farmers' field across over six location and were found to be 28% - 41% superior in yield over the control in six townships of Sagaing and Mandalay regions during 2009-2010 (Fig. 2). However, due to its purple seed coat color ICPH 2671 was not preferred by farmers and local brokers. ICPH 3461 and ICPH 2740 showed good yields with the preferred seed color. However, due to its photo and thermo sensitivity, these hybrids were late in maturity and pod setting was affected at low temperature, dropping of flowers and serious attacked by pod fly than local. Therefore the plant breeders considered to develop indeterminate type short duration hybrids which have photo and thermo insensitivity and suitable for different cropping system. In 2013, 10 short duration ICRISAT pigeonpea hybrids were conducted the experiment by

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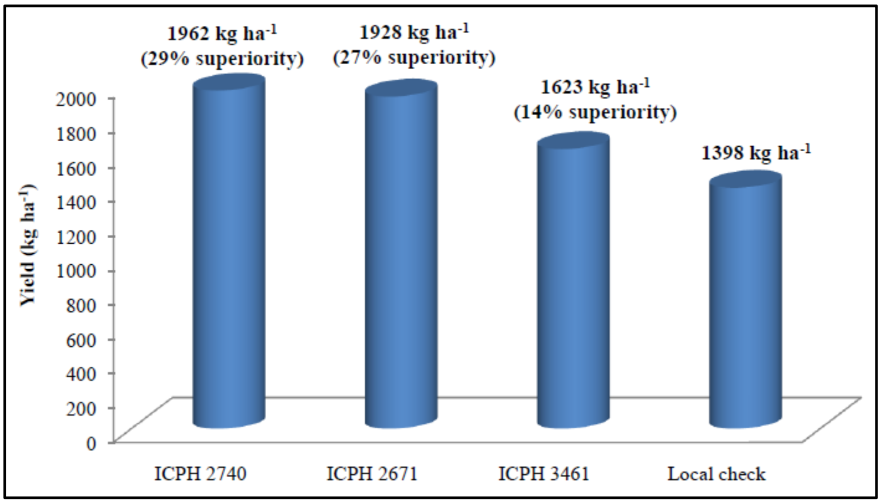

Figure 1. Performance of pigeonpea hybrids at Myingyan, Sebin and Zaloke Research Farms in Myanmar, 2008-2009

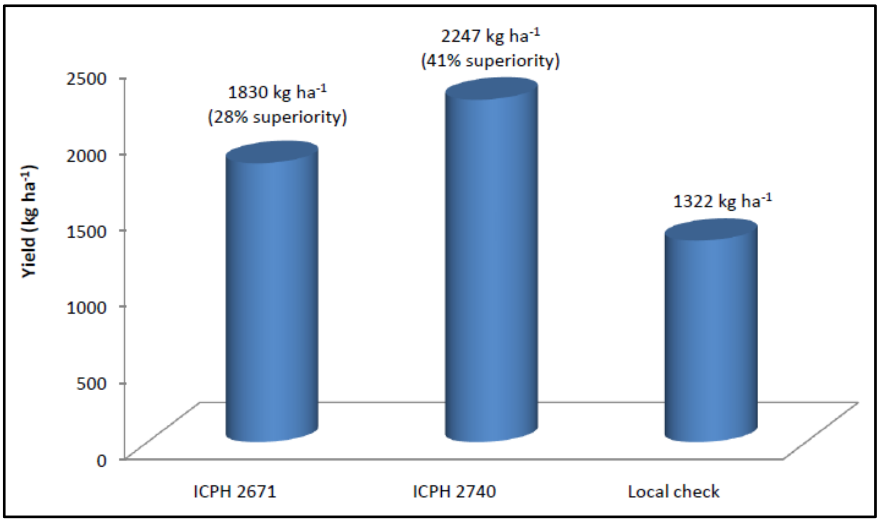

Figure 2. Performance of pigeonpea hybrids in farmers' fields across over six locations in Myanmar, 2009-2010

using 10 m × 2 m RBD at Yezin. ICPH 2433 (2507 kg ha^{-1}) was fully fertile and showed significant yield superiority (62.41%) over standard check, Yezin-3 (Table 2). In 2013, ICRISAT short duration CMS line ICPA 2039 was crossed with locally adapted germplasm lines; Layphatwai, Line-25, UPAS-120, Nyaungoo (MD) and Yezin-3. These combinations were screened at Zaloke research farm in 2014 monsoon season. The combination, ICPA 2039 × Line-25 (2239 kg ha^{-1}) restored 93% fertility in F$_1$ and exhibited 57% yield superiority over ICPL 88039 (Table 3). These finding showed the performance of short duration hybrids and their prospects in enhancing the productivity of pigeonpea in Myanmar.

Hybrid seed production. Hybrid seed production was also established successfully in the country. The first hybrid seed (A × R) production of ICPH 2671 was initiated at Tatkone and Pankone research farms in 2008-09 and produced 1069 kgha^{-1} of hybrid seed. During 2009-2010 seed production of the selected hybrids was undertaken using a row ratio of 3 female: 1 male, which produced 1569 kg ha^{-1} of ICPH 2740 and 2931 kg ha^{-1} of ICPH 3461. Therefore, it seems it may not be any problem for short duration pigeonpea hybrid seed production.

Conclusions

In Myanmar, pigeonpea is a favourite crop of small holder farmers in the dry zone area due to its multiple uses and its role in sustainable agriculture. Aberrant weather and climate abnormalities significantly reduce the crop productivity in present-day rainfed agriculture. Therefore, proper planning and adoption of location-specific pigeonpea short and medium duration varieties as well as hybrid varieties are needed to improve livelihood of vulnerable small holders.

Table 2. Performance of various morphological traits and yield attributes of short duration pigeonpea hybrids and check at Zaloke Research Farm, Sagaing Region, Myanmar, in 2014

Parentage	Number of days to maturity	Number of pods (plant^{-1})	Plot yield (g)	100-seed weight (g)	Yield (bsk ac^{-1})	Yield (kg ha^{-1})	Fertility restoration (%)	Yield superiority over check (%)
ICPA 2039 × Layphatwai	131	307	976	8.0	21.7	1754	82	22.7
ICPA 2039 × Line 25	128	281	1248	9.5	27.7	2239	93	56.9
ICPA 2039 × UPAS 120	115	360	1177	10.0	26.1	2110	88	48
ICPA 2039 × Nyaungoo (MD)	130	272	703	8.5	15.6	1261	40	
ICPA 2039 × Yezin-3	116	190	200	10.0	4.4	356	14	
ICPL 88039 (C)	126	253	795	8.5	17.7	1431		
Mean	124	277	850	9.0	18.9	1528		
CV (%)	5.7	20.4	24.9	9.5		20.8		
SE (±)	2.6	3.1	8.0	0.4	0.48	39		

Table 3. Performance of various morphological traits and yield attributes of short duration pigeonpea hybrids and check at Yezin, Nay Pyi Taw, Myanmar, in 2013

Hybrid	Number of days to 50% flower	Number of days to maturity	Plant height (cm)	Number of pods (plant^{-1})	Number of seeds (pod^{-1})	100-seed weight (g)	Number of primary branches (plant^{-1})	Number of secondary branches (plant^{-1})	Plant stand (13.5' × 10')	Yield (kg ha^{-1})	Yield superiority over check (%)	Fertility restoration (%)
ICPH 2441	115	149	159	256	3.5	7.7	13	6	24	1048		77
ICPH 3310	114	148	139	254	3.4	7.5	11	3	24	1055		91
ICPH 2438	117	151	149	459	3.5	7.7	12	7	26	1228		94
ICPH 2447	116	150	146	288	3.4	8.4	12	5	22	930		90
ICPH 2429	117	151	161	448	3.5	8.1	13	6	25	1476		95
ICPH 2431	117	151	172	503	3.2	7.9	14	13	26	1672		87
ICPH 2433	116	150	173	559	3.0	8.1	13	10	21	2507	62.41	100
ICPH 2363	122	156	170	500	3.4	8.8	15	9	24	1344		92
ICPH 2364	115	149	146	353	3.5	8.9	11	7	23	1304		100
Yezin-3 (C)	115	149	94	235	3.4	8.3	12	10	20	1544		
Mean	116	150	151	386	3.4	8.1	13	8	23	1411		
SE((±)	1.8	1.7	18.0	169.8	0.3	0.7	3.2	5.6	5.4	58		
CV%	0.9	0.7	6.9	15.7	5.4	4.7	14.6	21.9	13.6	17.9		

