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REVIEW ARTICLE

Cowpea: Breeding and Genomics

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Abstract

Cowpea (*Vigna unguiculata*) is a self-pollinating grain legume, fodder, and vegetable crop grown in a variety of tropical and subtropical climates around the world. Due to its nutritive value and soil-improving properties, it is also used as a fodder, green manure and cover crop. Being a legume crop, cowpea fits well in the inter-cropping system. Many biotic stresses, such as diseases caused by fungi, bacteria and viruses, significantly affect the crop yield in cowpeas. Apart from these, abiotic stresses such as drought, salinity stress and cold stresses are emerging problems. Therefore, it is required to breed many resistant varieties or genotypes through the identification of resistant gene pools**.** Vegetable cowpea breeding programs aim to develop cowpea varieties for vegetable purposes with tender pods in a bush or semi-determinate growth habits. Besides the development of high-yielding varieties, resistance to diseases such as golden mosaic disease, *Cercospora* leaf spot and anthracnose, resistance to insect pests such as bruchids pod borer and tolerance to abiotic stresses such as drought, salinity and high-temperature stresses is important. To achieve this traditional breeding combined with molecular approaches such as marker-assisted selection and genomic selection increases the precision of selection for desirable traits and also aids in the development of varieties with combined resistance to two or more diseases in less time. Genomic prediction and genomic selection schemes in cowpeas showed considerable improvement in predication accuracies and integrating with breeding schemes helps to enhance genetic gain.

Keywords: Cowpea, biotic and abiotic stress, marker-assisted selection and Genomic selection.

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Introduction

Cowpea (*Vigna unguiculata* L. Walp.) is one of the most important legume vegetables grown in tropical and subtropical regions of the world. It is also known as the southern pea, blacked-eyed pea and crowder pea. It is mainly cultivated as grain legume crop, vegetable crop and also as a fodder crop (Kongjaimun et al., 2013; Singh et al., 2018; da Silva et al., 2019). It is also cultivated as a green manuring crop, which improves the productivity of main crops (Singh et al. 2010) and as a main crop or intercropping with other crops like sorghum effectively controls soil erosion (Zougmore et al. 2000). The tender green pods are rich in crude protein (3.2%), iron (2.5 mg/100 g), calcium (80 mg/100 g), phosphorus (74 mg/100 g), vitamin A (941 IU/100 g), vitamin C (13 mg/100 g) and dietary fiber (2 g/100 g) making it an excellent vegetable (Singh et al., 2001). It is known as "Poor man's meat" owing to its major role in human nutrition in many developing countries (Jayathilake et al. 2018). Cowpea can play an important role in nutritional security in rural areas of the world.

Many biotic and abiotic stresses are major constraints in cowpea crop production. There are eleven major fungal diseases such as anthracnose, *Aschochyta* blight, black leaf spot, *Cercospora* leaf spot, blotch and many others cause significant yield loss in cowpea (Emechebe and Fiorini

1997). Bacterial diseases such as bacterial blight is a major constraint in cowpea production (Emechebe and Fiorini, 1997). More than twenty viruses are known to infect and cause diseases in cowpeas (Hampton et al. 1997). The infections caused by viruses in cowpeas stand out as they can reduce production from 60 to 80% in more susceptible cultivars. Among them, cowpea golden mosaic disease (CGMD), cowpea aphid-borne mosaic virus (CABMV), cowpea mottle virus (CMeV) and Southern bean mosaic virus (SBMV) are major viral diseases. In cowpea, insects are known to cause the crop damages through transmission of viral diseases and also feeding on crop plants. Striga is one of the major epiphytic flowering parasitic weed and a major constraint in cowpea crop production system. The abiotic stresses such as drought, salinity stress and cold stresses are emerging problems due to global warming or climate change (Mendelsohn 2014; Arora 2019).

