

Breeding perspectives of snap bean (*Phaseolus vulgaris* L.)

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Received: August, 2014 / Accepted: April, 2015

Abstract

Snap bean (*Phaseolus vulgaris* L.), a type of common bean whose fresh fleshy tender pods with reduced fibre content in pod-wall, is an important legume vegetable usually used for cooking or canning. Common bean has originated in southern Mexico to Central America (Mesoamerica) and Ecuador-Peru-Bolivia region is the secondary centre of origin, while snap bean is developed from Andean genetic resources in the southern Europe during 19th century. More than 260000 accessions of different species of *Phaseolus* are being maintained in >245 gene banks of various countries, moreover CIAT Colombia has the mandate for global germplasm collection and conservation of *Phaseolus* species and hosts the world's largest and most diverse collections. Globally, the breeders mainly focus on development of varieties having high yield potential; wider adaptability; earliness, better pod quality (bright and uniform colour, non-stringy, slender, long and straight, cylindrical, smooth, small seeded, less inter-locular cavitations and more flavour); tolerance to heat stress, particularly high night temperature; and resistance to major diseases such as bean common mosaic virus, bean golden mosaic virus, common bacterial blight, halo blight, *Sclerotinia* rot, anthracnose, angular leaf spot and root knot nematode. The favourable genes and QTL for various traits of economic importance are scattered across cultivated and wild populations in the primary, secondary, tertiary and other gene pools of common bean, and the efforts are being made to integrate two- or multi-tiered breeding approaches for broadening the genetic base, and introgressing and pyramiding the resistance genes and QTL.

Keywords: Snap bean, *Phaseolus* spp, breeding, improvement, legume vegetable, biotic and abiotic stresses

Introduction

Common bean (*Phaseolus vulgaris* L.) is an important

legume which is a rich source of protein, vitamins, minerals, and fibre, especially for the poorer populations of developing countries. The principal products of common beans, on the basis of uses, are dry beans (seeds harvested at complete maturity), shell beans (seeds harvested at physiological maturity) and snap beans (tender pods with reduced fibre harvested before the seed development phase). The later one is also known as French bean, garden bean, green bean, edible podded bean, string bean, fresh bean or vegetable bean. As the name implies, snap beans break easily when the pod is bent, giving off a distinct audible snap sound. The pods of snap beans (green, yellow and purple in colour) are harvested when they are rapidly growing, fleshy, tender (not tough and stringy), bright in colour, and the seeds are small and underdeveloped (8 to 10 days after flowering). After that period, excessive seed development reduces quality and the pod becomes fibrous, pithy and tough, and loses its bright colour. Snap bean seeds may also be used in dry static like the dry bean types. In that case pinto, kidney, pink, small red, etc. terms are used. In India, the dry bean type varieties are known as rajmash/rajmah. Common beans display a wide range of growth habits from bush determinate to pole indeterminate types. Bush types are the most widely grown and are a relatively short duration crop; but on the other hand, in smallholder agriculture or in kitchen garden where land is scarce, labour-intensive high-yielding climbing beans getting popularity now-a-days. Dry bean is the largest pulse crop in the world with 23.60 mt of annual production grown on 29.29 mha area; and the top ten producing countries are Myanmar (3.90 mt), India (3.63 mt), Brazil (2.79 mt), China (1.46 mt), USA (1.45 mt), Tanzania (1.20 mt), Mexico (1.08 mt), Kenya (0.61 mt), Ethiopia (0.46 mt) and Rwanda (0.43 mt). Moreover, snap beans' global annual production and area is about 20.74 mt and 1.54 mha, respectively with maximum production in China (16.20 mt) followed by Indonesia (0.87 mt), India (0.62 mt), Turkey (0.61 mt), Thailand (0.31 mt), Egypt (0.25 mt),

Spain (0.17 mt), Italy (0.14 mt), Morocco (0.13 mt) and Bangladesh (0.09 mt) [FAO 2012].

Origin, Evolution and Domestication

The genus *Phaseolus* is originated in the American continent and a large number of its species is found in Mesoamerica (Delgado-Salinas 1985; Freytag and Debouck 2002; Acosta-Gallegos *et al.* 2007). Moreover, common bean has originated in southern Mexico to Central America (Mesoamerica), while Ecuador-Peru-Bolivia region is the secondary centre of origin (Gepts 1998; Bitocchi *et al.* 2012; Bellucci *et al.* 2014). The wild beans from South America originated through migration from the Mesoamerica populations. The hypothesis of Mesoamerican origin of the common bean is supported by the observations that the closest relatives of wild *P. vulgaris* are distributed throughout Mesoamerica (Schmit *et al.* 1993; Freytag and Debouck 2002; Delgado-Salinas *et al.* 2006). Additionally, the higher diversity found in the Mesoamerican compared with the Andean gene pool as revealed by phaseolin types, allozyme alleles and molecular markers (Gepts *et al.* 1986; Koenig and Gepts 1989; Koenig *et al.* 1990; Becerra-Velasquez and Gepts 1994; Chacon *et al.* 2007) also support a Mesoamerican origin.

It is the most widely distributed and consumed legume species of the genus *Phaseolus* which comprised of about 70 species (Freytag and Debouck 2002) and has contributed to human welfare with five cultigens domesticated in pre-Columbian times: common bean (*P. vulgaris* L.), year bean (*P. dumosus* Macfad.), runner bean (*P. coccineus* L.), tepary bean (*P. acutifolius* A Gray) and lima bean (*P. lunatus* L.), and with a few additional species that show signs of incipient domestication (Delgado-Salinas *et al.* 2006). Among the five domesticated species, *P. vulgaris* is the most important economically that accounts for more than 90% of the cultivated *Phaseolus* worldwide (Singh 2001; Acosta-Gallegos *et al.* 2007). Each domesticated species constitutes a primary gene pool with its wild ancestral forms. Secondary and tertiary gene pools may exist for all the domesticated species, depending on the phylogenetic events that lead to the formation of the biological species (Debouck 1999).

The current distribution of the wild common bean encompasses a large geographical area: from northern Mexico to north-western Argentina. Prior to domestication, wild *P. vulgaris* had diverged into two major gene pools on the basis of geographic distribution: (i) the Mesoamerican i.e. Middle America and (ii) the Andean i.e. Andean South America (Figure 1; Gepts 1998; Bitocchi *et al.* 2012) which can be distinguished

at the morphological, biochemical and molecular levels (Gepts *et al.* 1986; Singh *et al.* 1991a), and also display partial reproductive isolation caused by F_1 lethality (Singh and Gutierrez 1984; Gepts and Bliss 1985). With the exceptions, no successful recombination has occurred between the two major gene pools. A first exception is provided by Chilean landraces which showed signs of introgression from the Mesoamerican gene pool based on phaseolin seed protein and allozymes (Paredes and Gepts 1995). The second exception is evolution of snap bean cultivars. Although they originated in the Andean gene pool, many varieties are actually intermediate between the two gene pools as evidenced by RAPD markers (Skroch and Nienhuis 1995). This intermediate position may be attributed to recent breeding efforts aimed at introducing disease resistance from the Mesoamerican gene pool into the snap bean cultivars (Gepts 1998). While only these two major gene pools are recognized in the domesticated population, the geographical structure of the wild form of the common bean is more complex, with an additional third gene pool that is localized between Peru and Ecuador, and characterized by a specific storage seed protein, phaseolin type I (Debouck *et al.* 1993; Kami *et al.* 1995). Generally, the Mesoamerican gene pool possesses higher content of lectin, Ca, P, S and Zn than the Andean gene pool but lower phaseolin and Fe (Islam *et al.* 2002). Further, the two major gene pools in *P. vulgaris* have been divided into six races (Mesoamerican gene pool: Mesoamerica, Durango and Jalisco; and

