**REVIEW ARTICLE**

**Legume Research- An International Journal, Volume 47 Issue 9: 1437-1445 (September 2024)**

# Population Breeding in Pigeonpea: A Review

K.B. Saxena[1], R. Sultana[2], P.I. Gangashetty[3], R.K. Srivastava[3], Zafar Imam[2], Rachit K. Saxena[3]

**10.18805/LR-4912**

## ABSTRACT

Issues related to the stagnation of yield in pigeonpea [*Cajanus cajan* (L). Millsp.] are as old as seven decades or even more. This may be a consequence a number of factors but ineffectiveness of pure line breeding appears on the top of the list as it was the only method used by each and every crop breeder. The natural out-crossing of the crop, always considered a bane, was never used in the pigeonpea breeding until mid-seventies, when a hybrid breeding programme was initiated jointly by ICRISAT and ICAR. Besides this, some population breeding schemes were also suggested and tried on a limited scale in pigeonpea. The authors in this paper have reviewed various aspects of these population breeding methods. It is concluded that the methods such as stratified mass selection and sybrid breeding have good technical base and can be tried for enhancing seed yield in pigeonpea.

**Key words:** *Cajanus cajan*, Genetic advancement, Hybrid vigour, Inter-mating, Recurrent selection, Sybrid breeding.

It is hard to believe that in spite of decades of breeding efforts, the productivity of pigeonpea [*Cajanus cajan* (L). Millsp.] - a pulse of multiple uses and international repute - has remained unacceptably low at around 700 kg/ha (FAO, 2021; Saxena *et al*., 2021a). To break this shackle pigeonpea breeders have used pure line breeding method internationally, but without any genuine reward with respect to its yield increases (Nigam *et al*., 2021). Recently, pigeonpea breeders also tried their hands at breeding hybrids in this partially cross-pollinated pulse (Saxena *et al*., 2018a). Although, the CMS-based hybrids recorded 40-50% on-farm yield gains, but due to a single bottleneck of seed quality control, the benefits of hybrid technology could not reach farmers (Saxena *et al*., 2021b). Some pigeonpea breeders also explored the third channel of crop breeding *i.e*. the development of composites and synthetics. Such activities, commonly known as “population breeding” were successfully applied in the past to open-pollinated cereals and fodder crops but not in any pulse. This breeding approach is primarily based on the concept of accumulating useful genes within a group of plants (population) from diverse germplasm. Within such a heterogeneous population, the frequencies of alleles (predominantly positive), following the “Hardy-Weinberg” theorem, are brought at equilibrium at each loci through random mating among the individuals. These are then maintained in isolation from generation after generation under open-pollination. In pigeonpea where, on average 25-30% cross-pollination takes place (Saxena *et al*., 2016), some population breeding methods were also tried or proposed. The scientific information generated from these research endeavors is dispersed in different journals and unpublished reports and they never received due attention about their destiny. In this paper the authors have made the first ever effort to compile information on the aspects of different population breeding methods with respect to their constraints, accomplishments and future prospects.

## The rudiments of population breeding

For planning and implementing any population breeding programme, a good understanding of two basic biological systems is important. These are understanding yield at genetic level and creation and selection of useful recombinants. These factors, in the context of pigeonpea are briefly discussed here in the following text.

### Genetic understanding of yield formation

Like other crops in pigeonpea also, various types of gene actions such as additive, dominance, epistasis, *etc*. have been reported to operate in determining its yield. In this crop, however, only limited research has been done in the past to elucidate the details of the genetic mechanisms. The reviews published earlier by Saxena and Sharma (1990), Sharma and Dwivedi (1995), Saxena and Sawargaonkar (2014) and Sawargaonkar and Saxena (2020) show that in pigeonpea mainly additive genetic followed by dominance and epistasis variances played key roles in determining yield. These variance components can be exploited by carefully designing appropriate population breeding schemes. For example, for extracting high-yielding inbred lines from the population, a method involving single plant selections can be prepared which will predominantly utilize the additive genetic variances.

---

[1]Al Mutaredh, Al Ain, Abu Dhabi, UAE.
[2]Bihar Agricultural University, Sabour-813 210, Bihar, India.
[3]International Crops Research Institute for the Semi-Arid Tropics, Patancheru-502 319, Telangana, India.

**Corresponding Author:** R. Sultana, Bihar Agricultural University, Sabour-813 210, Bihar, India. Email: rafat.hayat@gmail.com

**How to cite this article:** Saxena, K.B., Sultana, R., Gangashetty, P., Srivastava, R.K., Imam, Z. and Saxena, R.K. (2024). Population Breeding in Pigeonpea: A Review. Legume Research. 47(9): 1437-1445. doi: 10.18805/LR-4912.

**Submitted:** 06-03-2022 **Accepted:** 28-07-2022 **Online:** 17-08-2022

In contrast, for exploiting hybrid vigour the genes expressing additive, dominance or epistasis will be important.