Genetic Resources & Diversity

West or Central African regions were considered as the centre of origin of *V. unguiculata* based on genetic diversity. An overwhelming number of species of *Vigna* were found in tropical African regions (Faris 1965). There are four taxonomic taxa in *V. unguiculata viz.,* subsp. *unguiculata,* subsp. *dekindtiana* (var. *dekindtiana,* var. *mensensis,* var. *pubescens and* var. *protracta*) subsp. *tenuis and* subsp. *stenophylla.* Wild annuals of cowpea are crossable with cultivated cowpea and molecular characterization of accessions of cultivated and wild genetic resources also demonstrated extensive gene flow between cultivated and wild species (Coulibaly et al. 2002). Cultivated cowpea *V. unguiculata* subsp *unguiculata* has five cultivar groups such as cultivar group *biflora*, cultivar group *unguiculata*, cultivar group *sesquipedalis* and cultivar group *melanophthalmus* (Pasquet 1998), and cultivar group *textilis* (Smartt 1984; Pasquet 1996).

Yard long beans are a unique cultivar group (*Sesquipedialis*) of cowpea that produces very long pods and are widely consumed in Asia as a fresh green or "snapbean." Yardlong beans appear to have evolved in Asia and are rare in African landrace germplasm (Timkoo and Singh, 2008). They are grown extensively in Southeast Asia, South China and Africa. Fresh, tender green pods are eaten fresh as well as cooked. The indigenous varieties of yard long bean were climbing types. In recent times, many erect bushy varieties with increased yields have been developed. At a global level, IITA (International Institute for Tropical Agriculture) and USDA (United States Department of Agriculture) hold the largest collection of cowpea germplasm. In India, 3,720 cowpea accessions were maintained at ICAR-NBPGR, New Delhi (http://www.nbpgr.ernet.in/News_Details/aid/349.aspx).

Breeding objectives and varietal development

Vegetable cowpea breeding programs aim to develop cowpea varieties for vegetable purposes, bearing stringless tender pods in bush or semi-determinate growth habits. Besides the development of high-yielding varieties for tender pods, resistance to diseases such as golden mosaic disease, *Cercospora* leaf spot disease and anthracnose disease, resistance to insect pests such as bruchids, pod borer and tolerance to abiotic stresses such as drought, salinity and high-temperature stresses were other breeding objectives (Reddy et al. 2020). The genetics of major traits in cowpea and vegetable cowpea cultivars developed by various institutes in India are given in Tables 1 and 2, respectively.

Genetic improvement through traditional breeding

Breeding for suitable plant type, earliness and high yield

Yard long bean (*Vigna unguiculata* ssp. *sesquipedalis*) is usually grown as a traditional variety for vegetable purposes. Pods of the viny, indeterminate and long-duration cowpeas

Table 1: Genetics of major traits in cowpea

Traits	*Genetic architecture*	*Reference*
Early and medium earliness	3:1 ratio between early and medium earliness, governed by single dominant gene	(Owusu et al. 2018)
Cooking time	Fast-cooking was dominant over late cooking. Additive, dominant, additive×additive, additive× dominant, and dominant× dominant gene interaction was significant	(Addy et al. 2020)
Yield and component traits	Polygenic traits and transgressive segregation was observed in F_2 population	(Aryeetey and Laing 1973)
Cowpea aphid resistance	Segregated in 15:1 ratio indicating two dominant genes with additive effects governing resistance	(Ombakho et al. 1987)
Pod length and other traits	Additive gene effects with digenic and three digenic epistatic gene effects for pod length. Additive components were dominant for pod weight, number of seeds per pod and seed weight per pod	(Crosses et al. 2021)
Seed size	Small seeds were partially dominant over large seeds and additive, dominance and additive x additive epistatic gene actions were predominant	(Drabo et al. 1984)
Flower colour Stem colour Pod colour	Flower colour segregated in 1 purple: 2 light purple: 1 white or 3 purple : 1 white ratio in F_2 population and 1 purple: 1 white ratio in backcross population. Stem and stem colour segregated in 13 purple:3 green ratio ratio in F_2 population, 7 purple: 8 purple-white segregating: 1 white ratio in F_3 population	(Uguru 1995)

