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Review Paper

The decades-old fantasy of enhancing pigeonpea productivity

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ABSTRACT

Pigeonpea has long been perceived as a high-protein food that is low in its on-farm productivity. The research efforts made in the past half-century towards increasing its yields have not shown positive signs in achieving the goal. For example, in 1970-71, the mean yield of pigeonpea was 707 kg/ha, and now in 2024-25, it rests at only 856 kg/ha. This simply means that in the last 54 years of R&D, its average yield could crawl only 149 kg/ha. Considering the nutritional security and financial health of the subsistence farmers, concerted efforts are required to increase the yield of pigeonpea. In this context, although efforts have been made at various institutes, the same output has been achieved. Therefore, the research advances accomplished so far in the fields of plant breeding, seed quality control, genomics, and crop management should knit together again to form a new, broad-based platform for pigeonpea research and development. It is also true that past conventional research efforts successfully produced a number of widely adapted inbred cultivars, which, at the national level, led to a significant increase in pigeonpea-cropped area, but the on-farm productivity continued to lag far behind its potential. In recent times, two research accomplishments have shown promise. These include the development of (i) CMS-based hybrid breeding technology and (ii) the evolution of new and accurate genomics tools. It is expected that these may play a significant role in increasing the efficiency of plant breeding programmes. The development of high-yielding and climate-resilient pigeonpea varieties calls for accelerated genetic gains through the integration of modern plant breeding and genomics-enabled approaches. The merging of strategic approaches such as hybrid breeding, genomic selection, speed breeding, and sybrid populations offer positive scope to improve the breeding values of the end-products. Truly speaking, challenging the long-held myth of limited yield enhancement in pigeonpea would not only require an effective integration of advanced breeding tools but also a greater emphasis on the targeted use of genetic resources and resolution of seed system bottlenecks. Collectively, these amendments are likely to provide compelling evidence for enhanced productivity gains in this valuable pulse crop.

Key words: Yield stagnation, Genomics, Hybrid breeding, Production systems

INTRODUCTION

Pigeonpea production trends

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is known to play a significant role in the nutritional security of under-privileged masses due to its high-protein (22-24%) and valuable minerals (Saxena *et al*. 2023a). Pigeonpea seeds are consumed either as decorticated dry splits (*dal*), whole dry grains, or a fresh vegetable. The valuable by-products of the pigeonpea crop include nutritive fodder, feed, and fuel wood. Besides these, the cultivation of pigeonpea on a sustainable basis helps farmers in rejuvenating their fields through the natural processes of fixing atmospheric nitrogen, a deep penetrating root system, and a huge fall of nutrient-filled dry leaves (Saxena *et al*. 2018a). In spite of continuing crop improvement efforts over decades, the present average yields of pigeonpea hover at around 800 kg/ha. The low productivity of pigeonpea is attributed to the ill effects of various biotic and abiotic stresses, besides the non-availability of high-yielding cultivars and their quality seeds.

Globally, pigeonpea is cultivated on 5.38 m ha of land (FAOSTAT, 2024) in the tropical and sub-tropical regions of 22 countries (Figure 1). India, by far, is the largest producer and consumer of this pulse with a mean sown area of over 4 m ha and

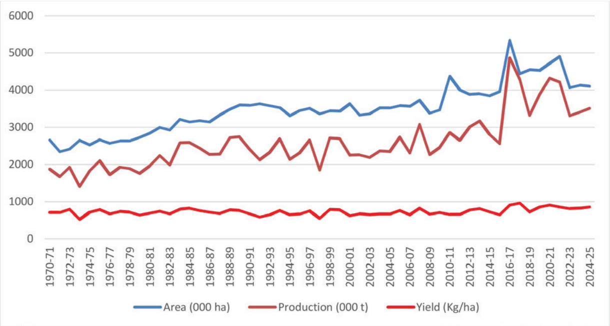

Fig 1. Pigeonpea production statistics from1970-71 to 2024-25

production of 3.5 m tonnes of grains (DoA-GOI, 2025). From 1961-63, pigeonpea production at the global level increased by 148 %, and this production enhancement is largely due to the addition of 2.6 m ha of land area. The annual growth rates recorded in pigeonpea area, production, and yield were 1.4%, 1.8%, and 0.4%, respectively (Nigam *et al*. 2021).

Africa, the other hub of pigeonpea cultivation, contributes 13% to the global pigeonpea area and 19% in the production volume. The major pigeonpea-producing African countries include Kenya, Tanzania, Uganda, Mozambique, and Malawi. In Africa, the production scenario is primarily driven by the export demand and prevailing market prices. The average pigeonpea yield in Africa (1,196 kg/ha) is marginally better than in India.

The South American and Caribbean Island countries constitute the third global centre for pigeonpea production. The countries included in this hub are Haiti, the Dominican Republic, Puerto Rico, and various small islands. In this part of the world, pigeonpea is grown primarily as a vegetable (green peas) crop for domestic and export markets. All the Caribbean Island countries grow pigeonpea on 0.15 m ha with 0.13 m t of total production with an average yield of 874 kg/ha. This region contributes 3% to each in global area and production. Pigeonpea production in this region has increased by 309%, mainly due to expansion in area by a huge margin of 409% (Nigam *et al*. 2021).

Pigeonpea utilization trends

The world's projected annual pigeonpea demand is expected to be at 5,580,000 tonnes by 2030, and it will escalate up to 6,415,000 tonnes by 2040. It is also projected that the two major pigeonpea-producing countries, India and Myanmar, will reach the level of self-sufficiency by 2030, and it will remain so for the next decade. However, the sub-Saharan African countries indicate a marginal gap between the projected demand and supply (Nigam *et al*. 2021).

KEY FACTORS RESPONSIBLE FOR LOW YIELDS

Genetic factors

The primary gene pool of pigeonpea houses over 15,000 accessions, and this carries a tremendous phenotypic variability, but the same is not true about their diversity at the molecular level (Yang *et al*. 2006). However, molecular diversity in the secondary gene pool is quite high, and this genetic resource deserves to be utilized in crop breeding programmes. But, unfortunately, pigeonpea breeders could not exploit it extensively due to strong linkage drag, besides the paucity of resources.

Kumar *et al*. (2003) and Saxena *et al*. (2018a), while studying the pedigrees of all the released Indian pigeonpea cultivars, revealed that in the past, only a limited number of parental lines from the primary gene pool were utilized in breeding. Based on this fact, they opined that the availability and utilization of limited genetic variability for some key traits may be responsible for low productivity in pigeonpea.

Key abiotic and biotic stress factors

Abiotic factors are non-living environmental stressors that often constrain the growth, development, productivity, and finally resilience. These factors include moisture (drought and waterlogging), temperature (high and low), and those arising from soil conditions (salinity, alkalinity, and mineral toxicity). These stresses, depending on the specificity of an ecosystem, affect crop productivity individually or in combination. In general, the losses from each of them are inconsistent, but in certain years/locations, they could be quite high.