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Pigeonpea seed systems in Asia

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Abstract: Pigeonpea seed systems consist of the formal and informal seed sector. However, the informal seed sector dominates the seed production system. Majority of rainfed farmers who grow pigeonpea (about 80% - 90%) save a part of their produce as seed requirement. In the formal seed sector, government agencies and private companies are involved in production and distribution of quality seeds of improved varieties and hybrids. Role of private sector diffusion in pigeonpea market is not encouraging owing to lack of commercial perspective in the crop and other factors. The integrated approach that takes into cognizance the formal and informal seed sector in breeding, seed production and distribution has shown to have promising potential for improving seed supply to smallholder farmers. Moreover, any seed system, for that matter, requires a regulatory framework as well as a seed policy that considers regulations of an expanding and diversifying seed sector for the benefit of the farmers engaged in the seed production system.

Key words: formal, informal, pigeonpea, seed system

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) plays an important role for sustainable agriculture in rainfed areas of Asia particularly in India, Myanmar, Philippines and Nepal. The increasing population growth and the poor productivity (800 kg ha^{-1}) have resulted in the reduction of per capita availability of this important pulse, which together with undue price hike has distorted consumption pattern of households. India has lion's share in terms of area and production and pigeonpea dal is source for predominant vegetarian population of the country (7). Production growth has not been able to keep pace with the population growth and, consequently, India's per capita net availability of pigoenpeas is around 2.88 kg $year^{-1}$ which is very low (1).

Current scenario

In spite of improved pigeonpea varieties and hybrids released for cultivation, their impact has not yet been fully realized by the resource-poor farmers in many countries. The accessibility of smallholder farmers to quality seed of improved varieties is hindered by both inadequate demand creation and limited supply (Fig. 1). This situation is also compounded by uncomplimentary and inadequate policy support and regulatory frameworks, inadequate institutional and organizational arrangements, and deficiencies in production and supply infrastructure and farmers' socio-economic situation (6). Numerous constraints limit the performance of seed systems including limited access of smallholder farmer to seed of improved varieties; limited supplies of quality (breeder, foundation and certified) seed of farmer and market-preferred varieties; lack of co-ordination among national seed production organizations and policy making institutions. In seed production chain, pigeonpea seed business generally does not attract large seed companies since profit margins are low (4). The seed replacement rate in India varies from 14% in chickpea (*Cicer arietinum* L.) to 35% in soybean (*Glycine max* (L.) Merr.), as presented at www.seednet.gov.in, thus indicating that a majority of the farmers still use their own saved seed. This situation is due to several factors including: the low seed multiplication rate of legumes; the reuse of grains from previous harvest as seeds and; often demand for specific varieties adapted to more narrow agro-ecologies and consumers' needs. Furthermore, when seed production takes place, it is often in higher potential areas, with seed stores being concentrated in zones of higher population density or those with better infrastructure (i.e. not the remote, stress-prone areas).

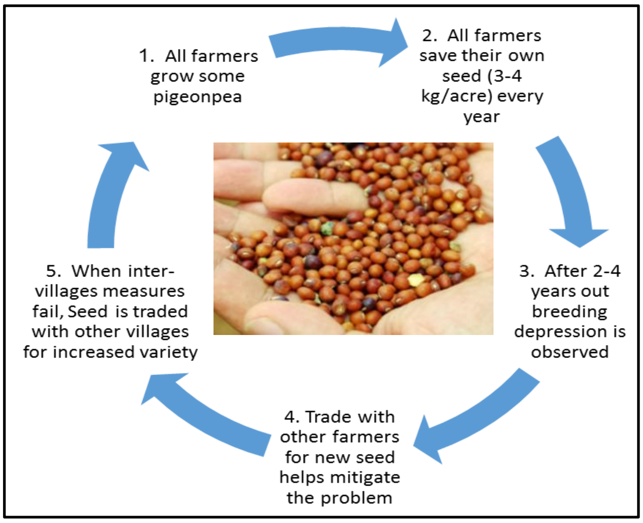

Figure 1. Existing pigeonpea smallholder farmers seed system model

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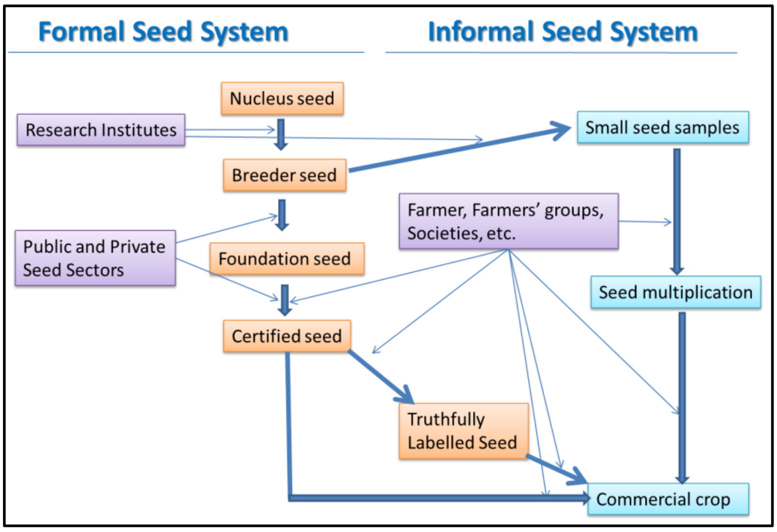

Figure 2. Pigeonpea seed production and delivery model in South Asia

As small and medium seed companies are emerging and gaining strength, they are also creating effective demand for improved varieties and hybrids in pigeonpea. However their capacities are still limited by the inadequate and discontinuous access to foundation seed, inadequate capital investment, and lack of appropriate marketing strategies including delivery systems targeting remote and small scale farmers. Public and private partnership would be the best approach to increase the availability of foundation seed need for subsequent seed classes. In the developing countries such as India, particularly for pigeonpea, the formal seed sector is highly subsidized and evolving at different stages of development. The informal seed sector is and will remain the dominant player in legumes. In recent past, development partners and researchers have realized the importance and significance of quality seed in agriculture and several projects have been implemented or are in progress to improve seed availability of improved farmer-preferred varieties to farmers. The main issue in resolving access to quality seed would be a thorough understanding and critical assessment of the status of existing seed sector (both formal and informal), their bottlenecks and comparative advantages and complementarity (2).

The cultivars under cultivation in pigeonpea used are invariably local landraces, and awareness about improved varieties, seed availability and seed access is poor. Seed is procured off-farm only when necessary as when own seed is not available due to drought, poverty or seed pests and diseases. The main sources of off-farm seed are local markets, relatives, other farmers and government relief agencies. However, these statements about the predominance of the informal seed sector cover significant differences between crops, villages, farmer groups and their socioeconomic conditions. Traditional seed systems are location-specific and vary greatly within farmer communities (2).

