16 Pigeonpea: From an Orphan to a Leader in Food Legumes

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More than six billion people of this planet are dependent on nurturing and harnessing agro-ecological biodiversity for food and nutritional security. Human life and civilizations have been influenced not only by cultivated taxa, but also by wild germplasm. The origin and fast-track evolution of agricultural crops aided by domestication have attracted considerable attention from evolutionary biologists, plant explorers, archaeobotanists, geneticists, and plant breeders worldwide in crops such as rice, wheat, and maize. However, legumes (barring soybean) have remained relatively neglected by the researchers.

Globally, pigeonpea is grown on an area of 4.64 million hectares (Mha) annually with production of 3.43 million tonnes, yielding 740 kg ha^{-1} (FAO 2008). In the past three decades India has contributed to more than 70% of global area and production of pigeonpea. India (cultivating 3.53 Mha), Myanmar (570,000 ha), China (150,000 ha), and Nepal (20,988 ha) are the most important Asian countries for pigeonpea production (Table 16.1). In Africa, Kenya (190,000 ha), Malawi (123,000 ha), Uganda (87,000 ha), and Tanzania (67,500 ha) are the leaders.

Pigeonpea is a versatile food legume. A dried decorticated split pea (*dhal*) is consumed as protein source in many Asian and African countries. Green seeds and pods are also consumed as a vegetable in parts of India and Africa. The seed husk and pod wall form quality animal feed. The dried stems of pigeonpea are a good source of fuel wood (the calorific value is about half that of coal (Panikkar 1950)), thatch, and material for basket making. Pigeonpea helps in release of soil-bound phosphorus (Ae *et al*. 1990). Like other legumes, pigeonpea fixes about 40 kg ha^{-1} nitrogen per season (Kumar Rao *et al*. 1983). There are also reports of up to 280 kg ha^{-1} of nitrogen fixation (Red de Grupos de Agricultura de Cobertura 2002). Pigeonpea has also been used as a green manure crop, a cover crop, and food for silkworms (Red de Grupos de Agricultura de Cobertura 2002) and as a host for the lac insect (*Kerria lacca*). The deep root system of pigeonpea breaks the soil hard-pan and helps in nutrient recycling from the deeper layers of soil. Long- and medium-duration pigeonpea varieties have also been successfully used for mountain slope stabilization in southern China and Northern India.

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Table 16.1. Global area, production, and productivity of pigeonpea during 2007

Country	Area (ha)	Production (tonnes)	Productivity (kg ha^{-1})
India	3,530,000	2,510,000	711
Myanmar	570,000	540,000	947
Kenya	190,000	105,000	553
Malawi	123,000	89,000	724
Uganda	87,000	79,000	908
Tanzania	67,500	48,500	719
Nepal	20,988	19,245	917
Dominican Republic	17,100	17,100	1,000
Congo	9,500	5,600	589
Haiti	6,200	2,500	403
Panama	5,000	2,100	420
Bolivarian Republic of Venezuela	3,400	3,100	912
Burundi	2,000	1,800	900
Bangladesh	1,600	1,000	625
Jamaica	900	1,000	1,111
Philippines	825	1,350	1,636
Grenada	550	530	964
Trinidad and Tobago	450	1,100	2,444
Comoros	440	320	727
Puerto Rico	285	230	807
Bahamas	200	135	675
Total/mean	**4.64 M**	**3.43 M**	**739**

Source: FAO 2008.

1 Origin and domestication

Following the origin of cultivated pigeonpea [*Cajanus cajan* (L.) Millspaugh; syn. *Cystisus cajan* L., *Cajanus bicolor* DC., *C. flavus* DC., *C. indicus* Spreng., *C. luteus* Bello], possibly from *C. cajanifolius* (Haines) van der Maesen (De 1974, van der Maesen 1980), it has undergone changes typical of the "domestication syndrome" (Harlan and de Wet 1971, Harlan 1975, 1976). These changes are similar to the domestication syndrome of some crops of the families Poaceae (rice, wheat, maize, barley, oats) and Fabaceae (peas, soybean, common bean) (Harlan 1992). The phylogenesis involved changes in the duration of maturity (from perennial to annual to a very short duration), seed dispersal (shattering to nonshattering types), seed dormancy (long dormancy to no dormancy), and harvest index (low to high harvest index). However, pigeonpea has also maintained some wild traits such as its deep root system, indeterminate growth habit and recovery from stresses.

