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# Legume Genetic Resources: Status and Opportunities for Sustainability

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## Abstract

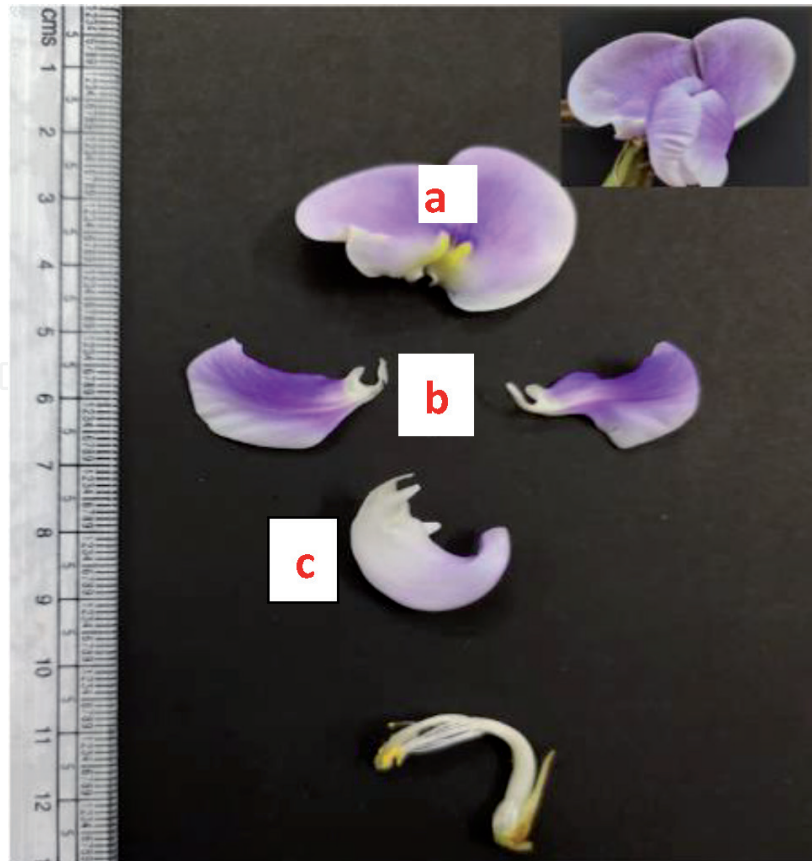
Legumes are one of the most valuable gifts of nature to man, animal, and environment. These are sustainable, affordable, water-efficient, and low-carbon footprint crop. Globally, the share of grain legume accessions is 15% of 7.4 million accessions conserved in genebanks, of which more than half of germplasm in genebanks are without characterization and evaluation data which ultimately limit the utilization of germplasm in legume improvement programs. Characterization of all genebank accessions should be of utmost priority for enhancing the utilization. The development of core, mini-core, reference sets, and trait-specific germplasm has provided route to crop breeders for mining genebanks. Identification of new sources of variation became easy with these subsets, but the entire collection also needs to be evaluated for unique and rare traits. In crop species with narrow genetic base, utilization of crop wild relatives as well as new resources aids to widen the genetic base of legume cultigens.

**Keywords:** core collection, crop wild relatives, diversity, genetic resources and legumes

## 1. Introduction

One of the biggest challenges in the twenty-first century is to produce sufficient nutritious food in the face of climate change, population explosion, and rapid urbanization and to do so in an environmentally sustainable manner. The United Nations Sustainable Development Goal number 2 explicitly recognizes the pivotal role that genetic diversity plays for food security, nutrition, and sustainable agriculture. Legumes, together with cereals, played a prominent role to the development of modern agriculture. The legume family, Fabaceae, is the third largest family of flowering plants, with 946 genera and 24,505 species [1]. Few domesticated ones have incontestably proven to be of crucial nutritional value for both humans and animals due to their protein content, causing them to be recognized as the second most valuable plant source of nutrients [2]. Legumes are extensively distributed in diverse agroclimatic zones globally, from alpine and arctic regions to the equatorial tropics.

The peculiar characteristics of the family are taproot system; bipinnate leaves; flower with corolla, standard petal (1), wing petal (2), and keel (2) (**Figure 1**); and



**Figure 1.** Floral dissection of papilionaceous family (*Vigna vexillata*): (a) standard petal, (b) wing petal, and (c) keel petal.