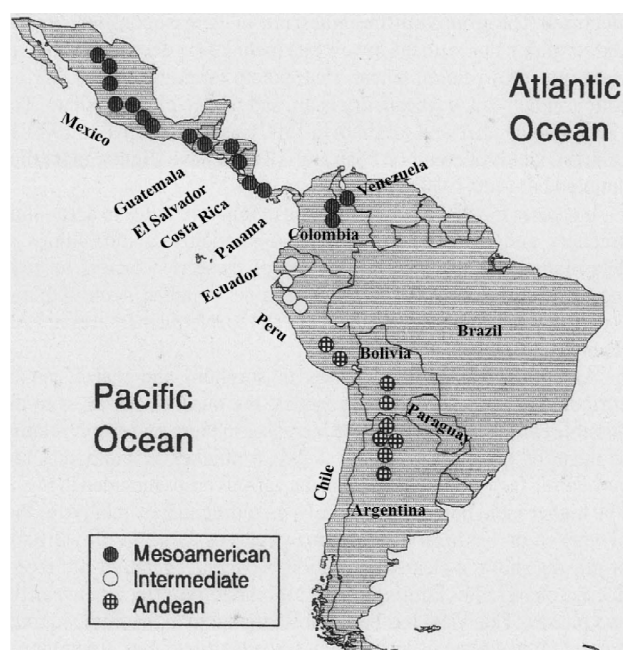


Figure 1: Distribution of wild *Phaseolus vulgaris* in Latin America (Gepts 1998)

Andean gene pool: Nueva Granada, Peru and Chile) as the members of each race share distinct morphological, agronomic, physiological and biochemical traits; and differ from other races in allelic frequencies of genes controlling these traits (Singh *et al.* 1991a; Kelly 2004). The divergence between two gene pools provides both an opportunity: for breeders to broaden the genetic basis of bean classes, and a challenge: to actually transfer quantitative traits from one gene pool to the other. Usually, the success rate has been quite low (Welsh *et al.* 1995; Johnson and Gepts 1999); but interracial crosses within the same gene pool have been the most effective strategy to improve the yield, adaptability, quality and resistance of common bean (Kelly *et al.* 1998). The changes under domestication are typically loss of pod dehiscence (dispersal ability) and seed dormancy; perennial to the annual life form; and a great change in seed size correlated with modified shoot architecture. Further, the stems tend to be thicker, leaves larger, branches fewer, short-days to day-neutral photoperiod, longer to shorter growing period, indeterminate to determinate growth habit (compact growth habit), the number of nodes may be reduced and shortened internode length. Pod dehiscence is characterized by the presence of fibres in the pods, both in the sutures (string) and in the walls (parchment). Loss of these fibres leads to indehiscence of the pods and lack of seed dispersal at maturity. This process culminates in evolution of self-supporting plants; and has also led to appearance of a vast variety of seed sizes, shapes and colours.

Snap bean cultivars have slender, long and cylindrical pods with greatly reduced fibre, thickened pod walls and smaller seeds. The extremely low pod fibre and pod shape could be used to morphologically distinguish between dry and snap beans in the archaeological records. With the available literatures, no such analyses have been reported. One reason for the lack of evidence is that the characteristic seed shape and low pod fibre may be a consequence of recent selection and breeding efforts. In addition, low-fibre in the pods may not persist well in the archaeological records. In a survey of common bean accessions available at International Centre for Tropical Agriculture (CIAT), Singh (1989) found very few examples of possible landrace of snap beans from the Mesoamerican and the Andean gene pools. Snap beans, if present at all in pre-Colombian times, were probably rare and subject to the capriciousness of the preservation process. Information on bean genetics may suggest that snap beans were derived from dry beans because more genetic changes were required to derive it from the wild beans compared to dry beans. Preference for the pods that remain edible

later into maturity would have selected for genes causing reduced fibre content. Genes that code for fleshy, tender and succulent pods would have been selected for as well (Myers and Baggett 1999). Based on phaseolin type, the snap beans are derived from the Andean centre of origin (Brown *et al.* 1982; Gepts *et al.* 1986). However, in some contemporary snap bean cultivars, the divisions between Andean and Mesoamerican centres of origin have been blurred from crossing between the two groups as shown by molecular markers (Skroch *et al.* 1992; Skroch and Nienhuis 1995). In the 19th century, the French made green beans a household vegetable, with the name haricot verts branding them as “French bean” in the minds of many Europeans (Andrews 2013). The traditional snap bean type of southern Europe ‘Romano’ (Flat pod beans) may be one of the predecessors to the contemporary snap bean. However, the stringless trait was discovered in 1870 by CN Keeney while working in Le Roy, New York; called the “father of the stringless bean”. He established a seed company at Le Roy as an outgrowth of his interest in green beans. Since then it is widely incorporated to develop new cultivars of snap bean (Myers and Baggett 1999; Ram 2005; Andrews 2013).

Taxonomy

Common beans belong to the family Fabaceae, order Fabales, sub-class Rosidae, class Magnoliopsida (dicotyledons), division Magnoliophyta (flowering plants) and super-division Spermatophyta (seed plants). It is a true autogamous diploid species with 22 chromosomes ($2n=2x=22$) and a haploid genome size is estimated to be between 587–637 Mbp (Arumuganathan and Earle 1991; Bennett and Leitch 2010). There are five cultivated species of genus *Phaseolus* (Table 1; Debouck 1988, 1991, 1999):

Classification

The common bean cultivars, rather than being bred in a systematic manner, were selected from variations generated by mutations and chance outcrosses in the older cultivars. These were grouped in three major distinct cultivars: snap beans, mature shell beans and dry beans. On the basis of growth habit, the common beans have been classified into two broader group viz. bush types and pole types; both types have green, wax and purple coloured pods with or without fibres.

Varieties: The snap bean genotypes comprise a group of common beans that have been selected for succulent tender pods with reduced fibres and strings; while common beans usually for seed characteristics (colour, shape and size). Names such as French bean, haricot

Table 1: Cultivated species of genus *Phaseolus* and their eecological requirements.

<i>Phaseolus</i> species	Common name	Altitude (m)	Temperature (°C)	Precipitation (mm/ year)	Growth cycle (day)
<i>P. vulgaris</i> L.	Common bean, dry bean, shell bean, snap bean, French bean	50–3000	14–26	400–1600	70–330
<i>P. polyanthus</i> Greenman	Yearlong bean	800–2600	14–24	1000–2600	110–365
<i>P. coccineus</i> L.	Runner or scarlet runner bean	1400–2800	12–22	400–2600	90–365
<i>P. acutifolius</i> A. Gray	Tepary bean	50–1900	20–32	200–400	60–110
<i>P. lunatus</i> L.	Lima bean (large seeded), sieve bean (small seeded), butter bean, Madagascar bean	50–2800	16–26	0–2800	90–365

bean, green bean, string bean, edible podded bean, wax bean or Romano (also known as Italian or Flat pod beans) describe subgroups or market classes of snap bean. Blue Lake Green Beans, varieties of snap bean, are named for the area in which they were developed in the early 1900s, the Blue Lake area near Ukiah, California, USA. They were originally developed for canning. By the mid-to-late 1920s, the beans had been developed into stringless bean for use as a green bean, probably in Oregon, USA. The Tendergreen variety of snap bean came on the scene in 1925 (Andrews 2013). The snap beans, especially vegetable-type genotypes, are slender, long, fleshy, tender, soft, free from the fibrous layer found in the pod wall (inedible fibre/parchment) and contain fewer parchment strings (present along the both pod-sutures but especially strong on ventral side which is made up of lignified sclerenchyma cells) whose immature pods and seeds are consumed as vegetable (Singh *et al.* 2014). Moreover, Romano bean pods are green in colour with flat cross-sectional shape and relatively fibre-free. In contrast to the Romano, green beans have fleshy pods that are generally oval to round in cross-section. Wax bean pods have similar shape to green bean pods, but are pale yellow to golden, instead of green in colour, because chlorophyll is absent from the pods, petioles and young stems (Myers and Baggett 1999). The term string bean refers to the older cultivars of snap bean that had fibre in the pod suture, which had to be removed manually before cooking. The tender

pods of snap bean (yellow, green and purple in colour) are harvested when they are rapidly growing, bright in colour, fleshy with small seeds, generally about 9-12 days after flowering. After that period, excessive seed development reduces quality, and the pod becomes pithy, tough and loses its bright colour. The pod traits are perhaps the most important economic parameter of snap bean cultivars. The traits of importance include colour, pod shape, length, cross-sectional shape, straightness, smoothness, fibre content, inter-locular cavitation, rate of seed development and point of detachment (Silbernagel 1986; Myers and Baggett 1999). Based on plant growth habit and colour of immature tender pods, the snap beans are classified in to following groups (Table 2; Myers and Baggett 1999; Ram 2005; Singh *et al.* 2011, 2013, 2014; Andrews 2013):