The primary pigeonpea center of diversity is found on the Indian subcontinent, with a large number of wild species, including the most closely related species *C. cajanifolius* (van der Maesen 1980). A very diverse cultivated gene pool and a few archaeological remains in India strongly suggest that India is also the center of

origin of pigeonpea. East Africa is regarded as a secondary center of origin. There have been some archaeological references to the presence of pigeonpea seeds in Egyptian tombs of the twelfth dynasty (2200–2400 BC) at Dra Abu Negga (Thebes) (Schweinfurth 1884). However, De (1974) and Vernon Royes (1976) reviewed the origin of pigeonpea and concluded that pigeonpea originated in India. Vavilov (1951) also supported the Indian origin theory of pigeonpea since he found the largest range of diversity of pigeonpea on the Indian subcontinent. The most recent conclusion is that the origin of pigeonpea was in India (van der Maesen 1980).

Pigeonpea belongs to the subtribe Cajaninae, tribe Phaseoleae in the subfamily Papilionoideae, of the family Fabaceae. Pigeonpea is the only cultivated food crop of the Cajaninae subtribe. The other members of the tribe Phaseoleae include many bean species (*Phaseolus, Vigna, Lablab, Macrotyloma*, etc.) consumed by humans. The updated genus *Cajanus* now comprises 32 species, with 18 species distributed in Asia, 15 in Australia, and one in West Africa (van der Maesen 1990). Of these, 13 are endemic to Australia, 8 to the Indian subcontinent and Myanmar, and one to West Africa. The rest of them occur in more than one country. Apart from cultivated pigeonpea, only one wild species, *C. scarabaeoides*, is common and widespread throughout South and Southeast Asia, the Pacific Islands, and northern Australia. The greatest diversity of wild species of *Cajanus* is found in Myanmar, southern China, and northern Australia.

The name pigeonpea originated in Barbados, where the seeds of *Cajanus* were used as pigeon feed. There are at least 350 recorded orthographic variants of the term pigeonpea. In India many ancient Sanskrit names (Adhaki, Adhuku) have modern equivalents as Arhar and Tur. It is also known as Angola pea, Congo pea, Kachang Bali, Ads Sudan, Cajanus des Indes, Frijol de árbol, Poisw cajan, Puerto Rican pea, Indircher Bohnenstrauch, Lentil du Sudan, Gandul, Gungo pea, Gunga pea, No-eye pea, and Red gram in different parts of the world.

2 Genepools in pigeonpea

The concept of the gene pool in pigeonpea was laid down by Harlan and de Wet (1971) and has undergone many revisions. Among the members of the Phaseoleae, Cajaninae is well distinguished by the presence of vesicular glands on the leaves, calyx, and pods. Currently, 11 genera are included in Cajaninae, including *Rhynchosia* Lour., *Eriosema* (DC.) G. Don, *Dunbaria* W. & A., and *Flemingia* Roxb. ex Aiton. The members of the earlier genus *Atylosia* closely resemble the genus *Cajanus* in vegetative and reproductive characters. However, they were relegated to two separate genera mainly on the basis of the presence or absence of a seed strophiole. Although the separation of these two genera was questioned by some researchers in the past, it was not taken seriously for want of taxonomic data. The establishment of ICRISAT in 1972 gave a big impetus not only to collect various *Atylosia* species but also for their utilization in the pigeonpea improvement. During the past three decades several researchers both at ICRISAT and in Indian

Table 16.2. Gene pools of pigeonpea

Primary gene pool	Cultivar collections
Secondary gene pool	*Cajanus acutifolius, C. albicans, C. cajanifolius, C. lanceolatus, C. latisepalus, C. lineatus, C. reticulates, C. scarabaeoides* var. *scarabaeoides, C. sericeus, C. trinervius*
Tertiary gene pool	*C. goensis, C. heynei, C. kerstingii (?), C. mollis, C. platycarpus, C. rugosus, C. volubilis, other Cajanus* spp. (?), other Cajaninae (e.g., *Rhynchosia, Dunbaria, Eriosema*)

national programs successfully produced fertile hybrids between pigeonpea and *Atylosia*. These studies provided the basis to merge the two genera following international rules of botanical nomenclature. Finally van der Maesen (1986) revised the taxonomy of *Cajanus* and merged the two genera under *Cajanus* following systematic analysis of morphological, cytological, and chemo-taxanomical data, which indicated the congenicity of the two genera. Primary (GP 1), secondary (GP 2) and tertiary (GP 3) gene pools have now been identified. These gene pools have been used in transferring agronomically superior traits such as disease resistance, high protein content, tolerance to drought, salinity, cold, waterlogging tolerance, *Helicoverpa* resistance, cytoplasmic-nuclear male sterility (CMS), etc. On the basis of crossability studies done at ICRISAT, different species have been assigned to their respective gene pools (Table 16.2).

