

Cowpea genetic resources and its utilization: Indian perspective – A review

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ABSTRACT

Cowpea is a multipurpose food legume of the tropics and is a crucial source of nutrition for rural and tribal communities in Africa and Asia. High protein content, nitrogen-fixing ability, drought tolerance and adaptability to challenging environment make cowpea, a promising climate resilient food legume of 21st century. This crop is grown as sole or mix-crop and in agro-forestry combinations for diverse uses as pulse, vegetable and fodder. Although cowpea has been used by indigenous people for centuries, its full potential has never been realized. Its production did not increase over the years due to narrow genetic base, biotic and abiotic stresses and non-adaptation to changing climate. Ultimate solution lies in its genetic resource which are the reservoir of useful genes. Lack of information on germplasm characterization and evaluation restricts the effective use of germplasm stored in the genebanks. Introgression of genes from closely related *Vigna* species and application of modern molecular tools may facilitate broadening the genetic base of cowpea.

Key words: Characterization, Evaluation, Genetic resources, Pre-breeding.

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.)Walp.] ($2n=2x=22$) belongs to the family Fabaceae, tribe Phaseoleae, genus *Vigna* and section Catiang (Verdcourt, 1970). This crop is emerging as one of the most important food legumes to eradicate malnutrition as it is high in protein, vitamins and minerals which makes it a key crop for food and nutritional security. It is also an important fodder crop grown during summer and rainy season in sole and mixed cropping systems. Annual global production of cowpea is over 7 million tonnes from an area of 14.5 million hectares (Singh, 2014). In India, cowpea is grown across the country primarily in Southern zone. *V. unguiculata* var. *spontanea* (formerly var. *dekindtiana*) is believed to be the progenitor of cowpea and it has been found in all low lying areas of Sub Saharan Africa (SSA) (Boukar, 2013). Padulosi and Ng (1997) reported Southern Africa as centre of origin for wild cowpea. Highest genetic diversity along with primitive forms of wild *V. unguiculata* are concentrated in the region from Namibia to Mozambique and Zambia to Cape Agulhas. *V. unguiculata*, *V. stenophylla*, *V. dekindtiana* and *V. tenuis* are the four subspecies of which *V. dekindtiana* is the cultivated species while others are wild relatives. Cultivated cowpea is categorized into four groups, namely *Biflora*, *Sesquipedalis*, *Textilis* and *Unguiculata* (Ng and Marechal, 1985). Yard-long bean belongs to culti-group *sesquipedalis* while grain type falls under *unguiculata*. They are easily crossable and crosses produce fertile and viable progeny. People from SSA, Latin America, Southern USA and Europe prefer grain type

over vegetable, while *sesquipedalis* is regularly cultivated in eastern hemisphere for long fleshy pods. It has been further reported that the yard-long bean has evolved in Asian region from cowpea following intense selection by farmers for long pods that are consumed as a vegetable. Jarvis *et al.* (2008) estimated the impact of climate change on the wild relatives of cowpea (*Vigna*), *Arachis* and *Solanum* and concluded that these species are under serious threat from climate change. Crop genetic resources are reservoir of gene and gene complexes for various stresses and provide basic raw material for genetic improvement of crops. The genetic improvement is achieved by screening appropriate germplasm for various traits of interest (Tripathi *et al.* 2012). Therefore, exploration and collection of cowpea germplasm, evaluation and conservation are the need of hour to accelerate crop improvement programmes in view of changing climate.

Historical overview in Hindustani centre: Cowpea has tag of ancient grain legume which is supported by excavation reports of Harappa (Indus -Saraswati civilization; 3200–2000 BC) (Mehra, 2002). It is mentioned as *rajmash* by Charaka during 700 BC and *lobhia* by Ain-i-Akbari during 1590 AD (Vidyalankar, 1994; Blochmann, 1873). Cowpea is popularly known as *chola* or *chorap*, *chavalya*, *alasanadolu*, *alasanade*, and *karamani* in different regional languages. Bhavamisra, an ayurvedic scholar reported diversity in the seed colour and described its nutritional importance to enhance milk production in livestock (Chunekar and Pandey, 1998). In India the plant exploration and germplasm collection work started in an efficient manner with the foundation of ICAR-