The way forward

Seed system for legumes in South Asia has a long way to go. However, in developing and strengthening formal and informal seed production and delivery systems to ensure quality seed of improved farmer preferred varieties and hybrids, we should do the following (3):

- Improving access to seed for smallholder farmers that focus on subsistence production through the enhancement of local village seed systems by testing a range of seed production and delivery options and searching for options to scale-out and scale-up alternative seed production and delivery schemes;
- Knowledge empowerment of farmers/ rural entrepreneurs in seed production, post-harvest and processing, and marketing;
- Exploiting market niches commercial (large scale) production by developing seed markets and identifying seed supply constraints and recommending options to improve its efficiency;
- Developing and/or strengthening seed regulatory framework as well as a seed policy that considers regulations of an expanding and diversifying seed sector for the benefit of the farmers engaged in the seed production system.

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Possibilities for introducing pigeonpea (*Cajanus cajan*) in Southeast Europe

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Abstract: Pigeon pea (*Cajanus cajan*) is a completely unknown crop in Southeast Europe, where the only large-scale cultivated warm season annual legume is soya bean (*Glycine max*). Since 2004, a small research programme assessing the possibility for introducing pigeon pea in temperate regions. A complex evaluation demonstrated a considerable potential of certain accessions for forage and grain production, with a neutral photoperiodic reaction as a necessary element in providing a reliable cultivation and market seed production. Pigeon pea may be useful as a source of quality forage during the summer and a complement to soya bean meal.

Key words: forage yield, grain yield, neutral photoperiodic reaction, pigeonpea, Southeast Europe, temperate climate

Introduction

In numerous Southeast European countries, such as Serbia, soya bean (*Glycine max* (L.) Merr.) is the most important grain legume crop, used for diverse purposes, as well as the only cultivated warm season annual legume species. Rather sporadically and still without a satisfactory explanation of their exact way and time of introduction, mutually isolated local landraces of hyacinth bean (*Lablab purpureus* (L.) Sweet) and cowpea (*Vigna unguiculata* (L.) Walp.) may be found, with no statistical records and grown solely for household needs (2).

Table 1. Results of evaluating forage yield components of pigeonpea accessions in field conditions at Rimski Šančevi, northern Serbia, from 2009 to 2012

Accession name	Plant height (cm)	Number of lateral branches (plant^{-1})	Number of leaves (plant^{-1})	Fresh forage yield (g plant^{-1})	Fresh forage yield (t ha^{-1})	Forage dry matter yield (t ha^{-1})
ICPL 88020	57	2.3	11.3	32	6.4	1.8
Hunt	94	6.5	19.0	169	33.9	9.5
Quantum	74	3.7	14.7	108	21.7	6.1
Quest	84	7.2	15.3	263	52.8	14.8
NI 470	125	3.8	14.7	137	45.9	12.9
Caqui	115	4.2	12.7	170	34.1	9.5
CAJ 012	91	4.5	16.5	135	31.9	9.3
$LSD_{0.05}$	27	1.7	3.8	46	14.6	2.9
$LSD_{0.01}$	36	2.2	5.2	62	19.2	4.0

Table 2. Results of evaluating grain yield components of pigeonpea accessions in field conditions at Rimski Šančevi, northern Serbia, from 2009 to 2012

Accession name	Plant height (cm)	Pod number (plant^{-1})	Grain number (plant^{-1})	Thousand grain mass (g)	Grain yield (g plant^{-1})	Harvest index	Grain yield (kg ha^{-1})
ICPL 88020	63	34.1	73.2	79	5.39	0.35	719
Hunt	105	35.1	68.3	105	6.97	0.07	930
Quantum	82	39.1	110.4	128	13.17	0.28	1756
Quest	94	38.1	79.1	20	15.40	0.33	1253
NI 470	187	0.0	0.0	-	0.00	0.00	0.00
Caqui	143	14.7	0.0	-	0.00	0.00	0.00
CAJ 012	124	48.2	124.0	111	16.40	0.48	2710
$LSD_{0.05}$	31	12.8	46.2	23	9.01	0.12	1479
$LSD_{0.01}$	39	17.3	62.4	31	12.21	0.16	2000

Establishing a collection

Inspired by the global pigeonpea collection at ICRISAT (6), India, the Institute of Field and Vegetable Crops launched a research programme in 2004 aimed at assessing the possibility for growing alternative annual legume crops. This produced a collection of pigeon pea (*Cajanus cajan* (L.) Huth), comprising several dozens of accessions of diverse geographic origin, status and biological characteristics.

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Evaluating the collection

The first steps following the establishment of the Novi Sad pigeon pea collection comprised developing the passport database, according to the FAO/IPGRI multi-crop descriptors (1), and characterising the accessions for the most significant morphological and other qualitative traits, such as flower colour and seed coat colour.

All the accessions have been evaluated for the economically most important characteristics in the field conditions, such as the number of day from sowing to cutting (if tested for forage production) or harvest (if assessed for grain production), plant height, number of branches. number of leaves, number of pods, number of seeds/grains, thousand grain weight, forage yield, grain yield, harvest index and crude protein content in forage and grain dry matter. The usual sowing time was identical to that of soya bean, that is, sometimes the last week of March or more often during the first decade of April (2, 3).

A certain number of the pigeon pea accessions were obviously inappropriate for introducing in the temperate regions, such as NI 470, a local landrace from Burundi, or Caqui, a cultivar from Brazil. Both accessions always remained in the vegetative stage until the late autumn, producing a rather abundant aboveground biomass and higher forage dry matter yields (Table 1) than pea (*Pisum sativum* L.), vetches (*Vicia* spp.) or other traditional European temperate annual forage legumes (3, 4).

On the other hand, a considerable number of the tested pigeon pea accessions showed a more neutral photoperiodic reaction, being able to transit from the vegetative into a full generative stage, forming pods and mature seeds until the first frosts in the second half of October (2). Some accessions, such as the Australian Quantum and Quest, have demonstrated a considerable potential for grain yield (Table 2).

Launching a breeding programme

Although the number of the accessions included in the evaluation of the economically interesting characteristics was not great, their diversity was sufficient enough for the preliminary attempts in developing the lines for three main purposes, namely, forage production, grain production and both forage and grain production.

Figure 1. The pigeonpea line CAJ 012, developed at the Institute of Field and Vegetable Crops, Novi Sad, Serbia; Rimski Šančevi, northern Serbia, second half of July 2012

Regardless of the breeding direction, the main goals still have remained either the neutral photoperiodic reaction or early maturity and an as stable as possible balance between forage and grain/seed yields (5).

The first outcome of these efforts was the line CAJ 012 (Fig. 1), developed by individual selection form a hybrid population of the parental accessions with desirable agronomic performance. In most seasons, this line achieved good results, being able to produce quite satisfactory forage and grain yields (Tables 1 and 2). It should be emphasized that a satisfactory grain yield also means a reliable seed yield, in terms of commercialisng this line as a potential forage cultivar, because many annual forage legumes, such as common (*V. sativa* L.) or hairy (*V. villosa* Roth) vetches may easily provide high forage yields and yet suffer from too low seed yields to find their niche on the market. It may be said that the Serbian pigeon pea breeding programme manages to continue its mission rather well.

Why pigeonpea in Southeast Europe?

Indeed, one may ask such a question, especially since the existing diversity of annual and perennial field legumes in this part of the world. However, it is also true that pigeon pea, if grown for forage, may provide animal husbandry with a quality feed in ruminant feeding during the summer, when the traditional crops, such as pea or vetches, have left the fields months before. Similarly, if cultivated for dry grain, pigeon pea may represent another complementary protein source to soya bean meal. Due to its high drought tolerance and other advantages, pigeon pea could find its place, however small, in the existing and novel cropping systems in temperate regions, such as Serbia, and the Southeast Europe.