Pigeonpea is a diploid species with $2n=2x=22$ somatic chromosomes. There has been no discrepancy in the chromosome numbers of pigeonpea across various reports. Most of the reserchers have found $2n=22$ for the entire genus *Cajanus*. The only exceptions came from *C. kerstingii*, which was reported to have $2n=32$ chromosomes (Lackey 1980; Gill and Husaini 1986). The meiotic behavior and pollen formation are normal in *C. cajan*, and the metaphase I behavior in pollen mother cells was found to be normal by many workers (Kumar *et al*. 1945; Bhattacharjee 1956; Dundas *et al*. 1987), or perfect pairing by Reddy and De (1983). The genome size (IC) of cultivated pigeonpea is reported to be 0.825 (Greilhuber and Obermayer 1998). This genome size corresponds to 808 Mbp.

Pigeonpea in an often cross-pollinated crop with natural outcrossing ranging from less than 1% to 70% (Saxena *et al*. 1990). Outcrossing is mediated by insects. Pathak (1970) reported *Apis mellifera* and *A. dorsata* as principal pollinating vectors.

3 Crop improvement

In spite of several useful traits, pigeonpea had remained by and large an "orphan" crop with many wild-type traits. Some of the wild traits in pigeonpea that were

Figure 16.1. A two-year-old pigeonpea tree in Antigua.

addressed by plant breeders were (i) long maturity duration, (ii) excessive plant height and low harvest index, (iii) photoperiod and temperature sensitivity, (iv) susceptibility to *Helicoverpa* and diseases (*Fusarium* wilt, sterility mosaic), and (v) low grain yield. Extensive trait-specific plant breeding research activities were directed towards these issues, with demonstrable progress.

3.1 Early maturity

Cultivated germplasm is of long-maturity duration type (200–300 days). Some perennial landraces may grow like a tree (Figure 16.1) in 2–3 years. Variation in maturity is almost continuous and has been classified into ten maturity groups on the basis of days to 50% flowering (Green *et al*. 1979) (Table 16.3). The long-duration varieties have low seedling vigor, thereby increasing exposure to stresses such as weeds, pests, and diseases. Breeding and selection have enabled development of a range of maturity types (Table 16.3) suitable for different agro-ecosystems and cropping systems.

Extra-short-duration (ESD) lines (Davis *et al*. 1995, Singh 1996) have opened up new cropping niches for pigeonpea. These lines (MN 1, MN 5, and MN 8) flowered in 45–50 days and matured in 70–85 days at ICRISAT, Patancheru (17°N latitude), and have served as an excellent source for earliness in many breeding programs globally.

Table 16.3. Ten maturity groups of pigeonpea

Note: Classification is based on days to 50% flowering at Patancheru (17°N).

Maturity group	Days to 50% flowering	Reference cultivars
0	<60	ICPL 88039
I	61–70	Prabhat
II	70–80	UPAS 120, ICPL 87
III	81–90	Pusa Ageti, T 21
IV	91–100	ICP 6
V	101–120	Maruti, BDN 1
VI	121–130	Asha, C 11
VII	131–140	Hy 3C, ICP 7035
VIII	141–160	Bahar
IX	>160	NDA 1, MAL 13

ESD lines are also grown as a catch-crop (Chauhan *et al*. 1993, Nam *et al*. 1993), and in rice fallows in the short-rainy season in Sri Lanka (Chauhan *et al*. 1999), India, and the Philippines. These lines are used for diversifying cereal-based crop rotations of rice–wheat cropping systems, particularly in the Indo-Gangetic plains. ESD line ICPL 88039 is presently grown on more than 40,000 ha in India and the Philippines, helping preserve the soil fertility and bringing about environmental sustainability to the farming systems.

3.2 Increasing harvest index

Most pigeonpea landraces are tall and grow up to 3 m or more. The harvest index associated with such tall landraces was quite low because of lower grain yield. Such tall lines posed difficulty in taking up plant protection measures such as spraying. Saxena and Sharma (1995) reported 12 types of genetic dwarf in pigeonpea. Dwarfness genes such as *d1* (Saxena *et al*. 1989) served as a source for breeding high-yielding genetically dwarf varieties. The lines bred with this gene were 30%–50% shorter in height and productivity compared with the tall varieties (Saxena 2005). The harvest index of these lines was about 30%–40% higher than that of the tall landraces.