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National Bureau of Plant Genetic Resources (NBPGR) in the year 1976. Enormous natural variability in cowpea has been tapped from different phyto-geographic regions and widely adapted landraces were selected for commercial cultivation in the country. Sporadic research efforts were in progress in several countries including India but cowpea improvement has received a great deal of attention worldwide from 1970 onwards when the International Institute of Tropical Agriculture (IITA) initiated breeding program in mission mode approach to develop cowpea varieties in collaboration with various ongoing programs in Asian and African countries. In India, the research and development on cowpea has got thrust with the conception of All India Coordinated Research Project (AICRP) on Arid Legumes in the year 1992 at Jodhpur. Subsequently, the AICRP on arid legumes was brought under National Network Research Project on Arid Legumes (NNRAL) which was later shifted to Indian Institute of Pulses Research, Kanpur, India.

Explorations and collection: Globally, agro-biodiversity and habitat loss have emerged as the biggest challenges for the agricultural diaspora (Lioi *et al.* 2019). Organized crop and region-specific cowpea germplasm exploration have resulted into collection of around 5270 accessions with diverse traits from different phyto-geographic regions of India. Maximum accessions were collected from Southern

peninsula (1,521) followed by eastern parts of India. Rich diversity exists in North-eastern state particularly in tribal dominated areas where it is consumed as both grain and vegetable. Lesser diversity was observed in Haryana, Punjab, West Bengal, Bihar and Andaman and Nicobar Islands. During the period from 1999 to 2007, NBPGR through explorations either alone or in collaboration with other ICAR institutes had collected a number of cowpea germplasm including its wild relatives from remote areas under the National Agricultural Technology Project on Plant Biodiversity (NATP-PB) (Abraham *et al.* 2008). The collections from the North-eastern region showed large variation in seed shape and seed-coat colour (Barua *et al.* 2006). Diversity mapping and identification of diversity rich areas for germplasm collection, *in-situ* conservation, exploring trait-specific germplasm for climate adaptive agriculture and bio-prospecting of genetic resources undoubtedly require the use of geographic information system (GIS) tools. Geo-referencing of germplasm depicts accurate collection sites of accessions and facilitate in understanding their distribution. It can be explained as the process of assigning latitude and longitude of each location to each accessions to aid in diversity distribution mapping (Hijmans *et al.* 2001; Van Hintum *et al.* 2011; Semwal *et al.* 2013). Geographic locality linked with germplasm leads to