Drought

Water deficiency or drought is the most common abiotic factor, particularly under subsistent agriculture, where the irrigation facilities are scarce or not available. According to Nigam *et al*. (2021), the estimated losses to pigeonpea due to drought alone often exceed 50%, and these are directly linked to the frequency, timing, and duration of drought stress and accompanying rate of evaporation and transpiration. Overall, the incidences of drought adversely affect plant growth, leaf area, photosynthetic capacity, symbiotic nitrogen fixation, and nutrient uptake. The drought stress that coincides with flowering and early pod-development stages often induces enhanced abscission of flowers and young pods.

The deep root system, perennial growth, long growth cycle of pigeonpea, and unpredictable nature of drought make the breeding of tolerant genotypes quite difficult. In this context, the studies conducted with pigeonpea hybrids have shown that the F_1 hybrids have a clear advantage over inbred cultivars in tolerating the incidences of water stresses (Saxena *et al*. 1992, Lopez *et al*. 1996). Besides pigeonpea, in other crops, in spite of serious resistance breeding efforts, true success in breeding drought-tolerant cultivars is still awaited. Hence, the issue of drought in field crops is still a big challenge to the scientific community.

Water-logging

Water-logging is another key abiotic stress of pigeonpea where both the short- and long-term water-logging cause severe yield losses, particularly in high rainfall areas and poorly drained soils. These losses are irreversible as the root system of the plants is damaged. In pigeonpea, it was observed that, in comparison to adult plants, the seed germination and early vegetative stages are more sensitive to waterlogging stress (Sultana *et al*. 2013).

The principal cause of plant mortality due to flooding is inadequate supply of oxygen to the submerged tissues, including roots. This anaerobic environment stops the normal functioning of root tissues, which leads to plant mortality. Hence, it is opined that any genetic mechanism that is able to restore oxygen supply to the flooded tissues would support the survival of submerged plants. Armstrong (1979) demonstrated that the formation of aerenchyma cells, hypertrophied lenticels, and adventitious roots facilitates gas diffusion to the roots and thus they contribute directly to the survival of plants under the water-logged environment.

Water-logging tolerance is a multi-faceted trait, controlled by various morphological, physiological, and biochemical processes, singly or in combination. The important morphological traits include the development of aerenchyma cells and adventitious roots (Figure 2), which facilitate the oxygen supply to submerged tissues. The key physiological mechanisms include stomatal regulation and photosynthetic adjustment, which help in maintaining different metabolic functions (Hingane *et al*. 2015, Sultana *et al*. 2013). Several germplasm accessions, advanced breeding lines, and hybrids have been screened for water-logging resistance under greenhouse environment and identified a few tolerant genotypes such as ICPLs 84023, 20241, 20092, and ICPH 2671.

Fig 2. Emergence of lenticels in the tolerant genotype under water-logged conditions

Soil salinity

Recently, soil salinity has emerged as an important limitation in cultivating pigeonpea, particularly in the irrigated rice-wheat areas and poorly drained coastal belt. In this eco-system the excessive accumulation of sodium (Na^+) and chloride (Cl^-) ions placed inside soil impairs water uptake, disrupts nutrient balance, and induces both ionic and osmotic stresses. This results in poor seedling establishment and plant growth. Pigeonpea, in general, is regarded as moderately sensitive to salinity because of its ability to maintain ionic balance, which protects photosynthetic efficiency and minimizes oxidative damage under saline conditions (Choudhary *et al*. 2011, Joshi *et al*. 2022).

Major biotic stresses

In pigeonpea, a few diseases (Fusarium wilt, sterility mosaic virus, and Phytophthora blight) and insects (*Helicoverpa armigera*, *Maruca vitrata,* and pod fly) are major biotic stresses. At present, a number of pigeonpea varieties resistant to wilt and sterility mosaic are available, and these are grown extensively by farmers in the major pigeonpea growing belts of the country. In case of insects, the two pod borers (*Helicoverpa armigera* and *Maruca* *vitrata)* cause significant yield losses year-after-year. Of these, the former insect is severe on all kinds of pigeonpea types, while the latter mostly damages early maturing genotypes. The pod fly often attacks the late-maturing types in the north Indian environment. Although the chemical control and Integrated pest management provide some relief to farmers, for sustainable insect management and high productivity, the development of new pigeonpea cultivars, which would have built-in genetic abilities to resist insect damage, is required.

The presence of low levels of pod borer resistance in pigeonpea germplasm has discouraged breeders from taking up the breeding programmes with high investments and priority. However, in spite of this limitation, some breeders started programmes using various genetic engineering and genomics tools, but these efforts also took scientists nowhere. As a result, the insects continue to wreak havoc on pigeonpea production. Considering the importance of pigeonpea towards nutritional security and the inability to breed pod borer-resistant cultivars, it has now become inevitable to try some alternative plant breeding and genomics tools so that the yield losses are minimized. To achieve this, Saxena (unpublished) proposed some amendments in the areas of pod borer screening technology, plant ideotype, and application of molecular breeding science to enhance the levels of genetic resistance against the pigeonpea pod borers.

Interaction of individual plants with the micro-environment

Theoretically, the maximum genotypic variability in a bi-parental mating of a cross is expressed in its F_2 generation. In contrast, the advanced generation (F_6 /F_7) inbred lines are homozygous for most quantitative as well as qualitative traits. The individual inbred bulk populations are very uniform, with the least intra-inbred variability. But surprisingly, this was not the case in pigeonpea, when crop breeders at ICRISAT found that the inbred bulks also exhibited high to very high intra-inbred population variability for yield/plant.

Saxena and Nigam (2022) investigated this surprising phenomenon in a few single crosses, their inbred parents, and F_2 bulks. The data collected on the yield/plant of these populations were used to estimate their phenotypic variances. They observed that the intra-population variances in the inbred populations were unexpectedly too large, and in some cases as good as their F_2s (Table 1). They opined that the variability observed within the genetically pure inbred populations was due to some non-genetic causes which were randomly distributed within the vicinity of each plant, and this creates a sphere of micro-environment in the vicinity of individual plants, both below and above the ground. These factors interact with individual plants at different growth stages and produce differential effects on productivity in one way or the other. In fact, these effects may or may not be visible at the phenotypic level. Because pigeonpea plants are plastic in nature, the resultant changes are irreversible. These play a significant role in shaping the phenology and grain yield of individual plants. Overall, the compound effect of such phenomena is that the inbred parental populations produced variable inter-plant yields and thereby, high variances. In such situations, the individual plants from segregating or non-segregating populations are likely to have poor heritability from one generation to the next.

Rossini *et al*. (2011) reported that the suppressed or stressed young plants present within the pure maize stands failed to recover from the initial stress shock, and the inter-plant differences were carried throughout their life cycle. It is believed that a similar situation exists in pigeonpea also. Such shocks are more frequent in pigeonpea owing to it being a long-duration rainfed crop. Consequently, genotype x micro-environment interactions adversely affected the heritability and breeding values of the single plants selected during the pedigree breeding exercise.