Table 2: Vegetable cowpea cultivars developed by various institutes in India

Institute	*Varieties developed*
ICAR-IIHR, Bengaluru	Arka Suman, Arka Samrudhi (Bush type), Arka Garima (Semi-determinate type), Arka Mangala (Yard long bean, Pole type)
ICAR-IIVR, Varanasi	Kashi Kanchan, Kashi Nidhi, Kashi Vishan, Kashi Gauri, Kashi Unnati, Kashi Shyamal (Bush type)
ICAR-IARI, New Delhi	Pusa Phalguni, Pusa Barsati, Pusa Dofasli, Pusa Rituraj, Pusa Komal (Bushtype)
KAU, Vellanikkara	Vyjayanti, Anaswara, Lola, Githika, Mithra, Vellayani Jyothika (Yard long bean, Pole type)
HARP, Ranchi	Swarna Harita, Swarna Suphala (Pole type)
PAU, Ludhiana	Selection-263 (Bush type)
BCKV, Kalyani	Bidhan Barati-1 (Bush type), Bidhan Barati-2 (Semi-determinate type)

Table 3: Desirable and undesirable traits of *Vigna unguiculata* subspecies *unguiculata* and *sesquipedalis*

Subspecies	*Desirable traits*	*Undesirable traits*
sesquipedalis	Better pod quality viz. soft, long, pulpy and parchment free pods.	Indeterminate growth habit needs staking, delayed flowering and fruiting, long duration, generally susceptible to cowpea golden mosaic virus cercospora diseases.
unguiculata	Determinate growth habit, earliness in flowering and fruiting,	Poor pod quality *viz.* hard, short and non-fleshy pods, presence of thick parchment

belonging to *Vigna unguiculata* ssp. *sesquipedalis* are of better quality, but their indeterminate growth habit restricts it to small-scale cultivation due to its vigorous viny growth which requires a trellis for the support of the plant. The cost of the trellis system is worked out to be Rs. 49000/- per ha (Lal et al., 2016). Growing bush type cowpeas can save this expenditure. The economic impact assessment of ICAR-IIVR developed bush type cowpea variety Kashi Kanchan gave net profit of Rs 36406/- during Kharif and Rs84942/- during summer with B:C ratio of 3.04 and 3.26 respectively, whereas the local variety had a B:C ratio of 1.43 (Vanitha et al., 2022). Delayed flowering and fruiting habit and long duration of yard long bean do not allow them to fit in the proper rice-wheat cropping system. In northern India, the rice-wheat cropping system occupies about 10 million ha potential area and there is 100-110 days gap between the harvest of wheat and the transplanting of rice. Development of determinate, early, short-duration and high-yielding genotypes would be profitable. In India, particularly IIVR, Varanasi and IIHR, Bengaluru, are still working in this direction and developed excellent vegetable cowpea varieties. The desirable and undesirable traits of *Vigna unguiculata* ssp. *unguiculata* and *sesquipedalis* are summarized in Table 3.

Breeding for product quality

Cowpea is important in the diet, and hence improvement of the nutritional quality is essential. According to Rachie (1985) the vegetable types should be developed to produce larger, string-free pods with more attractive cooking and taste qualities. The flatulence factor and metabolic inhibitors should be eliminated, and nutritional qualities should be enhanced mainly by increasing the content of sulfur-containing amino acids, calcium, iron etc. Pods of vegetable cowpea should be tender, pulpy and parchment-free.

Breeding for biotic stresses

There are several factors influencing the productivity of cowpeas, among them heavy biotic pressures *viz.* insects and diseases is one of the main reason. The important diseases in cowpea are *cercospora*, bacterial blight and mosaic, and the most injurious insect pests are jassids, aphids, pod borer and blister beetles. Nematodes are also a serious problem in cowpea cultivation. It is mentioned that photo-insensitive bacterial blight (eg. Pusa Komal) and cowpea golden mosaic virus resistant (eg. Kashi Kanchan, Kashi Nidhi, Arka Garima, Arka Samriddhi etc.) vegetable cowpea lines have been developed in India. Cowpea Sel.-263, KLS-10 and BC-244002 were screened near immune/symptomless and NDCP-8, VS-389 Arka garima as highly resistant to cowpea golden mosaic geminivirus (Chakraborty and Singh, 1999; Chakraborty et al., 2003). For *Maruca* pod borer, which causes severe damage and yield reduction in vegetable cowpeas, only low level of resistance have been reported. Jagginavan et al. (1995) observed cowpea lines P120 and C11 to be least damaged by *Maruca* and Veeranna and Hussain (1997) found TVx 7 to be most resistant to *Maruc*a and has a high density of trichomes (21.41/mm^2). Veerappa (1998) screened 45 cowpea lines for resistance to *Maruca* pod borer and observed that the tolerant lines had higher phenol and tannin contents compared to susceptible lines. This is in line with the general observation that cowpea varieties with pigmented calyx, petioles, pods, and pod tips suffer less damage due to *Maruca*.