Plant growth habit: Most cultivars and landraces grown in the highlands of Mexico, Central America and the Andes are often indeterminate in growth habit and highly sensitive to long photoperiods. However, photoperiod-insensitive genotypes of bush growth habit have been evolved during course of domestication and dissemination that allowed its spread in to non-traditional areas. Broadly, stem could be bush type or pole type depending upon growth and twining habits. Stem growth habit is governed by three genes such as L/l (long stem > short stem), A/a (indeterminate growth habit > determinate growth habit) and T/t (twining tendency >

Table 2: Classification of snap beans and their cultivars

Growth habit and pod colour	Cultivars/promising genotypes
1. Dwarf or bush types	
1 Green pods	Contender, Sparton Arrow, Premier, Tendergreen, King Green, Processor, Tendercrop, Topcrop, Cascade, Bountiful*, Plentiful*, Green Ruler*, GV 50, Quick Freezing, Siegerin, Prinsa, Lancet, Bush Blue Lake 92, GP-72-122, Bush Blue Lake, Blue Lake 47, Pusa Parvati, VL Boni 1, Arka Komal, Arka Suvidha, Arka Sarath, Arka Anoop, Arka Bold, Pant Anupama, Pant Bean 2, Kashi Sampann, Kashi Rajhans, VRFBB-91
2 Wax pods	Cherokee Wax, Uranus, Golden Ruler*, SUG131, Natal Sugar
3 Purple pods	Red Swan
4 Streaked	Dragon's Tongue
2. Climbing or pole types	
1 Green pods	Canadian Wonder, Kentucky Wonder, Pusa Himlata, Green Lake, Onatra, Blue Lake, Romano*, Phenomenal Long Podded, IC593590, IC593591, IC593592, IC593593, IC593594, IC593595
2 Wax pods	Kentucky Wonder Wax, Yellow Wax, Yellow Romano*, Gold Marie, Neckargold,
3 Purple pods	IC595238, Purple King
4 Streaked	Rattlesnake

*Flat pod

Table 3: Growth habit in *Phaseolus vulgaris*

Growth habit	Type of growth habit	Gene	Remark
Bush determinate	Type-I growth habit	llaatt	Determinate compact growth habit.
Bush indeterminate	Type-II growth habit	L- aatt	Determinate prostrate growth habit.
Pole determinate	Type-III growth habit	L-A-tt	Indeterminate prostrate growth with well-developed branching, but low or non-existent of climbing ability.
Pole indeterminate	Type-IV growth habit	L-A-T-	Indeterminate with long vine and high climbing ability.

Table 4: Gene pools, protein and distribution of various races of *Phaseolus vulgaris*

S. No.	Race	Phaseolin*	cpDNA haplotype#	Distribution
A. Mesoamerican race (Middle American race)				
A1.	Mesoamerica	S, Sd, B	K, L, I, J	Tropical lowlands and intermediate altitudes of Mexico, Central America, Colombia, Venezuela and Brazil.
A2.	Durango	S, Sd	K, L, J	Semi-arid central and northern highlands of Mexico and South-western USA
A3.	Jalisco	S	L, K	Humid highlands of Central Mexico and Guatemala.
A4.	Guatemala	S	I	Highlands of Guatemala and Chiapas, Mexico.
B. Andean race (South American race)				
B1.	Nueva Granada	T	C	Intermediate altitudes of the northern Andes (Colombia, Ecuador, and Peru), also in Argentina, Belize, Bolivia, Brazil, Chile, Panama and few Caribbean countries.
B2.	Chile	T, C	C	Drier regions of lower altitudes in the southern Andes (southern Peru, Bolivia, Chile and Argentina)
B3.	Peru	T, C, H	C, K	Northern Colombian highlands to Argentina.

*Phaseolin seed protein electrophoretic type (Gepts *et al.* 1986, 1988; Gepts and Bliss 1986; Koenig *et al.* 1990; Singh *et al.* 1991b, 1991c). #Frequency of haplotypes in descending order from left to right; distribution of haplotypes based on the survey of 127 Mesoamerican and Andean landraces (Chacon *et al.* 2005).

non-twining tendency). Thus, the common bean cultivars have four prototypes with respect to their growth habits (Table 3; Ram 2005):

Races: Common bean and its wild relatives showed a wide geographical distribution found in Middle America for the Mesoamerican race and South America for the Andean gene pools, but greater amounts of genetic variation were found among the Mesoamerican population as compared to Andean gene pool (Gepts *et al.* 1988; Chacón *et al.* 2005; Acosta-Gallegos *et al.* 2007). Within the two domesticated gene pools, several eco-geographic races have been identified in each gene pool based on plant morphology, eco-geographic and ecological distribution, isozyme and molecular information (Table 4; Singh *et al.* 1991a, 1991b, 1991c; Acosta-Gallegos *et al.* 2007). Additionally, Beebe *et al.* (2000) indicated that the races Durango and Mesoamerica could be further subdivided in two sub-races; and a distinct race was separated from the Jalisco race, namely 'Guatemala race' that includes the climbers found in the highlands of Guatemala and Chiapas, Mexico (Chacon *et al.* 2005). A brief description of six races is as follows (Ram 2005):

Plant Genetic Resources

More than 260000 accessions of different species of *Phaseolus* have been collected and are being maintained in >245 gene banks of various countries (Table 5; FAO 2010), including about 2900 accessions at NBPGR, New

Delhi. CIAT, Cali, Colombia has the mandate for global germplasm collection and conservation of *Phaseolus* species. The Germplasm Bank of CIAT hosts the world's largest and most diverse collection, with more than 36000 *Phaseolus* materials, corresponding to 44 taxa from 110 countries. Majority of these collections belong to primary centre of origin in the Neotropics (Mexico, Peru, Colombia and Guatemala). Moreover, there are also important collections from Europe and Africa, and to a lesser extent from Asia (<http://isa.ciat.cgiar.org/urg/beancollection.do>). In addition to these, ICAR-IIVR, Varanasi, Uttar Pradesh is maintaining 214 accessions of various *Phaseolus* species (202 of *P. vulgaris* both bush and pole types, 9 of *P. lunatus*, 2 of *P. coccineus* and one of *P. acutifolius*). Despite the wide diversity, the genetic base of commercial cultivars of green bean market classes, particularly snap bean, is narrow (Kelly 2004).

Breeding Objectives

The breeding objectives describe the characteristics that have ability to improve the yield, quality, adaptability, and profitability the most. Major breeding achievements of snap bean have been the modification of the plant growth habit, pod traits, photo-insensitivity and seed sizes. The breeding objectives describe the characteristics that have ability to improve the yield, quality, adaptability, uniformity, better tolerance to various stresses and profitability the most. The over-

Table 5: Global germplasm collection of *Phaseolus* species at various gene banks (FAO 2010).