Table 1. Comparative variances and means for yield in the inbred parents and their F2 bulks

S No.	Cross	Variance			Yield (g/pl)		
		P1	P2	F2	P1	P2	F2
Spreading x Spreading Crosses							
1	ICP 102 x BDN1	1205	882	665	65	66	66
2	ICP 102 x ICP1258	1205	646	975	65	36	36
Compact x Compact Cross							
3	TTB 7 x ICP 7977	214	393	202	29	30	26
Compact x Spreading Crosses							
4	NPWR 15 x ICP 102	344	1205	769	40	65	57
5	NPWR 15 x BDN 1	344	882	680	40	66	61
6	ICP 7086 x ICP 102	166	1205	854	22	65	59
7	KWR 1 x ICP 102	392	1205	975	32	65	52
8	KWR 1 x ICP 1258	392	646	427	32	36	37
9	TTB7 x ICP 1258	214	646	615	29	36	45

This table is modified from that reported by Saxena and Nigam (2022)

POTENTIAL PLANT BREEDING APPROACHES TO ENHANCE PIGEONPEA PRODUCTIVITY

Inability of inter-disciplinary scientific communities to overcome the hurdle of stagnant pigeonpea productivity has remained a matter of concern over the past half-century. This situation has arrived due to various biological, crop production, and research management factors. Among these, the genetic factors linked to a single or a few genes, such as disease resistance, earliness, seed size, and high protein, have been adequately addressed. But, in contrast, the issues relating to yield enhancement and stability of production persist. With the emergence of new breeding and genomics technologies, it has now become imperative to attend to these issues afresh using these tools. In this context, the authors have suggested the following research pathways, which may help in enhancing the on-farm productivity of pigeonpea.

Search and utilization of new genetic diversity

In case the desired trait is not available in the primary gene pool, then crop breeders often go to the next level of repository *i.e.,* the crossable wild species, and they plan to transfer them into the cultivated types. This breeding activity, however, is far from the comfort level of the breeders due to various bottlenecks encountered from hybridization to inbred development.

In pigeonpea also the story is the same, and some crossable wild species carry genes not available in the cultivated germplasm. Some potential crossable wild species include *Cajanus scarabaeoides, C. acutifolius, C. reticulatus*, and *C. sericeous,* etc. (Table 2)**.** This breeding approach looks like an attractive option, but on the ground, it is not only difficult but also consumes large amounts of time and resources.

Table 2. Trait-specific donors identified in crossable wild relatives of pigeonpea

Trait	Scientific name
Drought tolerance	*C. acutifolius, C. lineatus*
Heat tolerance	*C. acutifolius, C. cajanifolius*
Salinity tolerance	*C. albicans, C. sericeus*
Waterlogging tolerance.	*C. lineatus, C. sericeus*
Pod borer resistance	*C. scarabaeoides, C. sericeus*
Wilt resistance	*C. scarabaeoides*
Pod fly resistance	*C. albicans, C. scarabaeoides*
SM virus resistance	*C. acutifolius, C. scarabaeoides*
Pod wasp resistance	*C. albicans, C. scarabaeoides*
Bruchids resistance	*C. acutifolius; C. scarabaeoides;*
High seed protein	*C. scarabaeoides; C. albicans*

To overcome the complexities of inter-specific breeding programmes and ease this process. The plant breeders in the past had proposed to bifurcate the entire breeding project. In the first phase, the recipient genotype and wild species accessions are selected, and it follows the difficult job of hybridization. The hybrid plants are raised, and their subsequent generations are advanced up to the F_5/F_6 generation as the unselected bulk, which is temporarily lodged in a short-term storage for future use. This activity is designated as "pre-breeding"**.**

In the follow-up second breeding act, the unselected bulk is withdrawn from the storage, as and when required, for completing the breeding process. The stored inter-specific hybrid population is loaded with numerous recombinants carrying both useful as well as undesirable traits from the wild species. It has also been observed that certain wild species traits are strongly linked to each other and cannot be broken easily in succeeding generations. In plant breeding terms, this situation is termed "linkage drag". The selections in these populations are exercised for the required trait combinations to develop inbred lines which can be used as cultivars or parental lines for future breeding programmes.

Speed up the breeding activities

Most present-day pigeonpea cultivars are bred following the standard pedigree breeding method. This methodology is generally implemented either directly in the germplasm or diverse inter-varietal hybrid populations. Usually, it takes about 10-12 years to complete this assignment. To overcome the issue of extended periods, the plant breeders started growing the breeding populations in off-season to turn their second generation and reduce the variety breeding period. In order to reduce the breeding time further, the breeders attempt to take more than two generations per year using new breeding and genomics technologies. This varietal breeding act, called 'speed breeding', provides an ideal platform to accelerate the process of cultivar development (Aggarwal *et al*. 2025). In case of pigeonpea, no research was carried out until Saxena *et al*. (2017) demonstrated that in the early maturing group, four consecutive seed-to-seed generations can be taken within a calendar year. This speed breeding technology is based on the germination of immature seeds (30 days from flowering) and the "single pod descent method" of breeding. Following this methodology, the homozygous inbred lines can be developed in a short time of two years. This breeding approach can deliver new early maturing cultivars within a timeframe of 4-5 years.

Application of genetic transformation technology

Lawrence and Koundal (2001) were the first to generate putative transgenic lines expressing a *cowpea trypsin inhibitor* gene for pod borer resistance. Following this, (Surekha *et al*. 2005) incorporated gene *Cry1E-C* to confer resistance to *Spodoptera litura*. In an insect bioassay, a single T_1 progeny demonstrated 80% larval mortality. Soon, this technology was considered a potent tool for controlling insects in different crops. In pigeonpea, the *Agrobacterium*-mediated transformation and *in vitro* regeneration of leaf discs, shoot apices, and cotyledonary nodes were tried; so far, no genuine success has been witnessed (Ramu *et al*. 2012). However, some promising results were reported by Krishna *et al.* (2011). They introduced the Cry*1Ac* gene into pigeonpea and produced 17 primary transgenic lines, and of these, only two lines demonstrated 55% larval mortality. In conclusion, in spite of serious research efforts in the past, none of the experimental transgenics in pigeonpea has shown promise with respect to significant reduction in the growth and development of *Helicoverpa* pod borer larvae. However, since the transformation technology has a great potential to control insect damage, more concerted efforts are needed in pigeonpea, where the *Helicoverpa* pod borer is still a menace.

Rationalize the breeding of pigeonpea for intercrops

For centuries, pigeonpea has been cultivated on marginal lands under rainfed environments where risks of crop failure are quite high. In order to cover up such risks, most farmers cultivate pigeonpea as an intercrop with short-aged cereals or other food crops. (Nigam *et al*. 2021) estimated that at present, the intercropping system accounts for over 80% of the total pigeonpea area sown. Interestingly, Willey *et al*. (1981) revealed that a sole pigeonpea crop fails once in five years and a sole sorghum once in eight years; but the intercropping between the two fails only once in 35 years. Among legumes, the late maturing (170 - 250 d) pigeonpea is the most favourite crop for an intercrop cultivation system. This is due to its ability to recover from various stresses and to accommodate a range of species as a companion crop. In order to fetch high and stable performance of intercrop combinations, it is important that the specific production environment be assessed with respect to its productivity and potential risk factors. In fact, the probability of finding a pigeonpea cultivar that would adapt to different intercropping systems is very low due to their diversified agronomy and complex crop-environment interactions. Hence, in this grade of agriculture, the breeding of adaptive cultivars is the most difficult task.

