Chapter 8
Hyacinth Bean (*Lablab purpureus* L. Sweet): Genetics, Breeding and Genomics

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Abstract Hyacinth bean (*Lablab purpureus* (L.) Sweet) is widely distributed in the Indian subcontinent, Africa and Southeast Asia. It is a multipurpose tropical legume valued as a vegetable, pulse, fodder and green manure crop. Despite a wide range of adaptability and diversity, it remains an underutilized crop. Broadening the genetic base and enhancing crop cultivar diversity is the key to sustainable production of hyacinth bean. Development of purelines through pedigree breeding is the preferred method of breeding in the hyacinth bean, as in other grain legume crops. Screening of germplasm resources, identification of trait-specific material and their use in breeding could be a long-term strategy to addressing various existing and anticipated production constraints. With the advent of molecular marker/omic technology, the pace and efficiency of hyacinth bean breeding has attained considerable momentum. DNA marker-assisted diversity analysis, chromosomal localization and unraveling of the mode of action of genes controlling traits of economic importance, tagging genomic regions controlling economic traits etc., will complement phenotype-based selection and breeding. Furthermore, deployment of various genomic tools will help in introgression of superior alleles into elite agronomic backgrounds and hence sustainable production of hyacinth bean.

Keywords Core set · Diversity · Field bean · Germplasm · *Lablab* · Legume

8.1 Introduction

Hyacinth bean (*Lablab purpureus* L. Sweet) is one of the oldest grain legumes grown in Asia, Africa and Australia (Ayyangar and Nambiar 1935). It is a bushy semi-erect perennial herb belonging to the family Fabaceae, subfamily Faboideae, tribe Phaseoleae and subtribe Phaseolineae. It is predominantly a self-pollinated crop with 2n = 22 chromosomes (Goldblatt 1981; She and Xiang 2015). *Lablab* is a monotypic genuswith a diverse history of origin and domestication. It is believed to

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J. M. Al-Khayri et al. (eds.), *Advances in Plant Breeding Strategies: Legumes*,
https://doi.org/10.1007/978-3-030-23400-3_8

have originated in India (Kukade and Tidke 2014; Nene 2006) or Africa (Maass 2016) and later introduced into China, West Asia and Egypt (Ayyangar and Nambiar 1935). It is also commonly known as field bean, dolichos bean, lablab bean, Indian bean, sem, bonavista bean, lubia bean, butter bean and Egyptian kidney bean in different parts of the world.

Hyacinth bean is highly popular in South Asia, Southeast Asia and Africa, where it is grown in rainfed agroecosystems (Haque et al. 2003; Rahman et al. 2002) as a vegetable, pulse, forage, cover and green manure crop (Adebisi and Bosch 2004). In China, it is very popular and has been grown on fences and trellises in backyards for centuries. In Bangladesh, it is the third most important vegetable in the central and southwestern parts of the country with a total cultivation area of 48,000 ha (Rashid et al. 2007). In India, hyacinth bean is primarily grown as a vegetable cum pulse rainfed crop in southern states such as Karnataka, Tamil Nadu, Andhra Pradesh and Maharashtra (Mahadevu and Byregowda 2005; Shivashankar and Kulkarni 1989). Immature grains (as a vegetable), dry grains (as a pulse in foods and snacks) (Ayyangar and Nambiar 1935; Shivashankar and Kulkarni 1989; Viswanath et al. 1971) and whole plant before flowering (as fodder for mulch and draught animals) (Magoon et al. 1974), are the economic products from hyacinth bean. It is a good source of dietary protein to vegetarians in South India. Hyacinth bean is an important food source in tropical Africa as well. In Kenya, the bean is popular as *njahe* and has historically been the main dish for breastfeeding mothers. It is popular as an ornamental plant in the USA and as forage in Australia.

8.2 Origin and Distribution

The center of origin of hyacinth bean has long been the subject of debate. According to several researchers, it is a native of Indian subcontinent (Kukade and Tidke 2014; Nene 2006) as documented in archaeobotanical studies from Hallur (2000–1700 B.C.) and Veerapuram sites (1200–300 B.C.), India (Fuller 2003). It is believed to have been introduced into China, West Asia and Egypt from India (Ayyangar and Nambiar 1935). However, Maass et al. (2005) suggested eastern and or southern Africa as the center of origin. In addition, they reported the intermediate nature of Indian wild collections, suggesting a pattern of domestication and distribution of hyacinth bean from Africa to Asia. Maass and Usongo (2007) further affirmed this hypothesis by studying seed characteristics of wild and cultivated forms. A dual center of origin hypothesis (Africa and India) is also postulated for hyacinth bean. However, the African continent shows greater occurrence of natural diversity of wild and cultivated forms. During later periods, the crop was domesticated and distributed to many countries like China, Indonesia, Malaysia, Egypt, Philippines, Sudan, Papua New Guinea, East and West Africa, the Caribbean, Central and South America (Fig. 8.1). Hoshikawa (1981) documented the introduction of hyacinth bean to Japan from China in 1654 where it is called *fujimame* and the young pods are used as a vegetable.

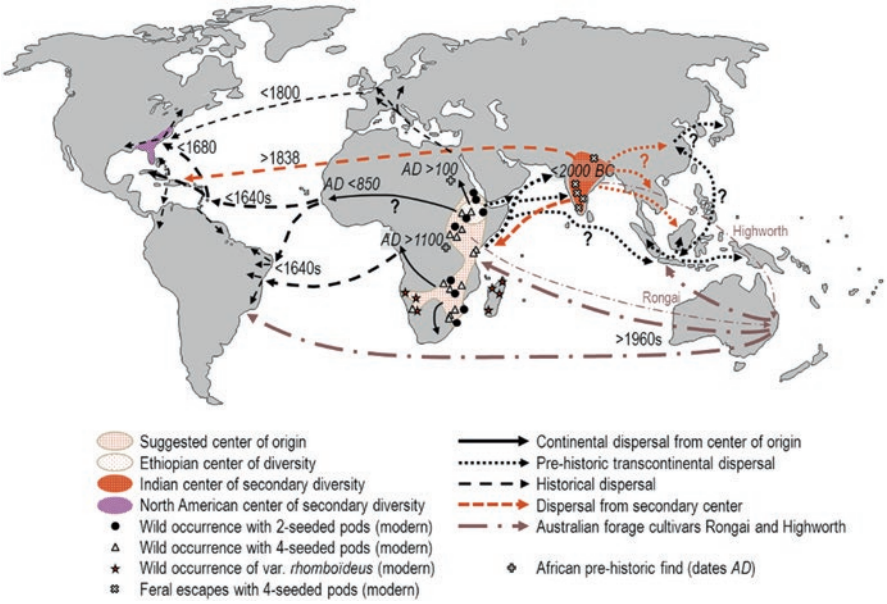

Fig. 8.1 Origin and distribution of hyacinth bean. (Source: Maass 2016)

8.3 Ecology

The hyacinth bean is remarkably adaptable to wide areas under diverse climatic conditions, such as arid, semiarid, subtropical and humid regions where temperatures are 22–35 °C, lowlands and uplands and many types of soils ranging from deep sands to heavy clays, and from acid to alkaline with a pH range of 4.4–7.8. Hyacinth bean prefers lower elevations but it can thrive up to 2100 m elevation. In the wild, hyacinth bean occurs in grassland, bushland and gallery forest, up to 2400 m elevation. It is a drought-tolerant crop, which grows well with the rainfall of 600–800 mm per annum. It has a deep tap root that can reach up to 2 m below the soil surface, permitting luxuriant growth in the dry season. It is normally a short-day plant, but day-neutral and long-day cultivars exist. Being a legume, it can fix atmospheric nitrogen to the level of 170 kg/ha (Ramesh and Byregowda 2016).