3.3 Reduced photoperiod and temperature sensitivity

The photoperiod and temperature sensitivity of pigeonpea was a constraint to its wider adaptation, and restricted it to the areas between latitudes 35°N and 35°S. Pigeonpea is a quantitative short-day plant, and requires long nights for induction of flowering. The photoperiod sensitivity in pigeonpea germplasm is not only linked to days-to-flowering but also to the amount of biomass produced (Wallis *et al*. 1981). ICRISAT scientists used the Kenya transect, which is near the equator, and selected experimental locations varying from 50 m to over 2,000 m in altitude. In these locations, temperature decreased with higher altitude, thus

providing an "open laboratory". Results indicated that medium-duration varieties would only flower under short days. Optimum temperature for early flowering and maturity was 22–24°C, indicating that they are suited to medium-altitude environments near the equator. On the other hand, long-duration varieties would flower under short days and low temperature. The optimum temperature for such lines was about 18°C. This material was suited for growing between 900 and 1500 m altitude near the equator and subtropics, where day length is short and temperature is low during autumn/winter (Omanga *et al*. 1995, Silim *et al*. 2006). This strategic research has helped scientists breed varieties for wider adaptability. Now it is possible to grow pigeonpea between latitudes 45°N and 45°S, and it can be cultivated up to 2000 m above mean sea level (msl) in tropics and subtropics.

3.4 Resistance to pests (*Helicoverpa*) and diseases (*Fusarium* wilt, sterility mosaic)

3.4.1 Resistance to *Helicoverpa*

Losses due to *Helicoverpa armigera* (pod borer) are estimated at US$310 M annually. A high level of resistance to *Helicoverpa* is not available in cultivated germplasm. Hence, the low-level of resistance is augmented by cultural and biological control means. Significant progress has been made towards transferring resistant genes from the secondary gene pool. Recent results show that while species like *C. albicans* and *C. scarabaeoides* are not preferred for oviposition, antibiosis is present in *C. sericeus*. Attempts are being made to combine these traits together. Some of the recent *C. acutifolius* derivatives registered less than 10% pod borer damage under field conditions.

Genetic transformation has been thought a more viable alternative towards solving this menace. Novel transformation protocols have been optimized for pigeonpea, otherwise considered a recalcitrant crop for obtaining transgenics by using *Agrobacterium tumefaciens*-based binary plasmids carrying *cry1Ab*, *cry1Ac*, and soybean trypsin inhibitor (*SBTI*) genes. A large number of putative transformants were generated for the first time and over 50% of them tested positive for the introduced genes. These transformants also showed high gene expression at the transcription level. Soon these will be available for field testing against pod borers (Kumar *et al*. 2004; Sreelatha *et al*. 2005; Sharma *et al*. 2006).

3.4.2 Resistance to wilt

Wilt caused by the soil-borne fungus *Fusarium udum* Butler can cause up to 100% yield loss under epidemic conditions. There are also reports of seed-borne infection under wilting during pod filling stages (Haware and Kannaiyan 1992). Wilt-sick plots have been used for large-scale screening of germplasm lines and breeding materials and a number of resistance sources have been identified at ICRISAT (Reddy *et al*. 1990). Several wilt-resistant varieties (such as Maruti and Asha in India) have been adopted by farmers on a large scale, leading to increased production. Now all advance breeding lines from ICRISAT carry resistance to wilt disease.

3.4.3 Resistance to sterility mosaic

The disease was reported in 1927 but its causal organism remained a mystery. In a relentless effort over decades, ICRISAT was able to identify the elusive causal agent, now named pigeonpea sterility mosaic virus (PPSMV) (Jones *et al*. 2004), which is transmitted by an eriophyid mite (*Aceria cajani*). This breakthrough research, coupled with effective resistance screening, has enabled the breeders to develop several resistant cultivars. ICRISAT has also developed effective and economical diagnostic kits to survey and determine the extent of the disease and the variability of the virus. ICRISAT has been able to deliver these outputs with effective partnerships with researchers in the Indian Council of Agricultural Research, India, and the Scottish Crops Research Institute, UK.

3.5 High yield potential

Until recently the grain yield levels of pigeonpea had remained stagnant between 700 and 800 kg ha^{-1} for five decades. Crop improvement methods, such as pure-line breeding, population breeding, mutation breeding, and interspecific crosses were used to develop improved varieties. More than 60 pure-line varieties bred in the past have had little or no impact on the productivity of pigeonpea. Therefore, scientists at ICRISAT envisaged breeding hybrids in pigeonpea to overcome the yield barrier. A genetic-male-sterility (GMS)-based hybrid breeding system using partial natural out-crossing (otherwise considered a constraint in varietal seed production) was initiated at ICRISAT (Reddy *et al*. 1978, Saxena *et al*. 1983). The world's first pigeonpea hybrid variety, ICPH 8 (Saxena *et al*. 1992) was released in 1992, targeted for diverse agro-ecological conditions, in which it recorded an average 30.5% yield advantage over the best existing variety. In spite of high yields, ICPH 8 could not become popular owing to difficulties in large-scale seed production. This spurred scientists to develop a more efficient cytoplasmic-nuclear male-sterility (CMS) system.