These genetic systems control the expression of a trait; and more so, on those traits controlled by minor effects; but their cumulative effects could be of significant consequences. In case of pigeonpea the quantitative traits such as yield, canopy growth, flowering, drought *etc*. are good examples where remarkable effect of environment has been recorded (Byth *et al*., 1981). Saxena *et al*. (1981) also demonstrated that the planting dates in pigeonpea significantly altered the estimates of gene effects. Based on this revelation and to minimize such effects and optimize the selection efficiency, Byth *et al*. (1981) suggested stratifying both the macro-environments and cropping systems and the breeding activities including population development should be done separately for each group. Besides this, Green *et al*. (1981) reported that in pigeonpea the intra-population variability for yield/plant is implausible large and mind-boggling. In their experiment they found that the observed phenotypic variability for single plant yield in the inbred parents was comparable to their $F_2$ populations. They opined that pigeonpea plants have great plasticity and their response to space, soil fertility, available moisture *etc*. induces irreversible changes in the plant canopy. Such incidences induce incredible non-heritable phenotypic variability among individual plants and thus result in poor heritability and breeding value to adversely affect response to selection. Therefore, it would be wise to assume that the population breeding programmes using single plant selections may also be adversely affected by this ill syndrome.

### Creation and selection of useful recombinants

A cost-effective cross-pollination mechanism is the backbone of any population breeding programme. This allows large-scale inter-mating and recombination among the constituent genotypes. Unlike other pulses, pigeonpea has a reputation of being a partially cross-pollinated pulse. The maximum reported out-crossing (Table 1) in different countries range between 20% and 60% (Saxena *et al*., 2016). Pigeonpea plants have profuse canopy and they produce loads of large attractive flowers spanning for about 25-30 days. These flowers produce nectar and some aromatic volatiles which attract a variety of insects. The most common insect species foraging on pigeonpea are *Apis mellifera, Apis dorsata* and *Megachile* species and these play a significant role in cross-pollination (Williams, 1977; Saxena *et al*., 2016).

A genetic male-sterility system can also be used to enhance recombination in population breeding programmes. It can be of immense use in pigeonpea where natural out-crossing is determined by the load of pollinating vectors. In cases where the male sterile plants are used as a vehicle for hybridization, high recombination rates can be expected even if insect population is moderate. This is because every pod harvested from the male sterile plants will be a hybrid pod with pollen received from the other genotypes.

In pigeonpea, two good sources of genetic mate sterility are available. These are characterized by easily identifiable sterile anthers. Each of them is controlled by a recessive gene pair. The male sterility with translucent anther is controlled by $ms_1ms_1$ (Reddy *et al*., 1978) while the brown anther shaped by $ms_2ms_2$ (Saxena *et al*., 1983) alleles. Both the male sterility systems are highly stable across environments and can be used for increasing recombination frequency.

## Overview of population breeding methods in pigeonpea

As an alternative to pure line cultivar breeding some pigeonpea breeders also tried to make use of natural cross-pollination of the crop to develop high-yielding heterogeneous populations. Considering a reasonable level of natural cross-pollination some population breeding methods were tried or simply proposed in pigeonpea for yield enhancement. Each method has its own positives and negatives. A short overview is presented here.

### Mixed-inbred population

Over a century ago, the pigeonpea breeders at Imperial Agricultural Research Institute, Pusa (Bihar), while engaged in breeding new cultivars, realized that in this crop it will be very difficult to breed and maintain high yielding inbred cultivars in pure form due to the contamination brought about by natural cross-pollination (Howard *et al*., 1919). They observed that in each generation purity of the selections was destroyed due to out-crossing brought about by insects and this resulted in their poor heritability and breeding value.

To overcome this breeding constraint, they recommended that some high-yielding inbred lines which match with each other in key plant and grain characters should be bulked together and maintained in isolation and released as cultivars. This was the first insight into the population breeding approach in pigeonpea and it was a well thought cost-effective suggestion for realizing high and stable pigeonpea yields.

### Mass selected population

Mass selection is the oldest and most popular breeding method where the superior genotypes (plants) from a

**Table 1:** Maximum natural out-crossing (%) reported in ten pigeonpea growing countries.

| Country | Out-crossing |
|---|---|
| Australia | 40 |
| Cameroon | 39 |
| China | 60 |
| India | 48 |
| Kenya | 46 |
| Myanmar | 40 |
| Nepal | 25 |
| Sri Lanka | 20 |
| Trinidad | 40 |
| Uganda | 22 |

(Source: Saxena *et al*., 2016).

landrace or cultivar are selected and bulked together to form a superior population. The mass selected populations in pigeonpea from germplasm were established in the past for disease resistance, plant type and yield. To reduce the effects of genotype - environment interactions and increase heritability, some changes in the selection procedures were also incorporated by some breeders in the mass selection schemes.

Harper (1967) and Dijkstara and De Vos (1972) stressed that varieties that are expected to grow in mixtures should be bred specifically for that purpose and under the same system. For pigeonpea also, the similar views were shared by Green *et al*. (1981) and Byth *et al*. (1981). Saxena *et al*. (2018b), while reviewing this subject, also concluded that in pigeonpea it is not always productive to breed cultivars under sole cropping for cultivation in inter-crop situations.

At ICRISAT, a mass selection programme was studied using grids in two crosses. Since the medium maturing pigeonpea is invariably grown under inter-cropping, two $F_2$ populations for mass selection under maize intercrop. At maturity and after the harvesting of maize, grids of 10 consecutive plants were made and from each grid two promising plants were harvested. The seeds harvested from the selected plants were bulked to run for another cycle of grid-based mass selection. This exercise was carried for two seasons (Green *et al*., 1981). The analysis of yield data revealed that this exercise failed to improve either mean or variance of the population over the period of two cycles. This failure in breeding mass selected populations was attributed to significant micro-environment effects and its interaction with the different genotypes as discussed in another section earlier.