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Plant growth-promotion traits of *Streptomyces* sp. in pigeonpea

by Subramaniam GOPALAKRISHNAN[*], Vadlamudi SRINIVAS and Chanda V. SAMEER KUMAR

Abstract: The aim of this study was to evaluate three strains of *Streptomyces* (CAI-21, CAI-26 and MMA-32), demonstrated previously to have potential for control of charcoal rot disease in sorghum and plant growth-promotion (PGP) in rice and chickpea, for their PGP traits in pigeonpea under field conditions in 2014 rainy-season. The *Streptomyces* enhanced the nodule number, nodule weight, root weight and shoot weight at 30 days after sowing (DAS) and branches, leaf area, stem weight and root weight at 60 DAS over the un-inoculated control. At crop maturity, the *Streptomyces* enhanced stover and grain yields over the un-inoculated control. The three *Streptomyces* were demonstrated for PGP activity in pigeonpea as well.

Key words: pigeonpea, plant growth promotion, *Streptomyces* sp., yield enhancement

Introduction

Pigeonpea (*Cajanus cajan* [L.] Millsp.) is an important grain legume crop in South Asia and East and Southern Africa. It is a rain-fed rainy season crop frequently subjected to both abiotic, such as drought and water logging, and biotic stresses, such as pod borer (*Helicoverpa armigera* Hübner), wilt (*Fusarium udum* Butler) and sterility mosaic diseases,resulting in severe yield losses. Global yields of pigeonpea have been relatively stagnant (762 kg ha^{-1}) (2) for the last five decades in spite of using various conventional and molecular breeding approaches.

Hence, in the present study, it was proposed to use the strains of the PGP genus *Streptomyces* Waksman & Henrici as a tool to enhance the plant growth and yield of pigeonpea. *Streptomyces* is a Gram positive bacterium found abundantly in rhizosphere of agriculturally important crops.PGP potential of *Streptomyces* was reported on wheat (*Triticum* aestivum L.; 8), rice (*Oryza sativa* L.; 5), bean (*Phaseolus* spp.; 7), pea (*Pisum sativum* L.; 9), chickpea (*Cicer arietinum* L.; 6) and tomato (*Solanum lycopersicum* L.; 1). Previously, we demonstrated a set of three *Streptomyces* strains (CAI-21, CAI-26 and MMA-32) isolated from herbal vermi-compost, with the potential for bio-control of charcoal-rot disease, caused by *Macrophomina phaseolina* (Tassi) Goid., in sorghum (*Sorghum bicolour* (L.) Moench; 3) and for PGP in rice (4).

The objective of the present investigation was to further ascertain the efficacy of the three *Streptomyces* strains for their PGP traits in pigeonpea under field conditions.

Materials and methods

The experiment was done in 2014 rainy season at ICRISAT, Patancheru in India on vertisols. The experiment was laid out with three replicates and subplot sizes of 4 m × 2 ridges (1.2 m) in a randomized complete block design (RCBD). Seeds of pigeonpea (variety ICPL 88039; short duration [120 days] which yields about 1.6 t ha-^{1}) were treated individually with a *Streptomyces* strain (either CAI-21 or CAI-26 or MMA-32; 10^8 CFU ml^{-1}) for 45 min and sown by hand planting on 30 June 2014 (in rows 60 cm apart and 10 cm between plants) at a depth of 5 cm. Control plots contained no *Streptomyces*.

All the agronomic practices were done as and when required. At 30 days after sowing (DAS), the nodule number (plant^{-1}), nodule weight (mg plant^{-1}), root weight (g plant^{-1}) and shoot weight (g plant^{-1}) and at 60 DAS, number of branches (plant^{-1}), leaf area (cm^{-2} plant^{-1}), leaf weight (g plant^{-1}), stem weight (g plant^{-1}) and root weight (g plant^{-1}) were recorded. The crop was harvested manually on 27 October 2014. At crop maturity, plant height (cm), number of primary branches (plant^{-1}), shoot weight (g plant^{-1}), pod weight (g), number of pods (plant^{-1}), 100 seed weight (g), number of seeds (plant^{-1}), stover yield (g plant^{-1} and t ha^{-1}) and grain yield (g plant^{-1} and t ha^{-1}) were recorded.

Data were analysed by analysis of variance (ANOVA) in the software package SAS considering isolates and replication as fixed in RCBD.

Results and discussion

The plots treated with *Streptomyces* strains CAI-21, CAI-26 and MMA-32 showed significantly enhanced agronomic performance of all the traits measured including nodule number (up to 47%), nodule weight (up to 34%), root weight (up to 28%) and shoot weight (up to 11%) at 30 DAS and number of branches (up to 23%), leaf weight (up to 13%), leaf area (up to 26%), stem weight (up to 22%), and root weight (up to 22%) at 60 DAS over the un-inoculated control plots (Tables 1 and 2).

At crop maturity, the *Streptomyces* strains enhanced the plant height (up to 12%), number of primary branches (up to 14%), shoot weight (up to 22%), pod weight (up to 21%), number of pods (up to 15%), 100 seed weight (up to 28%), seed number (up to 27%), grain yield (up to 36%) and stover yield (up to 25%) over the un-inoculated control plots (Table 3).

Among the three strains of *Streptomyces* studied, CAI-26 enhanced most of the PGP traits and yield parameters. The mechanism by which the three *Streptomyces* strains consistently enhanced agronomical and yield traits on sorghum and rice (from our previous study) and pigeonpea (from this study) could be attributed to their ability to produce indole acetic acid, siderophores and β-1,3-glucanase activities (3, 4).

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Table 1. Effect of the three *Streptomyces* sp. on agronomic performance of pigeonpea under field conditions at 30 days after sowing

Isolate	Nodule number (plant^{-1})	Nodule weight (mg plant^{-1})	Root weight (g plant^{-1})	Shoot weight (g plant^{-1})
CAI-21	4.6	1.3	254	2.27
CAI-26	5.4	2	214	2.12
MMA-32	7.8	2	203	2.18
Control	4.1	1.3	184	2.02
SE	0.25***	0.17*	9.5**	0.04**
LSD (5%)	0.87	0.6	33	0.15
CV%	8	18	8	4

SE = standard error; LSD = least significant differences; CV = coefficients of variation; *statistically significant at 0.05;**statistically significant at 0.01; ***statistically significant at 0.001

Table 2. Effect of the three *Streptomyces* sp. on agronomic performance of pigeonpea under field conditions at 60 days after sowing

Isolate	Number of branches (plant^{-1})	Leaf weight (g plant^{-1})	Leaf area (cm^{-2} plant^{-1})	Stem weight (g plant^{-1})	Root weight (g plant^{-1})	Total shoot weight (g plant^{-1})
CAI-21	10	9.98	2122	11.7	3.82	21.67
CAI-26	11.7	9.75	2031	10.61	3.29	20.37
MMA-32	10	8.76	1973	9.24	3.16	18.01
Control	9	8.73	1576	9.1	2.98	17.83
SE	0.17***	0.28*	84.8*	0.29**	0.13*	0.64**
LSD (5%)	0.58	0.96	293.6	0.99	0.46	2.21
CV%	3	5	8	5	7	6

SE = standard error; LSD = least significant differences; CV = coefficients of variation; *statistically significant at 0.05;**statistically significant at 0.01; ***statistically significant at 0.001

It is concluded that the *Streptomyces* strains studied in this investigation were apparently well adapted not only in sorghum and rice rhizosphere but also in the pigeonpea rhizosphere. Hence, these three strains are likely to be potential candidates for the discovery of novel secondary metabolites which may be of importance of various PGP and biocontrol applications. However, there is a need to do additional comprehensive research to exploit the potential of these PGP *Streptomyces* under different field conditions and commercialization.