ICRISAT scientists developed CMS lines by combining the cytoplasmic genome of wild relatives with the nuclear genome of cultivated pigeonpea. So far five CMS systems have been developed. A_1 cytoplasm was derived from *C. sericeus*, A_2 cytoplasm *from C. scarabaeoides*, A_3 cytoplasm from *C. volubilis*, A_4 cytoplasm *from C. cajanifolius, and* A_5 cytoplasm from *C. cajan*. A_4 cytoplasm has been most promising, and has offered stable male-sterile lines, excellent frequency of maintainers in the cultivated germplasm, and very high fertility restoration in the F_1 hybrids (Saxena 2008). Using this technology, ICRISAT developed the world's first CMS-based pigeonpea hybrid variety ICPH 2671 (Figure 16.2). The development of the pioneer CMS system and hybrid technology are major milestones in the history of breeding food legumes and hold the promise of breaking the productivity barrier. The CMS has now been introgressed into agronomically superior varieties for developing locally adapted hybrid varieties.

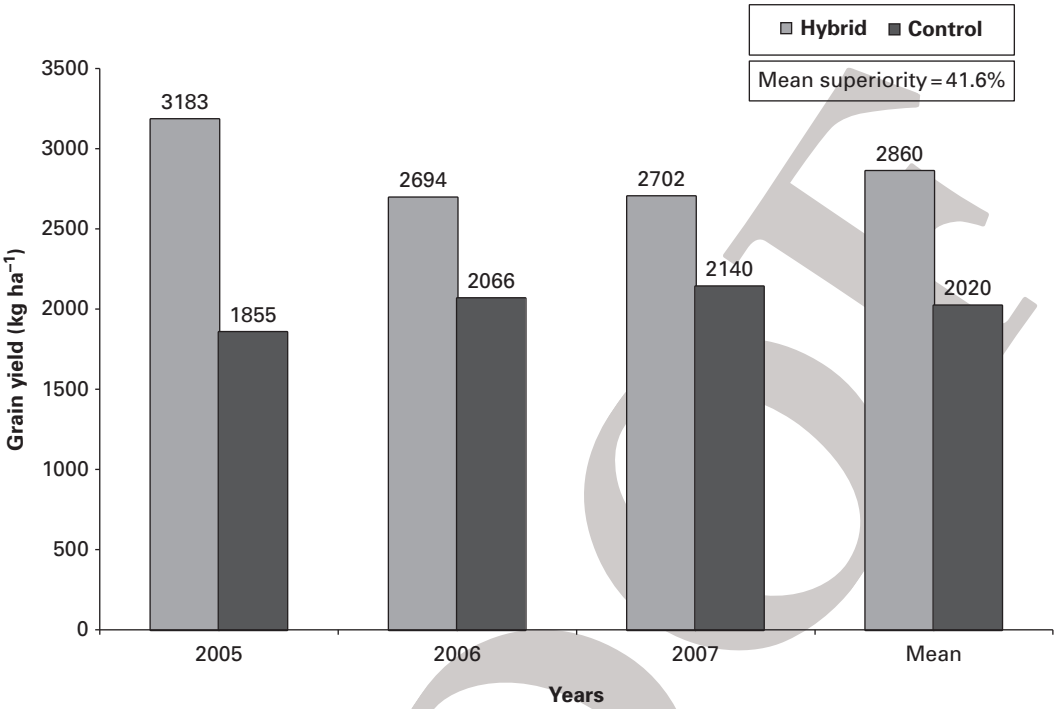

Figure 16.2. Performance of ICPH 2671 over three years and 21 locations in India.

4 Germplasm conservation, management, and utilization

The genebank at ICRISAT conserves 13,632 accessions of pigeonpea collected from 74 countries. India is the major contributor, with over 9,000 accessions. This is the single largest collection of pigeonpea germplasm assembled at any one place in the world. Landraces predominate the collection (8,215) followed by breeding materials (4,862) and wild relatives (555). ICRISAT has characterized, evaluated, and documented about 95% of the cultivated germplasm accessions. However, very few germplasm lines have been used by plant breeders.