Resistance to *Cercospora* leaf spot disease was governed by single dominant gene or two genes with inhibitory gene action. Yard-long bean susceptible genotype CSR12906 and resistant accession T90K-59-120 and their F_2 population were segregated in 3:1 and 13:3 ratio for susceptible: resistant types, whereas backcross population [(SR12906×IT90K-59-

120)×IT90K-59-120] were segregated in 1:1 ratio suggesting a single recessive gene or two genes with inhibitory gene action were determining the resistance for *Cercospora* leafspot disease in yard-long bean (Duangsong et al. 2018). Cowpea aphid-borne mosaic disease resistance governed by more than one recessive with additive effect as indicated by the predominance of CGA and continuous distribution indicates the significance of quantitative inheritance (Orawu et al. 2012). Seed weight was deduced to be controlled by five genes with a predominance of additive effects (Lopes et al. 2003).

Breeding for abiotic stresses

Abiotic stresses, including salinity/alkalinity, high moisture, drought and temperature extremes, are serious threats to crop survival, which somehow affect the crop yield. Several traditional methods are practiced for sustainable crop productivity but with the increasing abiotic stress due to changing climatic conditions and increasing pressure of population the traditional techniques of overcoming abiotic stress are not able to meet the demands. Hence, genetic engineering for developing stress-tolerant plants, based on the introduction and pyramiding of genes that are known to be involved in stress response and tolerance and may provide a promising track towards improving crop varieties, is required.

Molecular Breeding Approaches

Marker development

Simple sequence repeat (SSR) markers are simple and most commonly used in plant breeding in various crops. The SSR markers in cowpea, had shown high transferability (88%) to other crops (Gupta and Gopalakrishna 2010). Cross-transferability of SSR markers from cowpea to yard-long bean was studied and observed that microsatellite markers identified in cowpea are suitable for genetic diversity and marker-assisted selection in yard-long bean (Xu et al. 2010). Cowpea iSelect Consortium Array was developed by mapping 36 set of sequences derived from whole genome sequencing of 32 accessions with 12.5X coverage and other BAC clones against the whole genome sequence of T97K-499-35. Total of 60000 high-quality SNP markers were filtered through various bioinformatic tools and finally, 51128 SNPs were made available to the public through Cowpea iSelect Consortium Array (Munoz-Amatriain et al. 2017).

Linkage map construction

Genetic map or linkage map is a pre-requisite and essential requirement for QTL analysis and marker-assisted selection. SSR and SNP markers-based linkage map with a length of 745 cM was reported in 114 recombinant inbred lines derived from the cross between the landrace ZN016 and Chinese cultivar Zhijiang282 (Xu et al. 2011). A linkage map of 852.4 cM was from the population derived from BC_1F_1 ((JP81610 × TVnu457) × JP81610) population derived from yard-long bean and cowpea (Kongjaimun et al. 2012a, b, 2013). With the advance of Next-Generation Sequencing and with a reduction in cost of sequencing, NGS platforms were often used in the development of markers and construction of linkage map in the yard-long bean. SLAF (Specific locus amplified fragments) sequencing is an NGS-based genotyping methodology and has an advantage over whole genome sequencing due to the construction of a reduced representation library resulting in the identification of 5,225 SNP markers evenly distributed with an average distance of 0.35 cM across 11 linkage groups and resulted in linkage map of 1,850.81 cM (Huang et al. 2018). Restriction-site associated sequencing (RAD) is another NGS-based genotyping tool and genotyping of 168 F2:3 progenies derived from the crosses of vegetable cowpea and yard-long bean resulted in the identification of 17,996 SNP markers covering 1,194.25 cM with a mean distance of 0.066 cM/SNP marker locus (Pan et al. 2017). In cowpea, F_2 (IC-1 × BRS Marataoa) population was mapped with 51128 SNP markers and among them, 910 were polymorphic with a linkage map length of 1140.12 cM and 1.26 cM between markers (Seido and Santos 2019). In wild cowpea (*Vigna vexillata*) 300 F_2 population (Salt tolerant V1 ×salt sensitive V5) were mapped with 874 markers and the map spanned 511.5 cM with a distance of 7.2 cM between markers (Marubodee et al. 2015).