Table 3. Effect of the three *Streptomyces* sp. on agronomic performance and yield potential of pigeonpea under field conditions at harvest

Isolate	Plant height (cm)	Number of branches (plant^{-1})	Stover weight (g plant^{-1})	Pod weight (g plant^{-1})	Number of pods (plant^{-1})	100-seed weight (g plant^{-1})	Seed number (plant^{-1})	Grain yield (t ha^{-1})	Stover yield (t ha^{-1})
CAI-21	150	8.7	22.03	17.03	53	12.33	177	1.73	1.37
CAI-26	161	9.7	28.09	21.4	52	15.93	198	2.25	1.75
MMA-32	148	9	22.17	17.17	45	11.73	160	1.66	1.36
Control	142	8.3	21.91	16.93	45	11.47	144	1.43	1.31
SE	1.0***	0.19**	0.77**	0.58**	1.6*	0.64**	3.6***	0.08**	0.07**
LSD (5%)	3.5	0.64	2.65	2	5.5	2.21	12.3	0.28	0.23
CV%	1	4	6	6	6	9	4	8	8

SE = standard error; LSD = least significant differences; CV = coefficients of variation; *statistically significant at 0.05;**statistically significant at 0.01; ***statistically significant at 0.001

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Strategies for pigeonpea improvement

by Rachit K. SAXENA[1]*, Kulbhushan B. SAXENA[1], Chanda V. SAMEER KUMAR[1], Narendra P. SINGH[2] and Rajeev K. VARSHNEY[1]*

Abstract: In order to feed an ever-increasing population, it is essential to deal yield-reducing factors. Climate smart crop varieties that yield more with fewer inputs will be required to achieve the success. In this scenario pigeonpea plays an important role as it can stand in relatively harsh environmental conditions. Hybrid breeding along with the pure line breeding, genetic resources and genomics advances are enriching this crop. However, the pigeonpea improvement program must be re-oriented in order to deal with the yield-reducing factors and to break the yield plateau.

Key words: genomics assisted breeding, pigeonpea, quality control, value chain

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is rich in seed protein (20% - 22%) and its de-hulled split grains (dal) constitute a major supplement in the diets of most vegetarian families around the globe (5). In spite of extensive research and development activities in the last four decades, the yield levels remain stagnated in pigeonpea. The development of hybrid technology (6) has shown promise in this direction but its adoption is below the expectations due to some production and marketing reasons. Now the time has come to move forward more vigorously with backing of new technologies to overcome the present constraints and breed new cultivars at a rapid pace (4).

In this article we are sharing experiences and ideas to improve pigeonpea research for resource poor farmers in Asia and sub-Saharan Africa.

Integration R & D for hybrid and inbred cultivars

In a dynamic breeding program it is important that cultivars are released from time to time to cater the changing needs of farmers and market. In pigeonpea the technologies for breeding both hybrids and pure line cultivars are available and both types of products are in demand now. Considering the cost and resources involved in breeding, it is logical to integrate these two types of breeding programs. It should be done in such a way that the objectives and primary activities in either program are not compromised. For example breeding of inbred lines for variety development and breeding of new testers for hybrid program should go hand in hand. Selection of parents to develop breeding populations can be done together by considering their combining ability, genetic diversity, and market traits. Similarly screening of selections for biotic and abiotic stresses, their evaluation and maintenance for the two programs can be integrated together. In advance stages of pedigree selection, a set of high yielding inbreds can be picked to identify cultivars for a given region. On the other hand, a greater early generation selections from the same lot can be used as testers for hybrid breeding program to select potential fertility restorers and maintainers. The other research and development areas that would require serious attention are: exploitation of photo thermo sensitivity in hybrid breeding, diversification of hybrid parents, development of heterotic groups, refining seed technology and technology transfer to the farmers (Fig. 1).

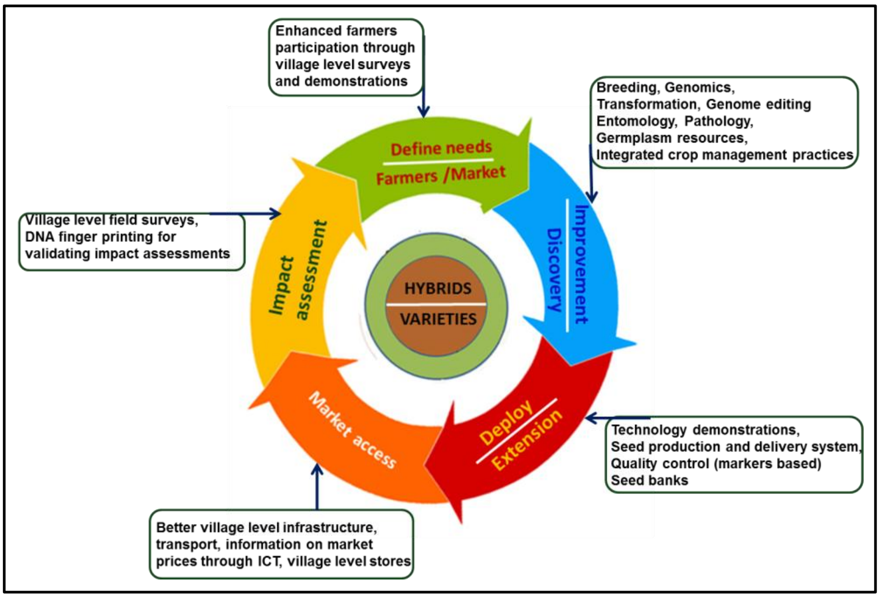

Figure 1. A schematic diagram representing different components for pigeonpea (hybrids and varieties) value chain

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Breeding high-yielding second-generation hybrids

The present set of hybrid parental lines has produced several good hybrids and showed high productivity in farmers' fields. In most places the hybrids have recorded the productivity between 2,500 kg ha^{-1} - 3,500 kg ha^{-1} with a yield advantage of 35% - 45% over ruling cultivars (6). This can be considered a good start to break the decades-old yield barrier, however, considering the potential of hybrid technology and realized yields from hybrids in other field crops, it is reasonable to believe that pigeonpea breeders would be aiming to produce new generation hybrids with yields of over 5,000 kg ha^{-1}. To achieve this, however, concerted efforts will be made to breed new hybrid parents using modern resources available in germplasm and genomics.

Enhanced participation of genomics and germplasm resources

For sustainable and rapid development in pigeonpea it is highly imperative to use genomics and germplasm resources in all possible breeding programs. In the case of genomics starting from markers based selection for key traits (biotic and abiotic stresses, fertility restoring genes, etc.), markers based purity testing of hybrids and parental lines, characterization and documentation of elite genotypes, understanding molecular basis of CMS systems and defining the heterotic groups are the prime targets. Recent advances in pigeonpea genomics have created an opportunity where we can deploy genomics in all above mentioned areas (4). For instance markers have been identified for fusarium wilt (7), sterility mosaic diseases (3), fertility restoration (2), and hybridity testing (1). Efforts are underway to detect markers for key agronomic traits. This will certainly enhanced the capacity of pigeonpea breeding programs. On the other hand initiatives to define heterotic groups and exploiting photo thermo sensitivity will certainly enrich the hybrid breeding.

Germplasm resource is very rich and contains a large variability with respect to various morphological traits. However limited resources from germplasm have been used in breeding programs. For continuous induction of new allelic combinations from germplasm in ongoing breeding programs, efforts have to be made to evaluate the situation and their systematic use. Genomics can play a major role in deployment of germplasm resources in breeding programs by fingerprinting and cataloging the desirable genes/genomic segments. Genomics data will be helpful in avoiding the linkage drag and the generation of well-planned breeding materials in collaboration with major disciplines involved in improving pigeonpea.

Outlook

In view of above it is evident that following are required to enhance the pigeonpea improvement program 1) research should be guided by farmers' needs, 2) advance breeding methodologies should be deployed by integrating genomics, genetic transformation for insect resistance and genome editing such as CRISPR/Cas9 multiplex editing for desirable traits, 3) improved seeds should be developed and seed delivery system should be strengthened and 4) agronomy and integrated crop management practices should be refined to achieve maximum yield potential of varieties or hybrids.