To overcome the obstacle of so many accessions, which may be inhibiting the use of the collection by breeders, scientists at ICRISAT developed a "core collection", consisting of about 10% of the entire collection, but representing the genetic variability of the entire collection (Reddy *et al*. 2005). However, it soon became evident that developing core collections will not solve the problem of low use of germplasm, as even the size of the core collection would be unwieldy for exploitation by crop improvement scientists. To overcome this, ICRISAT scientists (Upadhyaya and Ortiz 2001) proposed a "mini core collection" that contains 10% of the core or *c*. 1% of the entire collection and represents the diversity of the entire collection (Upadhyaya *et al*. 2006b). Owing to its greatly reduced size, the mini core collection provides an easy access to the germplasm

collection and scientists can evaluate the mini core collection easily and economically and identify trait-specific germplasm for use in their crop improvement programs (Upadhyaya *et al*. 2006a). A global composite collection of pigeonpea that included the mini core collection has been genotyped using 20 SSR markers, and a reference set of the 300 most diverse accessions has been selected and used in genomics studies. Systematic characterization and evaluation of germplasm accessions has resulted in the identification of several useful and new genotypes that have gone into the release of several varieties across the world.

5 Future

During the past 35 years, scientists have made significant contributions towards global pigeonpea research and development. Some of the constraints in the traditional landraces have been corrected, and these varieties are tailored to suit different cropping systems and new niches. ICRISAT maintains the world pigeonpea germplasm for present and future use. Further characterization of germplasm using molecular marker technology and greater sharing of pigeonpea germplasm with NARS partners needs to be done for better utilization of genetic resources.

While many biotic constraints such as *Fusarium* wilt and sterility mosaic diseases have been addressed, diseases such as *Phytophthora* blight are becoming important. New races of wilt and sterility mosaic are beginning to appear. These developments may be driven by climate change. The resistance levels of some wilt and sterility mosaic-resistant varieties are breaking down under new races of pathogens, and/or due to migration of races in newer geographical locations. Although a few sources of resistance towards *Fusarium* wilt, sterility mosaic, and *Phytophthora* blight are known, new sources of resistance need to be identified and introgressed in the pure lines, hybrids, and hybrid parental lines. Characterization and monitoring of the new races of wilt and sterility mosaic will be crucial towards development and deployment of the new varieties and hybrids. The evasive *Helicoverpa* resistance needs to be addressed through transgenics with optimized gene constructs with better temporal and spatial gene expression. We also need to breed for resistance to pod fly and *Maruca*, as these two pests are gaining importance in the wake of changing climate.

The new CMS-based hybrid technology calls for generating hybrids that combine high yield with resistance to major biotic and abiotic stresses. Resistance to major diseases (*Fusarium* wilt, sterility mosaic, *Phytophthora* blight), pests (*Helicoverpa*, pod fly, *Maruca*), drought, and salinity needs to be combined in the hybrid. This will require an enormous amount of research and cross-synergy in the fields of plant breeding, genetics, genetic engineering, genomics, and social science.

ICRISAT has demonstrated the power of partnership involving both private sector and government organizations. This approach exploits complementary expertise from various public and private partners in popularizing hybrids and pure line varieties for resource-poor farmers.

References

Ae N, J Arihara, K Okada, T Yoshihara, and C Johansen. 1990. Phosphorus uptake by pigeonpea and its role in cropping systems of the Indian sub-continent. *Science* **248**: 477–80.

Bhattacharjee SK. 1956. Study of autotetraploid *Cajanus cajan* (Linn.) Millsp. *Caryologia* **9**: 149–59.

Chauhan YS, WD Atukorala, KDA Perera *et al*. 1999. Potential of extra-short-duration pigeonpea in the short rainy season of a tropical bimodal rainfall environment. *Experimental Agriculture* **35**: 87–100.

Chauhan YS, C Johansen, and L Singh. 1993. Adaptation of extra-short-duration pigeonpea to rainfed semi-arid environments. *Experimental Agriculture* **29**: 233–43.

Davis DW, GR Gingera, and KJ Sautor. 1995. MN1, MN5, and MN8 early duration pigeonpea lines. *International Chickpea and Pigeonpea Newsletter* **2**: 57–8.

De DN. 1974. Pigeonpea. Pp. 79–87 *in* J Hutchinson (ed) *Evolutionary Studies in World Crops. Diversity and Change in the Indian Subcontinent*. London: Cambridge University Press.

Dundas IS, EJ Britten, DE Byth, and GH Gordon. 1987. Meiotic behavior of hybrids of pigeonpea and two Australian native *Atylosia* species. *Journal of Heredity* **78**: 261–5.

FAO. 2008. *FAOSTAT. Food and Agriculture Organization of the United Nations*. Rome, Italy. (http://faostat.fao.org/)

Gill LS and SWH Husaini. 1986. Cytological observations in Leguminosae from Southern Nigeria. *Willdenowia* **15**: 521–7.