S. No.	Gene bank	Accession		Type of accession (%)				
		Number	% share	WS	LR	BL	AC	OT
1	CIAT, Cali, Colombia	35891	13.70	6	85	2	7	-
2	USDA-ARS NPGS, Washington, USA	14674	5.60	6	67	3	21	4
3	CNPAF-EMBRAPA, Brazil	14460	5.52	-	-	-	-	100
4	INIPAF, Mexica	12752	4.87	17	-	-	-	83
5	IPK, Germany	8680	3.31	1	66	4	28	1
6	ICGR-CAAS, China	7365	2.81	-	-	-	-	100
7	VIR, Russia	6144	2.35	-	22	20	3	55
8	BCA, Malawi	6000	2.29	-	100	-	-	-
9	RCA, Hungary	4350	1.66	-	70	<1	<1	30
10	LBN, Indonesia	3846	1.47	-	-	-	-	100
11	KARI-NGBK, Kenya	3534	1.35	<1	34	3	35	28
12	IPGR, Bulgaria	3220	1.23	-	32	-	<1	68
13	DENAREF, Ecuador	3102	1.18	2	6	17	<1	75
14	ISAR, Rwanda	3075	1.17	-	-	-	-	100
15	INIACRF, Spain	3038	1.16	-	98	<1	<1	1
16	Other gene banks (231)	131832	50.32	-	30	5	13	52
	Total	261963	100.00	2	39	4	10	45

WS: wild species; LR: landraces/old cultivars; BL: breeding lines; AC: advanced cultivars; OT: others (the type is unknown or a mixture of two or more types).

expression of stress tolerance antioxidant enzymes (SOD-superoxide dismutase, CAT-catalase, GPOX-guaiacol peroxidase, APX-ascorbate peroxidase, GPX-glutathione peroxidase, GR-glutathione reductase, MDAR-monodehydroascorbate reductase, DHAR-dehydroascorbate reductase and GST-glutathione S-transferase) could play an imperative role in improving the tolerance to the various abiotic and biotic stresses. Few efforts have been made to enhance the antioxidant enzymes in vegetable crops through conventional breeding (Singh *et al.* 2009, 2010a, 2010b).

Breeding for Economic Traits, Yield and Quality

Pod yield is a complex quantitative trait with low heritability, and hence subject to be influenced considerably by various kinds of environmental conditions and their aberrations. Because of the additional pod quality factors involved in tender pod yield of snap beans, yield becomes even more complex as compare to dry beans. In snap bean, pod yield, its quality and stability are the most important economic traits which are mainly dependant on the plant architectures, pod traits, and resistance to abiotic and biotic stresses. The plant traits include yield and all the factors that are components of yield such as hypocotyl diameter, growth habit, plant height, leaf number and size, number of primary branches, intermodal length, days to flower, duration of flowering, number of reproductive nodes, number of flowers and pods per node and per plant, rate of pod filling and harvest index. Whereas the pod characteristics comprise length, colour, sieve size (pod width measuring through ventral and dorsal sutures), thickness (measuring through sidewall to sidewall), cross-sectional shape, straightness (curvature),

smoothness, rate of seed development, stringiness on sutures, fibre content in pod wall, presence of interlocular cavitation, point of detachment, shape and length of spur (remnant of the style), internal colour and texture, and flavour. Moreover, yield stability could be achieved by incorporating genes resistance to biotic and abiotic stresses, and by breeding for wider adaptation i.e. least value of genotype \times environment interactions.

The growth habit is a basic characteristic of plant traits responsible for canopy geometry. Most of the original edible podded beans (snap beans) were pole type with climbing growth habit (type IV), but presently most of the commercial cultivars belong to bush growth habit (type I) as it is easier to handle and don't require any support system for training. Lodging resistance, especially for bush/determinate genotypes, depends on number of internodes, internode length, root system and stem thickness. Moreover, seed size, leaf number and leaf size have negative association with yield as well as pod quality of snap bean. Higher the seed size triggers the bumpiness too, an undesirable trait of snap bean. However, leaf number and leaf size are inversely correlated with pod number and seed size, respectively. An intermediate number of primary branches and node number (12-15) and internode length (3.5-4.5 cm); thick hypocotyl and stem; and strong deeper root systems favour higher pod yield along with better plant stand or lodging resistance. Earliness is an economically important trait in snap bean breeding. Its constituent traits days to flowering, nodes to flowering and days to pod maturity are largely controlled by response to temperature (Tip), photoperiod (Ppd and Hr genes) and developmental rate (White *et al.* 1996). ICAR-IIVR, Varanasi has recently identified a genotype 'VRFB-91'

whose pods are ready to harvest during first fortnight of December (Singh 2014).

The colour of pods shows genetic variation for hue, and its intensity, brightness and uniformity. Most of the snap bean cultivars have pods with green colour, but yellow (wax) and purple/red colour also found. The green colour hue, and its intensity and brightness are ranging from light- to dark-green. The pods with wax colour are controlled by a monogenic recessive gene (*y*) which may be affected by a second modifier gene (*arg*) and perhaps other modifiers. The addition of *arg* gene causes near-white or silver-green pod colour. The breeders have to select for early yellowing of the pods that develop intense golden colour at tender pod stage. A few purple-podded cultivars do exist, but are not used commercially. These cultivars have *P* and *V* genes, and have pods which are solid coloured or striped depending on the allele at the *CPrp* locus (Bassett 1996). The anthocyanin pigments responsible for red and purple colours are water-soluble; hence they do not remain in a processed product. The purple-podded genotypes are rich in anthocyanin content, 15 times higher than the normal green-podded genotypes (Singh *et al.* 2011). With respect to snap bean breeding for fresh market and processing industry, the quality traits are more important than the total yield. Pod sieve size is one of the important quality factors pertaining to consumers' preference and acceptability. The various sieve size categories i.e. 1, 2, 3, 4, 5, 6 and 7 measure to <5.8, 5.8 to <7.3, 7.3 to <8.3, 8.3 to < 9.5, 9.5 to <10.7, 10.7 to <11.7 and >11.7 mm, respectively. The pods at both extremes of sieve size are of little value. Sieve size has negative association with total pod yield. Generally, full-sieve beans have 50% 1- to 4-sieve size at maturity. The pod cross-section (PCS) index or shape (the ratio of thickness to width) varies from 0.400-1.300 and classified as flat (elliptic: 0.400-0.700), oval (ovate: 0.850-0.950), round (circular: 0.950-1.100) and crease-back (eight-shaped: 1.150-1.300). At its most extreme, pod shape becomes crease-back, with the shorter distance between placental and ventral sutures than between the valves on an axis perpendicular to an axis through the sutures. Pod cross sectional shape is a function of pod wall thickness and timing of development. Most of the snap bean cultivars are oval to round in shape because these pods are fleshier and have higher transport durability (Myers and Baggett 1999). A cultivar harvested young may show oval pods, at maturity have round pods and when past prime have crease-back pods. Because cross sectional shape is a function of developmental time and absolute wall thickness; it shows quantitative variation and quantitative inheritance that are additive in nature.