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The most ancient words relating to pigeonpea (*Cajanus cajan*)

by Aleksandar MIKIĆ

Abstract: Historical linguistics may be of a remarkable assistance in casting more light onto the crop domestication. It is most likely that the first peoples cultivating pigeonpea (*Cajanus cajan*) belonged to the Dravidian ethnolinguistic family. There are two attested Proto-Dravidian roots relating to this legume, **ḳāj*-, meaning *fruit* and *pod* and and evolving into *cajan(us)*, and **toγar-*, denoting both dal and pigeonpea and bringing forth the modern *toor*.

Key words: *Cajanus cajan*, dal, historical linguistics, pigeonpea, toor

Origin and domestication

According to some earlier views, pigeonpea (*Cajanus cajan* (L.) Huth.) primarily originated in the African centre of diversity; however, various and more recent findings definitely positioned its homeland in the eastern parts of the Indian sub-continent (5, 7).

The oldest material evidence, as witnessed by the archaeological sites of Sanganakallu and Tuljapur Garhi in South India, suggests that pigeonpea has been cultivated for the last 3,500 years (2). It is most likely that by then the Indo-Aryan migrations still had not reached this region, meaning that pigeonpea was domesticated by the peoples belonging to the Dravidian ethnolinguistic family.

Fruit, pod, dal and pigeonpea

Past few decades demonstrated the possibility of casting more light on the earliest days of various crops by a joint effort of archaeobotany, palaeogenetics and historical linguistics (1, 4). Numerous analyses of existing and extinct Dravidian languages resulted in reconstructing the Proto-Dravidian language, their supposed common source.

Table 1. Evolution of the Proto-Dravidian root **toγar-*, denoting dal and relating to pigeonpea

Proto-language	Transitional languages			Modern languages	Modern words
Proto-Dravidian **toghar-* (dal)	Proto-Southern	Proto-South **tUvar-* (dal)	Proto-Tamil-Kannada	Kannada	*togari*; *tovari* (pigeonpea)
				Kodagu	*tōri bẽle* (pigeonpea)
				Malayalam	*tuvara* (dal; pigeonpea)
				Tamil	*tuvarai* (dal; pigeonpea)
				Toda	*tifiry* (jungle dal)
			Proto-Tulu	Tulu	*togari*, *togarè* (pigeonpea)
		Proto-South-Central **togar-* (dal; pigeon pea)	Proto-Gondi **tūr-i* (pigeonpea)	Adilabad	*tūri* (pigeonpea)
				Madiya	*tōri* (pigeonpea)
				Yavatmal	*tūriŋ* (pigeonpea)
			Proto-Telugu **togar-* (pigeonpea)	Telugu	*togari*; *togaru* (pigeonpea)
	Proto-Central **togar-* (dal)			Kolami	*togar* (pigeonpea)
				Naiki	*togari* (pigeonpea)

There are two attested Proto-Dravidian root words relating to pigeonpea (6). The first one is **ḳāj*- denoting both fruit and pod, with the original meaning preserved almost completely in the majority of the modern Dravidian languages (Fig. 1). The Telugu word *kandi* could be responsible for the Chinese 黄豆树 (*huang dou shu*), the Brazilian Portuguese *feijão-guandu* and the Portorican Spanish *frijol guandul*. In its neolatinised form of *cajan* and *Cajanus*, **ḳāj*- found its new life in botany and taxonomy.

Another Proto-Dravidian root, **toghar-*, denoted both dal and pigeonpea and brought forth numerous derivatives in both now extinct transitional languages and the contemporary ones, also with the retained primeval designation (Table 1). It is also responsible for the modern culinary name *toor* and was borrowed by the neighbouring non-Dravidian languages (3), as seen in the Sanskrit तुबरिका (*tubarikA*), the Hindi तूर (*toor*) or the Thai ถั่วแระ (*thua rae*). 

Acknowledgements

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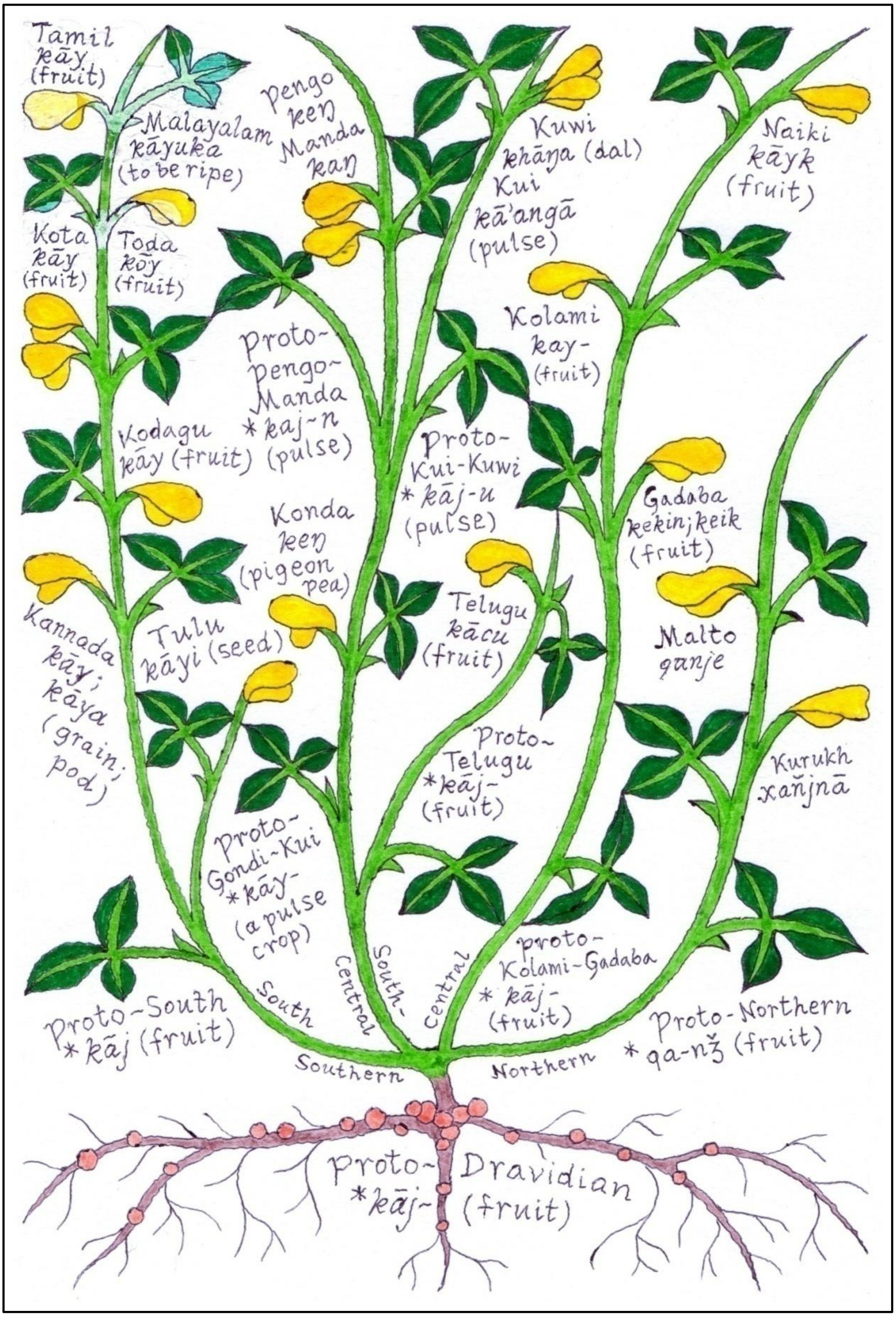

Figure 1. Evolution of the Proto-Dravidian root ***kāj-*, denoting fruit and relating to pigeonpea**

Journal of Food Legumes

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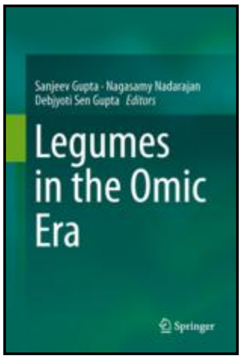
The Indian Society of Pulses Research and Development (ISPRD) has been publishing its official periodical continuously since 1987. The journal was published up to 2007 in the name of Indian Journal of Pulses Research. Later, it was renamed in 2008; since then, it has been published as Journal of Food Legumes quarterly.