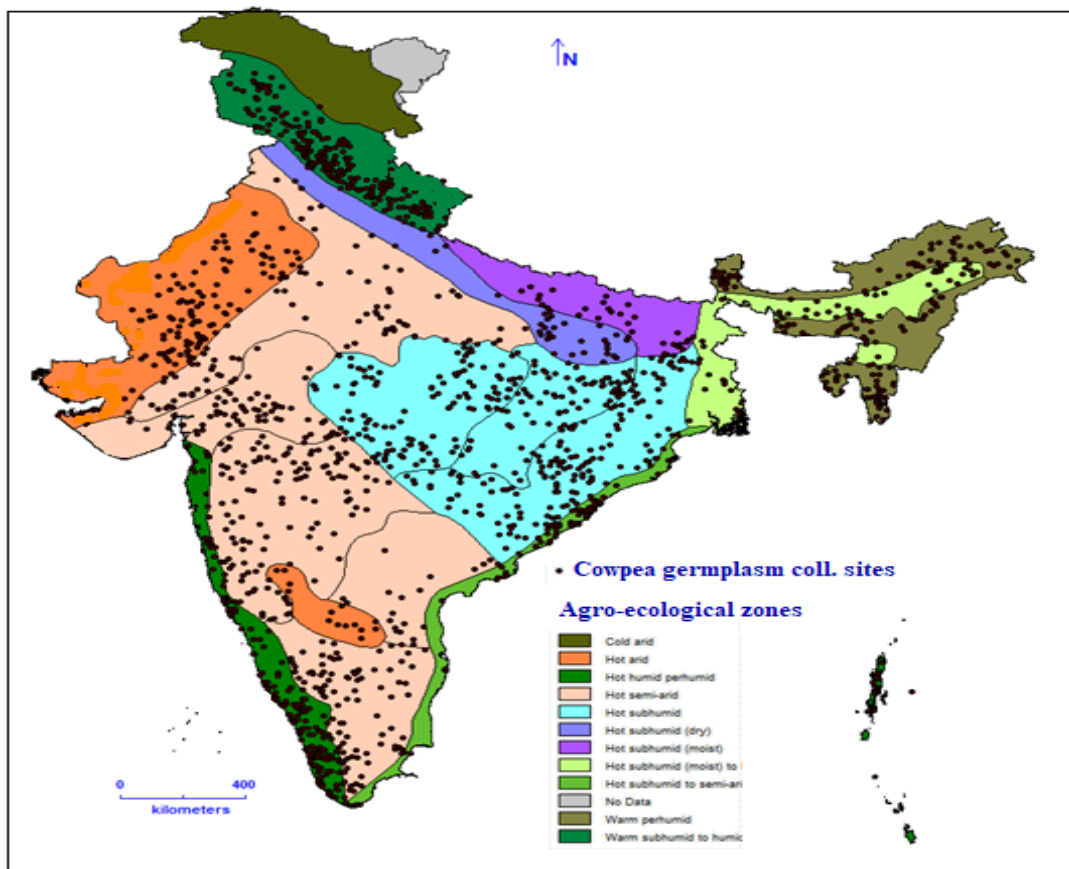


Fig 1: Distribution and collection of cowpea germplasm diversity over different agro-ecological zones of India.

Table 1: Trait specific exotic germplasm introduced in India.

EC Numbers	Country	Specific trait for which imported	Recipient Institute
EC120745-46	USA	<i>Cercospora</i> leaf blight resistance	IIHR, Bengaluru
EC130438	Nigeria	Multiple disease resistance	PAU, Ludhiana
EC157019	Nigeria	Extra early maturing (50-60 days)	PAU, Ludhiana
EC169717,20,21,22	Nigeria	Bruchid resistant	IARI, New Delhi
EC169718,19,23,24,25	Nigeria	Aphid resistant	IARI, New Delhi
EC493644-61	Nigeria	Resistant to black eye <i>Cowpea mosaic virus</i>	KAU, Thrissur
EC496737	USA	Heat tolerant and broad based resistance to Root Knot nematode	NBPGR, New Delhi
EC514421 and EC514422	USA	High bushy plant habit and early maturing (71 and 76 days respectively)	NBPGR, New Delhi
EC528457	USA	Extra early (50% of the plants produce their first flowering 37 days after sowing)	NBPGR, New Delhi
EC548850-549021	USA	Core set	IGFRI, Jhansi
EC738076-738278	Italy	Core set	NBPGR, New Delhi
EC723643- 725372	Nigeria	Core set	NBPGR, New Delhi

successful exploration programme and collection of diversity available in targeted crops. Indian map showing the distribution of cowpea germplasm over different agro-ecological zones is depicted in Fig 1.

Germplasm introduction and conservation: Probably, cowpea has entered into the Indian sub-continent more than 2000 years ago. India is believed to be the center of cowpea diversity because of two important “cultigroups” viz. *Biflora* and *Sesquipedalis* which have evolved from *Unguiculata* in India and Southeast Asia, respectively under intensive human selection (Ng and Marechal, 1985). ICAR-NBPGR is serving Indian cowpea breeders by introducing traits specific genetic resources (Table 1). During past 30 years, a total of 4,922 accessions have been imported by various Indian institutes for multiple purposes from IITA, Nigeria; Institute of Plant Breeding, University of Philippines; Department of Plant Industries, Australia; Plant Germplasm Quarantine Centre, Beltsville, Maryland, USA; Regional Plant Introduction Station, Georgia, USA; University of California, Riverside, California, USA and USDA-ARS, U.S. Vegetable Laboratory, South Carolina, USA. These accessions are also conserved in national gene bank with an aim of conservation through use. Introductions always have the risk of diseases and pests. Chalam *et al.* (2008) intercepted seed transmitted virus in 15 among 48 exotic cowpea accessions. Cowpea has orthodox seeds that can be dried and stored for a longer period with minimum loss of seed viability. The accessions meeting international standards, i.e. 2000 seeds with minimum viability of 85% are preserved in gene bank for long-term storage at -18°C . The most recent inventory includes 3764 accessions comprising 2671 indigenous and 1093 exotic introductions in the Indian National Seed bank of ICAR-NBPGR. Working collections are being conserved under medium-term storage (MTS) at NBPGR, New Delhi and its regional stations for supply to the indenters. Among CGIAR institutions, IITA, Nigeria holds the largest and diverse collection of cowpeas with 15,122 accessions from

88 countries. Global cowpea germplasm status of major genebanks is mentioned in Table 2.