S. no.	Tribe	Genus	a/b/c	Primary center of diversity
1	Phaseoleae	<i>Vigna</i>	107/26/24.3	Africa, Asia
		<i>Dolichos</i>	67/3/4.47	Africa, East Asia
		<i>Phaseolus</i>	50/3/6	America
		<i>Cajanus</i>	32/16/50	South Africa, South East Asia, and East Africa
		<i>Macrotyloma</i>	25/4/6.25	Tropical Africa and Asia
2	Cicereae	<i>Cicer</i>	44/5/8.8	Central Asia, Southwest Asia and Mediterranean countries, and Himalayas
3	Fabeae	<i>Lathyrus</i>	160/8/20	Europe, Asia and North America
		<i>Vicia</i>	160/15/10.6	Europe, Asia, and North America
		<i>Lens</i>	5/0/nil	Mediterranean countries and Central Asia
		<i>Pisum</i>	3/0/nil	Southern Europe, Mediterranean region, and West Asia

a, number of species present globally; b, number of species present in India; c, percentage of species found in India. Source: [15].

**Table 1.** List of important tribes with number of species.

root nodules that facilitate nitrogen fixation in the soil. The family is divided into three subfamilies, namely, Caesalpinoideae, Mimosoideae, and Papilionoideae [3]. Among them, subfamily Papilionoideae is economically very important as it contains most of the commercial leguminous crops. Among pulse crops, *Lathyrus* and *Vicia* are the largest genus comprising 160 species, which are naturally distributed

Sl. no.	Botanical name	Pulses	Oilseeds	Vegetable	Seed spice	Root/tuber	Forage
1	<i>Arachis hypogaea</i> L. (peanut)		√				√
2	<i>Cajanus cajan</i> (L.) Mills. (pigeonpea)	√		√			√
3	<i>Canavalia ensiformis</i> (L.) DC. (jack bean)	√					√
4	<i>Cicer arietinum</i> L. (chickpea)	√					
5	<i>Codariocalyx motorius</i> (Houtt.) H. Ohashi (telegraph plant)						√
6	<i>Cyamopsis tetragonoloba</i> (L.) Taub. (cluster bean)	√		√			√
7	<i>Flemingia procumbens</i> Roxb. (Sohphlang)					√	
8	<i>Glycine max</i> (L.) Merr. (soybean)	√	√				√
9	<i>Lablab purpureus</i> (L.) Sweet (hyacinth bean)	√		√			√
10	<i>Lathyrus sativus</i> L. (grass pea)	√		√			√
11	<i>Lens culinaris</i> Medik. (lentil)	√					
12	<i>Lupinus mutabilis</i> Sweet (tarwi)	√	√				√
13	<i>Macrotyloma uniflorum</i> (Lam.) Verdc. (horse gram)	√					√
14	<i>Medicago sativa</i> L. (lucerne)						√
15	<i>Melilotus indicus</i> (L.) All. (sweet clover)						√
16	<i>Periandra mediterranea</i> (Vell.) Taub. (sweet tuber)					√	
17	<i>Phaseolus lunatus</i> L. (lima bean)	√					
18	<i>Phaseolus vulgaris</i> L. (common bean)	√		√			√
19	<i>Pisum sativum</i> L. (garden pea)	√		√			√
20	<i>Psophocarpus tetragonolobus</i> (L.) DC. (winged bean)	√		√		√	√
21	<i>Psoralea esculenta</i> Pursh (bread root)					√	
22	<i>Pueraria tuberosa</i> (Willd.) DC. (Indian Kudzu)					√	

Sl. no.	Botanical name	Pulses	Oilseeds	Vegetable	Seed spice	Root/tuber	Forage
23	<i>Trifolium alexandrinum</i> L. (Egyptian clover)						√
24	<i>Trifolium resupinatum</i> L. (Persian clover)						√
25	<i>Trigonella foenum-graecum</i> L. (fenugreek)			√	√		√
26	<i>Vicia faba</i> L. (faba bean)	√		√			√
27	<i>Vigna aconitifolia</i> (Jacq.) Marechal (moth bean)	√					
28	<i>Vigna angularis</i> (Willd.) Ohwi & H. Ohashi (adzuki bean)	√		√			
29	<i>Vigna mungo</i> (L.) Hepper (black gram)	√					
30	<i>Vigna radiata</i> (L.) R. Wilczek (green gram)	√					
31	<i>Vigna subterranea</i> (L.) Verdc. (bambara groundnut)	√				√	
32	<i>Vigna umbellata</i> (Thunb.) Ohwi & H. Ohashi (rice bean)	√		√			
33	<i>Vigna unguiculata</i> (L.) Walp. (cowpea)	√		√			√
34	<i>Vigna vexillata</i> (L.) A. Rich. (zombi pea)	√		√		√	√

**Table 2.**  
List of important legume crops having diversified importance.

across temperate region of Europe, Asia, and America. *Vigna* has six subgenera. Ceratotropis is mostly referred to as Asiatic *Vigna*. Primary centers of diversity of major pulse genera are presented in **Table 1**.