8.4 Taxonomy

Linnaeus used an ancient Greek adjective *dolichos*, meaning *long*, to describe a group of about 60 species of herbaceous plants and shrubs (Aleksandar and Vesna 2016). The first scientific name of hyacinth bean was *Dolichos lablab* L. and it is still being used as a synonym of *Lablab purpureus*. Adanson and Mochel (1763) for

Fig. 8.2 Two *Dolichos lablab* varieties: (**a**) *D. lablab* var. *typicus* Prain (=*Lablab purpureus* (L.) Sweet, (**b**) *D. lablab* var. *lignosus* Prain (=*Lablab purpureus* (L.) Sweet

the first time assigned the name *Lablab* for *Dolichos* L. *Lablab* is an Arabic name describing the dull rattle of the seeds inside the dry-pod. Roxburgh (1832) described the genus *Dolichos*, listing 7 varieties, of which 5 were cultivated and 2 were wild. *Dolichos lablab* var. *typicus* Prain (=*Lablab purpureus* (L.) Sweet and *Dolichos lablab* var. *lignosus* Prain (=*Lablab purpureus* (L.) Sweet were two subdivisions of cultivated varieties of hyacinth bean recognized by Purseglove (1968).

Dolichos lablab **var.** *typicus* **Prain [=***Lablab purpureus* **(L.) Sweet]** This crop is commonly known as Indian butter bean (Fig. 8.2a). It is a perennial twining herb widely distributed throughout the tropical and temperate regions of Asia, Africa and America. Pods are flat, long and tapering with long axis of seeds parallel to the suture. Mainly grown as a garden crop, and trained on a pendal for green soft whole pods (used as vegetable). It produces white, green or purple-margined pods with varying seed color (white, yellow, brownish, purple, black seeds).

Dolichos lablab **var.** *lignosus* **Prain [=***Lablab purpureus* **(L.) Sweet]** This crop is commonly known as Australian pea or field bean (Fig. 8.2b). It is a semi-erect, perennial herb, showing little or no tendency to climb. It bears pinnately trifoliate leaves, which are smaller than those of var. *typicus*. Inflorescence is a terminal raceme and flowers open in succession. Pods oblong, flat and broad, firm-walled and fibrous contain 4–6 seeds, with their long axis at right angles to the suture. Seeds almost rounded white, brown or black. The plant emits a characteristic odor.

Rivals (1953) proposed another classification of the cultivated species as (a) short-day varieties (photoperiod of 10–11 h) and (b) others (relatively unaffected by day length). Verdcourt (1970) recognized 3 subspecies: *unicinatus*, *purpureus*, *bengalensis*. Subspecies *unicinatus* produces small pods (40 × 15 mm) and is distributed in East Africa representing an ancestral form. However, the cultivated form belongs to ssp. *purpureus* and produces large pods (100 × 400 mm); ssp. *bengalen-*

sis has linear oblong-shaped pods (140 × 10–25 mm) and was domesticated in Asia. Although there were significant differences with respect to pod shape, it is presumed that ssp. *purpureus* and ssp. *bengalensis* are genetically very similar and most of the domesticated material in India belongs either to ssp. *purpureus* or ssp. *bengalensis*. Subspecies *uncinatus* was domesticated only in Ethiopia (Magness et al. 1971). Verdcourt (1980) revised the monotypic genus *Lablab* by combining the subspecies under in *Lablab purpureus* (L.) Sweet.

8.5 Botany

Growth Habit It is a perennial herb twining up to 1.5–8.8 m. However, bushy, semi-erect, and prostrate forms exist. Wide variation in form and habit compared to other legumes (Figs. 8.3 and 8.4) (www.lablab.org).

Roots Well-developed tap root system with many lateral and adventitious roots.

Stem Cylindrical, twining, hairy or glabrous, usually 2–10 m.

Leaves Alternate, trifoliate, leaflets ovate, often hairy. Very broad leaflets, ovate, leaf tip acuminate, slender and laterally compressed petioles.

Inflorescence Axillary raceme with many flowers. Peduncle glabrescent, 1–5 flowers together form tubercles on rachis, deciduous, ovate to elliptic, short pedicels with 2 bracteoles attached at the base of the calyx.

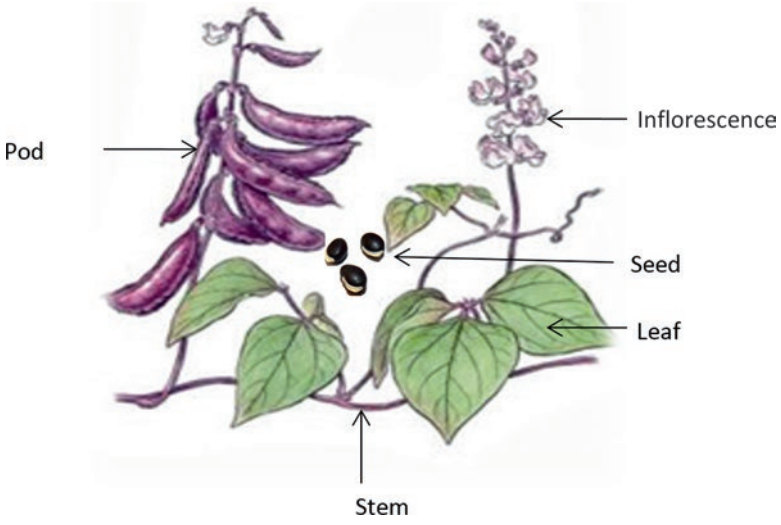

Fig. 8.3 Schematic representation of hyacinth bean plant

Fig. 8.4 Variability for growth habit among hyacinth bean germplasm collection

Flowers White, pink, red or purple colored, in clusters of 4–5, each with 2 large basal bracts, stamen free, long, flattening and geniculate near the base. Anthers are uniform, ellipsoid diadelphous (9 + 1), minutely denticulate and yellow. Sessile, finely pubescent ovary with 4 brown speckled ovules. Style abruptly upturned, laterally compressed, apical part thinly pubescent, persistent on pod, stigma capitate and glandular (www.lablab.org).

Pods Flat or inflated, pubescent or smooth, papery, straight, curved or crescent-shaped, white, green or purplish in color and approximately 5–20 cm long (Fig. 8.5) (www.lablab.org). Cultivars grown as a vegetable have thick fleshy pods with less fiber. Pods may be septate (each seed occupies a separate compartment in the pod) or nonseptate (pods have a bloated appearance).

Seed Each pod normally encloses 3–6 round, oval or flattened seeds. Seeds are variable in size and color (Fig. 8.6) ranging from white, red, brown, black or speckled hilum white, prominent and oblong, usually covering 1/3 of the seed. Germination is epigeal (www.lablab.org).