Germplasm evaluation: Lack of information on range of variability in traits of interest is the foremost constraint for efficient utilization of cowpea genetic resources. Therefore, characterization and trait specific evaluation programs are being conducted in India that identifies various promising lines which are being used in crop improvement programmes

Table 2: Cowpea accessions maintained ex-situ by national institutions across the world.

Country	Cowpea
Angola (SADC)	172
AVRDC-Taiwan	322
Belgium	331 ^c
Benin	155
Cote d'Ivoire	126
Germany	291
IITA, Nigeria	15004 ^a
India (NBPGR)	3648 ^b
Kenya	875
Namibia (SADC)	57
Nigeria	384
Russia	1945
South Africa	886
South Korea	910
Spain	466
Swaziland (SADC)	45
Tanzania	386
Zambia (SADC)	305
UC Riverside	5600
USDA-ARS	8255 ^a

Source: Global Crop Diversity Trust (2017).

^aInformation on total germplasm accessions held (as per May 2017) in IITA and USDA-ARS genebanks taken from SINGER (<http://singer.cgiar.org/index.jsp>) and USDA-ARS GRIN (<http://www.ars-grin.gov/npgs/stats/>) databases, respectively.

^bInformation taken from genebank dashboard of NBPGR (<http://genebank.nbpgr.ernet.in/CropSpecieswithICECwise.aspx?CropCode=730>)

Table 3: Trait specific accessions identified in India.

Traits	Accessions
Early flowering (< 50 Days)	EC723666, EC723684, EC723690
Early maturity (< 87 Days)	EC724381, EC723746, EC723797
Erect habit (< 66 cm)	EC723894, EC723684, EC724381
High number of pods per plant	EC724307, EC724366, EC725116, EC724547, EC724770
High pod length	EC723681, EC725162, EC724327, EC724045, EC724536
High number of seeds per pod	EC725164, EC723741, EC723971, EC725180
Nematode resistance(<10 galls/ root system)	EC517140, EC723886, EC724523, EC725122,
Higher protein content (>25%)	IC536626, IC536637, IC397807
Fodder type	EC723771, EC725106, EC723662, EC723995, EC723908
Large seeded and stay green	IC202793

Source: (ICAR-NBPGR, 2016; ICAR-NBPGR, 2018; Rana *et al.* 2016).

globally. Catalogues on cowpea accessions were published internationally and nationally by IITA, Nigeria (IITA, 1974) and ICAR-NBPGR (Sardana *et al.* 2000), respectively. Descriptors for cowpea genetic resources were developed by IBPGR (now Bioversity International, Rome) in 1983 (IBPGR, 1983) while minimal descriptors (for characterization and evaluation) of cowpea were primarily developed to describe Indian germplasm (Mahajan *et al.* 2000). Key access and utilization descriptors for cowpea genetic resources were developed after comparing with different descriptors published before like 'Descriptors for Cowpea' published by IBPGR; Descriptors for Characterization and Evaluation of Cowpea by National Institute of Agrobiological Sciences, Genebank of Japan; Descriptors for *Vigna* (USDA, ARS, GRIN) and this key set was later validated by a core advisory group led by NBPGR and IITA. Evaluation for agro-morphological traits in selected accessions of vegetable type cowpea revealed variability in pod length, plant type, pod weight, seed colour, number of pods per plant, number of seeds per pod and peduncle length (Chattopadhyay *et al.* 1996). Significant variation for agro-morphological traits was observed by several researchers (Verma, 2016; Sardana *et al.* 2000; Makanur *et al.* 2013). Variability in cowpea seeds and leaves is depicted in Fig 2 and 3 respectively. A total of 845 accessions of cowpea were characterized for agro-morphological traits in ICAR-NBPGR and promising lines were identified (ICAR-NBPGR, 2016). Trait specific accessions identified in India were listed in Table 3. Mishra *et al.* (2008) evaluated the experimental materials comprising 1100 germplasm accessions of indigenous and exotic origin and observed wide range of diversity for targeted traits (Table 4). In a comparative study of cowpea and horse gram flours with chickpea flour traits, Sreerama *et al.* (2012) recommended that the mixture of cowpea and horse gram flours can be used in place of chickpea flour in some food products formulations. Core set of cowpea have been developed by Mahalakshmi *et al.* (2007) from germplasm originating from 89 countries. Accessions were characterized for 28 agro-morphological descriptors and 2,062 accessions