The spurs vary in length and shape with some cultivars possessing a short broad-based spur and others having a long tapered spur. Commercially, the spurs that are short and straight get more preference because they are easier to remove during preparation for packing and cooking. Inherently, the pods may be straight, curved, fish-hooked or S-shaped. The straightness of pods is also affected by plant growth habit i.e. upright bush types and pole beans tend to have straighter pods. Pod straightness is inversely associated with sieve-size. With respect to fibre content in the walls of pod, three major genes control the switch from the highly fibrous dry bean type pod to a relatively fibre free pod of the typical snap bean (Leakey 1988). Fibre content also increases with sieve size and maturity. Moreover, pod suture stringlessness governed by a single dominant gene (*St*; Prakken 1934). Drifjhout (1978) confirmed the *St* gene and also described a temperature sensitive dominant gene (*Ts*) forms strings at higher temperature. Pod smoothness and fleshiness are related to pod wall fibre, rate of seed development and seed size. Snap beans have relatively smooth pods than dry beans. Seed size and shape does affect pod smoothness in that large seeds or oval or round seeds will produce bumps on the pod surface. Selection of genotypes having slower rates of seed development, and smaller and cylindrical seeds can minimise wall bumpiness and increase smoothness (Myers and Baggett 1999). Interlocular cavitation, long spacing or cavities between the seeds in a pod, may be because of rapid pod growth (Kuksal and Seth 1981). It is associated with cooler nights at the early pin pod stage of growth, and has a genetic component. Generally, interlocular cavitation is not visible in young pods but develop as pod and seed size increases. The main chemical constituents responsible for flavours in snap beans are 1-octen-3-ol and linalool. The pole cultivar Romano contained high levels of these compounds, while FM-1L Blue Lake contained relatively high levels of 1-octen-3-ol but low levels of linalool. Moreover, Gallatin 50, a white seeded selection from Tendercrop, had low levels of 1-octen-3-ol but high levels of linalool. The level of 1-octen-3-ol and linalool is governed by monogenic dominant and additive gene, respectively.

Breeding for Disease Resistance

More than 50 species of bacteria, fungi and viruses that limit the quality of bean production have been reported (Sofkova *et al.* 2010). The pathogen management alone by pesticides has not been achieved satisfactorily; hence integrated disease management such as use of resistant cultivars, disease-free seeds, pesticides, suitable crop rotations, planting adjustment, deep ploughing of bean debris, etc are recommended.

Among them, the use of resistant cultivars, if available, is the most efficient, eco-friendly and economically viable option. Hence, development of disease resistant cultivars of common bean has been the overall objective at almost all the institutes involved in bean improvement programmes. Breeding the durable disease resistant cultivars and maintaining its continuity should always stick on three points continually: (i) investigation of the pathogens variability and virulence, (ii) search and studying new sources of resistance to pathogenic agents, (iii) developing cultivars/ advance lines resistant to economically important diseases. Globally, there are nearly 30 major diseases of common bean and the more important ones are as follows: bean common mosaic virus (BCMV), bean golden mosaic virus (BGMV), bean yellow mosaic virus (BYMV), bean curly top virus (BCTV), Southern bean mosaic virus (SBMV), pod mottle virus (PMV), common bacterial blight i.e. CBB (*Xanthomonas axonopodis* pv. *phaseoli*), halo blight i.e. HB (*Pseudomonas syringae* pv. *phaseolicola* i.e. Psp), bacterial wilt (*Corynebacterium flaccumfaciens*), bacterial brown spot (*Pseudomonas syringae* pv. *syringae*), anthracnose (*Colletotrichum lindemuthianum*), angular leaf spot i.e. ALS (*Phaeoisariopsis griseola* i.e. Phg), white mold (*Sclerotinia sclerotiorum*), rust (*Uromyces appendiculatus*), *Fusarium* root rot (*Fusarium solani* sp. *phaseoli*), *Rhizoctonia* root rot (*Rhizoctonia solani*), black root rot (*Thielaviopsis basicola*), *Pythium* blight (*Pythium* spp.), powdery mildew (*Erysiphe polygoni*) and root knot nematode (*Meloidogyne incognita*).

Viral disease: The viruses occur nearly worldwide and historically have been responsible for serious yield losses in common bean. The only effective means for controlling viral disease is through utilization of resistant cultivars (Sofkova *et al.* 2010). BCMV is one of the most serious seed-borne viral diseases caused by an aphid-vectored potyvirus in a non-persistent manner causing great yield losses (Sofkova *et al.* 2010). Genetic resistance to BCMV is conditioned by a series of independent multi-allelic loci (Drijfhout 1978). At least 19 different strains of BCMV have been identified and biologically authenticated. The dominant I gene resistance to BCMV and related potyviruses discovered by Ali (1950), originally found in the cv. Corbett Refugee. It conditions either an immune or temperature-dependent hypersensitive resistance. Therefore, this gene has been widely backcrossed into many bean varieties. The I gene located on B2 (Kelly *et al.* 2003) is independent of recessive resistance conditioned by three different bc genes. The bc-3 gene is located on B6 (Johnson *et al.* 1997; Miklas *et al.* 2000b; Mukeshimana *et al.* 2005), whereas the bc-1² allele was mapped to B3 (Miklas *et*

al. 2000a). The non-specific bc-u allele, needed for expression of bc-2² resistance, also resides on B3 based on the loose linkage with the bc-1 locus (Strausbaugh *et al.* 1999). In the presence of the I gene, the bc genes will confer broad resistance. The breeders recognize that the combination of the dominant I gene with recessive bc genes offers broad and durable resistance over single gene resistance to BCMV because the two types of genes have distinctly different mechanisms of resistance. At CIAT, MAS was used extensively based primarily on the SCAR marker ROC11 developed for the bc-3 gene (Johnson *et al.* 1997) and the SCAR marker SW13 for the I gene (Melotto *et al.* 1996). The bc-3 resistance was successfully transferred into a background of cream mottled and red mottled seed types through triple-, double- and back-crosses (Santana *et al.* 2004).

Bacterial disease: Among bacterial diseases, CBB is one of the most serious seed-borne disease that plague bean production worldwide, especially in the warmer areas with high humidity and plant wounds during and after flowering. The bacteria usually affect the leaves, causing leaf spots that may coalesce and result in leaf blight, and are also capable of invading the vascular tissue of the plant and infecting stems, pods and seeds. Breeding for genetic resistance is complex as revealed by identification of at least 24 QTL distributed across all 11 linkage groups or chromosomes, and the expression of these QTL are influenced by environment, disease pressure, plant maturity and plant organs affected (Miklas *et al.* 2006; Yu *et al.* 2012). However, a dominant gene Xap conferring resistance to CBB was found in the small white bean line PR 0313-58 (Zapata *et al.* 2010). Tepary bean accessions such as PI 319443, PI 44079 and G 40001 are sources of the major CBB resistance gene(s)/or QTL. Because tepary bean has the highest level of resistance to CBB (Singh and Munoz 1999), efforts have been made successfully to transfer the genetic factors controlling CBB resistance from tepary bean into common bean through inter-specific hybridizations (Scott and Michaels 1992; Singh and Munoz 1999). The resistant XAN lines, XAN 159, XAN 160 and XAN 161 were developed at CIAT (Thomas and Waines 1984; Jung *et al.* 1997). SCAR markers BC420, SU91 and SAP6 linked with three major QTL on B6, B8, and B10, respectively (Kelly *et al.* 2003), and are being used for MAS of CBB resistance (Mutlu *et al.* 2005; Yu *et al.* 2000).