Onim (1981) implemented two population improvement schemes, namely stratified mass selection and mass selection with progeny testing in long duration pigeonpea grown under marginal rainfall environmental conditions of Kenya. After each cycle of mass selection, the recorded yield gains were 2.3% and 4.3%, respectively. Almost similar results were obtained by Gardner (1961) in corn. Onim (1981) concluded that in this breeding approach the scattered alleles contributing to yield and stability can be accumulated for developing high yielding adapted cultivar.

## Composite population

Khan (1973) opined that pigeonpea, being a partially cross-pollinated crop, offers scope to breed composite cultivars. This methodology is based on the approach of enhancing gene frequency of favourable alleles from diverse sources and then maintaining them in a single heterogeneous population through random mating using natural cross-pollination in adequately isolated plots. He recommended that after 3-4 generations of random mating these composites can be improved to provide a high yielding heterogeneous population. These populations can be released as heterogeneous population for cultivation, especially for stressed rain-fed environments. Besides this, the composite can also serve as a gene pool for deriving useful variability.

## Sybrid population

Saxena (2020) recently proposed a new population breeding method and named it as “sybrid breeding”. This approach integrates the concepts of breeding synthetic and hybrid cultivars and uses natural cross-pollination for producing the hybrid plants. At genetic level, the sybrid population is benefitted from additive, dominance and epistatic variance with no yield loss on account of inbreeding depression in the population, as it happens in composites.

The sybrid breeding procedure is outlined in Fig 1. In brief, to start the programme 4-6 inbred lines are selected and these are crossed in a half-diallel and the top most hybrid is selected for sybrid breeding. The sowing of the two parents of the selected hybrid is done in isolation in a row ratio of 2F:1M. The crop is allowed to cross pollinate and at maturity the female rows are harvested; and this will be a sybrid population. This population is in fact a mixture of hybrid ($P_1 \times P_2$) and self-pollinated seed of the female parent ($P_1$). The proportion of hybrid plants in this population will be determined by the extent of natural out-crossing. In comparison to pure line or hybrid cultivar, a sybrid is easy to breed and will house relatively broader spectrum of genetic variability and therefore, will express greater buffering capacity.

## Recurrent selection population

Jenkins (1940) introduced recurrent selection for general combining ability to improve a parental population before isolating inbred lines for their use as parents in hybrid breeding programmes. He opined that the heterosis is the consequence of complete to partial dominance gene action; and combining ability of a line is established in early generation of inbreeding. Its breeding involves three major steps including (i) selfing and crossing of superior plants to a heterogeneous tester; (ii) evaluation of the testcrosses in yield trial and selection of lines on the basis of testcross performance and (iii) inter-crossing of selected ($S_1$) lines in all combinations to generate an improved version of the population. This cyclic procedure is repeated in the next level ($S_2$) of selection and thus, a further enhanced population is created. In this manner cycles of selection and inter-mating are implemented.

Hull (1945) modified the above breeding approach by replacing the broad-based tester with an inbred line or single-cross tester. This procedure is based recurrent selection for specific combining ability. Its breeding involves (i) self-pollination of about 100 superior plants from a heterogeneous population and crossing them separately to a number of inbred tester plants, (ii) evaluate the performance of testcrosses and select 10 or more parental plants that produced superior testcrosses and (iii) inter-mate the selected selfed parental lines (see ii) to generate the improved new population. The above procedure is repeated in a cyclic form to generate the advanced superior population.

In pigeonpea intra-population recurrent selection was attempted by Reddy *et al*. (1981). They created 10

| Jobs | Activities |
|---|---|
| Selection of parents | Select 4-6 lines on the basis of diversity yield etc. Select 4-6 lines for final crossing |
| Hybridization | Cross in a half-diallel. Produce about 100 seeds/ cross. |
| Selection of cross for breeding sybrid | Conduct hybrid trial. Select a hybrid on the basis of vigour, combining ability and yield. |
| Select isolated plots | Isolation 500 m. it should be well drained, preferably near bushes |
| Plant the parent seed | Use row ratio of 2 female and 1 male row |
| Cross pollination | Allow cross-pollination. |
| Harvesting | Harvest female rows. This will be the sybrid population for sowing. |

**Fig 1:** A diagram showing the process of developing a sybrid population.

**Table 2:** Germplasm groups synthesized to start recurrent selection breeding programs.

| Group | Maturity | Growth habit | Plant type | Other traits |
|---|---|---|---|---|
| G-1 | Early | Determinate | Compact | Variable |
| G-2 | Early | Non-determinate | Semi-spreading | Variable |
| G-3 | Medium | Non-determinate | Compact, tall | Variable |
| G-4 | Medium | Non-determinate | Semi-spreading, tall | Variable |
| G-5 | Medium | Non-determinate | Spreading, tall | Variable |
| G-6 | Medium | Non-determinate | Compact, large seeds | Variable |
| G-7 | Medium | Non-determinate | Spreading, dwarf | Variable |
| G-8 | Late | Non-determinate | Compact, tall | Variable |
| G-9 | Late | Non-determinate | Spreading, dwarf | Variable |
| G-10 | Late | Non-determinate | Spreading, tall | Variable |

germplasm groups (Table 2) from the available germplasm on the basis of key morphological traits, mainly maturity and plant type. In each group the number of genotypes varied but their equal number of seeds was bulked to launch the population breeding programme.