Table 4: Range of variability recorded in 1100 accessions of cowpea.

Characters	Range	
	Minimum	Maximum
Days to flowering	37 (C 480)	119 (C 577)
Days to maturity	62 (C 62)	152 (C 577)
Plant height (cm)	30 (C 653)	421 (C 579)
Pod length (cm)	07 (C 102)	53 (C 626)
Number of pods/peduncle	01 (C 565)	04 (C 421)
Number of pods/plant	10 (C 42)	130 (C 482)
Number of seeds/pod	5.6 (C 504)	20.7 (C 589)
100-seed weight (g)	4.3 (C 619)	24.42 (C 607)
Seed yield/plant (g)	08 (C 625)	110 (C 440)

Source: Mishra *et al.* (2008).

Table 5: Composition of global cowpea core developed by IITA, Nigeria.

Genetic resources	Total accessions (Number)	IITA Core set (Number)
Landraces	10227	1701
Advance lines	1422	225
Unknown biological status	838	130
Wild and weedy	64	06
Total	12,551	2,062

Source: Mahalakshmi *et al.* (2007).

of different groups were finally selected to serve as base material for use in breeding programmes (Table 5). Cowpea core set is served as ideal working collection which is distributed by IITA to various countries including India for accelerating the cowpea improvement program.

Molecular characterization: Molecular markers are an essential tool for detection of the structure and extent of genetic variation in crops and their wild relatives. Genetic diversity information is extremely important for cowpea breeding which makes conservation and utilization easy for improvement of cultivars. The RAPD markers have proved to be a constructive tool in molecular characterization of cowpea cultivars (Prasanthi *et al.* 2012; Malviya *et al.* 2012; Pandey *et al.*, 2004). Anatala *et al.* (2014) compared ISSR and RAPD primers on genotypes of cowpea and found that ISSR and RAPD markers gave differentiated diversity to



Fig 2: Variability in seeds of cowpea germplasm.



Fig 3: Variability in leaves of cowpea germplasm.

distinguished genotypes, individually with specific band. Xiong *et al.* (2016) estimated genetic diversity and population structure of 768 cowpea accessions from 11 geographic regions including India using 1,048 SNP markers. Highest PIC value (0.32) was observed for Indian region, which was akin to the gene diversity, indicating that the accessions from India varied the most. This study also supported the theories of previous researchers, Africa as the first domestication regions of cowpea and India as a sub-domestication region. Uma *et al.* (2009) characterized 83 cowpea genotypes with 15 micro satellite markers to test the genetic variation and reported its efficient use in the detection of polymorphism among the local landraces and cultivated varieties. EST were found valuable in genetic diversity and phylogenetic studies in cowpea as well as in the other *Vigna* species (Gupta *et al.* 2012). Mondal *et al.* (2013) characterized gene encoding putative β -carbonic anhydrase (CA) from cowpea and designated it as *VuCA1* (GenBank ID: JQ429799). Transgenic cowpea

was developed by inoculating *in vitro*-germinated seedlings of cultivar Pusa Komal with *Agrobacterium tumefaciens* strain and reported that this transformation method is efficient and reproducible and could be used to introduce desirable genes into cowpea for biotic and abiotic stress tolerance (Chaudhury *et al.* 2007; Bakshi *et al.* 2011; Bakshi *et al.* 2012). *Callosobruchus maculatus* and *C. chinensis* are the major storage pest, causing severe damage to the cowpea seeds during storage and α -amylase inhibitor-1 (α AI-1) gene of bean (*Phaseolus vulgaris*) provides resistance to both the storage pests. Solleti *et al.* (2008a and 2008b) used *Agrobacterium* mediated transformation method to insert α -amylase inhibitor-1 (α AI-1) gene from bean to Pusa Komal and generated fertile transgenic cowpea.