Journal of Food Legumes publishes articles in all the disciplines (Breeding, Genetics, Biotechnology, Biochemistry, Physiology, Agronomy, Soil Science, Economics, Extension Education, Statistics and Computer Application, Agricultural Engineering and Post Harvest Technology, etc.) of food legumes (including arid legumes). It is a peer reviewed Journal receiving articles from national and international organizations. It has more than 100 national and foreign subscribers. It has well-structured editorial board.

The contribution to the Journal, except in case of invited articles, is open to the members of the Society only. Any non-member submitting a manuscript will be required to become at least annual member. Members will be entitled to receive the Journal and other communications issued by the Society from time to time.



Legumes in the Omics Era

Editors: Sanjeev Gupta, Nagasamy Nadarajan and Debjyoti Sen Gupta

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Year: 2014

ISBN: 978-1-4614-8369-4

Legumes in the Omic Era provides a timely review of recent advances in legume genomics research and application. In this post-genomic era enormous amount of biological information is available which could be of huge potential use for crop improvement applications. This aspect of genomics assisted plant breeding is focused throughout the book for all the important grain legume crops. Role of functional genomics and importance of bioinformatics tools in present day genomics and molecular breeding research is also discussed in detail. Use of molecular tools for nutritional fortification of grain legume is briefly presented. The book contains fifteen chapters contributed by 50 scientists from different countries who are actively involved in analyzing and improving particular legume genome. This book will serve as reference resource to legumes researchers for use of genome information in improvement of major legume crops.

Second International Legume Society Conference (ILS2) *2016: Legumes for a Sustainable World*

Tróia, Portugal, 12-14 October 2016

http://www.itqb.unl.pt/meetings-and-courses/legumes-for-a-sustainable-world/welcome#content

The International Legume Society and the Instituto de Tecnologia Química e Biológica of the Universidade Nova de Lisboa cordially invite you to join us at the Second International Legume Society Conference, scheduled from 12-14 October, 2016 at Tróia resort, in the vicinity of Lisbon, Portugal.

In a world urgently requiring more sustainable agriculture, food security and healthier diets the demand for legume crops is on the rise. This growth is fostered by the increasing need for plant protein and for sound agricultural practices that are more adaptable and environmentally sensitive. Food, feed, fiber and even fuel are all products that come from legumes – plants that grow with low nitrogen inputs and in harsh environmental conditions. The Second Legume Society Conference will be held during 2016 - the United Nations' International Year of Pulses. The goals of this UN International Year include: the encouragement of connections throughout the food chain that would better utilize pulse based proteins; increase global production of pulses; better utilization of crop rotations; and to address challenges in the trade of pulses.

The conference will address the following themes: Legume Quality and Nutrition; Farming Systems/Agronomy; Abiotic and Biotic Stress Responses and Breeding; Legume Genetic Resources; and New “Omics” Resources for Legumes. The health and environment benefits, as well as, the marketing of legumes will be transversal topics throughout the conference. Special attention will be given to foster the interaction of researchers and research programs with different stakeholders including farmers and farmer associations, seed/feed and food industries, and consumers. For this, the conference will also be the site of the Final Meeting of the EU-FP7 ABSTRESS project, the Annual Meeting of EU-FP7 LEGATO project; and final dissemination events of EU-FP7-ERANets MEDILEG and REFORMA. The results and conclusions from these four important research programs will be shared with conference attendees.

Please join us in beautiful Tróia, Portugal from 12-14 October, 2016! Plan now to include the Second ILS Conference in your busy agenda. Kindly share this information with any colleagues dealing with legumes.

Diego Rubiales, on behalf of the Scientific Committee
Pedro Fevereiro, Carlota Vaz Patto and Susana Araújo, on behalf of the Organizing Committee

Local Organizers

The Instituto de Tecnologia Química e Biológica / Universidade Nova de Lisboa (ITQB/UNL) will be responsible for organising the Conference, in cooperation with the International Legume Society. The official language of the Conference will be the English.

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Venue

The conference will be held in Tróia in the vicinity of Lisbon, Portugal. Tróia is a beautiful sand peninsula dividing the Sado River from the Atlantic Ocean.

The nearest airport is the Lisbon International Airport, about 50 Km away. Shuttles will be made available from and to Lisbon International Airport.

During the period of Roman occupation, date from the 1st century to the 6th century AD, Tróia was an island of Sado delta, called Ácala Island.

The Sado Estuary Nature Reserve, where dolphins swim, and the Serra da Arrábida Natural Park, where a full developed Mediterranean forest can be seen, are two of the main natural attractions nearby Tróia peninsula.

The Tróia Golf Championship Course is considered the best course in Portugal in the categories of difficulty and variety. It also stands in 20th place in the list of the best golf courses in Europe drawn up by the Golf World magazine.

International Year of Pulses 2016

Global Pulse Confederation (CICILS-IPTIC)

CICILS – IPTIC, shortly to be renamed Global Pulse Confederation is head quartered in Dubai and licenced under the Dubai Government authority, Dubai Multi Commodity Centre (DMCC). CICILS is the not for profit peak body for the whole global pulses industry value chain. As the sole international confederation for the industry it enjoys membership from 18 national associations (federations) and over 600 private sector members in an industry worth over $100 Billion at the retail level and over 60 million tonnes in pulse production and distribution in over 55 countries. The organisation represents the common good of all sectors of the global pulse industry value chain from growers and researchers, through input and logistics suppliers, traders, exporters and importers to government bodies, multilateral bodies, processors, canners and consumers. CICILS works for transparency and sustainability in all sectors and aspires to contribute in as many ways possible to global food security and improved health and nutrition. The CICILS Executive Board consists of up to 30 members from all over the world elected from the membership. Board positions are voluntary, non-profit and carry no remuneration.

OUR VISION

To create an inclusive global pulse organization recognized for its integrity, professionalism and ability to work together across the entire pulse value chain to resolve issues and grow the industry.

OUR MISSION

To lead the global pulse industry to major crop status by facilitating free and fair trade and increasing production and consumption of pulse crops worldwide.

OUR GOALS

- To expand the permanent membership of CICILS to include the broadest base of organisations and companies involved both directly and indirectly in the global trade of pulses.
- To ensure a reliable, consistent and safe pulse value chain delivering pulses that meet the requirements of the industry's existing and future customers and consumers - and to encourage all industry sectors that impact on production, marketing and service delivery for Pulses to operate ethically and at world's best practice.
- To identify, select, fund and/or otherwise support approved research and development activity that leads to increased production and consumption of pulse crops to address the critical health, sustainability and food security issues around the world.
- To work towards harmonisation of the global pulse trade and removal of all barriers to trade for pulses world wide, and where possible develop new markets.
- To hold annual conventions of the highest calibre, that unite CICILS-IPTIC global membership in friendship, provide a focus for exchange of ideas and information, and a forum for discussion and amicable resolution of industry issues.
- To support national and regional member associations through active participation in local country activities by local CICILS members ("Ambassadors").