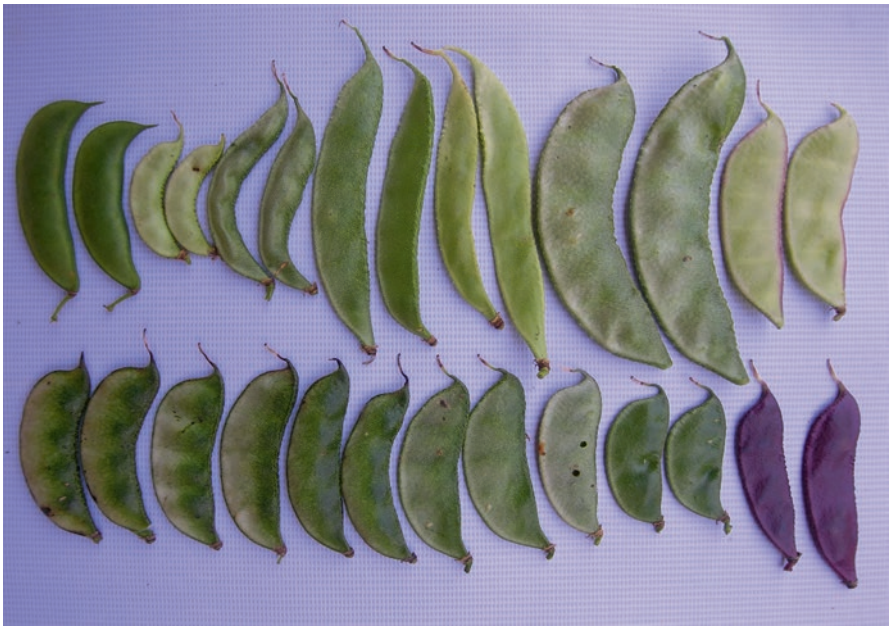

Fig. 8.5 Variability for pod size, shape and color among hyacinth bean germplasm collection

Fig. 8.6 Variability for seed size, shape and color among hyacinth bean germplasm collection

8.6 Cytology

Cytogenetic studies of hyacinth bean were primarily based on conventional staining techniques. Root tips from germinated seeds were collected, pretreated and fixed in acetic alcohol for slide preparation. Karyotype studies showed somatic chromosome number of 2n = 22 for hyacinth bean (Ali et al. 2011; Chen 2003). The chromosomal length varied from 1.17–3.00 μ (Ali et al. 2011). The haploid complement consisted of 11 metacentric chromosomes with 5 individually identifiable ones. Recently, FISH mapping of 5S and 45S rDNA in *Lablab purpureus* was reported (Iwata et al. 2013). She and Xiang, (2015) demonstrated genomic organization of hyacinth bean using sequential CPD staining and FISH with 5S and 45S rDNA probes. They depicted karyotype of hyacinth bean as $2n = 2x = 22 = 14$ m (2SAT) + 6sm + 2st (2SAT). These studies also revealed the presence of centromeric AT-rich heterochromatin and proximal GC-rich heterochromatin in hyacinth bean chromosomes. However, a molecular cytogenetic karyotype of this species is still unavailable.

8.7 Germplasm Collection, Conservation and Utilization

8.7.1 Germplasm Collection and Conservation

Diversifying the genetic base of crop cultivars is a prerequisite for continued genetic improvement to enhance productivity and to address various production constraints. More than 3000 hyacinth bean accessions have been collected worldwide (Maass et al. 2010); these genetic resources are preserved in the form of seeds in ex situ gene banks globally.

Table 8.1 Summary of hyacinth bean germplasm maintained in different countries, regions and institutes of the world

Countries/region/institute	Number of accessions	Source
South America	134	BI (2008)
North America, United States Department of Agriculture (USDA)	52	GRIN (2009)
Europe	82	BI(2008) and VIR (2009)
Oceania including Australia at Common Wealth Scientific and Industrial Research Organization (CSIRO)	104	BI (2008)
China	410	BI (2008)
Philippines	209	Engle and Altoveros (2000)
Taiwan at Asian Vegetable Research and Development Center (AVRDC)	423	AVRDC (2009)
Southeast Asia (countries other than Bangladesh and India)	82	BI (2008) and NIAS (2009)
Bangladesh	551	Islam (2008)
India at National Bureau of Plant Genetic Resources (NBPGR), New Delhi	221	BI (2008)
South Asia	93	BI (2008)
Ethiopia including International Livestock Research Institute (ILRI)	223	BI (2008)
Kenya	403	BI (2008)
Sub-Saharan Africa including International Institute of Tropical Agriculture (IITA), Nigeria	67	BI (2008)
University of Agricultural Sciences (UAS), Bengaluru, India	650	Byregowda et al. (2015) and Vaijayanthi et al. (2015a)

The National Gene bank of Kenya, Commonwealth Scientific and Industrial Research Organization (CSIRO-Australia), International Livestock Research Institute (ILRI-Ethiopia), International Institute of Tropical Agriculture (IITA-Nigeria), National Bureau of Plant Genetic Resources (NBPGR-New Delhi) and the University of Agricultural Sciences, Bengaluru (UAS (B)-India) hold the largest working germplasm collections of hyacinth bean. In Australia and New Zealand, only fodder types are maintained. Systematic efforts to collect, evaluate, catalogue, document and conserve hyacinth bean genetic resources in several countries/regions/institutes are summarized in Table 8.1 (Ramesh and Byregowda 2016).

8.7.2 Germplasm Utilization

From the above discussion, it is evident that the UAS, Bengaluru, India holds the largest working germplasm (650 accessions) of hyacinth bean. These accessions were characterized and evaluated for a set of 70 descriptors (16 vegetative, 14

Table 8.2 Status of hyacinth bean germplasm conserved at UAS, Bangalore, India

Sl. no	Geographical origin	Base collection[a]
1	Indian collections	544 (83.95%)
	(a) Karnataka	449
	(b) Andhra Pradesh	36
	(c) Maharashtra	14
	(d) Gujarat	36
	(e) Tamil Nadu	7
	(f) Kerala	2
2	Exotic collections	24 (3.7%)
3	Unknown Origin	80 (12.35%)
Total		648

[a]Figures within parenthesis indicate percentage of accessions

inflorescence, 20 pod, 20 seed traits) considering the spectrum of variability for these traits following the guidelines of Bioversity International (BI), (Byregowda et al. 2015). These descriptors can be used as diagnostic markers of germplasm accessions to maintain their identity and purity. They are also useful in conducting distinctness, uniformity and stability (DUS) testing, a mandatory requirement for protecting varieties under the Protection of Plant Varieties and Farmers' Rights (PPA & FR) Act of India, and similar laws in force in other countries (Byregowda et al. 2015).

Most traits of economic importance often exhibit high genotype × environment interactions and require multi-locational and multi-year evaluation, which is a resource-demanding task owing to the large size of the germplasm collections. Hence, Frankel (1984) proposed the concept of the *core collection*, a manageable representation of the base collection. A core collection is a subset of the entire collection chosen to represent the maximum genetic diversity with minimum redundancy (Brown 1989). Considering that the plant genetic resource collections being maintained at UAS, Bengaluru (Table 8.2) are large and pose difficulties in effective management and evaluation of accessions for quantitative traits, a core set (n = 64) which captures ≥90% of variability in the entire collection (n = 648) was developed (Vaijayanthi et al. 2015b) using Power Core (v.1), a program that applies advanced M-strategy with a heuristic search (Kim et al. 2007). The procedure adapted for the development of a representative core set is depicted in Fig. 8.7.

In similar efforts to reduce size and possible duplication, Bruce and Maass (2001) in Ethiopia and Islam et al. (2014) in Bangladesh, also developed core sets of 47–36 accessions from the base collections of 251–484 accessions, respectively. The core sets are considered a first look at sources of genetic resources for use in crop improvement programs. Because of their small size, core sets can be effectively characterized and evaluated across many locations/years and are considered ideal for discovering new sources of variation, identification of trait-specific accessions, gene discovery, allele mining and as an association mapping panel (Qiu et al. 2013; Upadhyaya 2015).