In view of the above and to ease the variety breeding programmes, (Saxena *et al*. 2022) proposed that different inter-cropping systems be aggregated into 2-3 major groups. The basis of such grouping should be their cultural practices and the level of competition between the two inter-cropped species. Then, for each group, appropriate variety development breeding strategies should be developed. For example, in the intercrops such as cotton-pigeonpea and groundnut-pigeonpea, traditionally, the space between the two pigeonpea rows is as wide as 2.0-2.5 m, and in these systems, the competition between the main and companion crop species is less. Therefore, for this group of intercrops, ideally, the pigeonpea genotypes should have a spreading growth habit with a greater number of primary and secondary branches. In contrast to the above, in the other group of intercrops, such as pigeonpea-maize, pigeonpea-pearl millet, and pigeonpea-sorghum, the spacing between the two pigeonpea rows is comparatively less (about 1.5 m), and the level of competition between the two component crops of a pair with respect to nutrients and sunlight is intense. Such competition starts right from the early growth stage till the cereal (companion) crop is harvested. Therefore, in this intercrop system, the tall pigeonpea genotypes with compact branching and relatively large pods are likely to perform well. Also in this intercrop system, the aspect of rapid seedling growth can also be harnessed through hybrids, which are characterized by faster germination and rapid seedling growth.

Considering the above discussion, it can be concluded that an exercise of cropping systems aggregation may ease the breeding of pigeonpea cultivars adapted to different intercropping systems. Such varieties can replace the traditional cultivars, which are often used in all the intercrop systems.

Look for rapid and uniform pod development traits

Most pigeonpea cultivars take about a month and a half from flowering to pod maturity. This extended reproductive period exposes the critical period of fertilization and pod development to pod borers, pod fly etc. It is believed that if this period is reduced to a month or less, then the induced uniformity in flowering and podding will not only reduce the period of insect visitation but also make chemical control easy and economical.

In order to achieve this, pigeonpea breeders at ICRISAT were on the lookout for the natural variability for this trait in the germplasm and advanced breeding lines. A breakthrough in this direction was achieved when Srivastava and Saxena (2019) found that some of the genotypes took only about a month from flowering to maturity as compared to the mean value of 48.6 days for most pigeonpea cultivars. (Pazhamala *et al*. 2016) opined that such differences may appear due to the presence of different genetic regulatory mechanisms that control the photoperiod reaction. These genes induce indeterminateness in the plants, and thereby, extend their reproductive phase, resulting in significant delays in pod setting, its growth, and maturity. Using an RNA-sequence, they revealed that these genes remain functional only during the period of flowering to pod setting. This rapid pod and seed development are valuable trait and available in the primary gene pool, but has not been exploited so far by the breeders. In fact, selection for such a unique trait will help in breeding cultivars with synchronous flowering and maturity. Once introduced in the new varieties, the mechanisation of pigeonpea production would also be a reality**.**

Attempt an ideotype-based breeding approach

Donald (1968) conceptualized the idea of appropriately combining different yield contributing traits through plant breeding and creating the most productive plant type. He referred to this activity as "Breeding for plant ideotype". Theoretically, this concept appears to be very sound, but its execution is equally difficult. This is because in a given ecosystem, various natural parameters such as amount and distribution of rainfall, sunshine hours, evapotranspiration, soil properties etc., determine the specificity of adaptation. Therefore, it becomes difficult to develop a widely adapted plant type. Also, in this endeavour, the crop breeders, physiologists, and agronomists need to design and tailor a variety together which could meet most of the expectations.

In the case of pigeonpea, no plant architecture has been deciphered so far towards maximizing grain yield. Since, at the global level, the factors such as plant phenology, maturity, and stress resistance are directly linked to adaptation, they vary a lot. Also, since the majority of pigeonpea at the global level is cultivated as an intercrop with different combinations, it is important that these are given high priority. In this context, Saxena *et al*. (2022) suggested that for inter-cropping agriculture, the pigeonpea ideotype should be indeterminate, semi-spreading, and with a greater number of primary and secondary branches and a large number of fruiting points.

Pigeonpea is a short-day species, and for harvesting high yield, its planting is done around the longest day (Saxena *et al*. 2021a). The canopy size of the same genotype, however, reduces proportionately to the delay in the planting time. Such changes in the plant canopy are always associated with corresponding changes in the yield components, such as days to flower, plant height, plant spread, number of branches, number of pods, and yield. Hence, designing the plant ideotype for a rainy season crop will not suit to the post-rainy sowings; and for each planting date, it would require a different plant ideotype for maximizing its productivity.

EXPLOITATION OF HETEROSIS FOR PRODUCTIVITY ENHANCEMENT

The persistence of the low-yield plateau (Figure 1) has been haunting the pigeonpea breeders for a long time, and, therefore, they were on the lookout for any technology that could break this yield barrier. In this context, the CMS-based hybrid technology appeared to fill the bill. Soon after the successful breeding of CMS systems (Bohra et al. 2025, Saxena *et al*. 2005, Tikka *et al*. 1997), concerted efforts were made to exploit hybrid vigour in this crop.

Realized heterosis in different maturity groups

The recent review on breeding hybrids (Saxena *et al*. 2025a) revealed that many hybrid combinations had significant levels of exploitable heterosis for yield (Table 3). The details related to various aspects of hybrid breeding are comprehensively presented by Saxena *et al.* (2018b).

The first set of early-maturing hybrids was evaluated in multi-location trials for four years, and hybrids ICPHs 2433, 2438, and 2383 were found promising, with respectively 54%, 42%, and 36% superiority over the control. The highest mean yield (2300 kg/ha) was recorded by hybrid ICPH 2433. It was also found that the unit productivity (yield/ha/day) of the hybrids (17-22 kg/ha/day) was far superior to that of the control (13 kg/ha/day).

Table 3 Hybrid advantage for yield recorded in early, medium and late maturing hybrids in multi-location trials

Maturity group	Hybrid number	No. of locations	Yield (kg/ha)	Stand. Hete (%)
Early	ICPH 2433	25	2306^{**}	54
	ICPH 2438	25	2127^{**}	42
	ICPH 2363	25	2048^{**}	36
Medium	ICPH 3491	18	2919^{**}	57
	ICPH 3497	18	2686^{**}	44
	ICPH 3481	18	2637^{**}	41
Late	ICPH 2307	05	2855^{**}	53
	ICPH 2306	05	2600^{**}	39
	ICPH 2896	05	2579^{**}	38

Source: Various ICRISAT Pigeonpea Breeding Reports

The largest pigeonpea area is sown with medium maturing cultivars, and therefore, this maturity group was given the highest priority in breeding. In this group also some hybrids, such as ICPH 3491 (57% heterosis), ICPH 3497 (44% heterosis), and ICPH 3481 (41% heterosis), were highly promising. Traditionally, the long-duration (>200 days) pigeonpea varieties are restricted to deep Vertisols with high moisture-holding capacity. In this group, there has been limited research on hybrids, and hybrids ICPHs 2307, 2306, and 2896, with respectively 53%, 39%, and 38% standard heterosis were found promising. The hybrid research programmes at ICRISAT and ICAR centres witnessed the release of seven pigeonpea hybrids. These hybrids performed well both in the station and on-farm trials (Table 4). The detailed information is presented by Saxena *et al*. (2025a), and its brief run follows:

GTH 1

This is the first early-maturing CMS-based hybrid. In the multi-location trials, it recorded >50% yield advantage over the best control. In the following year, hybrid GTH 1 recorded 25.3% standard heterosis in the on-farm demonstrations. This hybrid was released for cultivation in Gujarat state.