Induced variations: India is a pioneer centre for mutation research on grain legumes. The mutant cultivars have contributed immensely in augmenting the efforts of Indian plant breeders in accomplishing the aim of food security and

vibrant economic growth (Kharkwal *et al.* 2009). Mutation induced experiments on various grain legume species have been conducted at the ICAR-IARI, New Delhi since long time with an objective to improve existing germplasm and develop superior varieties. These efforts have culminated as the development of a number of improved cultivars such as V-16 (Amba), V-38 (Swarna) and V-240. Dhanavel *et al.* (2012) reported higher frequency of chromosomal aberrations in cowpea with gamma irradiation. The effects include changes in the cellular structure and metabolism of the plant which increased with increasing doses of gamma rays. Ethyl methane sulphonate (EMS) and Gamma rays are most frequently used mutagens to alter genes. Variation was created and observed for various agro-morphological traits of cowpea using different mutagens (Girija *et al.* 2009; Girija *et al.* 2013; Singh *et al.* 2013). Lower and intermediate doses of EMS (0.25% and 0.30%) and gamma rays (200 and 300 Gy) are most effective for inducing variability and isolating promising mutants (Nair *et al.* 2014).

Resistance to biotic and abiotic stresses: *Aphis craccivora* Koch is the major pest of *V. unguiculata* in India causing direct feeding and indirect damage by transmitting a virus. Chari *et al.* (1976) reported antibiosis, a mechanism of resistance by screening 104 multiple-disease-resistant exotic lines against *A. craccivora* and identified six lines as free from infestation at a density of 20 aphids per plant. Galaxy of studies have reported aphid tolerant cowpea germplasm (Pathak, 1988; Singh *et al.* 1990). Jayappa *et al.* (1988), in a study of 408 cowpea germplasms with considerable variability, reported that five accessions possessing aphid resistance were Mandya local, MS370, TVU2740, P912 and P1475. In storage, pulse beetle (bruchids), causes considerable damage in addition to other pests. The estimated losses due to bruchids in various pulses ranges from 30-40 per cent within a period of six months and the post harvest seed losses due to bruchids results in economic damage up to 100 per cent during periods of severe infestation (Gore *et al.* 2015). Tripathi *et al.* (2015) evaluated 52 accessions of cowpea for resistance to bruchid, *Callosobruchus chinensis* under no-choice test method and IC328859 has shown higher level of resistance while IC106033 was observed most susceptible. Further, variability in seed parameters *viz.*, colour, shape, texture, length, width, hardness, 100 seed weight and biochemical parameters namely phenols, tannins and α -amylase inhibitor activity was found as the possible factors for resistance against storage pest (Tripathi *et al.*, 2016). Also, positive correlation between GI of beetle and seed length-width ratio, 100 seed weight while negative correlation between seed hardness, phenol and tannin with Growth Index (GI) of *C. chinensis* was recorded (Tripathi *et al.* 2013). A total of 350 accessions of cowpea were screened for root-knot nematode resistance, of which six (EC0517140, EC0528391, EC0723686, EC0724523, EC0725122, and IC0253277 (<10 galls/ root systems) were

identified as promising accessions (Khan *et al.* 2018). In a pot experiment, Devi *et al.* (1991) evaluated cowpea varieties for their resistance to pigeonpea cyst nematode, *Heterodera cajani* and found Orissa Red and IFG8505 as source of resistance. Manjunatha *et al.* (2016) studied effect of *Bean common mosaic virus* (BCMV) disease incidence on yield and nodulation of cowpea genotypes and reported IC8996 as resistant to BCMV and good grain yielder (15.5 q ha⁻¹) with maximum height (68.3 cm). Among the 188 diverse cowpea genotypes screened for insect pest resistance, fifteen genotypes were identified as tolerant genotypes while EC549012, IC438372 and IC438373 showed superior insect tolerance (Roy *et al.* 2011).