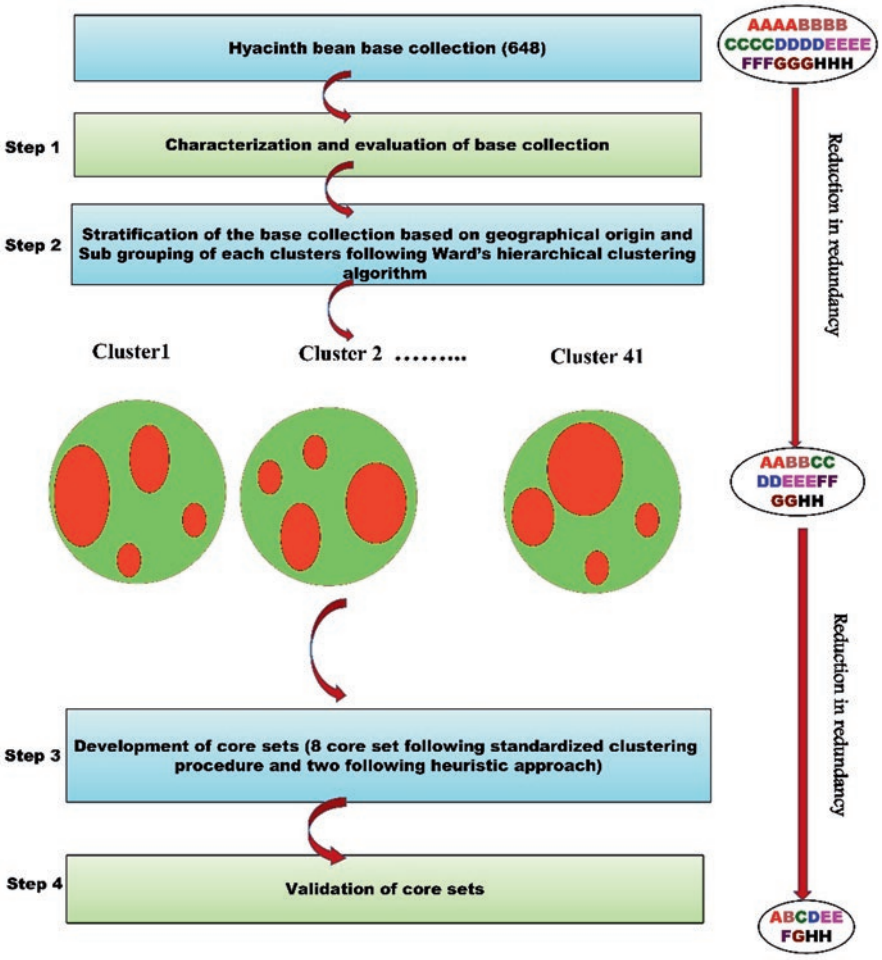

Fig. 8.7 Flow diagram depicting establishment of 10 core sets from 648 hyacinth bean accessions

In order to identify promising trait-specific germplasm accessions, the core set at UAS, Bengaluru was evaluated for 2 years (2012–2014) and those promising for per se productivity traits (Table 8.3) and multi-traits (Table 8.4) identified (Vaijayanthi et al. 2016a). Furthermore, promising germplasm accessions for multi-traits were evaluated in multi-locations to identify those widely/specifically adaptable to different agroclimatic zones. Accessions such as GL 250, FPB 35 and Kadalavare were found widely adaptable with a relatively high fresh pod yield (Vaijyayanthi et al. 2016b, 2017). These accessions are suggested for preferential use in breeding hyacinth bean varieties widely adaptable to different agroclimatic zones.

Table 8.3 Promising trait-specific germplasm accessions identified from core set

Traits	Germplasm accessions
Days to 50% flowering	HA-11-3, GL 326, HA-12-9, GL 432, GL 661
Primary branches plant^{-1}	GL 621, GL 199, GL 147, GL 228, GL 110, GL 12, GL 252, GL 205, GL 606, GL 527
Racemes plant^{-1}	GL 326, GL 142, GL 205, GL 447, GL 12, GL 530, GL 606, GL 199, GL 110, GL 438, GL 412
Fresh pods plant^{-1}	GL 447, FPB 35, GL 576, GL 418, KA, GL 142, GL 633, GL 527, GL 250, GL 66, GL 444
Fresh pod yield plant^{-1} (g)	GL 576, FPB 35, GL 527, GL 447, GL 142, GL 441, GL 66, GL 12, GL 418, GL 579
Fresh seed yield plant^{-1} (g)	FPB 35, GL 576, GL 527, GL 142, GL 447, GL 12
100 fresh seed weight (g)	GL 441, GL 6, GL 12, HA-12-9, GL 579, GL 142, GL 527, GL 68, GL 658, GL 66, GL 439, FPB 35

Table 8.4 Promising multiple traits specific germplasm accessions identified from core set

Identity of accessions	Traits
GL 576	Fresh pods plant^{-1}, fresh pod yield plant^{-1}, fresh seed yield plant^{-1}
GL 110	Primary branches plant^{-1}, racemes plant^{-1}
GL 527	Primary branches plant^{-1}, fresh pods plant^{-1}, fresh pod yield plant^{-1}, fresh seed yield plant^{-1}
GL 447	Racemes plant^{-1}, fresh pods plant^{-1}, fresh pod yield plant^{-1}, fresh seed yield plant^{-1}
GL 142	Racemes plant^{-1}, fresh pods plant^{-1}, fresh pod yield plant^{-1}, fresh seed yield plant^{-1}, 100 fresh seed weight
GL 441	Fresh pod yield plant^{-1}, 100 fresh seed weight
FPB 35	Fresh pods plant^{-1}, fresh pod yield plant^{-1}, fresh seed yield plant^{-1}, 100 fresh seed weight.
GL 66	Fresh pods plant^{-1}, fresh pod yield plant^{-1},100 fresh seed weight
GL 12	Racemes plant^{-1}, fresh pod yield plant^{-1}, fresh seed yield plant^{-1}, 100 fresh seed weight.

8.8 Genetics of Important Productivity Traits

8.8.1 Qualitative Traits

Several researchers have reported the number and mode of action of genes controlling easily-observable/assayable growth traits, leaf traits, inflorescence traits, pod traits and seed traits in hyacinth bean (Table 8.5). Joint segregation analysis showed linkage among the genes controlling various qualitative traits. Independently segregating genes controlling direction of inter-nodal hairs, pod width, orientation of dry pods on the branches and seed color in hyacinth bean were found (Patil and Chavan

1961). On the contrary, genes controlling pod width and seed shape and those controlling orientation of dry pods and nature of pod surface are closely kinked without recovery of recombinants (Patil and Chavan 1961). This is possible because of the pleiotropic effect of a single gene. Raut and Patil (1985) reported a close linkage between genes controlling stem color and flower color, and between genes controlling flower color and leaf margin. The genes controlling photoperiod sensitivity and petiole color are linked with recombination of 33.16% and those controlling petiole color and growth habit and photoperiod sensitivity and growth habit are also linked with recombination of 32.92% and 6.14%, respectively (Rao 1987). The genes controlling growth habit and photoperiod sensitivity are linked with recombination of 7.82% (Rao 1987). On the other hand, genes controlling photoperiod sensitivity and stem color, growth habit and stem color segregated independently (Rao 1987). While the genes controlling photoperiod sensitivity and growth habit, photoperiod sensitivity and raceme emergence from the foliage and growth habit and raceme emergence from the foliage are linked in coupling phases with recombination of 29%, 24% and 21%, respectively; those controlling flower color and pod curvature are un-linked (Keerthi et al. 2016). The qualitative traits controlled by single/oligogenes could be used to identify true F_1s, to rule out the possibility of selfing due to the occurrence of pollination before opening of the flowers (Ayynagar and Nambiar 1935; Harland 1920; Kukade and Tidke 2014).