The recurrent breeding programme was started by growing bulked seeds of groups 3, 4 and 5 in isolation plots. Within each population over 200 single plants with good pod load were selected visually and their open-pollinated seeds harvested. In the following season their single plant progenies were grown in an isolated plot to start the second round of random mating and selection. The progenies with apparently undesirable traits such as high level of susceptibility to phytophthora blight, water-logging or delayed germination were discarded.

In this population again open-pollinated promising single plants were harvest to move into the next cycle of selection. The process was repeated. In the fourth round a disastrous struck due to an outbreak of sterility mosaic disease and in each population no flowering occurred in most plants. Therefore, the entire population breeding activities were abandoned.

### Male sterility-based recurrent selection population

In a partially cross-pollinated crop like pigeonpea sometimes the recombination process may fall short of the expectations due to limited population of pollinators. Therefore, to ensure high degree of recombination, the genetic male sterility is an ideal tool.

Byth *et al.* (1981) presented a population improvement scheme (Fig 2) which utilizes both the cross-pollination and genetic male sterility. The process involves identification of constituent genotypes with desirable traits. Each genotype is crossed with the male sterile line to produce $F_1$ hybrid seeds. This scheme incorporates a composite cross backup population and recurrent selection

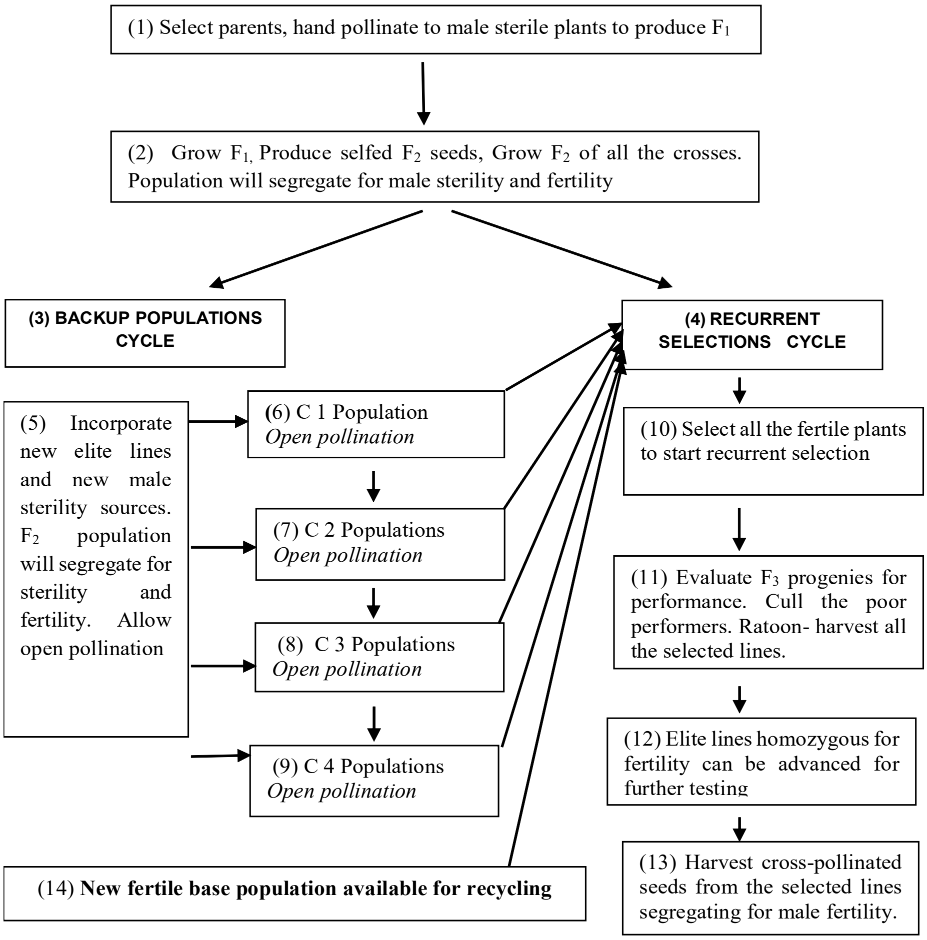

**Fig 2:** A population improvement breeding scheme utilizing open pollination and genetic male sterility.

of $F_3$ line progeny tests. The population would be recycled using open-pollinated progeny of male-sterile segregants within the elite progenies. Here every seed harvested will be a product of cross-pollination. From such populations the promising individual plants can also be drawn for pure line cultivar development. Alternatively, the fertile bulks can also be formulated for using them as a heterozygous population for cultivation.