Moreover, halo blight (HB) is a seed-borne bacterial disease that attacks the foliage and pods of beans in the regions with cooler and humid climate i.e. 24-28 °C and > 95% relative humidity for minimum 24 h. The

yield losses due to HB and CBB may range from 30-100%, especially when adverse environmental conditions persist during the early growth and flowering stages (Schwartz *et al.* 2001). Nine races of the pathogen HB (Psp race 1- Psp race 9) have been reported based on their reactions on differential cultivars and lines (Taylor *et al.* 1996a). The cultivars Red Mexican UI 3, GN Nebraska #1 Sel. 27 and UI 35 have hypersensitive resistance to race 1 isolate, controlled by a single dominant gene (Taylor *et al.* 1996b; Beebe and Pastor-Corrales 1991). A recessive gene controlling tolerance to Psp races 1 and 2 was reported in genotype PI 150414 from USA, while a two complementally gene model was found in a USA variety Montcalm. A series of three recessive alleles complementally to either of two other genes were identified in a Malawian bean line 1212D (Msuku 1984; Kelly *et al.* 1985). Furthermore, Chataika *et al.* (2011) reported monogenic dominance of resistance to HB in a genotype CAL 143. The QTL and genes with monogenic inheritance for resistance to halo blight have been observed within the same gene cluster similar to observations with anthracnose (Geffroy *et al.* 2000). In a RIL population of BelNeb-RR-1 \times A 55, Fourie *et al.* (2004) observed that three of the QTL corresponded with the location of Pse-1, Pse-3, and Pse-4 genes on linkage group B4, B2, and B4, respectively. The Pse-1 gene; which conditions resistance to Psp races 1, 7 and 9; resides within the B4 cluster of genes and QTL conditioning anthracnose, rust, ashy stem blight and bacterial brown spot (caused by *P. syringae* pv. *syringae*) resistance. Moreover, Pse-3 gene which conditions resistance to Races 3 and 4 is tightly linked with the I gene (Taylor *et al.* 1996b). Both genes condition a hypersensitive reaction, Pse-3 to Psp races 3 and 4, and I gene to certain strains of BCMV expressing temperature-sensitive necrosis. Given a similar hypersensitive mode of action for both Pse-3 and I genes and the lack of recombination between genes, it is possible that I gene is conditioning resistance to both diseases—HB and BCMV.

Fungal disease: ALS is a severe fungal disease in the tropical and subtropical countries, caused by *Phaeoisariopsis griseola* (Sacc.) Ferraris. The fungus infects most aerial parts of the plant, especially pods, seeds, leaf petioles and lower surfaces of leaflets causing premature leaf drop, foliar and stem necrosis that culminate in poorly filled seeds and reduced seed quality. The screening under field experiments and laboratory are discussed in details by Mahuku *et al.* (2003). Genetic resistance is mostly monogenic and race-specific, but because the pathogen is highly variable with many different races characterized (Mahuku *et al.* 2002), combinations of genes from diverse sources are needed

to provide broad resistance. The secondary gene pool (*P. coccineus* and *P. polyanthus*) has abundant source of resistance to ALS (Busogoro *et al.* 1999; Mahuku *et al.* 2003). The disease resistance is primarily governed by single dominant genes (Ferreira *et al.* 2000; Caixeta *et al.* 2003; Mahuku *et al.* 2004); but monogenic resistance genes conditioned with recessive inheritance have also been reported (Correa *et al.* 2001). RAPD or SCAR markers linked with many of the dominant resistance genes have been obtained (Miklas 2005). The SN02 SCAR marker linked with Phg-2 gene was identified in Mexico 54 (Sartorato *et al.* 2000) and co-segregated with a dominant resistance gene in Cornell 49-242 (Nietsche *et al.* 2000); while Phg-1 gene identified in AND 277 (Carvalho *et al.* 1998; Queiroz *et al.* 2004). Five QTL were identified in the cross population of DOR 364 \times G 19833 that mapped to linkage groups B4 and B10 (Lopez *et al.* 2003).

The fungus *Colletotrichum lindemuthianum* causes anthracnose disease, a seed-borne pathogen, found on all the continents, especially in the areas with high relative humidity and mild temperatures. The pathogen attacks aerial parts of the plant and produces lesions containing masses of conidia with a mucilaginous coating which are capable of being disseminated and infecting healthy tissues. The successful development of anthracnose resistant cultivars depends on understanding of the levels of variability within and among populations of the pathogen. More than 100 pathotypes or races of *C. lindemuthianum* have been identified worldwide (Sicard *et al.* 1997). The resistance is governed by monogenic independent genes Co-1 to Co-10, and multiple alleles exist at the Co-1, Co-3, Co-4 and Co-9 (Kelly and Vallejo 2004; Mendez-Vigo *et al.* 2005). Molecular markers linked to the majority of major Co-genes have been widely reported and these provide the opportunity to enhance disease resistance through MAS which has been successfully employed to breed new cultivars such as Perola in Brazil (Ragagnin *et al.* 2003) and in pinto beans in the USA (Miklas *et al.* 2003).

White mold, caused by necrotrophic fungus *Sclerotinia sclerotiorum*, is another fungal disease which causes considerable yield damage. Wet and cool weather, particularly winter crop during rains at the bloom period, favours infection. The lack of long-term crop rotation to avoid the buildup of the pathogen, and the use of furrow and sprinkle irrigation systems make additional risk of disease epidemic. It occurs on all aerial plant parts. The lesions on pods, leaves, branches, and stems are initially small, circular, dark green and water soaked, but rapidly increase in size; may become slimy and eventually encompass and kill the entire organ. Under

moist conditions, these lesions may also develop a white and cottony growth of external mycelium. Colonies of white mycelium (immature sclerotia) develop into hard, black sclerotia in and on infected tissues (Schwartz and Singh 2013). Resistance to white mold in bean is quantitatively inherited (Genchev and Kiryakov 2002; Kolkman and Kelly 2003), consisting of physiological resistance and avoidance. Plant avoidance of white mold can be due to plant architectural traits which allow a drier and warmer microclimate under the canopy (bush indeterminate plants i.e. Type II growth habit, resistant to lodging, stay-green stem character, and open porous canopy and branching pattern) or agronomic management practices (Sofkova *et al.* 2010). Partial physiological resistance, controlled quantitatively both by dominant and recessive genes, is found in the germplasm of small-seeded Middle American (ICA Bunsí, AB 136, PI 313850) and large seeded Andean (A 195, G 122, PC 50, PI 318695, VA 19, Xana) common bean, wild bean (PI 318695), and *Phaseolus* species of the secondary gene pool such as *P. coccineus* (G 35172, PI 255956, PI 439534) and *P. costaricensis* (G 40604). Twenty-seven QTL for partial physiological resistance and 36 QTL that coalesced into 18 genomic regions for avoidance traits have been reported (Schwartz and Singh 2013).

Bean rust, caused by the fungus *Uromyces appendiculatus*, is distributed throughout the world, especially in humid tropical and subtropical regions. It is highly variable in nature due to rapid breakdown of major gene resistance which ultimately challenged bean breeders to develop durable resistance to bean rust. Pyramiding of different race-specific resistance genes in association with other genes conferring plant resistance, slow rusting and reduced pustule size would be important strategy for obtaining effective and durable genetic resistance. Resistance to rust is mainly controlled by single dominant genes (Augustin *et al.* 1972; Alzate-Marín *et al.* 2004; Souza *et al.* 2007a, 2007b). In a review of Souza *et al.* (2013), at least 14 major dominant RR genes have been identified (Ur-1 to Ur-14) in various genotypes such as B 1627, B 2090, B 2055, AXS 37, Aurora, NEP 2, Mexico 235, Early Gallatin, Mexico 309, B 190, Golden Gate Wax, Olathe, Great Northern 1140, US 3, PC 50, Cape, Resisto, PI 181996, Kranskop, Redlands Pioneer and Ouro Negro. In addition to these 14 genes, other important unnamed RR genes have also been identified in many lines such as Montcalm, BAC 6, Dorado, CNC and PI 260418 (Souza *et al.* 2013). Besides, various molecular markers associated with mentioned genes conferring rust resistance have been described in details (Souza *et al.* 2013).