Table 4. Yield gain of released pigeonpea hybrids over the control

Maturity group	Hybrid Name	Sterility System	Year released	Yield (kg/ha)	
				hybrid	%gain
Early	ICPH 8	GMS	1991	1800	31
Early	IPH 09-5	A2 CMS	2012	1863	>33
Early	IPH 15-03	A2 CMS	2020	1600	28-55
Early	PAH 5	A2 CMS	2023	2546	25
Medium	ICPH 2671	A4 CMS	2010	2850	35
Medium	ICPH 2740	A4 CMS	2012	1816	37
Medium	ICPH 3762	A4CMS	2021	1726	112

IPH 09-5

This pigeonpea hybrid exhibited >33% yield advantage over the best existing check variety UPAS 120. It has been reported to exhibit over 30% standard heterosis for yield.

IPH 15-03

This early maturing hybrid showed 28-55% standard heterosis for yield. In the All India Coordinated trials, it recorded a maximum yield of about 2200 kg/ha.

Pusa Arhar Hybrid 5

This early maturing hybrid produced a 2546 kg/ha yield. The multi-location testing of this hybrid, it revealed 25% standard heterosis over the control Pusa 992.

ICPH 2671

This is the first medium maturing hybrid released in Madhya Pradesh. In multi-location trials, it recorded 35% yield superiority over the control (2000 kg/ha). In 1,829 on-farm trials, conducted in five provinces, the hybrid ICPH 2671 (1400 kg/ha) produced 52% more yield over the local check.

ICPH 3762

This medium maturing hybrid, which recorded 112% standard heterosis in the station trials. In 114 on-farm trials, this hybrid witnessed 112% superiority over the control and was released in Odisha state.

ICPH 2740

In the station trials, this recorded 40.7% standard heterosis; while in the on-farm trials, ICPH 2740 recorded 36.2% yield advantage in four provinces. This hybrid was released in the Telangana state.

Performance of hybrids in diverse farming environments

Since the hybrid technology was new, the on-farm validation of the first medium-maturing hybrid was essential. For this purpose, a series of on-farm trials was undertaken in different states. Overall, the hybrids were evaluated in 1829 on-farm trials using farmers' own cultural practices. The highest number (782) of tests was conducted in Maharashtra state, and, on average, the hybrid demonstrated 35% superiority over the best local control (Table 5). The performance of this hybrid in three other states was also equally good. Similarly, the on-farm

Table 5. Yield of ICPH 2671 in the on-farm trials in four states

State	Farmers (no.)	Mean yield (kg/ha)		Standard het (%)
		Hybrid	Control	
Maharashtra	782	969	717	35
Andhra Pradesh	399	1,411	907	56
Jharkhand	288	1,460	864	69
Madhya Pradesh	360	1,940	1,326	46
Total/Mean	1829	1,445	954	52

productivity data of ICPH 2740 (220 trials) and ICPH 3762 (144 trials) were equally outstanding, with respectively 45 and 112% standard heterosis.

Advantages of cultivating hybrid cultivars

In pigeonpea, the hybrids are known to enhance both the biomass and yield (Figure 3). Such heterotic effects are visible right from seed germination to yield formation. The recent reviews on this aspect by Saxena *et al.* (2025a) revealed the following positive points about the hybrids.

- The expression of heterosis is independent of maturity and plant type.
- In comparison to inbred cultivars, the hybrid seeds germinate faster and produce 20-40% longer radicles and 7-14% greater seedling vigour indices.
- Hybrid seedlings produce about 44% more shoot mass and 43% more root mass than the control.
- Under inter-crop cultivation, the hybrids compete well with weeds and companion crops.
- The roots of hybrid plants maintain relatively high water content even under adverse conditions, which contributes to their ability to tolerate drought.
- Both the hybrid and inbred plants exhibit almost similar dry matter partitioning, but the former utilise various critical inputs effectively to produce more carbohydrates than inbreds, which leads to producing greater yields in the former.
- Inherently, the hybrid plants are more productive (22 kg/ha/day) than inbred cultivars (12.5 kg/ha/day).

Fig 3. Comparative shoot and root biomass produced by a hybrid ICPH 2671 (left) and inbred (right) cultivar

Hybrid adoption scenario

Pigeonpea hybrids are not only high-yielding; however, their seed production remains challenging. The transfer of this technology to farmer clients is critical for reaping the benefits of this endeavour. Interestingly, both the farmers and researchers are convinced about the performance of hybrids, but unfortunately, its adoption has failed to take off. This happened because the seed growers were unable to ensure the genetic purity of F_1 hybrid seeds. This was linked to the practical problems in conducting the standard grow-out tests (GoT) due to the requirements of pigeonpea of short days, necessary for inducing the flowers. To overcome this critical issue, (Saxena *et al.* 2022) suggested that in the future the investments in hybrid-related technologies should be made in (i) breeding early maturing hybrids because in this maturity group GoT can be applied with ease due to photo-insensitivity of the plants, and (ii) encourage seed producers to undertake the application of seed quality control genomics tools. These two approaches can easily bring the pigeonpea hybrid programmes back on rails.

CONSTRUCTION OF HETEROTIC GROUPS

The value of genetically distinct parents in plant breeding has been demonstrated by numerous researchers, and identifying the genetically diverse parents is a serious business. In order to achieve this, the breeders collect data on key plant parameters and process them through different statistical and genomics tools to form diverse groups, and these clusters are called "heterotic groups". For breeding purposes and to maximise genetic gains, the parental lines are selected from the most diverse heterotic groups.

For the first time in pigeonpea, this breeding technology was developed and applied by Saxena and Sawargaonkar (2014). They formulated seven heterotic groups based on multi-location specific combining ability data, and demonstrated that heterosis for seed yield was much greater when the parental lines represented the two most diverse heterotic groups. This approach has since been refined using genomic tools. In this context, Saxena RK *et al*. (2021) used genome-wide SNP markers to categorise a global collection of pigeonpea lines into three heterotic groups. This genomics approach is quite reliable since it eliminates the confounding effects of the environment on the phenotypic expression of any given trait. They further validated the usefulness of this technology with multi-location hybrid performance data. The diverse genotypes were found to produce high-yielding hybrids and vice versa (Figure 4). The above specialized research on heterotic groupings in pigeonpea also provides a robust framework for selecting the most useful parental germplasm for developing both high-yielding inbred and hybrid cultivars.