QTL mapping

Quantitative trait analysis is an additive difference between marker genotype against recombination frequency between marker allele and a putative QTL (Kearsey and Hyne 1994) and, QTL identification is a pre-requisite for marker-assisted selection and further map-based cloning (Remington et al. 2001). There are several studies or reports on QTL identification for various traits in cowpeas, including yardlong bean, summarized in Table 4. Fine mapping of QTLs is required to locate the genomic regions harboring candidate genes. In cowpea, rust-resistant QTL 'Ruv2' was fine-mapped using 119 RILs derived from the cross ZN016 × Zhijiang 282 and genotyping with 49194 SNP markers resulted in 193 Kb genomic regions harboring 23 genes and this genomic region was highly enriched with nucleotide binding site (NBS). This genomic region was flanked by SNP markers with distance of 0.45 cM and PCR based CAPS marker was developed. This CAPS marker is suitable for marker-assisted selection for rust resistant genes in cowpea (Wu et al. 2018). However, fine mapping of QTL was reported only in fewer traits and further studies are required to candidate genes controlling many economic traits in cowpeas.

Association and genome-wide association studies

Genome-wide association mapping helps to dissect out the causal genomic regions or candidate genes associated with

Table 4: Identification of quantitative trait loci for various traits in cowpea

Trait	*Number of QTLs*	*Mapping population*	*Marker used for genotyping*	*Methods of QTL analysis*	*POV (%)*	*References*
Yard-long bean						
Pod tenderness and total soluble solids	Three QTLs for pod tenderness two QTLs for TSS	BC1F1 ((JP81610 × JP89083) × JP81610) F_2 (JP81610 × JP89083)	226SSR	Composite interval mapping	Pod tenderness: 5.6–50% TSS: 7 - 9 %	(Kongjaimun et al. 2013)
Domestication related traits	121 QTLs	BC1F1 ((JP81610 × JP89083) × JP81610) F_2 (JP81610 × JP89083)	226SSR	Multiple Interval mapping	-	(Kongjaimun et al. 2012a)
Pod length	One major and six minor QTLs	BC1F1 ((JP81610 × JP89083) × JP81610) F_2 (JP81610 × JP89083)	226SSR	Multiple Interval mapping	3.2 to 30.5%	(Kongjaimun et al. 2012b)
Resistance to *Cercospora* leaf spot	1 QTL- qCLS9.1	190 F_2 (yardlong bean CSR12906 × cowpea IT90K-59-120)	165 SSR	Inclusive composite interval mapping	25.40-89.26%	(Duangsong et al. 2016)
Salt Tolerance	six major QTLs	143 F_2 population (Suzi 41 × Sujiang 1419)	103 InDels	Composite interval mapping	9.9% ~ 72.7%	(Zhang et al. 2020)
Cowpea						
Domestication related traits						
Floral scent	63 QTLs	159 RILs (524B × 219-01)	202 SSR Four morphological markers	composite interval mapping	60%	(Andargie et al. 2014)
Flowering time	5 QTLs	159 RILs (524B × 219-01)	202 SSR Four morphological markers	composite interval mapping	8.8–29.8%	(Andargie et al. 2013)
Domestication related traits	16 QTLs	215 RILs (IT99K-573-1-1 × TVNu-1158)	17739 SNPs	Linear mixed model	18.32 - 85.65%	(Lo et al. 2019)
Days to flowering and plant height	Flowering: qDTF9.1, Plant height: qPH9.1, qPH4.1)	175 RILs (Golden Eye Cream × IT98K-476-8)	4154 SNPs	SNP linkage map	qDTF9.1: 29.3% qPH9.1: 29.5%	(Angira et al. 2020)
Biotic stresses						
Bacterial blight resistance	*qtlblb-1*- LG8 *qtlblb-2* - LG 11 *qtlblb-3 - LG11*	194 $F_{2:3}$ (C-152 × V-16)	80 SSR 40 conserved intron-scanning primers (CISP)	composite interval mapping	*qtlblb-1:* 30.58% qtlblb-*2:* 10.77% *qtlblb-3:* 10.63%,	(Dinesh et al. 2016)
Resistance to root knot nematode	1 QTL	87 RILs (CB27 × 24-125B-1) 170 F2:3 (IT84S-2049 × UCR779) 132 F2:3 (T93K-503-1 × UCR779)	1536 SNPs	QTL IciMapping,	52.4-72.9 %	(Huynh et al. 2016)
Brown blotch resistance	One major and three minor QTLs	200 F_2 (KN1 × Tiligre)	99 allele-specific markers (AS-PCR)	multiple interval mapping	-	(Ohlson et al. 2018)
Abiotic stresses						
Heat tolerance	5 QTLs	141 RILs (CB27 ×IT82E-18).	48 transcript SNPs	Interval mapping	11.5–18.1 %	(Lucas et al. 2013)
Drought stress (premature senescence and maturity)	12 QTLs	127 RILs (IT93K503-1 × CB46)	306 AFLP	Multiple interval mapping	4.7-24.2%	(Muchero et al. 2009)