### Single pod descent population

This population breeding method is unique for pigeonpea. In fact, it is a modification over the popular single seed descent method of breeding self-pollinated crops (Brim, 1966). In this method limited recombination occurs in successive generations pending the selection of inbred lines in $F_6$ generation. Green *et al.* (1981) used this method in pigeonpea. To implement this, the two parental lines were selected and single cross made. The $F_1$ population was grown under controlled pollination. In $F_2$ generation, with a population size of 2000 plants, under open pollination was grown and one fully grown mature pod (without any borer damage) was harvested. The pods from all the plants were bulked and their seed was used to advance the generation. The process was repeated in $F_3$ to $F_5$ generations. In order to accommodate more plants per unit area, the sowing time was shifted towards shorter days. The delayed plantings under reducing photo-periods resulted in early flowering and development of short canopy. Further, to allow insect-aided intra-population inter-mating among plants, the sowing was done in a square plot. In $F_5$ generation 1000 plants were selected randomly and $F_6$ progeny rows were grown at the normal sowing time along with intermittent controls. The harvesting was done by ratooning. Of these, 48 lines were found better than the control and their ratooned planted were bagged using selfing bags. The selfed seed (obtained from ratooned bagged plants) used for pedigree and population breeding. The selfed seed were also bulked to develop a genetically enhanced population. This bulked performed well in the station and multi-location trials with yield gains of 11% over the control. This population was advanced in isolation for further inter-mating and selection. Overall, this population breeding method appeared quite promising.

### Dual populations

With the objective of increasing recombination through inter-mating, a dual-population breeding schemes as proposed by Rachie and Gardner (1975). Green *et al.* (1981) used this population improvement method in peagonpea. In this method a pair of parental genotype with easily identifiable recessive (obcordate) and dominant (lanceolate) leaf shape markers were used. The obcordate leaf trait is rare in the germplasm and it is controlled by a single recessive gene pair. The naturally cross-pollinated hybrid plants with pollen from the lanceolate plant can easily be identified in the population of obcordate type plants because these hybrid plants will have lanceolate leaves.

To start the population breeding programme (Table 3) crosses were made manually using the genotype carrying the recessive marker as female parent with some known high-yielding specific combiners having lanceolate (normal) leaves. The $F_1$ plants characterized by lanceolate leaves were self-pollinated to advance the generation. The $F_2$ populations, grown in isolation under open pollination, segregated for the marker phenotype and the plants with the recessive marker (obcordate leaves) were tagged and their seed harvested. In the alternate generation the heterozygote plants with normal leaves were harvested. In the following generation the progenies of heterozygous plants will segregate for dominant and recessive traits; but seed from all the recessive plants were harvested. This alteration ensures that in each generation only cross-pollinated plants are selected and advanced. This exercise was carried out up to $F_5$ generation. Unfortunately, the bulk populations derived from this exercise were either at par or inferior to the control and failed to meet the expectations.

### Selective mating populations

To release new recombinants in the highly self-pollinated crops like wheat Jensen (1970) proposed a breeding scheme that was based on inter-mating of selected individual plants. This will produce new recombinants through multiple parents input involving inter-mating and selection of promising plants. This scheme also permits mass selection within the inter-mated population. This breeding procedure also provides options to enrich the variability of the population by incorporating new germplasm from time to time. Besides this, some useful genetic materials can be withdrawn from the synthesized populations to develop high yielding inbred lines.

In case of pigeonpea, this gene pool concept was implemented at ICRISAT. To start the programme, an $F_1$ diallel hybrid trial was grown to select the heterotic cross. After recording the data on yield other traits, the crop was harvested by ratooning at the height of about 50-60 cm from the ground level. After the analysis of the diallel data, most heterotic hybrid combination was identified for selective mating. After about three weeks from harvesting, new flowers emerged on the ratooned stumps and inter-plant crosses were made. The recombinant population was grown in the subsequent season. Some visually promising plants were selected and the inter-plant crosses were made on the ratooned growth. This cycle was repeated and the populations were advanced through four successive generations.

In the following season the inter-mated seeds of the selected populations were multiplied under controlled pollination. This was followed by growing the population in an isolated plot and at maturity gridded mass selection was exercised for one generation to obtain a genetically-rich pool of individuals. This bulk was evaluated at nine locations along with other elite breeding materials for two years. But unfortunately, the results were discouraging. The mass selected populations were statistically at par with the control cultivar C-11. It was concluded that the heterosis observed in the $F_1$ generation was perhaps due predominantly to non-additive variance and to lesser extent by additive variances.

## Factors influencing genetic gains in population breeding

### Limited molecular diversity

An important factor that needs consideration while breeding populations is the genetic divergence among the constituent genotypes. In pigeonpea, gene banks at ICRISAT and NBPGR hold >15,000 accessions and these, as a group, cuddle tremendous phenotypic variability for various traits (Singh *et al*., 2014; Upadhyaya *et al*., 2016). However against the expectations, the scenario related to the molecular diversity within the germplasm is not the same order and does not exhibit high divergence (Yang *et al*., 2006; Saxena *et al*., 2014; Varshney *et al*., 2017). This indicates that in this crop the relationship between the two diversity indicators is not strong. Hence, the selections of parental lines based on phenotypic diversity in the population breeding programmes may not produce significantly superior populations. Instead, the use of genomic tools may be more useful.

### Restricted recombination

Variation for flowering in pigeonpea germplasm is quite large (45-150 days) and therefore, the population breeding involving parents of diverse flowering may pose difficulties in cross-pollinations to produce new recombinants. This is likely to adversely affect the expected gains from this exercise. Therefore, the primary structures in the population breeding programmes should be built separately for early, medium and late maturity groups.

### Poor response to selection

The response to individual plant selection is important to maintain the gains made in during breeding exercising. Such responses are erratic in case of pigeonpea which results in poor heritability. The reasons related to this issue have been discussed earlier under section.