Legumes play a major role in fulfilling human, animal food, and nutritional needs. The major grain legumes include dry beans, chickpea, cowpea, faba bean, lentil, field pea and pigeonpea, green gram, and black gram. Soybean and peanut are predominantly oil-producing legume. Beans, yard long bean, and garden pea where immature seeds and pods are eaten are vegetable types of legumes. Lucerne, berseem, grass pea, and cowpea are the forage legumes, while tuber legume includes zombi pea, winged bean, Sohphlang, etc. *Abrus precatorius* is having poisonous seeds which contain toxin *abrin*. In addition to these primary grain legumes, several underutilized potential legumes like cluster bean, horse gram, moth bean, and pillipsera, primarily grown in the Indian subcontinent, China, and South East Asia, are also equally important for ensuring food and nutritional security.

Legumes are the reservoir of the protein, carbohydrate, fiber, and minerals. In addition to that, low glycemic index (GI) makes them super food that provides long-term health benefits. The isoflavone content of legumes plays a role in plant defense [4] and root nodulation and is also beneficial in human health. In addition to the human health, legumes also serve as fodder for livestock. The best advantage of legumes is nitrogen fixation, through which they enrich soil fertility and improve soil texture for other crops, and, hence, plays an important role in cropping system [5]. Legumes with their economic use are presented as follows (Table 2).

## 2. Conservation

Despite their significant contribution in global food and nutrition security, it has also been reported that their production rate becomes static mainly due to biotic factors like viruses, insects, parasitic weeds, nematodes, fungi, bacteria, and abiotic factors, viz., extreme temperatures, drought, flood, mineral imbalance, etc. [6, 7]. Therefore, there is a need to explore sustainable alternative strategies to improve

Crop	USDA	NBPGR**	VIR	CGIAR institutes			SGSV*
				ICARDA	ICRISAT	IITA	
Chickpea	7000	14,626		15,246	20,764		47
Pigeonpea	4806	11,321			13,783		13,177
Green gram	3931	3935	856				8620
Pea	6161	4436		6113			11,929
Cowpea	1287	3671	1493			15,933	19,355
French bean	17,223	3919					42,314
Cluster bean		4051					61
Horse gram		2557					47
Rice bean		2032					
Zombi pea	32		1				460
Lucerne	1748	230					
Black gram	304	2200	220				363
Soybean	33,208	4779				4575	28,034
Grass pea		2613		4220			2537
Clovers		606		5152			—
Lentil		2515		12,477			13,591
Faba bean		866		10,029			4154
Groundnut		13,406			15,622		14,583
Bambara groundnut		2				1890	1528
Wild <i>Vigna</i>		565				1878	—
Adzuki bean		187					1562

\*Ref. [16].

\*\*Ref. [17].

**Table 3.**  
 Legume germplasm holdings in major genebanks.

and diversify their production. For that, the use of diverse legume genetic resources in crop improvement is one of the most sustainable strategies and ways to conserve valuable genetic resources for the future. Crop improvement programs are always depending upon genetic diversity available in genebank. Globally, genebanks hold ~1 million accessions of leguminous crop. Legume germplasm conserved in major genebank in the world has been presented in **Table 3**.

A large number of genetic resources are conserved *ex situ* in genebanks; a considerable amount of diversity remains untapped in the nature. Hence it became a priority to collect maximum amount of diverse germplasm before it lasts forever. Crop wild relatives (CWR) are reservoir of genes for breeding [8–10]. To explore the potential of CWRs in today's changing climate, collection and conservation become of utmost priority.

### 3. Utilization

For sustainable growth in agriculture production “Conservation through use” approach is the only way. Storing the genetic resources will not solve the purpose until it is utilized. In genebanks, genetic integrity is maintained over the periods with the aim to utilize this variability in the future and bring them to the main-stream breeding programs. More than 80% of genetic resources conserved in genebanks are without characterization and evaluation data. Huge collection size with large duplicates or triplicates is again a big constraint for systematic characterization and evaluation in multi-environment experiments. To tackle this situation, the concept of core collection [11] and mini-core collection [12] are considered as the best solution for characterization of samples that represent most of the variability of the germplasm collections. Core collection represents maximum genetic diversity with minimum repetitiveness of germplasm; hence, the size of germplasm became manageable without affecting the extent of genetic diversity of the germplasm (**Figure 2**).