trait variations and dissect the true association between markers and traits even for rare variants with low frequency and small effects (Brachi et al. 2011; Korte and Farlow 2013). In yard-long bean, GWAS was performed for drought stress tolerance in mini-core germplasm consisting of 95 accessions of yard-long bean for soil moisture stress and genotyping with 1127 SNPs resulted in the identification of 39 SNP markers tightly linked to soil moisture stress. Among them, many genes related to abscisic acid and phospholipid signaling, aquaporin genes and hormonal genes were identified for soil moisture stress (Xu et al. 2012). Further studies are required for many other traits,

Table 5: Genome-wide associated studies for various traits in cowpea

Traits	*Association panels*	*Genome wide markers*	*Putative candidate gene*	*Functional annotation*	*References*
Bacterial Blight	249 USDA germplasm	1031 SNP (GBS)		Four SNP showed 70% selection accuracy	(Shi et al., 2016)
Aphid resistance	338 cowpea USDA germplasm panel	1047 SNPs	Ten SNPs were identified for aphid resistance	Two SNPs viz., C35011941_894 and scaffold30061 _3363 were strongly linked to Aphid tolerance	(Qin et al. 2017)
Seed size	368 cowpea diverse accessions panel	51,128 SNPs (51K Cowpea iSelect Consortium Array)	Six candidate genes: *Vigun05g036000,* *Vigun05g039600,* *Vigun05g204200,* *Vigun08g217000,* *Vigun11g187000,* *Vigun11g191300*	Candidate genes were annotated to cell wall protein, phosphate transporter PHO1, fertilization-independent endosperm, histidine kinase 2, WD repeat-containing protein 61-like isoform 1 and delta (24)-sterol reductase-like protein	(Lo et al. 2019)
Bruchids	217 mini-core accession panel	51,128 SNPs (51K Cowpea iSelect Consortium Array)	Six candidate genes: *Vigun08g132300,* *Vigun08g158000,* *Vigun06g053700,* *Vigun02g131000,* *Vigun01g234900,* *Vigun01g201900*	Candidate genes were annotated to Chloroplast envelope transporter (Tic110), Interacting selectively and noncovalently with any protein or protein complex, WRKY DNA -binding domain, Alpha/beta hydrolase fold-containing protein (ABH), Glutamate-prephenate Aminotransferase, Transcription factor activity PTHR	(Miesho et al. 2019)
Flowering time	384 cowpea germplasm panel	51,128 SNPs (51K Cowpea iSelect Consortium Array)	Four candidate genes: *Vigun01g084000,* *Vigun01g227200,* *Vigun02g062600,* *Vigun03g296800*	Candidate genes were annotated to flowering locus T, early flowering 4, F-box/KELCH-repeat protein SKIP11 and casein kinase II	(Seo et al. 2020)
Flowering time	368 mini-core panel	seven reliable SNPs	Twelve candidate genes were identified for flowering time	*Candidate genes were functionally annotated and some them are Flowering locusT, Gigantea, Cryptochrome-2, Light-dependent short hypocotyls 3 and Rebelote*	(Paudel et al. 2021)