### Plant density losses

Being a rainy season long duration crop, pigeonpea often encounters various biotic and abiotic stresses at different stages of its growth. The main factors include waterlogging, soil salinity and diseases like fusarium wilt, sterility mosaic virus and stem blight which often cause serious damage to the standing crop in patches of various sizes. This means that in certain years some proportion of the potential recombinants within the population may be lost. Further, it is to be noted that the resistance to these stresses is controlled by recessive alleles (Saxena and Sharma, 1990) and this will also complicate the population breeding process. In case if any parent of the population is susceptible then the population will produce more and more susceptible (dominant) segregants in the passing generations. This may lead to increased proportion of susceptible genotypes and if the isolation plot has disease inoculums then the population breeding programme will be adversely affected.

### Damage by pod borers

Among the crop damaging insects, *Helicoverpa* pod borers cause huge losses in pigeonpea. Such losses on individual plant basis may be as high as 100%. Since there is no resistance available for this insect their control is dependent on chemical sprays. This job needs a lot of care and proper scheduling so that the pollinating insects remain safe.

Pigeonpea, when cooked as *dal*, *samber* or vegetable, makes excellent protein food for both rural and urban masses. The national agricultural statistics show that the demand of this pulse out-scores the production and this affects the per capita availability of much needed protein constituent. Besides this, the adaptation of pigeonpea to low inputs/ stressed environments, ability to perform well with diverse intercrops and various other on-farm and domestic uses (Saxena *et al*., 2021c) makes it a favourite crop of rural communities. For the genetic the breeders made serious efforts to develop high-yielding cultivars (Ramanujam and Singh, 1981) but, unfortunately, the productivity graph of the crop showed no upward movement (Nigam *et al*., 2021) and it has been lingering at around 700 kg/ha.

The breeders, in this endeavour, predominantly used pedigree breeding. Some breeders, however, also opted to use of its natural cross-pollination to enhance yield and alternative methods such as hybrid and population breeding were used. The literature on hybrid breeding has been splendidly compiled and is available in "Plant Breeding Reviews" (Volume 44).

Since yield is quantitative in nature, it is not possible to produce an ideal genotype with all of the desirable alleles though classical pedigree breeding (Falconer, 1981). The population breeding, on the other hand, has potential for genetic enhancement of the partially self-pollinated crop like pigeonpea; and it needs to be explored. According to Comstock (1996) the population breeding permits the accumulation of a large number of alleles with positive effects within a group of plants through recurrent cycles of recombination among the most desirable phenotypes and

**Table 3:** A dual population breeding scheme developed at ICRISAT.

| Step | Activity | Remarks |
|---|---|---|
| 1 | Cross recessive obcordate leaf type line as female with dominant lanceolate leaf type cultivars. | Produce 50 seeds /cross by manual emasculation and pollinations. |
| 2 | Grow $F_1$s plants and produce self-pollinated $F_2$ seeds. | $F_1$ plants will have dominant lanceolate leaves. |
| 3 | Grow $F_2$ population in isolation. | Segregation for leaf types observed.<br>Select obcordate plants and collect OP seeds. |
| 4 | Grow the cross-pollinated seeds harvested from the obcordate plants. | Population will have both selfed and cross-pollinated pods.<br>Select lanceolate leaf type hybrid plants. |
| 5 | Grow selected lanceolate selections. | Population will segregate for leaf types. Select obcordate plants. |
| 6 | Grow obcordate plants. | Select the hybrid lanceolate plants. |
| 7 | Repeat the cycles by sowing the harvested cross-pollinated seeds and selecting alternatively for obcordate and lanceolate leaf types for recombination. | |

Repeat the cycles
Select lanceolate leaf type plants
Purify the selections. Multiply seeds for yield testing of bulks

**Table 4**: Suggested populations which can be created through breeding.

| Priority | Maturity | Population name | Adaptation area | Proposed method |
|---|---|---|---|---|
| High | Medium | Wilt and sterility mosaic resistant, brown, medium-bold seeds | Telangana Andhra Pradesh, Maharashtra, Odisha, Karnataka | Sybrid breeding, Mass selection, SPD bulks |
| High | Medium | Wilt and sterility mosaic resistant, white bold seeds | Gujarat, Karnataka, Odisha | Sybrid breeding Mass selection, SPD bulks |
| High | Late | Wilt and sterility mosaic, resistant medium-bold brown seed | Madhya Pradesh,<br>Uttar Pradesh, Bihar | Sybrid breeding<br>Mass selection<br>Inbred mixture |

follow-up selections. The prime advantage of population breeding is that it exploits additive, additive × additive and epistatic genetic variances to impart a strong built-in buffering capacity to the population leading to wide adaptation. In addition, the continuum of population breeding also allows pulling-out of elite genotypes for pure line breeding and incorporating new variability into the system.

Overall, in case of pigeonpea the population breeding is a cumbersome procedure since it would require selection of desirable individuals, proper inter-mating of genotypes and maintenance of an appropriate population size. For increasing the randomness in mating and to accumulate a range of positive alleles, some population breeders also recommend the use of genetic male sterility. They however, need to maintain the male sterility gene while advancing each cycle of generations. This will sustain high intra-population recombination. The most difficult and unreliable part of population breeding in pigeonpea is the selection of individual plants for generation advance. Such a limitation is posed by its canopy, mainly the plant height (≥2m) and the configuration of its large number of primary and secondary branches. These make it very difficult for a breeder to move freely inside the field and exercise fair single plant selections.