Expensive and unreliable screening methods to select drought tolerant progenies from the segregating populations masked the progress in drought tolerance breeding in cowpea. Singh (2000) developed simple box screening method for drought tolerance in shoot of cowpea and root-box pin-board method to study two dimensional root architecture of individual plants. Kumar *et al.* (2008) assessed the association of leaf water content with yield-attributes using midday drop of leaf relative water content (RWC), and significant genotypic variation was observed, which was correlated with yield-attributes. This method is recommended to select and screen the trait for drought tolerance in cowpea germplasm. Anantharaju *et al.* (2008) reported VCP 16 and CO 6 as most drought tolerant on the basis of seed yield, pod and proline contents after screening cowpea germplasm for drought tolerance in a pot culture experiment.

Pre-breeding and genetic enhancement: Numerous cowpea breeding programs have been initiated to alleviate hunger and poverty in developing countries through widening its genetic base in the last decades (Timko *et al.* 2007; Singh, 2016). Large scale and repeated monocropping of improved cultivars and changing climate have increased the susceptibility of cowpea to a range of parasites like bacteria, virus, fungi, nematodes and weeds (*Striga gesnerioides* and *Alectra vogelii*). *Vigna vexillata* (L.) A.Rich. is a tuberous legume which is closest to the *V. unguiculata*. Besides other agronomic characters of interest, *V. vexillata* are resistant to cowpea weevil, cowpea pod borer and sucking bugs (Fatokun, 1991). Baudoin and Marechal (1988) reported *V. vexillata* as intermediate type between the African and Asiatic *Vigna* species but there is lesser chance of cross compatibility between *V. vexillata* and cowpea despite of phylogenetic proximity (Fatokun, 2002). In addition, interspecific hybridization was reported between *V. unguiculata* and its hairy wild relatives *V. pubescens* (Fatokun and Singh, 1987) and between *V. unguiculata* and *V. vexillata* (Gomathinayagam *et al.* 1998). Hybrid embryos were rescued by culturing in Murashige and Skoog medium and produced F₁ plants, sharing traits from both the parents. Further, researchers have also described pre-zygotic barriers

Table 6: Cowpea genetic stocks registered in India.

National identity	Donor identity	Year	Developing institute	Novel unique features
IC299972	CAZC-B	2004	ICAR-CAZRI, Jodhpur, Rajasthan	Black seed coat colour
IC202803	KM-5501	2008	ICAR-NBPGR, Pusa Campus, New Delhi	Bold seed
IC519745	KDRS-205	2008	ICAR-NBPGR, Regional Station, Hyderabad, Telangana	Resistance to black eye cowpea mosaic virus

Source: <http://www.nbpgr.ernet.in:8080/ircg/index.htm>.

Table 7: Improved varieties developed through germplasm utilization.

Variety	Source	Breeding method	Area of Adaptation	Unique Traits
Kohinoor	IGFRI, Jhansi	Single plant selection from Itan (IL-68-786)	HR, PJ, GJ and UP	Red and bold seeds
NP 3	IARI, New Delhi	Selection from exotic material	Delhi	Erect to semi-erect
Arka Garima	IIHR, Bengaluru	Derivative of the cross TUV 762 x <i>V. unguiculata</i> subsp. <i>sesquipedalis</i>	South zone	Photoinsensitive, suitable for vegetable purpose, tolerant to heat, drought and low moisture stress.
UPC-4200	GBPUAT, Pantnagar	Pure line selection from CK-76-4200	North east zone	Green fodder and suitable for drier areas
Kashi Nidhi, (VRCP-6)	IIVR, Varanasi	Pedigree selection (Kashi Unnati x Cowpea-263)	UP, BR, PJ and Jharkhand	Golden mosaic virus resistant
Pusa Do-Fasli	IARI, New Delhi	A derivative of the cross Pusa Phalguni x EC-21622	Delhi and NCR	Bushy growth habit and photo-sensitive. First picking in 50 days
UPC- 9202	GBPUAT, Pantnagar	Pedigree selection from intervarietal cross (V-260 x UPC 9805-7-2-4)	Central zone	Medium late variety which matures in 80–85 days
Swarna Harita (IC285143)	ICAR-RC for eastern region, Patna	Selection from germplasm line collected from Jamalpur of Burdwan district of West Bengal	WB, AS, BR, JH, UP and PJ	Resistant to rust and mosaic viral disease and tolerant to pod borer
Kashi Shyamal (IVREP-1)	IIVR, Varanasi	Selection from local collection (Kala Jhamla)	BR, PJ and Delhi	Early maturity (40 to 42 days); average yield under normal condition: 79qt/ha (fruit)
TC-901	BARC, Mumbai	Mutant of EC394763	Summer Season	Early maturity (70 days) with semi determinate with semi determinate habit and field resistance to mosaic & root rot