A general procedure for the selection of a core collection can be divided into five steps, which are described in the following sections:

- i. Identify the material (collection) that will be represented.
- ii. Decide on the size of the core collection.
- iii. Divide the set of material used into distinct groups.
- iv. Decide on the number of entries per group.
- v. Choose the entries from each group that will be included in the core.

Conventional core and mini-core collections have been developed in many legume crops. **Table 4** represents the core and mini-core developed in legumes.

Trait-specific reference set is also developed by various genebanks which offers huge opportunities to identify novel sources of variation for use in breeding program. Discovery of new traits is also possible during large-scale characterization program which resulted into unique genotypes for its further exploitation in breeding programs. For example, unique seed morphotype with extended funiculus was found during lentil characterization of 2600 accessions of lentil, and this trait is associated with fast water uptake [13].



**Figure 2.**  
 Field view of lentil characterization program at ICAR-NBPGR, India.

Sl. no.	Crop	Core/mini-core	References
1	Soybean	Core and mini-core	[18–23]
2	Peanut	Core and mini-core	[24–28]
3	Chickpea	Core and mini-core	[12, 29, 30]
4	Pigeonpea	Core and mini-core	[30, 31]
5	Lentil	Core	[30, 32]
6	Mungbean	Core and mini-core	[33, 34]
7	Adzuki bean	Core	[35]
8	Common bean	Core	[36–42]
9	Cowpea	Core	[43]
10	Moth bean	Core	[44]
11	Pea	Core	[45]
12	Hyacinth bean	Core	[46]
13	<i>Medicago</i> spp.	Core	[47–49]

**Table 4.**  
 List of cores and mini-cores developed in legume crops.

Crop wild relatives (CWR) are wild plant species genetically more or less closely related to a particular crop, but unlike the crop species has not been domesticated and remain untouched by humans. Being progenitors of crop, they contain enormous genetic variation, which are readily available to plant breeders to use in crop improvement programs and to meet the challenge of global food security along with enhancing agricultural production and sustainability in the context of a rapidly growing world population and accelerated climate change. CWRs can be categorized based on the genealogy that explains the extent to which CWRs can exchange genes with the crop. The Taxon Group (TG) concept is as follows: TG1a comprises crop species; TG1b, the taxa within the same species as crop; TG2, taxa in the same series or section as crop; TG3, taxa within the same subgenus as crop; TG4, taxa