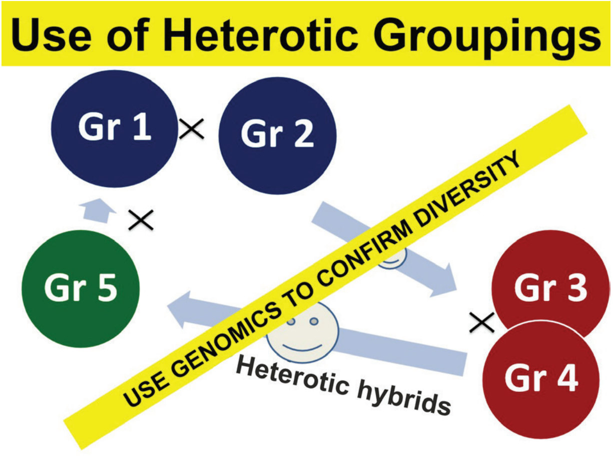

Fig 4. Schematic presentation of using diversity-based heterotic groups in breeding

EXPLOIT HETEROSIS THROUGH BREEDING SYBRID POPULATIONS

To exploit heterosis, besides hybrid breeding, an alternate breeding approach was also proposed by Hays and Garber (1919). In pigeonpea also, a considerable level of hybrid vigour is present, and this subject has already been discussed herein (Saxena *et al*. 2025b) proposed a new genetic enhancement scheme called "sybrid population breeding" which exploits a part of heterosis. This scheme (Figure 5) amalgamates the two established plant breeding concepts – the hybrids and synthetics into a single product. This breeding method has been designed in such a way that portions of both additive and non-additive genetic variances are exploited for enhancing the productivity in the often-cross-pollinated crops. The primary breeding tool, however, remains the insect-aided cross-pollination.

In comparison to a three-parent (A-, B-, R-) hybrid system, the sybrid breeding involves two fertile inbreds (P_1 and P_2) and excludes any male-sterile system. In this breeding programme, the natural cross-pollination produces hybrid pods on each of the two inbred parents (i.e. $P_1 \times P_2$ and $P_2 \times P_1$). Since the cross-pollination in plants takes place only in some flowers, each plant will have both the self- as well as cross-pollinated (hybrid) pods. But the proportion of the two pod types would vary and depend on the visits of pollen-loaded insect pollinators to different plants.

Since the seed production of sybrids does not involve any male-sterile and fertility restorer, the issues related to poor pod-setting and pollen-shedding do not arise. Hence, in comparison to the three-parent hybrids, the seed production of sybrids

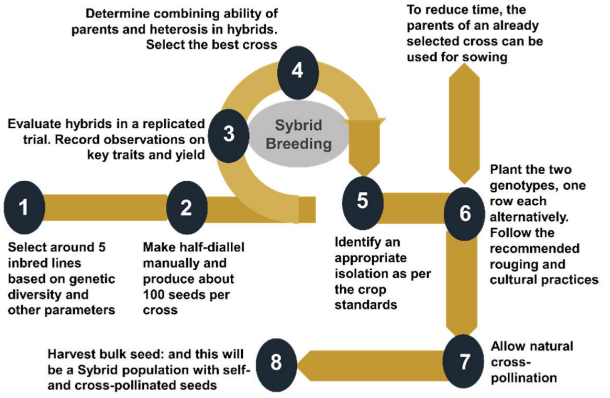

Fig 5. Schematic diagram showing eight chronological steps involved in breeding a sybrid population (source: Saxena *et al*., 2024)

is very easy, cost-effective, hassle-free, and does not require highly skilled technical personnel. With respect to commercial yields, a sybrid population is expected to be inferior to hybrids but superior to inbred and synthetic cultivars. Thus, this breeding approach could be used to enhance pigeonpea yields.

The sybrid breeding technology utilizes natural cross-pollination to harness portions of dominance, epistasis, and additive genetic variances to harvest more grain yields to augment the conventional inbred breeding programmes. Also, it is estimated that one hectare of sybrid seed production plot can easily yield about 1500-2000 kg seed (Table 6). This high seed-to-seed ratio can help in making the sybrid seed available to farmers at affordable costs. Like a hybrid, the sybrid seed is also designed for a single use, and hence, it should be able to attract the private seed sector as well.

Table 6. Expected yield of sybrid populations at different levels of out-crossing and heterosis

No.	Genotype	% out-crossing	Yield (kg/ha) at different levels of heterosis			
			40 %	50 %	60 %	100%
1	Inbred line	00	2000	2000	2000	2000
2	Sybrid	10	2080	2100	2120	2200
3	Sybrid	20	2160	2200	2240	2400
4	Sybrid	30	2240	2300	2360	2600
5	Sybrid	40	2320	2400	2480	2800
6	Sybrid	50	2400	2500	2600	3000
7	Hybrid (C)	100	2800	3000	3200	4000

POTENTIAL ROLE OF GENOMICS IN ENHANCING PIGEONPEA PRODUCTIVITY

The potential transition of pigeonpea breeding from conventional phenotypic selection to genomics-enabled strategies can help in reshaping hybrid development, genetic resource utilization, and breeding efficiency. The success of the hybrid breeding system relies critically on the maintenance of genetic purity of parental lines and hybrid seed, as even minor contamination from pollen shedders or physical admixtures during seed production and processing can erode heterosis and compromise hybrid performance. The integration of molecular markers has provided an effective solution to these limitations. Mitochondrial genome comparisons between CMS and maintainer lines led to the identification of diagnostic chimeric open reading frames and a characteristic 10 bp deletion in the nad7a gene specific to CMS cytoplasm. This deletion was converted into a robust PCR-based indel marker that enables rapid and reliable identification of CMS lines and routine monitoring of genetic purity (Sinha *et al.* 2015). Parallel advances in understanding fertility restoration genetics resulted in the development of QTL-based markers capable of distinguishing fertility restorers from non-restorers in the A_4 hybrid system (Saxena *et al.* 2018c). These markers substantially reduce reliance on phenotypic evaluation, lower operational costs, and enable early-generation selection of parental lines. Hybrid seed purity testing has similarly evolved from low-throughput SSR-based assays to cost-effective SNP genotyping platforms (Bohra *et al.* 2011, 2020, Saxena *et al.* 2010). While SSR markers initially enabled molecular purity testing of several pigeonpea hybrids, their application at scale proved economically limiting. The development and deployment of diagnostic SNP panels on high-throughput platforms have significantly reduced per-sample genotyping costs, allowing routine purity testing of large seed lots. These SNP-based assays offer rapid, and scalable alternatives to conventional GOT.

Beyond hybrid purity, sustained genetic gains in pigeonpea require systematic exploitation of heterosis through the development of heterotic pools and heterotic patterns. Traditionally, heterotic grouping relied on estimates of combining ability, heterosis, and pedigree information, approaches that are labor-intensive and context-specific. In pigeonpea, only limited efforts have been made to define heterotic groups using such methods. The availability of genome-wide molecular markers has added a powerful dimension to this process by enabling estimation of genetic relatedness among parental lines. Integrating molecular diversity data with hybrid performance information provides a more predictive framework for parental selection and lays the foundation for stable heterotic patterns that can be exploited over breeding cycles.

The effective construction of heterotic pools is closely linked to the broader challenge of unlocking genetic diversity of breeding relevance. Conventional assessments of diversity based on morphological traits are confounded by genotype–environment interactions and often fail to reflect true genetic relationships. Molecular marker technologies, and more recently high-throughput genotyping, have revealed critical insights into pigeonpea diversity and have shown that breeding over recent decades has largely recycled a narrow genetic base (Saxena *et al.* 2018a). Comparative genomics has further revealed extensive gene loss in domesticated pigeonpea relative to wild relatives, underscoring the urgency of reintroducing lost alleles to enhance yield stability, stress tolerance, and climate resilience (Varshney *et al*. 2017).