Green JM, D Sharma, KB Saxena, LJ Reddy, and SC Gupta. 1979. *Pigeonpea Breeding at ICRISAT*. Paper presented at the Regional Workshop on Tropical Grain Legumes. University of West Indies, St. Augustine, Trinidad, 18–22 June 1979.

Greilhuber J and R Obermayer. 1998. Genome size variation in *Cajanus cajan* (Fabaceae): a reconsideration. *Plant Systematics and Evolution* **212**: 135–41.

Harlan JR. 1975. *Crops and Man*. Madison, WI: American Society of Agronomy.

Harlan JR. 1976. Genetic resources in wild relatives of crops. *Crop Science* **16**: 329–33.

Harlan JR. 1992. *Crops and Man*, 2nd edition. Madison, WI: American Society of Agronomy, Inc.

Harlan JR and JMJ de Wet. 1971. Towards a rational classification of cultivated plants. *Taxon* **20**: 509–17.

Haware MP and J Kannaiyan. 1992. Seed transmission of *Fusarium udum* in pigeonpea and its control by seed-treatment fungicides. *Seed Science Technology* **20**: 597–601.

Jones AT, PL Kumar, KB Saxena *et al*. 2004. Sterility mosaic disease – the 'green plague' of pigeonpea. *Plant Disease* **88**: 436–45.

Kumar LSS, A Abraham, and VK Srinivasan. 1945. Preliminary note on autotetraploidy in *Cajanus indicus* Spreng. *Proceedings of the Indian Academy of Science*. Section B, **21**: 301–6.

Kumar SM, D Syamala, KK Sharma, and P Devi. 2004. *Agrobacterium tumefaciens* mediated genetic transformation of pigeonpea (*C. cajan* L. Millsp.). *Journal of Plant Biotechnology* **6**: 69–75.

Kumar Rao JVDK, PJ Dart, and PVSS Sastry. 1983. Residual effect of pigeonpea (*Cajanus cajan* (L.) Millsp.) on yield and nitrogen response of maize. *Experimental Agriculture* **19**: 131–41.

Lackey JA. 1980. Chromosome numbers in the *Phaseoleae* (*Fabaceae: Faboideae*) and their relation to taxonomy. *American Journal of Botany* **67**: 595–602.

Nam NH, YS Chauhan, and C Johansen. 1993. Comparison of extra-short-duration pigeonpea with short-season legumes under rainfed conditions on Alfisol. *Experimental Agriculture* **29**: 307–16.

Omanga PA., RJ Summerfield, and A Qi. 1995. Flowering of pigeonpea (*Cajanus cajan*) in Kenya: Response of early maturing genotypes to location and date of sowing. *Field Crops Research* **41**: 25–34.

Panikkar MR. 1950. Alternate fuel-arhar stalk. *Indian Farming* **11**: 496.

Pathak GN. 1970. Red gram. Pp. 14–53 *in* P Kachroo (ed) *Pulse Crops of India*. New Delhi: Indian Council of Agriculture Research.

Red de Grupos de Agricultura de Cobertura. 2002. *Base de información sobre especies con potential de abonos verdes y cultivos de cobertura*. New York, NY: Rockefeller Foundation.

Reddy BVS, JM Green, and SS Bisen. 1978. Genetic male-sterility in pigeonpea. *Crop Science* **18**: 362–4.

Reddy LJ and DN De. 1983. Cytomorphological studies in *Cajanus cajan* x *Atylosia lineata*. *Indian Journal of Genetics and Plant Breeding* **43**: 96–103.

Reddy LJ, HD Upadhyaya, CLL Gowda, and Sube Singh. 2005. Development of core collection in pigeonpea [*Cajanus cajan* (L.) Millsp.] using geographic and qualitative morphological descriptors. *Genetic Resources and Crop Evolution* **52**: 1049–56.

Reddy MV, SB Sharma, and YL Nene. 1990. Pigeonpea: disease management. Pp. 303–47 *in* YL Nene, SD Hall, and VK Sheila (eds) *The Pigeonpea*. Wallingford: CAB International.

Saxena KB. 2005. Pigeonpea (*Cajanus cajan* (L.) Millsp.). Pp. 86–115 *in* RJ Singh and PR Jauhar (eds) *Genetic Resources, Chromosome Engineering, and Crop Improvement*. Volume 1. *Grain Legumes*. Boca Raton, FL: Taylor and Francis.

Saxena KB. 2008. Genetic improvement of pigeonpea – a review. *Tropical Plant Biology* **1**: 159–78.