Crop	Gene pool			References
	GP1	GP2	GP3	
Chickpea	<i>C. reticulatum</i>	<i>C. echinospermum</i>	<i>C. judaicum</i> , <i>C. pinnatifidum</i> , <i>C. bijugum</i> , <i>C. cumeatum</i> , <i>C. chorassanicum</i> , and <i>C. yamashitae</i>	[50]
Cluster bean	<i>C. senegalensis</i>	—	—	[50]
Lentil	<i>L. culinaris</i> , <i>L. orientalis</i> , <i>L. tomentosus</i>	<i>L. lamottei</i> , <i>L. odemensis</i>	<i>L. ervoides</i>	[51]
Green gram	<i>V. radiata</i> var. <i>radiata</i> , <i>V. radiata</i> var. <i>sublobata</i> , <i>V. radiata</i> var. <i>setulosa</i>	<i>V. mungo</i> var. <i>mungo</i> , <i>V. mungo</i> var. <i>silvestris</i> , <i>V. aconitifolia</i> , <i>V. trilobata</i>	<i>V. angularis</i> , <i>V. dalzelliana</i> , <i>V. glabrescens</i> , <i>V. grandis</i> , <i>V. umbellata</i> , <i>V. vexillata</i>	[14, 52–55]
Black gram	<i>V. mungo</i> var. <i>mungo</i> , <i>V. mungo</i> var. <i>silvestris</i>	<i>V. radiata</i> var. <i>radiata</i> , <i>V. radiata</i> var. <i>sublobata</i> , <i>V. radiata</i> var. <i>setulosa</i> , <i>V. aconitifolia</i> , <i>V. trilobata</i>	<i>V. angularis</i> , <i>V. dalzelliana</i> , <i>V. glabrescens</i> , <i>V. grandis</i> , <i>V. umbellata</i> , <i>V. vexillata</i>	[14, 52, 53]
Cowpea	<i>V. unguiculata</i> var. <i>unguiculata</i> (L.) Walp (cv. <i>unguiculata</i> , cv. <i>biflora</i> , cv. <i>sesquipedalis</i> , cv. <i>melanophthalmus</i> , cv. <i>textilis</i> ), <i>V. unguiculata</i> var. <i>spontanea</i> (Schweinf.), <i>V. unguiculata</i> subsp. <i>alba</i> , <i>V. unguiculata</i> subsp. <i>dekinditiana</i> (Harms.), <i>V. unguiculata</i> subsp. <i>pubescence</i> , <i>V. unguiculata</i> subsp. <i>stenophylla</i> , <i>V.</i> <i>unguiculata</i> subsp. <i>tenuis</i>	<i>V. unguiculata</i> subsp. <i>aduensis</i> , <i>V. unguiculata</i> subsp. <i>baoulensis</i> , <i>V. unguiculata</i> subsp. <i>burundiensis</i> , <i>V. unguiculata</i> subsp. <i>letouzeyi</i> , <i>V. unguiculata</i> subsp. <i>pawekiae</i>		[55]
Faba bean	—	<i>V. narbonensis</i> , <i>V. hyaeniscyamus</i> , <i>V. galilaea</i> , <i>V.</i> <i>johannis</i> , <i>V. bithynic</i>		[56]
Pigeonpea	<i>C. cajanifolius</i>	<i>C. lineatus</i> , <i>C. sericeus</i> , <i>C. scarabaeoides</i> , <i>C. albicans</i> , <i>C. trinervius</i> , <i>C. reticulatus</i> , <i>C. confertiflorus</i> , <i>C. latisepalous</i>	<i>C. platycarpus</i> , <i>C. lanceolatus</i> , <i>C. acutifolius</i>	[57]
Adzuki bean	<i>V. angularis</i> var. <i>nipponensis</i> and wild types of <i>V. umbellata</i>	<i>V. dalzelliana</i> , <i>V. glabrescence</i> , <i>V. minima</i>	<i>V. aconitifolia</i> , <i>V. mungo</i> , <i>V. radiata</i> , <i>V. trilobata</i> , <i>V. grandis</i>	[14]
Rice bean	<i>V. angularis</i>	<i>V. dalzelliana</i> , <i>V. glabrescence</i> , <i>V. minima</i>	<i>V. aconitifolia</i> , <i>V. mungo</i> , <i>V. radiata</i> , <i>V. trilobata</i> , <i>V. grandis</i>	[14]

**Table 5.**  
Gene pool of major legumes.

Crop	Wild relative	Trait	Reference
Chickpea	<i>C. microphyllum</i>	Resistant to legume pod borer ( <i>Helicoverpa armigera</i> )	[57]
	<i>C. echinospermum</i> , <i>C. pinnatifidum</i> , <i>C. bijugum</i> , <i>C. judaicum</i> , and <i>C. montbretii</i>	<i>Ascochyta</i> blight resistance	[58, 59]
	<i>C. bijugum</i> , <i>C. judaicum</i> , <i>C. pinnatifidum</i> , <i>C. reticulatum</i> , <i>C. echinospermum</i> , and <i>C. cuneatum</i>	<i>Fusarium</i> wilt resistance	[59, 60]
	<i>C. judaicum</i> , <i>C. pinnatifidum</i>	Gray mold resistance	[60]
	<i>C. echinospermum</i>	<i>Phytophthora</i> root rot	[61]
	<i>C. pinnatifidum</i> , <i>C. bijugum</i> , and <i>C. reticulatum</i>	Cyst nematode	[59]
	Green gram	<i>V. aconitifolia</i> , <i>V. glabrascence</i> , <i>V. sublobata</i> <i>V. umbellate</i>	<i>Cercospora</i> leaf spot disease resistant
<i>V. radiata</i> var. <i>sublobata</i>		Bruchid resistant	[62, 63]
<i>V. luteola</i> , <i>V. trilobata</i>		Salt stress resistant	[64]
Black gram	<i>V. mungo</i> var. <i>silvestris</i>	Mungbean yellow mosaic virus (MYMV) resistance	[65]
	<i>V. mungo</i> var. <i>silvestris</i>	Bruchid resistance	[65]
Cowpea	<i>V. pubescence</i> , <i>V. vexillata</i> , <i>V. reticulata</i> , <i>V. oblongifolia</i> , <i>V. luteola</i>	Insects Resistance	[65]
	<i>V. ambacensis</i> , <i>V. davyi</i> , <i>V. glabrescens</i> , <i>V. marina</i> , <i>V. mungo</i> , <i>V. oblongifolia</i> , <i>V. parkeri</i> , <i>V. racemosa</i> , <i>V. reticulata</i> , <i>V. vexillata</i> , and <i>V. unguiculata</i> subsp. <i>dekindtiana</i>	Resistance to <i>Striga gesnerioides</i>	[66]
Pigeonpea	<i>C. scarabaeoides</i> , <i>C. sericeus</i> , <i>C. acutifolius</i> , <i>C. lineatus</i> , <i>C. albicans</i>	Pod fly ( <i>Melanagromyza obtusa</i> )	[67]
	<i>C. scarabaeoides</i> , <i>C. albicans</i>	Pod wasp ( <i>Tanaostigmodes cajaninae</i> )	[68]
	<i>C. acutifolius</i>	Sterility mosaic disease resistance, salt tolerance	[68]
	<i>C. albicans</i>	Pod borer resistance, sterility mosaic disease resistance, salt tolerance	[68]
	<i>C. cajanifolius</i>	Nuclear male sterility, cytoplasmic male sterility	[68]
	<i>C. sericeus</i>	Cytoplasmic male sterility, <i>Phytophthora</i> blight resistance	[68]
Pea	<i>P. fulvum</i>	Pea weevil, rust, powdery mildew and <i>Ascochyta</i> blight	[69]
	<i>P. sativum</i> subsp. <i>elatius</i>	Resistant to nematodes, weevil, broomrape, powdery mildew, <i>Fusarium</i> wilt, root rot, <i>Ascochyta</i> blight and white wilt	[69]