8.8.2 Quantitative Traits

Jacob (1981) reported partial dominance with a duplicate type of epistasis for green pod yield plant^{-1} and predominance of additive gene action for seed yield plant^{-1}. Rao (1981) reported the importance of all the three types of gene action (additive, dominant, epistatic) in different proportions in the inheritance of pod yield plant^{-1}, pods plant^{-1}, seed yield plant^{-1}, raceme length, pods raceme^{-1} and plant height. Muralidharan (1980) reported complementary epistasis with preponderance of dominance genetic variance (σ^2_D) in the inheritance of seed yield, while Reddy et al. (1992) documented the preponderance of additive genetic variance (σ^2_A) for number of pods plant^{-1}. Khondker and Newaz (1998) reported the predominant role of additive variance in the inheritance of days to flowering, pod width, seeds pod^{-1} and 20-pod weight. On the other hand, traits such as number of inflorescences plant^{-1}, number of pods inflorescence^{-1} and pod yield plant^{-1} were mostly governed by σ^2_D.

Sakina and Newaz (2003) reported the preponderance of σ^2_A in the inheritance of all the characters considered for the study and presence of complete dominance in controlling flowering time and partial dominance for raceme plant^{-1} and number of flowers raceme^{-1}. Alam and Newaz (2005) reported the importance of both σ^2_A and σ^2_D in the expression of flower and pod traits. Raihan and Newaz (2008) also documented the importance of both σ^2_A and σ^2_D with a preponderance of σ^2_A in the expression of all the traits except number of inflorescences plant^{-1}. Desai et al. (2013) reported preponderance of σ^2_A for all the traits considered for the study

Table 8.5 Summary of genetics of different traits in hyacinth bean

Traits and different states	Number of genes	F_2 ratio	Mode of action	References
Growth traits				
Orientation of stem inter-nodal hairs	1	3 Downward:1 upward	Downward > upward	Ayynagar and Nambiar (1935)
Upwards/downwards				
Orientation of inter-nodal hairs	1	3 Downward: 1 upward	Downward > upward	Patil and Chavan (1961)
Upwards/downwards				
Stem pigmentation on nodes and internodes	3	27 Pigmented: 37 non-pigmented	Pigmented > non-pigmented	Manjunath et al. (1973)
			Complementary epistasis	
Growth habit	1	3 Spreading: 1 compact	Spreading > compact	Rao (1987)
Spreading/compact				
Growth habit	3	57 Erect: 7 prostrate	Erect > prostrate	Girish and Byregowda (2009)
Erect/prostrate				
Growth habit	2 or 3	9 Indeterminate: 7 determinate (two complementary genes)	Indeterminate > determinate	Keerthi et al. (2014a) and Keerthi et al. (2016)
Determinate/indeterminate		57 Indeterminate: 7 determinate (1 basic and two complementary genes)	Complementary epistasis	
Stem color	1	3 Purple: 1 green	Purple > green	Raut and Patil (1985)
Purple/green				
Stem color	3	57 Purple: 7 green	Purple > green	Rao (1987)
Purple/green			Complementary epistasis	
Leaf traits				
Leaf margin color	1	3 Purple: 1 green	Purple > green	Raut and Patil (1985)
Purple/green				

Leaf vein color	2	9 Purple: 7 green	Purple > green	Raut and Patil (1985)
Purple/green			Complementary epistasis	
Petiole color	2	9 Purple: 7 green	Purple > green	Rao (1987)
Purple/green			Complementary epistasis	
Leaf color	3	54 Dark green: 10 green	Dark green > green	Girish and Byregowda (2009)
Dark green/green			Complementary epistasis	
Leaf texture	2	9 Rough:7 smooth	Rough > smooth	Girish and Byregowda (2009)
Rough/smooth			Complementary epistasis	
Inflorescence traits				
Photoperiod sensitivity to flowering	1	3 Sensitive: 1 insensitive	Sensitivity > insensitivity	Rao (1987)
Sensitive/insensitive				
Photoperiod sensitivity to flowering	1	3 Sensitive: 1 insensitive	Sensitivity > insensitivity	Prashanti (2005)
Sensitive/insensitive				
Photoperiod sensitivity to flowering	1	3 Sensitive: 1 insensitive	Sensitivity > insensitivity	Keerthi et al. (2014a) and Keerthi et al. (2016)
Sensitive/insensitive				
Flower color	1	3 Purple: 1 white	Purple > white	Raut and Patil 1985)
Purple/white				
Flower color	1	3 Purple: 1 white	Purple > white	Keerthi et al.(2016)
Purple/white				

(continued)

Table 8.5 (continued)

Traits and different states	Number of genes	F_2 ratio	Mode of action	References
Raceme emergence from foliage	2	13 Emerge out of the foliage: 3 remain within the foliage	Emergence > remaining within the foliage	Keerthi et al. (2016)
Emerge out of the foliage/ remain within the foliage			Inhibitory epistasis	
Pod traits				
Orientation of dry pods to branches	1	3 Erect: 1 dropping	Erect > drooping	Ayynagar and Nambiar (1935)
Erect/drooping				
Width of pods	1	3 Medium: 1 narrow	Medium width > narrow width	Ayynagar and Nambiar (1935)
Medium/narrow				
Pod width	1	3 Broad: 1narrow	Broad > narrow	Patil and Chavan (1961)
Broad/narrow				
Nature of surface of narrow pods	1	3 Septate: 1 nonseptate	Septate > non-septate	Ayynagar and Nambiar (1935)
Septate/non-septate				
Pod position after drying	2	15 Erect: 1 dropping	Erect > drooping	Patil and Chavan (1961)
Erect/drooping			Duplicate dominant	
Nature of pod surface	2	15 Smooth: 1 shriveled	Smooth > shriveled	Patil and Chavan (1961)
Smooth/shriveled			Duplicate dominant	
Pod color	1	3 Green: 1 light green	Green > light green	D' cruz and Ponnaiya (1968)
Green/light green				
Pod shape	1	3 Flat: 1 bloated	Flat > bloated	D' cruz and Ponnaiya (1968)
Flat/bloated				

Pod curvature	4	117 Straight: 139 curved	Curved > straight	Girish and Byregowda (2009)
Straight/curved			Two complementary, one inhibitory and one anti-inhibitory	
Pod curvature	2	9 Straight: 7 curved	Straight > curved complementary, epistasis	Keerthi et al. (2016)
Straight/curved				
Pod fragrance	2	13 High: 3 low	High > low	Girish and Byregowda (2009)
High/low			Inhibitory epistais	
Seed traits				
Seed coat color	1 or 2	9 Khaki: 3 chocolate: 1 buff	Khaki > chocolate > black > buff	Ayynagar and Nambiar (1936 a, b)
Khaki/chocolate/black/buff			Supplementary epistasis	
Seed shape	1	3 Fat: 1 round	3 Flat > 1Round	Patil and Chavan (1961)
Round/flat				
Seed color	1	3 Red: 1 white	Red > 1white	Patil and Chavan (1961)
Red/white				
Seed coat color	1	3 Chocolate: 1 brown	Chocolate > brown	D' Cruz and Ponnaiya (1968)
Chocolate/brown				