Wild *Cajanus* species represent a rich reservoir of adaptive variation, and their systematic utilization, supported by high-density genotyping and precise phenotyping, offers substantial opportunities for crop improvement. Combining genomic data with phenotypic information across diverse germplasm panels enables the identification of favorable alleles and selection sweeps associated with key agronomic traits (Varshney *et al.* 2017). The efficient introgression of such alleles into elite backgrounds can be accelerated through modern breeding tools, including marker-assisted backcrossing, genomic selection, and speed breeding. At the same time, strategic and targeted germplasm collection, guided by ecological and geographic gap analyses, is essential to ensure long-term conservation and utilization of underrepresented genetic diversity in pigeonpea.

While marker-assisted backcrossing has proven effective for traits controlled by major-effect QTLs, many agronomically important traits in pigeonpea, including yield and stress adaptation, are polygenic in nature. Genomic selection offers a powerful alternative by enabling the prediction of breeding values using genome-wide marker data, thereby capturing both major and minor effect loci. By reducing dependence on extensive phenotyping and allowing early selection of superior genotypes, genomic selection has the potential to substantially enhance breeding efficiency. Although its application in pigeonpea is still emerging, experiences from other crops demonstrate its promise for accelerating genetic gain in complex traits.

Looking ahead, the convergence of high-throughput sequencing, advanced analytics, and modern breeding methodologies points toward sequence-based breeding as a next-generation strategy for pigeonpea improvement (Bohra *et al*. 2020). Sequence-based breeding emphasizes continuous population improvement through deep sequencing of diverse founder germplasm, identification of favorable alleles using genome-wide association approaches, and recurrent selection guided by genomic estimated breeding values. Superior individuals emerging from these cycles can be rapidly advanced for release or recycled as parents for subsequent breeding cycles, creating a dynamic and data-driven improvement pipeline. By integrating genomic resources directly into practical breeding workflows, sequence-based breeding bridges the genotype–phenotype gap and enables a more precise understanding of genome dynamics under selection. In pigeonpea, the adoption of such integrative approaches holds considerable promise for delivering resilient, high-yielding cultivars capable of meeting future food security challenges under changing climatic and production environments.

GENERAL DISCUSSION

In 2023, the Food and Agriculture Organization sadly revealed that in the year 2022, over 700 million people across the world encountered the ill effects of hunger. This event highlights the fact that there is a severe shortage of food worldwide, especially carbohydrates, protein, and vital nutrients. The FAO (2023) also projected that by 2030, almost 600 million people will be chronically undernourished. This scenario has now assumed even greater significance in the backdrop of population growth, reduction in agricultural land areas, declining per capita protein availability, unpredictable precipitation, rising temperatures, and other destructive effects of climate change, particularly in the tropical and subtropical regions.

Enhancement of protein content

Pigeonpea, among the legumes, is rated high because of its high-protein and adaptation to stressed environments. It is assumed that increasing the protein harvests from a unit area by breeding new high-protein varieties could be one of the potent strategies in combating the malnutrition of the masses. In this context, the recent success in breeding high-yielding high-protein pigeonpea genotypes by Saxena *et al.* (2023a) has shown the way. In this programme, some inbreds with 26-28% seed protein and high yields were successfully bred (Table 7). Besides this, a transgressive segregant with the highest-ever protein (35.6%) content was

Table 7. Seed and protein yields harvested from high protein lines

Genotype	Maturity (days)	100-seed wt. (g)	Yield (kg/ha)	Protein (%)	Protein yield (kg/ha)
HPL 40-5	169	9.6	2100	26.9	452
HPL 40- 17	169	8.5	2070	26.5	440
BDN 1 (C)	168	9.6	2020	23.2	373
SEm±	0.9	0.18	160	0.46	-
CV (%)	0.9	3.4	17.3	3	-

Source: Saxena *et a*l. (2025)

also selected from an interspecific cross between cv. Baigani and *C. scarabaeoids* (Saxena *et al.* 2023b). The horizontal expansion in pigeonpea area is an alternate approach to enhance the protein harvests. This can be achieved by developing and promoting new high-yielding cultivars in early, medium, and late maturity groups.

Enhancing adaptation

In pigeonpea, the response to changing photoperiods plays a significant role in its adaptation. (Saxena *et al*. 2021b, c) demonstrated that both the response to photoperiod and flowering time in pigeonpea were controlled by the same genetic system, and hence, these are strongly linked with each other. In order to take pigeonpea to new areas, some early maturing types, which are relatively photo-insensitive, including UPAS 120, Manak, and ICPL 88039 etc. were bred under the aegis of ICAR and ICRISAT. Such genotypes can produce flowers and pods under the long photoperiods of 46°N latitudes (Saxena *et al*. 2019) and hence can be promoted in the non-conventional areas to broaden the global spectrum of pigeonpea-based cropping systems.

Crop diversification

According to Khoury *et al*. (2012), the crop diversification in the country in the past 5-6 decades has narrowed down significantly. Of the over two dozen cropping systems prevalent in India, the rice-wheat rotation is the most profitable and widely spread crop combination. The long-term use of this system is now showing its ill effects on soil health and, consequently, on productivity. This situation has now warranted crop diversification of this area. Among various crop combinations tried, the "pigeonpea-wheat rotation" was found ideal, wherein the water-sucking paddy was replaced by pigeonpea – a crop that is characterised by its reduced water requirements, deep tap roots, and fixing about 40-60 kg atmospheric nitrogen. This crop rotation has been adopted on a large scale in Punjab, Haryana, western Uttar Pradesh, and parts of the Indo-Gangetic plains. The early maturing pigeonpea cultivars can also be used for diversification in the new niches such as rice-fallows, rain-fed hilly regions, rainfed high altitudes (1200 m), wastelands (Saxena *et al.* 2011), and low rainfall (about 300 mm) areas (Singh *et al*. 2025).

Breeding photo-insensitive cultivars

It is well known that the traditional long-duration pigeonpea cultivars cannot be cultivated beyond 30° latitudes due to their strict short-day (photo-period) requirements. The long photo-period the plants produce more biomass, and vice versa (Figure 6). This situation, however, can be reversed if the sensitive germplasm could be converted to photo-insensitive or partially photo-sensitive by incorporating some independent photo-insensitive genes. In this context, the search of photo-insensitivity gene (Saxena *et al.* 2023c) has shown a ray of hope. They discovered this gene in cv. Pant A-3, and it exhibited partial dominance of photo-insensitivity (Table 8). This gene could be transferred to elite late-maturing cultivars through breeding, and this will allow the cultivation of such genotypes at wider latitudes to extend pigeonpea cultivation to some non-traditional areas.