**Table 6.**  
 Wild genetic resources as trait donor in few pulse crops [70–77].

within the same genus as crop; and TG5, different genus to the crop [8]. CWRs have been categorized into three gene pools as primary gene pool (GP1) contains close relatives that readily intercross with the crop. Secondary gene pool (GP2) contains

all the biological species that can be crossed with the crop but where hybrids are usually sterile. Tertiary gene pool (GP3) comprises those species that can be crossed with the crop with difficulty and where gene transfer is only possible with radical techniques. Another way is taxonomic which is based on taxonomic relationship of CWR with the crop [12]. Gene pools of some of the major legumes are represented (**Table 5**).

CWRs have provided vital genetic diversity for crop improvement since the twentieth century. They imparted resistance to numerous pests and diseases and tolerance to many abiotic stresses, viz., extreme temperatures, drought, and flood, and to improve nutrition, flavor, color, texture, and yield stability [13]. Almost all modern varieties of crops contain one or more genes derived from a CWR and contributed significantly to the agricultural and horticultural industries and to the world economy [14]. Furthermore, being components of natural ecosystems, they also play a role in functioning and maintaining the ecosystem services. However, many of CWRs remain unexplored. To explore the unexplored potential of CWRs, collection, conservation, characterization, and evaluation are the only powerful ways. Some examples of the use of CWRs in providing resistance to abiotic and biotic stress yield and quality improvement are listed in **Table 6**.

#### **4. Conclusions**

Genetic resources are recognized as the fourth essential input after water, soil, and light. It is the need of hour to utilize leguminous genetic resources to meet the global challenges like population explosion, malnutrition, and hunger. Legumes are dominated by rice-wheat system in the past with the major focus on cereal production worldwide. This has led to a substantial decrease in research on legumes. In view of the current climate change scenario and environmental disturbances, research on landraces and CWR is strengthened in effective and efficient manner. Legumes have the potential to contribute significantly to eco-friendly agricultural land use and sustainable forage production in the tropics. Earlier, genebanks were focusing on the conservation of genetic resources, but emphasis has been shifted to conservation through utilization. Overall, legume genetic resources provide the new potential climate smart crops, viz., zombi pea, winged bean, and grass pea, and also new alleles which help in developing biotic and abiotic stress-tolerant varieties. It is much needed to identify the bottleneck for the utilization of the valuable germplasm of the legumes. With the advancement of the modern molecular technologies, the trait discovery and the markers linked to the traits need to be explored so that a large-scale screening would become possible and eventually help to reveal the real genetic potential of the germplasm conserved in the gene banks.

#### **Acknowledgements**

We greatly thank Director of ICAR-NBPGR for his guidance in the management of legume genetic resources at ICAR-NBPGR, New Delhi, India.

#### **Conflict of interest**

The authors declare no conflict of interest.

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