Keeping this constraint, it seems that the among the population breeding methods so far tried or proposed for pigeonpea, only mass selection and sybrid breeding (Table 4) appear to have high practical appeal. The former for its simplicity and in the latter no single plant selection is exercised. In the sybrid population breeding, the required time is short and the process is easy and simple (Saxena and Gangashetty, 2021).

## CONCLUSION

Genetic enhancement of yield in pigeonpea in the past and at present is being attempted using pure line breeding by almost all the crop breeders. But unfortunately, in the last seven decades hardly any yield gain is visible. This gives a clear message that for some reasons the individual plant selection for yield is not working. The decades of plateauing pigeonpea yields is a matter of real concern when it comes to nutritional security of under-privileged masses. Considering the consistent failures in yield enhancement efforts, it seems that now the time is ripe to look beyond pedigree breeding and try some alternative breeding tools. In this context, it is interesting to note that the reproductive biology of pigeonpea permits the use of breeding methods, traditionally assigned to both self- and cross-pollinated crops. Of these, at present the broad choice reclines towards hybrid and population breeding. But considering the issues related to the hybrids, the population breeding based on mass selection and sybrid breeding appear to be the most appropriate options for genetic improvement of yield. The experience with population breeding has taught an important lesson to breeders. This is related to the selection of initial germplasm. To maintain the populations year after year, the germplasm should have resistance to the most prevalent diseases. This, however, will restrict the gene pool mass and will go against the primary concept of population breeding.

### Conflict of Interest

All authors declared that there is no conflict of interest.

## REFERENCES

Brim, C.A. (1966). A modified pedigree method of selection in soybeans. Crop Science. 6: 220.

Byth, D.E., Wallis, E.S. and Saxena, K.B. (1981). Adaptation and Breeding Strategies for Pigeonpea. Proceedings of the International Workshop on Pigeonpeas, In: [Nene YL, Kumble V (eds)]. vol 1. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, pp 450-465.

Comstock, R.E. (1996). Quantitative Genetics with Special Reference to Plant and Animal Breeding. Iowa State University. Press. pp. 421.

Dijkstara, J. and De vos, A.L.F. (1972). The evaluation of selections of white clover (*Trifolium repens* L.) in monoculture and in mixture with grass. Euphytica. 21: 432-449.

F.A.O. (2021). http://faostat.fao.org

Falconer, D.S. (1981). Introduction to Quantitative Genetics. (2nd Edition). John Wiley and Sons, New York, USA. pp. 340.

Gardner, C.O. (1961). An evaluation of effects of mass selection and seed irradiation with thermal neutrons. Crop Science. 1: 241-245.

Green, J.M., Sharma, D., Reddy, L.J., Saxena, K.B., Gupta, S.C., Jain, K.C., Reddy, B.V.S. and Rao, M.R. (1981). Methdology and Progress in the ICRISAT Pigeonpea Breeding Program. In: Proceedings of the International Workshop on Pigeonpeas, Volume 1, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru. pp. 437-449.

Harper, J.L. (1967). A Darwinian approach to plant ecology. Journal of Ecology. 55: 247-270.

Howard, A., Howard, G.L.C. and Khan, A.R. (1919). Studying the Pollination of Indian Crops I. Memoirs. Department of Agriculture (Botanical Series). 10: 195-200.

Hull, F.H. (1945). Recurrent selection for specific combining ability in corn. Journal of the American Society of Agronomy. 37: 134-145.

Jenkins, M.T. (1940). The segregation of genes affecting yield of grain in maize. Journal of the American Society of Agronomy. 32: 55-63.

Jensen, N.F. (1970). A diallel selective mating system for cereal breeding. Crop Science. 10: 629-635.

Khan, T.N. (1973). A new approach to the breeding of pigeonpea [*Cajanus cajan* (L.) Millsp.] formation of composites. Euphytica. 22: 373-377.

Nigam, S.N., Chaudhary, S., Deevei, K.C., Saxena, K.B. and Janila, P. (2021). Trends in Legume Production and Future Outlook. In: Genetic Enhancement in Major Food Legumes. [KB Saxena *et al.* (eds)]. Springer Nature Switzerland. pp. 7-48. doi.org/ 10.1007/978-3-030-64500-7_2.

Onim, J.F.M. (1981). Pigeonpea Improvement Research in Kenya. In: Proceedings of the International Workshop on Pigeonpeas, Vol 1. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, pp. 450-465.

Rachie, K.O., Gardner, C.O. (1975). Increasing Efficiency in Breeding Partially Out-crossing Grain Legumes. In: Proceedings International Workshop on Grain Legumes. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. pp. 285-297.

Ramanujam, S. and Singh, S.P. (1981). Pigeonpea Breeding in the All India Coordinated Programme. In: Proceedings of the International Workshop on Pigeonpeas. vol 1. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. pp. 403-414.

Reddy, B.V.S., Green, J.M. and Bisen, S.S. (1978). Genetic male sterility in pigeonpea. Crop Science. 18: 362-364.

Reddy, L.J., Saxena, K.B., Sharma, D. and Green, J.M. (1981). Some Combining Ability Analyses in Pigeonpea [*Cajanus cajan* (L.) Millsp.]. In: Proceedings of the International Workshop on Pigeonpeas, Vol 2. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. pp. 93-104.