Maintaining genetic purity

Once new varieties are developed, their genetic purity must be maintained year-after-year. In fact, the insect-aided natural cross-pollination has been ruining the genetic purity of pigeonpea germplasm and genetic stocks. It is also a serious bottleneck in the genetic enhancement programmes and maintaining productivity levels of released cultivars (Saxena *et al.* 2012). At present, the national quality seed production efforts are also being made under the aegis of various public and private seed

Fig 6. Effects of changing photoperiods on pigeonpea canopy. The July sowing (left) produces tall plants while in September sowings the canopy (right) is significantly reduced.

Table 8. Days to first flower in the parents (P_1, P_2) and their hybrids (F_1) in three planting dates, showing presence of a partial dominant photosensitivity gene in cv. Pant A 3 (Data source: Saxena et al., 2023)

Sowing	Day length	P1	P2	F1	MPV
Cross: Prabhat (E) x T 7 (L). Note: Dominance of photosensitivity of var T 7					
Jul-07	Long (nor)	73.4±3.3	147.9±11.7	96.7± 6.3	110.7
Nov-30	Short (late)	70.1±3.0	118.1±12.4	89.2±5.1	94.1
Feb-20	Long (v. late)	**63.4 ±4.5**	**250.3±8.2**	**194.9±8.1**	156.9
Cross: Pant A 3 (E) x T 7 (L). Note: Partial dominance of photo-insensitivity of var T 7					
Jul-07	Long (nor)	64.3±4.1	147.9±11.7	90.7± 5.0	106.1
Nov-30	Short (late)	69.1±3.0	118.1±12.4	89.2±5.7	93.6
Feb-20	Long (v. late)	**55.7±5.6**	**250.3±8.2**	**83.6±3.7**	153

agencies, but the quantum of output is inadequate to meet the domestic requirements. Besides this, the maintenance of diverse sources of resistance to various stresses and quality traits is also equally important for genetic enhancement of the crop.

To overcome this constraint, the pigeonpea breeders were on the lookout for a permanent solution to maintain the seed purity at the genetic level. In this context, a floral mutant (Figure 7), identified as "cleistogamous flowers," appears to be the most promising. The natural out-crossing in this genetic material is <2% as compared to 20-40% in the cultivars with normal flowers (Saxena *et al*. 1994). Since this mutant is easy to identify and controlled by a single recessive gene pair, it can be incorporated into elite germplasm and cultivars with ease. Recently, Yadav *et al*. (2017) have also identified this gene at the molecular level. Hence, transforming the allogamous plants to autogamous types will prove an asset in the genetic enhancement of pigeonpea, and it could provide a long-lasting solution for maintaining the genetic purity.

Fig 7. A modified pigeonpea flower (left) with all 10 free stamen which restricts out-crossing to <2% and a normal (9+1) flower(right) which registers >30% out-crossing.

Stability of production

Besides yielding, stability of production is equally important. To achieve this milestone, first of all, the key destabilizing factors should be identified and ranked according to their importance. Subsequently, plans should be made to overcome them through targeted breeding programmes. In the case of pigeonpea, the key plant diseases such as Fusarium wilt and sterility mosaic virus were given high importance (Patil *et al.* 2017), while Phytophthora and Alternaria diseases are put on the secondary priority list. Similarly, insects such as *Helicoverpa armigera*, *Maruca testulalis,* and pod fly are given the top research priority.

For wilt and sterility mosaic diseases, a number of resistance sources have been identified in the past, and new cultivars have been bred by different ICAR institutions and ICRISAT. Also, a few biotypes (= races) for both diseases have already been identified. At present, attempts are being made to identify new resistance sources to breed stable cultivars. For insects, although some success has been achieved in identifying tolerant sources, the success in breeding resistant cultivars is still elusive.

Enhancing productivity per se

Considering the stagnation of pigeonpea productivity and complexities of production systems related to maturity and diversity, it is well understood that the present set of varieties will not adapt well to all ecosystems. Hence, the productivity scenario of pigeonpea is not likely to rise enough to influence the national statistics. The authors hereby propose two potential ways to overcome this serious productivity bottleneck.

The first crop improvement approach for enhancing the adaptation and yield is breeding pigeonpea cultivars that are adapted to a specific cropping system. The vast diversification found with respect to plant type and maturity of pigeonpea has led to the evolution of a number of cropping systems where pigeonpea is treated as the main companion crop. Broadly, these production systems are classified into pure crop and inter-crop. Based on diverse regional agro-ecological conditions, the inter-cropping systems were further classified on the basis of crop combinations, rainfall distribution, soil type, and domestic needs. Further, the plant-type requirements, availability of resources, and agronomical practices of these crop combinations may vary considerably for optimizing the productivity of a given system.

Saxena *et al*. (1981) reported that the genetic parameters of pigeonpea were inconsistent across the production environments and the photo-sensitivity parents. These variable parameters would influence the breeding value of different traits of the selections in either direction. Considering the above facts, Byth *et al*. (1981) and Green *et al*. (1981) proposed that the pigeonpea breeding programmes should be designed to suit a particular production system. To achieve this, pigeonpea breeding activities should be carried out in the same production environment. This would help with increasing heritability and, finally, the breeding values also.

The second important breeding approach relates to the exploitation of hybrid vigour. Since the critical inputs of this technology are already available, it can enhance yield significantly as a term approach. Research institutions like ICAR and ICRISAT need to take this challenge very seriously and revisit the entire technology, including the accomplishments and limitations of the hybrid technology, and come out with a strong joint workplan of course, with the active participation of the private sector.

CONCLUDING REMARKS

Pigeonpea is a popular pulse and farmers across the country grow the crop because it can sustain the vagaries of weather and other stresses and provide protein-rich grains even under very odd agricultural conditions. Regarding its genetic improvement, the records show that this activity started in 1920 with germplasm collection at Pusa in Bihar. This initial research was followed by low-key systematic research at different ICAR centres (Ramanujam and Singh, 1981), and this activity was largely confined to selecting disease-resistant plants from landraces, and there was hardly any emphasis on yield improvement in 1965. The Indian Council of Agricultural Research took a significant step to launch a nation-wide pigeonpea improvement programme with multiple objectives, including yield enhancement. Since then, the research activities were strengthened year-after-year with liberal funding resources and are still continuing with equally good support from ICRISAT. During this long period, a number of accomplishments were achieved, but the enhancement of yield remained elusive. These have been well documented by Wanjari (2016), Saxena *et al*. (2018c, 2025a), and many more. In 1970-71, the recorded mean yield of pigeonpea was 707 kg/ha, and in 2024-25 it rests at only 856 kg/ha (Figure 1), meaning that in 54 years of R&D, the mean yield could crawl only 149 kg/ha (FAO, 2025). Considering the resources made available to the research projects of pigeonpea, this meager yield gain is not worth mentioning. Considering the stagnation of pigeonpea productivity and complexities of production systems related to maturity and diversity, it is well understood that the present set of varieties will not adapt well to all ecosystems. Hence, the productivity scenario of pigeonpea is not likely to rise enough to influence the national statistics. The authors hereby propose two potential ways to overcome the productivity bottleneck. The first approach for enhancing the adaptation and yield would be to breed pigeonpea cultivars under the agro-ecologies and production systems for which breeding of cultivars is targeted. The second important and viable breeding approach would be to exploit the hybrid vigour present in the crop. A couple of alternatives to address the issues related to seed quality control of hybrids are presented by Saxena *et al*. (2021c).

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