Breeding for Insect Resistance

Various insect pests and nematodes cause substantial loss globally (35-100%) to the yield and quality of dry and snap beans depending on the occurrence and severity (Singh and Schwartz 2011). The key insect pests of *Phaseolus vulgaris* are the leafhoppers (*Empoasca kraemeri*, *E. fabae*), thrips (*Thrips palmi*), weevils (*Apion godmani*, *A. aurichalceum*), whitefly (*Bemisia tabaci*), bean fly (*Ophiomyia phaseoli*), aphid (*Aphis fabae*), chrysomelid (*Ootheca* species), pod borer (*Maruca testulalis*), bruchids (*Zabrotes subfasciatus*, *Acanthoscelides obtectus*) and mites (*Tetranychus cinnabarinus*, *Polyphagotarsonemus latus*) (Karel and Autrique 1989; Schwartz and Peairs 1999). In addition to causing direct damage to vegetative plant parts, flowers, pods, seeds and quality; insects are important as vector of numerous common bean viruses such as BCMV, BCMNV and BYMV by aphid-vectored potyviruses; BGMV, BGYMV and bean dwarf mosaic virus by whitefly-transmitted geminiviruses; and BCTV by leafhopper-vectored curtovirus. Adequate levels of resistance to bean pod weevil are found in the common bean landraces from the Mexican highlands belonging to race Jalisco. But resistance to bruchids *Z. subfasciatus* was found only in wild *P. vulgaris* (Sparvoli and Bollini 1998), *P. acutifolius* and other *Phaseolus* species (Cardona and Kornegay 1999). *Phaseolus acutifolius* also has the highest levels of resistance to *A. obtectus* (Dobie *et al.* 1990) and *E. kraemeri* (Cardona and Kornegay 1999). Thus, favourable genes and QTL are scattered across cultivated and wild populations in the primary, secondary, tertiary, and other gene pools of common bean. Given the diversity and genetic distance between the cultivars to be improved and the resistance donor germplasm, generally two- or multi-tiered integrated breeding approach (multiple-parent crosses) are often used to broaden the genetic base, and introgress and pyramid resistance genes and QTL (Singh and Schwartz 2011).

Breeding for Tolerance to Abiotic Stresses

The physio-biochemical responses that allow plants to be most productive in the environmental stress conditions must be better defined, and the genetic factors that control these responses should be discovered and introgressed into new varieties. Important environmental stresses are drought, heat and cold. Drought tolerance is often associated with a well-developed root system. High temperature stress (> 35 °C) adversely affects plant physio-biochemical processes: limiting plant growth, flowering, pollens, pod setting and development. At anthesis and pod setting,

high temperatures may result in reduced activity of pollen and anther, sluggish growth of pollen tubes, slower embryo development and restrict pod enlargement and thereby leading to reductions in pod yield. In order to adopt high temperature stress, plants employ various adaptive mechanisms such as earliness, cooler canopies, high transpiration rate, stay-green trait and reduced photosynthetic rates. Early maturity provides an escape mechanism under late incidence of high temperature which would be a good approach for snap bean breeding for North Indian Plains that suffers from terminal high temperature from mid-March and onwards. Another important trait is cooler canopy temperature which enables plants to maintain physiological functions in balance under elevated temperature. Maintaining higher content of leaf chlorophyll (stay-green) is also considered desirable trait as it indicates a low degree of photo-inhibition of the photosynthetic apparatus at high temperature. Thus, physiological characterization under higher temperature may provide a better understanding of adaptive traits that can be integrated into breeding programmes. A breeding line 5 BP 7 has been reported to be heat tolerant. There is a need to develop varieties which are able to grow more vigorously and reach flowering earlier under low temperature conditions. The characters contributing towards cold tolerance are large embryonic axis, rapid hypocotyl elongation, rapid mobilization of cotyledonary reserves, leaf area and production of surplus photosynthate. Tolerance to drought and high temperature has been reported in the few populations of *P. acutifolius* (Parsons and Howe 1984; Markhart 1985; Federici *et al.* 1990). Also, over-expression of antioxidant enzymes could play an imperative role in improving the effects of various types

of abiotic and biotic stresses. A few efforts have been made to enhance the antioxidant enzymes in vegetable crops through conventional breeding (Singh 2007; Singh *et al.* 2009; 2010a; 2010b). Moreover, the expression of barley HVA1 gene in five varieties (Condor, Matterhorn, Sedona, Olathe and Montcalm), via the Biolistic bombardment of the apical shoot meristem primordium, resulted in drought tolerance due to increase in root length of transgenic plants (Kwapata *et al.* 2012).

Sources of Tolerance/ Resistance

An important task in the breeding programme is to find the resistant sources. In India, Pantnagar and the North-east states are hot-spot for several diseases of snap bean to screen the efficient germplasm. Detailed screening techniques have been described by Schuster and Coyne (1981) and Silbernagel (1986). It may, however, be emphasized that considerations of time, space, expense, and the requirements for large numbers often dictate that screening be done under field conditions. However, for confirmation of resistance with identified pathogen controlled greenhouse or growth chamber conditions are needed (Silbernagel 1986). It is, therefore, suggested that screening for resistance should normally be carried out in the field preferably under hot-spot conditions, and laboratory and glasshouse procedures should be developed as a supplement to field screening. Breeders have recognized that a vast amount of genetic diversity among *Phaseolus* species (wild common bean as well as wild and domesticated germplasm of alien species) which are a promising source of tolerance to biotic and abiotic stresses that can be exploited for the improvement of yield and its stability in domesticated common bean

Table 6: Sources of tolerance/resistance found in domesticated and wild *Phaseolus* species.

Tolerance/ resistant trait	Species	Reference
ALS	<i>P. coccineus</i> and <i>P. polyanthus</i>	Busogoro <i>et al.</i> (1999a), Mahuku <i>et al.</i> (2003)
Anthraxnose	<i>P. coccineus</i> and <i>P. dumosus</i>	Mahuku <i>et al.</i> (2002)
White mold	<i>P. coccineus</i> and <i>P. costaricensis</i>	Sofkova <i>et al.</i> (2010)
CBB	<i>P. acutifolius</i>	Singh and Munoz (1999)
BYMV and BGMV	<i>P. coccineus</i>	Osorno <i>et al.</i> (2003)
High temperature and drought	<i>P. acutifolius</i>	Parsons and Howe (1984), Markhart (1985), Federici <i>et al.</i> (1990)
Freezing	<i>P. angustissimus</i>	Balasubramanian <i>et al.</i> (2004)
Root rots	<i>P. coccineus</i>	Silbernagel and Hannan (1992)
Weevil	Jalisco race	Sparvoli and Bollini (1998)
Bruchid, <i>Zabrotes subfaciatus</i>	wild <i>P. vulgaris</i> and <i>P. acutifolius</i>	Sparvoli and Bollini (1998), Cardona and Kornegay (1999)
Bruchid, <i>A. obtectus</i>	<i>Phaseolus acutifolius</i>	Dobie <i>et al.</i> (1990)
Leaf hopper, <i>E. kraemeri</i>	<i>Phaseolus acutifolius</i>	Cardona and Kornegay (1999)
Bruchids, <i>Zabrotes</i> spp.	wild <i>P. vulgaris</i>	Schmit and Baudoin (1992), Debouck (1999), Singh (1999), Baudoin <i>et al.</i> (2001)
Anthraxnose, root rots, white mold, BYMV and BGMV	<i>P. coccineus</i>	
Leaf hoppers	<i>P. acutifolius</i>	
CBB and bruchids	Some accessions of tepary bean	
Salt	<i>P. macvaguui</i> , <i>P. micranthus</i> and <i>P. filiformis</i>	Bayuelo-Jimenez <i>et al.</i> (2002)

Table 7: *Phaseolus vulgaris* germplasm/lines/cultivars resistant to various diseases