Source: <https://seednet.gov.in/SeedVarieties/CentralVariety.aspx>.

(States in India: AP-Andhra Pradesh, AS-Assam, BR-Bihar, CG-Chandigarh, GJ-Gujrat, HR-Haryana, JH-Jharkhand, MP-Madhya Pradesh, OD-Odisha, PJ-Punjab, UP-Uttar Pradesh and WB-West Bengal).

at intraspecific level after crossing *V. unguiculata* with subspecies *baoulensis*, *letouzeyi* and *tenuis* (Echikh, 2000; Kouadio *et al.* 2006). Kouadio *et al.* (2006) reported that more than 4 % of the ovules fertilized in the cross *V. unguiculata* x subspecies *baoulensis*.

Germplasm utilization: Germplasm utilization can be enhanced by identification of trait specific germplasm and their registration as genetic stock. Germplasm registration is needed to inventorize, document and bring all the important genetic stocks into public domain, facilitating their safe and enhanced use in research and crop improvement. ICAR-NBPGR, New Delhi is a nodal institute for registering

genetic stocks and trait specific germplasm. So far, only three cowpea accessions have been registered for unique traits (Table 6). Cowpea landraces were found to be an important source of genetic variability for number of pods per plant, number of pods/peduncle, better pod filling ability, grain yield/ plant as well as drought and heat tolerance and rust resistance. Hegde *et al.* (2009) reported DWDC-016, a landrace collected from peninsular India, can be utilized to improve cultivated varieties by transferring the desirable traits like number of pods/ peduncle. Hybridization between C-152 and DWDC-016 (landrace) resulted higher yield than both the parents. Direct utilization of cowpea germplasm

resulted in the release of many varieties since 1950 in India. EC4216, an introduced germplasm from USA was directly released as a variety in 1978, suitable for entire country. Its average green fodder yield is 280-300 qt/ ha. TVX-Cowpea (TVX-944-026), Pusa Barsati and Pusa Phalguni were also notified as varieties developed by the direct selection of exotic germplasm introduced from Nigeria, Philippines and Canada, respectively. Many varieties released in India by selection from indigenous germplasm *viz.* Kankamani (Kerala), JC-5 and JC-10 (Rajasthan), GFC-1(Gujarat), UP-5286 (selection from germplasm line 5286), Shweta (selection from introduction received from ICAR-NBPGR) and Gomti (Ranchi). The improved varieties and some promising selections of cowpea are presented in Table 7.

Future perspectives: In order to break the yield plateau caused by narrow genetic base, biotic and abiotic stresses, the productivity of grain type cowpea should be enhanced over current yield potential within 60 to 70 days maturity period. Focussed exploration and germplasm collection programs on endangered and wild relatives from diversity

rich and threatened areas will help in the discovery of trait specific germplasm. Multi-location characterization and trait specific evaluation are required to enhance their utilization. There is a need to strengthen the adaptive potential of cowpea over marginalized areas by combining multiple traits of drought tolerance, heat tolerance, high biological nitrogen fixation, efficient acquisition and use of limited availability of phosphorus in the soil. Breeding efforts may be developed to improve cowpea varieties having high protein content, high fibre, low glycemic index and high levels of antioxidants to tackle the potential threat of malnutrition and non-communicable diseases in Asia and Africa. Extra-early input responsive varieties can fit into the niches of cereal based cropping systems. High nitrogen fixation ability should be aimed to maximize grain and fodder production in marginal drought prone areas. DNA profiling of superior accessions, including released varieties and registration of germplasm can help in better utilization.

Declaration

The authors declare no conflict of interest.

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