Saxena KB, YS Chauhan, C Johansen, and L Singh. 1992. Recent developments in hybrid pigeonpea research. Pp. 58–69 *in* B Napompeth and S Subhadrabandhu (eds) *New Frontiers in Pulses Research and Development*. 10–12 November 1989. Kanpur, India: Indian Institute of Pulses Research.

Saxena KB, SM Githri, L Singh, and PM Kimani. 1989. Characterization and inheritance of dwarfing genes of pigeonpea. *Crop Science* **29**: 1199–202.

Saxena KB and D Sharma. 1995. Sources of dwarfism in pigeonpea. *Indian Journal of Pulses Research* **8**: 1–6.

Saxena KB, L Singh, and MD Gupta. 1990. Variation for natural out-crossing in pigeonpea. *Euphytica* **46**: 143–8.

Saxena KB, Wallis ES, and Byth DE. 1983. A new gene for male sterility in pigeonpeas. *Heredity* **51**: 419–21.

Schweinfurth G. 1884. Further discoveries in flora of ancient Egypt. *Nature* **29**: 312–15.

Sharma KK, M Lavanya, and V Anjaiah. 2006. *Agrobacterium*-mediated production of transgenic pigeonpea (*Cajanus cajan* L. Millsp.) expressing the synthetic *Bt cry1Ab* gene. *In Vitro Cellular and Developmental Biology – Plant* **42**: 165–73.

Silim SN, Coe R, Omanga PA, and Gwata ET. 2006. The response of pigeonpea genotypes of different duration types to variation in temperature and photoperiod under field conditions in Kenya. *Journal of Food, Agriculture and Environment* **4**: 209–14.

Singh L. 1996. The development of and adoption prospects of extra-short-duration pigeonpea. Pp. 1–5 *in* L Singh, YS Chauhan, C Johansen, and SP Singh (eds) *Prospects for Growing Extra-Short-Duration Pigeonpea in Rotation with Winter Crops:* Proceedings of the IARI/ICRISAT workshop and monitoring tour, New Delhi, India. 16–18 Oct 1995. New Delhi: IARI, and Patancheru: ICRISAT.

Sreelatha G, HC Sharma, D Manohar Rao, M Royer, and KK Sharma. 2005. Genetic transformation of pigeonpea [*Cajanus cajan* (L.) Millsp.] with *Bt cry1Ac* gene and the evaluation of transgenic plants for resistance to *Helicoverpa armigera*. P. 58. Abstract *in* MC Kharkwal (ed) *IVth International Food Legumes Research Conference: Food Legumes for Nutritional Security and Sustainable Agriculture*, 18–22 October 2005. New Delhi: Indian Agricultural Research Institute.

Upadhyaya HD, CLL Gowda, HK Buhariwalla, and JH Crouch. 2006a. Efficient use of crop germplasm resources: identifying useful germplasm for crop improvement through core and min-core collections and molecular marker approaches. *Plant Genetic Resources* **4**: 25–35.

Upadhyaya HD and R Ortiz. 2001. A mini core subset for capturing diversity and promoting utilization of chickpea genetic resources in crop improvement. *Theoretical and Applied Genetics* **102**: 1292–8.

Upadhyaya HD, LJ Reddy, CLL Gowda, KN Reddy, and Sube Singh. 2006b. Development of mini core subset for enhanced and diversified utilization of pigeonpea germplasm resources. *Crop Science* **46**: 2127–32.

van der Maesen LJG. 1980. India is the native home of the pigeonpea. Pp. 257–62 *in* JC Arends, G Boelama, CT de Grant, and AJM Leeuwenberg (eds) *Libergratulatorius in honerem HCD de Wit. Agricultural University Miscellaneous Paper*, vol **19**. Wageningen, The Netherlands: Agricultural University.

van der Maesen LJG.1986. *Cajanus* D.C. and *Atylosia* W. and A. (Leguminosae). *Agricultural University Wageningen Miscellaneous Papers 85–4*. Wageningen, The Netherlands: Agricultural University.

van der Maesen LJG. 1990. Pigeonpea: Origin, history, evolution and taxonomy. Pp. 15–46 *in* YL Nene, SD Hall, and VK Sheila (eds) *The Pigeonpea*. Wallingford: CAB International.

Vavilov NI. 1951. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica* **13**: 1–366.

Vernon Royes W. 1976. Pigeonpea. Pp. 154–6 *in* NW Simmonds (ed). *Evolution of Crop Plants*. London and New York: Longmans.

Wallis ES, DE Byth, and KB Saxena. 1981. Flowering responses of thirty-seven early maturing lines of pigeonpea. Pp. 143–150 *in* YL Nene and V Kumble (eds) *International Workshop on Pigeonpeas*, Vol **2**, 15–19 Dec 1980. Patancheru: ICRISAT.