Source: Ramesh and Byregowda (2016)

except days to 50% flowering and number of pods cluster^{-1}. Das et al. (2014) reported the importance of σ^2_A in the inheritance of number of inflorescences plant^{-1} and number of nodes inflorescence^{-1}. On the contrary, length of inflorescence, number of pods inflorescence^{-1}, pod length and number of seeds pod^{-1} were influenced by σ^2_D, while the characters such as days to 50% flowering, number of pods plant^{-1}, pod weight and pod yield plant^{-1} were controlled by both σ^2_A and σ^2_D. Keerthi et al. (2015) reported the predominance of σ^2_A in the inheritance of racemes plant^{-1} and predominance of σ^2_D in the inheritance of pod weight plant^{-1}. Additive genetic variance was found to be very important in the inheritance of days to flowering and seed weight plant^{-1}. Furthermore, Keerthi et al. (2015) documented not only the important role of epistasis but also significant bias in the estimates of both σ^2_A and σ^2_D for most of the traits investigated. It is therefore not advisable to ignore epistasis in studies designed to estimate σ^2_A and σ^2_D controlling quantitative traits. Identification and non-inclusion of the genotypes that contribute significantly to epistasis could be a better strategy to obtain unbiased estimates σ^2_A and σ^2_D. Selection based on unbiased estimates σ^2_A and σ^2_D is expected to be reliable and effective. Alternatively, one or two cycles of bi-parental mating in the F_2 generation is expected to dissipate epistasis and selection will be effective (Chandrakant et al. 2015).

8.9 Breeding for Hyacinth Bean Improvement

Hyacinth bean has evolved as a highly-photoperiod-sensitive crop requiring long-nights (short-days) for switching over from a vegetative to a reproductive phase (Ayyangar and Nambiar 1935; Kim and Okubo 1995; Kim et al. 1992; Schaaffhausen 1963; Shivashankar and Kulkarni 1989; Viswanath et al. 1971). Most varieties grown by Indian and African farmers are landraces which are highly-photoperiod sensitive (PS) and display indeterminate growth habit. Indeterminacy is advantageous for subsistence production of hyacinth bean as it enables harvesting of pods in several pickings ensuring continuous availability for a longer time. However, the market-led economy has necessitated production of hyacinth bean throughout the year and development of cultivars with synchronous pod-bearing ability to enable single harvest, which is possible only from photoperiod-insensitive cultivars (PIS) with a determinate growth habit (Keerthi et al. 2014b, 2016). Hence, major emphasis/objective of hyacinth bean breeding has been to develop PIS determinate cultivars. When using PIS cultivars, farmers can control the date of flowering, and hence maturity, simply by either varying the sowing date or choosing cultivars with different heat-unit requirements. However, selection for photoperiod insensitivity most often results in reduced vegetative phase, fewer braches, racemes and pods and hence reduced economic product yield. Although yields of such PIS varieties could be maximized by high-density planting (Shivashankar and Kulkarni 1989; Viswanath et al. 1971), developing PIS varieties with a minimum of 45 days from seedling emergence to early blooming would enable vegetative growth adequate enough to produce an acceptable economic product yield, even under normal density of planting as is practiced for PS cultivars (Keerthi et al. 2016).

Most of the improvement work on *typicus* and *lignosus* types is concentrated in India. Desired qualities in improved cultivars are high yield, short duration, determinate growth habit, day-length neutrality, uniform maturity and disease and pest resistance (Ramesh and Byregowda 2016). In Bangladesh, hyacinth bean breeding is being carried out in Mymensingh (Alam and Newaz 2005; Arifin et al. 2005). These programs are aimed at developing improved photoperiod insensitive determinate pureline varieties for year-round production of hyacinth bean for food use. On the other hand, in India at the Indian Grass Land and Fodder Research Institute (IGFRI) (Magoon et al. 1974) and in Australia (Whitbread and Pengelly 2004), hyacinth bean breeding programs are focused on developing pureline varieties for fodder use. In Australia, the strategy is to combine the traits of widespread forage variety Rongai with those of African wild perennial germplasm accessions (Whitbread and Pengelly 2004).

Development of pureline varieties is the major breeding option in hyacinth bean since it is a predominantly a self-pollinated crop (Chaudhury et al. 1989; Kukade and Tidke 2014) lacking pollination control systems. As in the case of other grain legumes, pedigree breeding is the preferred method of developing pureline varieties in hyacinth bean. Some varieties developed for food and fodder use in India, China, Australia and the USA are summarized in Tables 8.6 and 8.7 (Ramesh and Byregowda 2016).

Of the several biotic stresses, anthracnose and dolichos yellow mosaic virus (DVMV) diseases and pod borers (*Heliothis armigera* and *Adisura atkinsoni*) and bruchids (*Callosobruchus theobrome*), are major biotic production constraints in hyacinth bean (Ramesh and Byregowda 2016). While pod borers cause damage in the field, bruchids cause damage both in the field and in storage. Losses to pod borers and bruchids can be up to 100%. Breeding for resistance to these insect pests is currently limited to screening and identification of resistance sources in germplasm and breeding lines. Jagadeesh Babu et al. (2008) identified germplasm accessions such as GL 1, GL 24, GL 61, GL 69, GL 82, GL 89, GL 196, GL 121, GL 135, GL 412, and GL 413 with <10% insect damage as resistant to pod borers (*Heliothis armigera* and *Adisura atkinsoni*) and bruchids (*Callosobruchus chinensis*) based on field screening of 133 germplasm accessions. Based on laboratory screening of 28 selected germplasm accessions, Rajendra Prasad et al. (2013) identified resistant accessions, GL 77, GL 233 and GL 63 with least seed damages of 13.4, 14.69 and 18.34%, respectively. The germplasm accession GL 187 was identified as resistant to *Helicoverpa armigera, Adisura atkinsoni* and bruchids infestation (Rajendra Prasad 2015). In another study at UAS, Bengaluru, antixenosis and antibiosis mechanisms of resistance are highlighted against *Helicoverpa* and germplasm accessions GL 233, GL 426, GL 357 and GL 187 which were found moderately tolerant (Rajendra Prasad 2015).

Dolichos yellow mosaic virus (DYMV) is characterized by yellow to bright yellow patches and vein clearing on leaves (Maruthi et al. 2006); it is caused by the gemini virus and transmitted by whiteflies (Capoor and Verma 1950). The disease causes up to 80% crop loss (Muniyappa et al. 2003). As is the case with insect pests, breeding hyacinth bean for DYMV resistance is confined to identification of resis-

Table 8.6 Summary of hyacinth bean grain purpose varieties developed for commercial production

Varieties	Pedigree	Location	References
Hebbal Avare (HA) 1	Photoperiod sensitive local land race × photoperiod insensitive red *typicus*	University of Agricultural Sciences (UAS), Bengaluru, India	Viswanath et al. (1971)
HA 3	HA 1 × US 67–31 (an introduction from USDA	UAS, Bengaluru, India	Shivashankar et al. (1975)
HA 4	HA 3 × CO 8 (*typicus*, photoperiod insensitive	UAS, Bengaluru, India	Hiremath et al. (1979) and Mahadevu and Byregowda (2005)
Selections 1 & 2	Not reported	Indian Institute of Horticulture Research (IIHR), Bengaluru, India	Anon (1988)
Koala	Selection from accession introduced from France to Australia as Q 6680	Australia	Holland and Mullen (1995)
IPSA Seam -1 & IPSA Seam -2	Not reported	Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh	Rokhsana et al. (2006)
Xiangbiandou 1	Not reported	China	Peng et al. (2001)
RioVerde	Not reported	USA	Smith et al. (2008)

Source: Ramesh and Byregowda (2016)

Table 8.7 Summary of hyacinth bean forage varieties developed for commercial production

Varieties	Pedigree	Location	References
IGFRI -1- S- 2214 and IGFRI-1-S-2218	Not reported	IGFRI, India	Magoon et al. (1974)
Rongai	Pureline selection from germplasm accession, CPI 17883 introduced from Kenya	Australia	Wilson and Murtagh (1962)
Endurance	Rongai × African wild perennial germplasm accession, CPI 24973	Australia	Liu (1998)
Highworth	Pureline selection from germplasm accession, CPI 30212 introduced from south India to Australia	Australia	Liu (1998)

Source: Ramesh and Byregowda (2016)

tance sources. Singh et al. (2012) identified accessions VRSEM 894, VRSEM 887 and VRSEM 860 as resistance to DYMV among 300 germplasm accessions.