Disease	Resistant source
BCMV	Corbett Refugee, RH 13, ARS 6BP 5, ARS 5 BP 7, Viva, Roza, Gloria, NW 410, NW 590, Seafarer, Swan Valley, Robust, Turkish Brown, Plovdiv, Zarya,
BYMV	RH 13
BCTV	ARS 6 BP 5, ARS 5 BP 7, NW 410, NW 590 Apollo, Blue Mountain, Gold Crop, Wonder Green
CBB	GN Tara, GN Valley, Pea Bean MSU 4 lines, CIAT lines, Wis. 71 -3938, GN Nebraska, Sel. 27, PI 207262, PI 150414, Wis HBR 13, Wis HBR 72, RH 13, Rusenski Ran, Plovdiv 564, Fonura 332, PI 197032, PI 319443, IG 238, XAN 159, XAN 160, XAN 161, PI 165421, A-8-12, A-8-40, RH 13, RH 26, PR0313-58, PI 319443, PI 44079, G 40001
Hallo blight	Redkote, Redcloud, Montcalm, Mecosta, Lumarep, Starland, Wis HBR 40, Wis HBR 72, OSU 1040, Seafarer, Wis HBR 13, RH 13, RH 26, Red Mexican UI 3, GN Nebraska #1 Sel. 27, UI 35, PI 150414, 1212D, CAL 143,
Anthraxnose	RH 13, Nairobi Acc. No. 16, 84, 86, Seafarer, Wells Red Kidney, HR 45, A 769, XAN 273, Prelom, Abritus, Oreol, Perola, G 122
White mold	EX Rico 23, C 20, Dunav 1, Padez 1, Izavella, IIRR 7585, A 195, NAB 19, SIN 11, ICA Bunsu, AB 136, PI 313850, A 195, G 122, PC 50, PI 318695, VA 19, Xana, PI 318695, G 35172, PI 255956, PI 439534, G 40604,
ALS	G 4691, G 14016, G 23578A, Argfunai, G 2328C, G 4380, G 12806, G 2359, G 19120, G 18780A, G 21135, G 855, G 13550, G 2726, G 16267, G 18970, G 19227A, G 18256, G 3005, G 2769, G 16291, G 1727, G 3970, G 18141, G 15846, G 23614, G 8719, G 9836, G 14675, G 22542A, G 14056, G 148, MAR 2, MAR 3, AND 277, CAL 143, BAT 332, Cornell 49-242, Ouro Negro, G 10474, Mexico 54
Root rots	Footlong, Wisconsin 4B, Wisconsin 77, Wisconsin 78, NW 410, NW 590, PI 203958, Pindak
Bacterial wilt	GN Star, GN Emerson
Rust	B 4175, PR 190, BARC 1, 8 BP 3, Laker, C 20, Kentucky Wonder, VL Boni 1, L 226-10, Dunav 1, Biser, Trudovec, Cornell 49-242, TO, TU, AB 136, PI 207262, B 1627, B 2090, B 2055, AXS 37, Aurora, NEP 2, Mexico 235, Early Gallatin, Mexico 309, B 190, Golden Gate Wax, Olathe, Great Northern 1140, US 3, PC 50, Cape, Resisto, PI 181996, Kranskop, Redlands Pioneer, Ouro Negro, Montcalm, BAC 6, Dorado, CNC, PI 260418
Brown spot	BBSR 130, WBR 133

as well as snap bean (Table 6; Acosta-Gallegos *et al.* 2007):

Also, to be more specific, the sources of resistance to various diseases have been found in the population of *Phaseolus vulgaris* (Table 7) by various researchers such as Ali (1950), Mihov *et al.* (1975), Schuster and Coyne (1981), Ockendon (1983), Poryazov *et al.* (1984), Thomas and Waines (1984), Msuku (1984), Kelly *et al.* (1985), Silbernagel (1986), Nene (1988), Poryazov (1990), Beebe and Pastor-Corrales (1991), Sharma and Joshi (1993), Kiryakov and Genchev (1996, 2000), Taylor *et al.* (1996b), Jung *et al.* (1997), Kmiecik and Nienhuis (1998), Singh and Munoz (1999), Nietsche *et al.* (2000), Sartorato *et al.* (2000), Kiryakov (2000, 2002), Mahuku *et al.* (2003), Ragagnin *et al.* (2003), Queiroz *et al.* (2004), Kiryakov and Genchev (2002, 2004a, 2004b, 2009), Ram (2005), Sofkova *et al.* (2010), Zapata *et al.* (2010), Chataika *et al.* (2011).

Future Strategies

The important future strategies that have relevance to snap bean breeding are—

- Sturdy and upright plants that hold their pods in the upper half of the canopy.
- Bush indeterminate (Type-II) or pole type (Type-IV) growth habit along with photo-insensitive.
- Early pod harvesting and wider adaptability.
- High tender pod yield along with following traits such as bright and uniform colour, non-stringy, slender fleshy, long and straight, cylindrical (round

in cross-section), smooth, small seeded and less inter-ocular cavitations.

- Tolerance to heat stress, particularly high night temperature.
- Resistance to major biotic stresses: bean common mosaic virus, common bacterial blight, *Sclerotinia* rot, anthracnose, angular leaf spot, pea stem fly and pod borer.

सारांश

सनेप बीन (फैजियोलस बुल्वैरिस एल.) एक सामान्य बीन है जो गूदेदार मूलायम एवं फल भित्ति में कम मात्रा में रेशा बनने वाली दलहनी सब्जी फसल है जिसका उपयोग पकाने अथवा डिब्बाबन्दी के लिए भी किया जाता है। इसकी उत्पत्ति दक्षिण मैक्सिको से सेंट्रल अमेरिका (मेजोअमेरिका) तथा इक्वाडोर-पेरू बोलिविया क्षेत्र द्वितीयक उत्पत्ति स्थल माना जाता है जबकि सनेप बीन का विकास एण्डियन अनुवांशिक संसाधनों से दक्षिण यूरोप में 19वीं शताब्दी के दौरान हुआ। फैजियोलस प्रजातियों की 260000 से ज्यादा जनन द्रव्यों का संरक्षण >245 जीन बैंक जो विश्व के कई देशों में है, किया जाता है। सीआईएटी कोलम्बिया का मुख्य उद्देश्य विश्व के जननद्रव्यों का एकत्रीकरण एवं फैजियोलस प्रजातियों का संरक्षण है। यहाँ विश्व का सबसे अधिक विभिन्न जननद्रव्य रखकर सेवा प्रदान करना है। पूरे विश्व में प्रजनक मुख्य अधिक उपज देने वाली विस्तृत परिस्थिति अनुकूलन अगेतीपन, उत्तम फली गुणवत्ता (चमकीला एवं एकसार रंग, गैर रेशेदार पतला, लम्बा व सीधा, बेलनाकार, चिकना, छोटे बीज वाले, दो प्रकोष्ठों के बीच कम दूरी तथा ज्यादा सुगन्ध); उष्ण प्रतिबल सहनशीलता, विशेष उच्च तापमान पर तथा मुख्य रोगों के प्रति प्रतिरोधिता जैसे— बीन कामन मौजैक वायरस, बीन गोल्डेन मौजैक वायरस, कामन बैक्टेरियल ब्लाइट, हेलो ब्लाइट, स्कलेरोशिनिया गलन, एन्थ्रोक्नोज, एन्गुलर लीफ स्पॉट तथा जड़ सूत्र कृमि। वांछित जीन एवं अनेक गुणों के लिए फ्लै क्यू टी एल तथा जंगली पौध

समूहों जो प्राथमिक, द्वितीयक, तृतीयक तथा कामन बीन के अन्य जीन समूह को एक जगह, द्वि- या बहु-स्तरीय प्रजनन में अनुवांशिक आधार को विस्तृत करने के लिए उपयोग किया जा सके जिससे इन्हें एक साथ मिलाकर, प्रतिरोधी जीन को पिरामिड तथा क्यू टी एल तैयार कर सकें।

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