Themes

CICILS and its IYOP partners have identified a series of thematic areas that will be the focus for activities during the International Year. These areas represent the key issues where new and increased efforts could help make a difference in promoting sustainable agriculture and livelihoods, as well as healthy diets, through increased production, trade and consumption of pulses.

We are working on more than 100 activities and projects related to 2016, four of them have already been launched in the areas of branding, school programs, recipes, and market access. Fifteen external partners have been recruited to work on the year, from major science centres, health institutes, academia to farm groups. Additionally, a total of 30 national committees have begun activities in every continent.

These activities will be built around four thematic areas:

1) Creating Awareness

IYOP 2016 is an opportunity to increase awareness and global demand for pulses. We aim to reach an audience of 20-40 million people worldwide using social media, websites and global media outreach.

2) Food & Nutrition Security & Innovation

IYOP has set the ambitious targets of helping initiate:

- 20 governments to commit to including pulses as part of their food security policies.
- 100 research projects substantiating the ability of pulses to combat nutrition and health issues.
- 100 research projects into functional and nutritional properties for food product advancement.

3) Market Access & Stability

IYOP is an excellent opportunity to open a dialogue on improving the regulatory framework in which trade occurs. We hope to reduce trade barrier costs that are borne by farmers, processors, traders and consumers while introducing greater efficiencies to enhance food security, reduce price volatility and enhance the return to growers.

4) Productivity & Environmental Sustainability

IYOP 2016 is a perfect chance to draw the focus of the scientific community. We hope to see the completion of a 10-year plan of action on pulse research by the end of 2016 and the genome sequencing of three pulse crops by 2018.

National Committees

CICILS has convened a worldwide network of promotional teams to ensure wide-reaching and global coordination of activities on the 2016 International Year of Pulses. The National Groups are made up of experts with “great ideas” who plan and coordinate the most important activities of IYoP outreach, from the ground up. Their work is essential to the successful dissemination of the key thematic areas of the Year.

The Groups will meet via a conference call every two months. The purpose of the calls is to provide an update on activities, exchange ideas, identify gaps and coordinate a global approach on the key themes of the IYoP. As of February 2015, there were 30 countries on the National Promotions Group mailing list and additions to this list will follow over the course of 2015 and 2016.

Join Us!

We know you all love pulses, which is why we want to give you 10 ideas on what you and/or company can do to help promote the 2016 International Year of Pulses.

1. Include a link to iyop.net in your website.
2. Spread the word! Have your communications team promote pulse stories in the media. Messages like: "What Are Pulses and Why Are They Important?" can help.
3. Donate your recipes to the global collection, and feature the recipes on your web site. Send your recipes to IYOP@emergingag.com.
4. Donate your photos to our Photo Gallery.
5. Be social and talk about us! Follow us on Twitter and use the hashtag#IYOP2016.
6. Make use of your own connections to get more supporters. Do you know a local company who could be a sponsor? Perhaps you know someone in the Agricultural Department in your country? We are here to coach you and to provide you materials on how to get them on board.
7. Share your news. Send us your pulse related news to include in the News pages of iyop.net.
8. Submit your event to iyop.net to include on our Event Calendar.
9. Translate materials on iyop.net into your national language.
10. And finally… to welcome the Year, have an Event on January 5th, 2016 and serve pulses!

INDIA PULSES AND GRAINS ASSOCIATION

The Pulses Conclave

Jaipur, India, 17-19 February 2016

http://www.ipga.co.in/pulses-conclave

2016 INTERNATIONAL YEAR OF PULSES

Joint Pan-African Grain Legume and World Cowpea Conference

Livingstone, Zambia, 28 February - 4 March 2016

http://gl2016conf.iita.org

good for planet, good for people

International Conference on Pulses

Rabat, Morocco, 13-15 April 2016

http://www.icarda.org/sites/default/files/u158/Pulses_brochure.pdf

GPC 2016 Global Pulse Convention

Global Pulse Convention

Izmir, Turkey, 19-22 May 2016

http://globalpulseconvention2016.com

ENNFC2016

12th European Nitrogen Fixation Conference

Budapest, Hungary, 25-28 August 2016

http://enfc2016.hu/

XIV Congress of the European Society for Agronomy
Edinburgh, UK, 5-9 September 2016
http://esa14.org.uk

हर कदम, हर डगर
किसानों का हमसफर
भारतीय कृषि अनुसंधान परिषद
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ICAR
Agrisearch with a human touch

International Conference on "Pulses for Nutritional Security and Agricultural Sustainability"
New Delhi, India, 12-14 November 2016
http://www.icar.org.in/files/PulsCon2016-IIPR-22-09-2015.pdf

InterDrought-V
Hyderabad International Convention Center (HICC)
Hyderabad, India
21-25 February, 2017
ID-V

Fifth International Conference InterDrought-V
Hyderabad, India, 21-25 February 2017
http://ceg.icrisat.org/idV/home.html

ICLGG VIII

8th International Conference on Legume Genomics and Genetics
Siofok, Hungary, September 2017

10-16 September, 2017
WSRC 2017 10
SAVANNAH | GEORGIA | USA
CELEBRATING 250 YEARS OF

10th World Soybean Research Conference
Savannah, USA, 10-16 September 2017
http:// www.wsrc10.com

Legume Perspectives is an international peer-reviewed journal aiming to interest and inform a worldwide multidisciplinary readership on the most diverse aspects of various research topics and use of all kinds of legume plants and crops.

The scope of *Legume Perspectives* comprises a vast number of disciplines, including biodiversity, plant evolution, crop history, genetics, genomics, breeding, human nutrition, animal feeding, non-food uses, health, agroecology, beneficial legume-microorganism interactions, agronomy, abiotic and biotic stresses, agroeconomy, sociology, scientometrics and networking.

The issues of *Legume Perspectives* are usually thematic and devoted to specific legume species or crop, research topic or some other issue. They are defined by the Editorial Board, led by the Editor-in-Chief with the help from Assistant Editors, who select and invite one or more Managing Editors for each issue. Having accepted the invitation, the Managing Editor agrees with the Editorial Board the details, such as the deadline for collecting the articles and a list of the tentative contributors, from whom he, according to his own and free choice, solicit the articles fitting into the defined theme of an issue.

There is a possibility that every member of the global legume research community, with a preference of the International Legume Society members or established authorities in their field of interest, may apply to the Editorial Board to be a Managing Editor and suggest a theme for his issue, done simply by contacting the Editor-in-Chief by e-mail, with a clearly presented idea, structure and authors of the potential issue.

The articles published in *Legume Perspectives* are usually concise, clear and up-to-date reviews on the topic solicited by the Managing Editor from each author. Managing Editor is solely responsible for collecting the articles from the authors, anonymous peer-review, communicating with the Technical Editor and providing the authors with the proofs of their manuscript prior to the publication.

Legume Perspectives prefers a clear, simple and comprehensive writing style that would make its articles interesting and useful for both academic and amateur audience.

Legume Perspectives welcomes either longer (900-1,100 words + up to 3 tables, figures or photos + up to 10 references) or shorter (400-500 words + 1 table, figure, photograph or drawing + up to 4 references) manuscripts. The Editor-in-Chief, depending on the opinion of the Managing Editor, may allow any variation in length or structure, from case to case.

The manuscripts for *Legume Perspectives* should be prepared in Microsoft Office Word, using Times New Roman font, 12 points size and single spacing. Please provide each manuscript with a 100-word abstract and 4-6 key words listed alphabetically. The references should follow the style of the published papers in this issue, be given in full and listed alphabetically. The tables may be incorporated in the manuscript, while figures, photographs or drawings should be submitted separately as jpg files with a resolution of at least 300 dpi. The authors whose native language is not English are strongly advised to have their manuscripts checked by a native English speaker prior to submission.

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