Hyacinth bean has better inherent capacity to withstand moisture stress than other legumes such as cowpea, horse gram, etc. (Ewansiha and Singh 2006; Maass et al. 2010; Nworgu and Ajayi 2005) and adapt to acidic (Mugwira and Haque 1993) and saline soils (Murphy and Colucci 1999). With its deep root system, hyacinth bean is not only drought tolerant (Cameron 1988; Hendricksen and Minson 1985; Kay 1979), but also has the ability to harvest soil minerals which are otherwise unavailable to annual crops (Schaaffhausen 1963). However, research on breeding hyacinth bean for resistance to abiotic stresses is limited. In the event of the imminent extremes of abiotic stresses driven by climate change, hyacinth bean would be a better alternative to more popular legumes. Thus, breeding and enhancing the economic value of hyacinth bean would provide a competitive edge to hyacinth bean producers. In this backdrop, hyacinth bean is regarded as one of the promising future crops for sustainable agricultural production.

8.10 Application of Genomic Tools

8.10.1 Molecular Genetic Diversity

The use of genomic tools such as DNA markers in hyacinth bean breeding is at an early stage due to their unavailability in large numbers. Nevertheless, independent marker systems based on sequence information such as RAPD and AFLP have been used to detect and characterize genetic variation among germplasm accessions and breeding lines. Literature on the use of DNA markers in analysis of genetic diversity is summarized in Table 8.8; it suggests the presence of ample variation in the gene pool of hyacinth bean.

DNA marker allele-based variation present in germplasm would be useful for determining whether morphometric traits-based variation reflect variations at DNA sequence level as well. It would also provide information on the population structure, allelic richness and parameters that specify diversity among germplasm to help breeders to choose the appropriate genetic resources for cultivar development more effectively. Most studies on genetic diversity analysis are based on RAPD and AFLP. However, the information obtained from these markers is not reliable due to poor reproducibility. Hence, sequence dependent simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) are highly preferred by researchers owing to their simple inheritance and amenability for automation and high reproducibility. SSR marker assay helps to understand genetic relationship among germplasm accessions/breeding lines, selection of parents for hybridization, organization of variation in germplasm accessions and identification of cultivars (Benabdelmouna et al. 2001).

Table 8.8 Summary of DNA marker-based genetic diversity analysis in hyacinth bean

Genetic material used	Marker used	References
CSIRO: 40 accessions	RAPD	Liu (1996)
Mapping population (cross of 2 CSIRO accessions)	RFLP, RAPD	Konduri et al. (2000)
Bangladesh/Japan germplasm +60 CSIRO accessions	RAPD	Sultana and Ozakiy (2000)
Mapping population for comparative mapping with mung bean (*Vigna radiata)*	RFLP	Humphry et al. (2002)
103 CSIRO accessions	AFLP	Maass et al. (2005)
11 varieties from Hunan province of China	RAPD	Tian et al. (2005)
12 landraces from southern India	RAPD	Gnanesh et al. (2006)
28 accessions + Tanzanian landraces	AFLP	Tefera (2006)
30 germplasm accessions of USDA	SSR	Wang et al. (2007)
62 landraces collected from southern India and core collection accessions	AFLP, SSR	Venkatesha et al. (2007)
47 accessions of USDA	SSR	Wang et al. (2007)
40 accessions from India	AFLP	Patil et al. (2009)
10 insect tolerant and susceptible landraces from India	RAPD	Sujithra et al. (2009)
Mapping population from cross of 2 Chinese accessions	RAPD	Yuan et al. (2009)
30 Indian accessions	RAPD	Rai et al. (2010)
22 accessions from India	AFLP	Venkatesh et al. (2010)
11 genotypes of hyacinth bean	RAPD	Biswas et al. (2012)
50 Kenya accessions	AFLP	Kimani et al. (2012)
13 Kenyan germplasm	SSR	Shivachi et al. (2012)
24 hyacinth bean accessions collected from China and Africa	EST-SSR	Guwen Zhang et al (2013)
36 hyacinth bean accessions	SSR	Laxmi et al. (2016)

8.10.2 Cross Legume Species/Genera Transferability of Markers

The use of transferable cross-species/genera SSR markers is an alternative strategy to ensure the availability of markers in genomic resource-limited crops such as hyacinth bean. Taking a clue from several successful examples of cross-transferability of SSR markers, Yao et al. (2012) demonstrated that all tested EST-SSR markers from soybean were cross-transferable to hyacinth bean. At the UAS, Bengaluru, transferability of SSR markers from cowpea, soybean, *Medicago truncatula,* green gram and chickpea to hyacinth bean were examined (Shivakumar and Ramesh 2015). Wang et al. (2004) also reported transferability of 1/3 (30.78%) of the SSR primers from *Medicago*, soybean, cowpea and groundnut to hyacinth bean. Venkatesh et al. (2007) examined the transferability of AFLP and EST-derived markers from a range of legumes to hyacinth beans collected from India, Australia

and Ethiopia. The results suggested that there is a good source of legume-related primers in databases from well-characterized species that can readily be used in diversity and genome analysis of hyacinth bean. Uday kumar et al. (2016) used 100 cross-legume species/genera SSR markers (65 from soybean, 12 from medicago, 14 from green gram, 9 from chickpea) to check parental polymorphism and found 18 of them (41.86%) were polymorphic between the parents of RILs. A total of 275 cross-legume species/genera SSR markers were examined for their transferability to hyacinth bean (Shivakumar et al. 2016). They found that 126 of 275 cross-legume species/genera SSR markers (45.81%) were transferable to hyacinth bean. The extent of transferability of SSR markers based on simple di−/tri-nucleotide repeat motifs was higher than those based on penta−/tetra−/complex nucleotide repeat motifs.

8.10.3 Mapping Genomic Regions Controlling Economically Important Traits

Conventional hyacinth bean breeding based on phenotype-based selection for yield and its component traits is rather less effective owing to their crop-stage specific expression, complex inheritance and significant cross-over genotype-by-environment interaction. DNA markers owing to their crop stage non-specificity, simple inheritance and environment neutrality have proven to be powerful surrogates of such difficult-to-select traits. Besides analysis of genetic diversity, DNA markers have also been used to develop a linkage map, a prelude to identifying DNA markers linked to genomic regions controlling target traits. DNA marker-assisted identification and introgression of QTLs into elite genetic background is expected to complement phenotype-based selection and help enhance the pace and efficiency of hyacinth bean breeding.

Konduri et al. (2000) were pioneers in the construction of a linkage map of hyacinth bean consisting of 127 RFLP and 91 RAPD loci in 119 F_2 population (Rongai× CPI 24973) of hyacinth bean. The map comprised 17 linkage groups (LG) and covered 1610.0 cM, with an average inter-marker distance of 7.0 cM. Later, Humphry et al. (2002) compared a linkage map of mung bean with hyacinth bean using a common set of 65 RFLP probes. A significantly high level of homology was noticed between mung bean and hyacinth bean.