Sawargaonkar, S.L. and Saxena, K.B. (2020). Application of heterotic grouping, standard heterosis and performance in breeding high yielding inbred and hybrid cultivars. Indian Journal of Genetics and Plant Breeding. 79: 704-712.

Saxena, K. B., Tikle, A. N., Mishra, A. K., Saxena, R. K., Srivastava, R.K. and Varshney, R.K. (2021b). Persuasive solutions to bring back hybrid pigeonpea breeding programmes on the rails. Journal of Food Legumes. 34(3): 166-172.

Saxena, K.B. (2020). SyBrid - A new breeding method for food legumes. International Journal of Scientific Research. 9: 199-200.

Saxena, K.B. and Gangashetty, P. (2021). A breeding recipe for exploiting hybrid vigour in pigeonpea through sybrids. International Journal of Scientific Research. 10(7): 20-21. doi: 10.36106/ijsr.

Saxena, K.B. and Sawargaonkar, S.L. (2014). First information on heterotic groups in pigeonpea [*Cajanus cajanus* (L.) Millsp.]. Euphytica. 200: 187-196.

Saxena, K.B. and Sharma, D. (1990). Pigeonpea Genetics. In: The Pigeonpea [Nene Y.L. Hall S.D. and Sheila V.K., (eds.)]. Wallingford, UK: CAB International. pp. 137-158.

Saxena, K.B., Byth, D.E., Wallis, E.S. and Delacy, I.H. (1981). Genetic Analysis of a Diallel Crosses of Early Flowering Pigeonpea Lines. In: Proceedings of the International Workshop on Pigeonpeas, Vol 2. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. pp. 81-92.

Saxena, K.B., Choudhary, A.K., Dalvi, V.A., Saxena, R.K., Ghosh, J., Singh, S., Verma, P. and Kumar, S. (2021c). Pigeonpea is significantly more than just a delicious pulse. Journal of Agri Search. 8: 177-187.

Saxena, K.B., Dalvi, V.A., Saxena, R.K. and Varshney, R.K. (2021a). Hybrid Breeding in Food Legumes with Special Reference to Pigeonpea, Faba Bean and Soybean. In: Genetic Enhancement in Major Food Legumes. [K.B. Saxena *et al.* (eds)]. Springer Nature Switzerland. pp. 123-148. doi.org/10.1007/978-3-030-64500-7_5.

Saxena, K.B., Sharma, D. and Vales, M.V. (2018a). Development and commercialization of CMS pigeonpea hybrids. Plant Breeding Reviews. 41: 103-167.

Saxena, K.B., Tikle, A.N., Kumar, R.V., Choudhary, A.K. and Bahadur B. (2016). Nectarivore-aided hybridization and its exploitation for productivity enhancement in pigeonpea. International Journal of Scientific and Research. 6: 321-331.

Saxena, K.B., Choudhary, A.K., Saxena, R.K. and Varshney, R.K. (2018b). Breeding pigeonpea cultivars for intercropping: synthesis and strategies. Breeding Science. 68: 159-167. ISSN 1344-7610.

Saxena, K.B., Wallis, E.S. and Byth, D.E. (1983). A new gene for male sterility in pigeonpea [*Cajanus cajan* (L). Millsp.]. Heredity. 51: 419-421.

Saxena, R.K., von Wettberg, E., Upadhyaya, H.D., Sanchez, V., Songok, S., Saxena, K.B., Kimurto, P. and Varshney, R.K. (2014). Genetic diversity and demographic history of *Cajanus* spp. illustrated from genome-wide SNPs. PloS One. 9: e88568.

Sharma, D. and Dwivedi, S. (1995). Heterosis in grain Legume Crops-scope and Use. In: Genetic Research and Education: Current Trends and the Next Fifty Years. Indian Society Genetics and Plant Breeding. IARI, New Delhi. India. pp. 960-970.

Singh, M., Gautam, K.N., Rana, M.K., Dahiya, O.P., Dutta, M. and Bansal, K.C. (2014). Pigeonpea genetic resources and its utilization in India: Current status and future prospects. Journal of Plant Sciences and Research. 1: 107. ISSN: 2349.

Upadhyaya, H.D., Reddy, K. N., Sharma, S., Dwivedi, S. L. and Ramchandran, S. (2016). Enhancing the value of genetic resources for use in pigeonpea improvement. Legume Perspectives. 11: 1-4.

Varshney, R.K., Saxena, R.K., Upadhyaya, H.D., Khan, A.W., Yu, Y., Kim, C., Rathore, A., Kim, D., Kim, J., An, S., Kumar, V., Anuradha, G., Yamini, K.N., Zhang, W., Muniswamy, S., Kim, J.S., Penmetsa, R.V., von Wettberg, E. and Datta, S.K. (2017). Whole genome resequensing of 292 peagonpea accesions identifies genomic regions associated with domestication and agronomic traits. Nature Genetics. 49: 1082-1088.

Williams, I.H. (1977). Behaviour of insects foraging on pigeonpea [*Cajanus cajan* (L.) Millsp.] in India. Tropical Agriculture (Trinidad). 54: 353-363.

Yang, S., Pang, W., Ash, G., Harper, J., Carling, J., Wenzl, P., Huttner, E., Zong, X. and Kilian, A. (2006). Low level of genetic diversity in cultivated pigeonpea compared to its wild relatives is revealed by diversity arrays technology. Theoretical and Applied Genetics. 113: 585-595.