such as pod quality-related traits, salinity stress tolerance, and major diseases such as anthracnose, rust and other viral diseases. In cowpea, there are many studies on genome-wide association studies and presented in Table 5.

Transcriptome and whole genome sequencing in yard long bean

Next-generation sequencing (NGS) platforms are frequently used in many crops for the identification of a total number of protein-coding genes and to assess the global expression analysis for various biotic and abiotic stresses (Ray and Satya 2014; Vlk and Repkova 2017). In yard-long bean, whole genome sequences developed through a shot-gun sequencing approach were assembled into 632.8 Mb and assigned to 11 pseudo linkage groups anchoring 94.42% of scaffolds. A total of 42,609 and 3,579 protein and non-protein coding genes were identified from the assembly (Xia et al. 2019). Through transcriptome studies, a total of 1,21,138 unigenes for salinity stress (Id et al. 2019) and 88,869 unigenes for cold stress tolerance (Tan et al. 2016) were identified. Further transcriptome studies are required for other horticultural and pod quality traits for the identification of functional genes associated with various traits. These genomic resources have high significance for breeders for the development of genome-wide markers and further utilization in crop improvement or marker-assisted selection program in the yard-long bean.

Transcriptome and whole genome sequencing

In yard long bean, whole genome long-read sequencing of elite breeding line IT97K-499-35 by using PacBio Sequencing resulted in the generation of 56.8 Gb sequencing data. These sequences were assembled to 519 Mb and a total of 29773 protein-coding genes were identified from the assembly. More than half of the genome was represented by repetitive elements and as compared to other legumes, NBS-LRR overrepresented cowpea genome, SAUR-like auxin superfamilies and genomic regions associated with interaction with other plants such as *Striga gesnerioides* was also identified (Lonardi et al. 2019). Besides, the sum total of genes controlling specific environmental stimuli was reported in cowpeas. Many genes related to photosynthesis, photo-oxidation, reactive oxygen species and other metabolic pathways-related genes were identified in gamma irradiation through transcriptome analysis (Kang et al. 2021). A total of 19922 genes were identified for nematode tolerance in through comparative transcriptome analysis in resistant and susceptible near-isogenic lines (Santos et al. 2018). A total of 47,899 unigenes were identified for drought stress through transcriptome analysis and 500 genic SSR markers were mined from the transcriptome data (Chen et al. 2017). The genomic resources developed through whole genome and transcriptome sequencing are useful in the development of genomic and genic markers and further utilization in crop improvement programs.

Moreover, in cowpeas, genomic selection is an indirect selection of desirable plant types based on genomic estimated breeding values and is very useful in enhancing genetic gain. Genomic selection is a multi-disciplinary science and pre-requisite for implementation of genomic selection are genome-wide distributed markers, robust genomic prediction models, training and testing populations with heritable traits (Meuwissen et al. 2001; Rincent et al. 2012, 2017; Crossa et al. 2016). The benefits of genomic selection to enhance the genetic gain in crop breeding programs has been demonstrated in many vegetable crops (Cappetta et al. 2021; Liu et al. 2021) and fewer examples in cowpea are described below. A total of 305 RILs derived from eight-way magic populations derived from eight founding parents were genotyped with 51K Illumina Cowpea Consortium Array (Huynh et al. 2018) and genetic architecture for days to flowering, days to maturity and seed size (Olatoye et al., 2019). Additive and epistatic modules were incorporated into the genomic models of RR-BLUP and RKHS, revealing the presence of large and moderate epistatic interactions for these traits. Candidate genes such as Phytoclock1 and Phytochrome A were co-localized in the flowering QTLs. Flowering adaptation to photoperiodism was also regulated by distinct epistatic genes (Olatoye et al. 2019). Further, genomic prediction studies on this MAGIC RIL population revealed the presence of large genetic variation for drought tolerant indices, identified many SNPs associated with drought tolerance attributing traits through GWAS and genomic prediction revealed low to moderate prediction accuracies for drought attributing traits (Ravelombola et al. 2021). Genomic prediction and genomic selection schemes in cowpeas showed considerable improvement in predication accuracies and integrating with breeding schemes helps to enhance genetic gain.