In order to map the QTLs for various agronomic and phonological traits in hyacinth bean, Yuan et al. (2009) designed an F_2 population derived from the contrasting parents-Meidou 2012 and Nanhui 23. The molecular map was constructed with 131 loci (122 RAPD and 9 morphological markers) covering 1302.4 cM and 14 linkage groups. A total of 41 main effect QTLs (19 for fruit traits and 22 for growth phonological traits) were detected on 11 linkage groups. They also reported stable QTLs for pod length, pod diameter, pod fresh thickness, flowering time, podding time and harvest maturity period. Yuan et al.

(2011) also identified QTLs associated with various quantitative traits such as inflorescence length, peduncle length from branch to axil, peduncle length from axil to lowermost flowering node, rachis length, node number of inflorescence, rachis internode length, node order of the first inflorescence and node order of lowest inflorescence. In another study at UAS, Bangalore, 91 SSR markers out of 465 in-house developed hyacinth bean specific SSR markers were found to be polymorphic between the parents (HA 4 and CPI 60125) of HACPI 6-derived RIL population. The linkage map was constructed using genotypic data of 58 polymorphic markers in HACPI 6-derived 109 RIL populations; 58 markers were anchored on to 11 linkage groups (LGs). The total length of the map spanned 2008.55 cM of the hyacinth bean genome with an average marker density of 34.63 cM. The linkage map length varied from 118.77 cM (LG 10) to 261.06 cM (LG 4). A total of 5 QTLs, 1 controlling days to 50% flowering, 2 each controlling dry seed yield plant^{-1} and test weight were detected (Chandrakant 2018). Furthermore, the linkage of markers with QTLs controlling days to 50% flowering; raceme length; pods plant^{-1} and dry seed yield plant^{-1} in HACPI 6-derived RIL population was confirmed in HACPI 3-derived RIL population. However, it is suggested to saturate the linkage map of HACPI 6-derived RIL population for high-resolution mapping of QTLs controlling productivity per se traits for use in marker-assisted selection after their validation (Chandrakant 2018).

Association mapping (AM) is an alternative method of QTL discovery which exploits historic linkage disequilibrium (LD) present in natural populations. AM is effective in self-pollinated crops such as hyacinth bean as LD extends over a longer genomic distance driven by a low rate of recombination and thereby requiring fewer markers for exploring marker-trait associations. Vaijayanthi (2016) evaluated a core set of hyacinth bean germplasm consisting of 64 accessions for 9 quantitative traits (QTs) and genotyped it using 234 SSR markers. Substantial diversity was observed among the core set accessions at loci controlling QTs and 95 of the 234 SSR markers were found to be polymorphic. The structure analysis based on 95 polymorphic SSR markers revealed weak population structure, low magnitude of the estimates of fixation indices, which in turn indicated low possibility of false discovery rates in marker-QTs association. The marker alleles' scores were further regressed onto phenotypes at 9 QTs following general linear model (GLM) and mixed linear model (MLM) for exploring marker-QTs associations. A few of the significantly associated markers such as KTD 200 for days to 50% flowering, KTD 273 for fresh pod yield plant^{-1} and KTD 130 for fresh pods plant^{-1} explained $\geq$10% of the trait variations. These linked SSR markers are suggested for validation for their use in marker-assisted hyacinth bean improvement programs.

Marker-assisted selection (MAS) is most effective for improvement of traits controlled by a few large effect genes. QTs are controlled by both large and small effect QTLs. Genomic selection (GS), proposed by Meuwissen et al. (2001), captures both small and large effects QTLs (Bernardo and Yu 2007; Bernardo 2010) and is emerg-

ing as a powerful alternative to MAS for improving QTs. GS is defined as the selection of a genotyped-only breeding population (BP) of individuals based on their genomic breeding values (GBVs) predicted using marker effects estimated by fitting statistical models calibrated to both genotyped and phenotyped populations referred to as a training population (TP), preferably related to a breeding population (BP). Recently GS was attempted in hyacinth bean (Chandrakant 2018). A total of 109 RILs derived from HACPI-6 were used as the training population (TP). The 2 year phenotypic data (BLUPs) and genotypic data (91 SSR markers) of TP were used to calibrate the ridge regression (RR) to estimate the effects of 91 SSR markers. The study necessitated an optimizing prediction model, composition and size of the training population and marker density for implementing genomic selection in hyacinth bean.

Application of modern crop improvement techniques like plant tissue culture, genetic engineering and omic-driven technologies are in their infancy in hyacinth bean. However, genetic manipulation based on such modern techniques can add a competitive edge and direction to selective breeding programs to evolve better hyacinth bean varieties.

8.11 Conclusion and Prospects

Despite being a multipurpose adaptable legume crop, hyacinth bean is considered an underutilized crop owing to the small area under cultivation and limited efforts towards its genetic improvement. However, it can contribute enormously to food security and better nutrition, ecosystem stability and cultural diversity. It is often called the *poor-man's* bean, a kind of confirmation of its low-input production and an essential contribution to the human diet in certain regions. Conservation and utilization of plant genetic resources is the key to attain sustainable hyacinth bean productivity and production. Systematic evaluation of germplasm resources, identification of trait-specific accessions, unraveling the inheritance of productivity traits and the use of both conventional and genomic tools to combine desired traits will provide competency in hyacinth bean improvement programs. The SSR and SNP markers should be routinely used for genomic selection to complement phenotype-based selection. Furthermore, genome sequencing and other omic approaches help to identify novel and useful genes and their introgression into an elite agronomic background.

Appendices

Appendix 1: List of Major Institutes Engaged in Research on Hyacinth Bean

Institution	Specialization and research activities	Website
University of Agricultural Sciences (UAS), Bengaluru, India	Germplasm collection, Conservation and utilization	www.lablab.org
	Conventional and marker-assisted hyacinth bean improvement	www.uasbangalore.edu.in
	Breeding for pod borer resistance	
CSIRO, Australia	Breeding hyacinth bean for forage purpose	www.csiro.au
IITA, Nigeria	Germplasm collection, Conservation and utilization	www.iita.org
	Breeding for biotic and abiotic stress	
Bangladesh Agriculture Research Institute (BARI), Bangladesh	Hyacinth bean improvement using conventional and molecular tools	www.bari.gov.bd
Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India	Breeding hyacinth bean for vegetable purpose	www.icar.org.in
		www.iivr.org.in
Indian Institute of Horticulture Research (IIHR), Hesarugatta, Bangalore, India	Improvement of *Lablab purpureus* var. *typicus* and of *L. purpureus* var. *lignosus*	www.iihr.res.in
		www.icar.org.in
Tamil Nadu Agriculture University, India	Hyacinth bean improvement using conventional and molecular tools	www.tnau.ac.in
Kenya Agriculture Research Institute, Kenya, Africa	Germplasm collection, evaluation and breeding for African countries	www.kalro.org
		www.ilri.org
USDA-ARS,USA	Hyacinth bean conservation and improvement	www.ars.usda.gov

Appendix 2: Genetic Resources of Hyacinth Bean

Cultivar	Cultivation location
HA-1, HA-3, HA-4,Co-1, Co-2, Arka-Vijay, Kalyanpur type-2, Jawahar Sem-37, Deepali, Wal Konkan-1, Hima, Grace, Pusa sem1 & 2	India
CPI 30212 (High worth), Rongai, CPI 24973 (Endurance)	Australia
Local varieties and landraces	Bangladesh
Amora-guaya, Gerenga, Njahe	Africa

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