Future prospects

Future breeding programs in cowpeas must aim to widen the genetic base of working germplasm and deploy new cultivars with new or novel alleles and genes for agronomic traits and resistance to biotic and abiotic stress tolerance. Therefore, breeding programs for cowpeas must focus on the following aspects:

- Characterization of germplasm using genome-wide markers is required to assess total genetic diversity in cowpea and further combining them with genomic prediction methods helps to identify trait-specific accessions with specific genomic regions.
- GWAS studies are required in cowpea for dissecting causative genomic regions or candidate genes for various agronomically important traits that help to enhance the utilization of germplasm in breeding programmes.
- Integration of genomic selection schemes in cowpea breeding programs can certainly help breeders enhance the higher genetic gain and effectively utilise germplasm or genetic diversity.

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सारांश

लोबिया एक स्व-परागण करने वाली अनाज की फलियों, चारे और सब्जियों की फसल है, जिसे दुनिया भर में विभिन्न उष्णकटिबंधीय और उपोष्णकटिबंधीय जलवायु में उगाया जाता है। इसकी पौष्टिकता और मृदा सुधार गुणों के कारण, इसे चारे, हरी खाद और आवरण फसल के रूप में भी इस्तेमाल किया जाता है। एक दलहनी फसल होने के नाते, लोबिया इंटर-क्रॉपिंग प्रणाली में अच्छी तरह से फिट होती है। कई जैविक तनाव जैसे कि कवक, बैक्टीरिया और वायरस के कारण होने वाली बीमारियाँ, लोबिया की फसल की पैदावार को काफी प्रभावित करती हैं। इन समस्याओं के अलावा, सूखा, लवणता और ठंड जैसे अजैविक तनाव उभरती हुई समस्याएं हैं। इसलिए, प्रतिरोधी जीनपूलों की पहचान करके कई प्रतिरोधी किस्मों या जीनोटाइपों का विकास आवश्यक है। सब्जी लोबिया प्रजनन कार्यक्रम का उद्देश्य सब्जी के रूप में उपयोग के लिए कोमल फली वाली झाड़ी या अर्ध-निर्धारित वृद्धि वाली लोबिया की किस्मों का विकास करना है। उच्च उपज वाली किस्मों के विकास के अलावा, गोल्डन मोज़ेक रोग, सर्कोस्पोरा पत्ती धब्बा और एन्थ्रेक्नोज जैसी बीमारियों के प्रतिरोध, ब्रूचिड्स, पॉड बोरर जैसे कीटों के प्रतिरोध और सूखा, लवणता और उच्च तापमान तनाव जैसे अजैविक तनावों के प्रति सहनशीलता महत्वपूर्ण है। इसे प्राप्त करने के लिए पारंपरिक प्रजनन के साथ-साथ मार्कर असिस्टेड चयन और जीनोमिक चयन जैसी आणविक विधियाँ वांछनीय गुणों के चयन की उपयोगिता को बढ़ाती हैं और दो या दो से अधिक बीमारियों के संयुक्त प्रतिरोध के साथ कम समय में किस्मों के विकास में भी मदद करती हैं। लोबिया में जीनोमिक प्रिडिक्शन और जीनोमिक चयन योजनाओं ने प्रिडिक्शन सटीकता में काफी सुधार दिखाया है और प्रजनन योजनाओं के साथ एकीकृत करने से आनुवंशिक लाभ को बढ़ाने में मदद मिलती है।