Vegetable Science (2015) 42 (1) : 1-17

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

BK Singh and B Singh

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 Mayanmar (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 Rawanda (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),

ICAR-Indian Institute of Vegetable Research (ICAR-IIVR), Shahanshahpur-221305, Varanasi, Uttar Pradesh
E-mail: bksinghkushinagar@yahoo.co.in

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 (Debuck *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

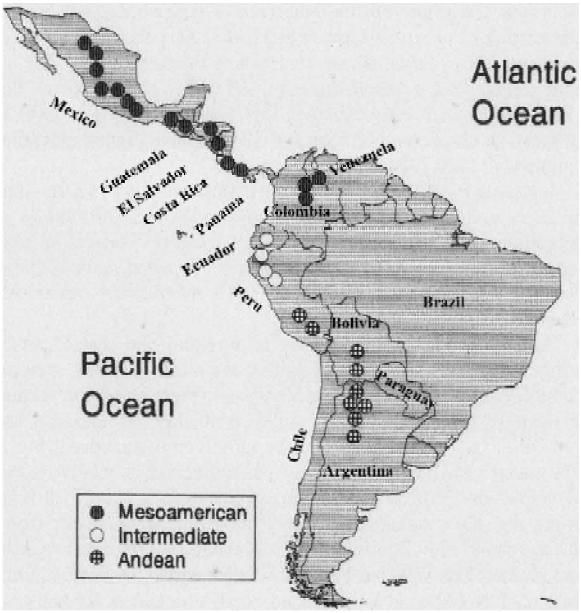

Figure 1: Distribution of wild Phaseolus vulgaris in Latin America (Gepts 1998)

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.

Phaseolus species	Common name	Altitude (m)	Temperature (°C)	Precipitation (mm/ year)	Growth cycle (day)
P. vulgaris L.	Common bean, dry bean, shell bean, snap bean, French bean	50–3000	14–26	400–1600	70–330
P. polyanthus Greenman	Yearlong bean	800–2600	14–24	1000–2600	110–365
P. coccineus L.	Runner or scarlet runner bean	1400–2800	12–22	400–2600	90–365
P. acutifolius A. Gray	Tepary bean	50–1900	20–32	200–400	60–110
P. lunatus 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 Poded, 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	Semiarid 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 peroxidise, 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 × 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 'VRFBB-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, iterlocular 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 bean 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 (*Erisyphe 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-1^2 allele was mapped to B3 (Miklas *et al.* 2000a). The non-specific bc-u allele, needed for expression of bc-2^2 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 × 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 × 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 Bunsi, 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-Marin *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 subfaciatus*, *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. subfaciatus* 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 been 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 he 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	*P. coccineus* and *P. polyanthus*	Busogoro *et al.* (1999a), Mahuku *et al.* (2003)
Anthracnose	*P. coccineus* and *P. dumosus*	Mahuku *et al.* (2002)
White mold	*P. coccineus* and *P. costaricensis*	Sofkova *et al.* (2010)
CBB	*P. acutifolius*	Singh and Munoz (1999)
BYMV and BGMV	*P. coccineus*	Osorno *et al.* (2003)
High temperature and drought	*P. acutifolius*	Parsons and Howe (1984), Markhart (1985), Federici *et al.* (1990)
Freezing	*P. angustissimus*	Balasubramanian *et al.* (2004)
Root rots	*P. coccineus*	Silbernagel and Hannan (1992)
Weevil	Jalisco race	Sparvoli and Bollini (1998)
Bruchid, *Zabrotes subfaciatus*	wild *P. vulgaris* and *P. acutifolius*	Sparvoli and Bollini (1998), Cardona and Kornegay (1999)
Bruchid, *A. obtectus*	*Phaseolus acutifolius*	Dobie *et al.* (1990)
Leaf hopper, *E. kraemeri*	*Phaseolus acutifolius*	Cardona and Kornegay (1999)
Bruchids, *Zabrotes* spp.	wild *P. vulgaris*	Schmit and Baudoin (1992), Debouck (1999), Singh (1999), Baudoin *et al.* (2001)
Anthracnose, root rots, white mold, BYMV and BGMV	*P. coccineus*	
Leaf hoppers	*P. acutifolius*	
CBB and bruchids	Some accessions of tepary bean	
Salt	*P. macvaguii, P. micranthus* and *P. filiformis*	Bayuelo-Jimenez *et al.* (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, Redkloud, 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,
Anthracnose	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 Bunsi, 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 l4016, G 23578A, Argfunei, G 2328C, G 4380, G l2806, 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 l4675, G 22542A, G l4056, G l48, 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 el 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-locular 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

स्नैप बीन (फैजियोलस बुल्गैरिस 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 सेन्ट्रल अमेरिका (मेजोअमेरिका) तथा इक्वाडोर–पेरू बोलिविया क्षेत्र द्वितीयक उत्पत्ति स्थल माना जाता है जबकि स्नैप 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। यहां विश्व का सबसे अधिक व 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 प्रकोष्ठो के बीच कम दूरी तथा ज्यादा सुगन्ध); उष्ण प्रतिबल सहनशीलता, विशेष उच्च तापमान पर तथा मुख्य रोगों के प्रति प्रतिरोधिता जैसे– बीन कामन मोजैक वायरस, बीन गोल्डेन मोजैक वायरस, कामन बैक्टेरियल ब्लाइट, हेलो ब्लाइट, स्कलेरोशिनिया गलन, एन्थ्रोक्नोज, एन्गुलर लीफ स्पाट तथा जड़ सूत्र कृमि। वांछित जीन एवं अनेक गुणों के लिए फैले क्यू टी एल तथा जंगली पौध

समूहों जो प्राथमिक, द्वितीयक, तृतियक 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।

References

Acosta-Gallegos JA, Kelly JD, Gepts P (2007) Pre-breeding and genetic diversity in common bean (*Phaseolus vulgaris*). Crop Science 47 (Supplement 3): S44-S59.

Alzate-Marin AL, Souza TLPO, Ragagnin VA, Moreira MA, Barros EG (2004) Allelism tests between the rust resistance gene present in common bean cultivar Ouro Negro and genes Ur-5 and Ur-11. Journal of Phytopathology 152: 60-64.

Andrews SA (2013) Snapping green beans. http://humanelivingnet.net/2013/12/17/snapping-green-beans (accessed on 22.09.2014).

Arumuganathan K, Earle ED (1991) Nuclear DNA content of some important plant species. Plant Molecular Biology Reporters 9 (3): 208-218.

Augustin E, Coyne DP, Schuster ML (1972) Inheritance of resistance in *Phaseolus vulgaris* to *Uromyces phaseoli* typical Brazilian rust race B11 and of plant habit. Journal of the American Society for Horticultural Science 97: 526-529.

Basset MJ (1996) List of genes–*Phaseolus vulgaris* L. Annual Report of the Bean Improvement Cooperative 39: 1-19.

Baudoin JP, Camarena F, Lobo M, Mergeai G (2001) Breeding *Phaseolus* for intercrop combinations in Andean highlands. In: Broadening the Genetic Bases of Crop (Cooper HD, Spillane C and Hodgkin T eds). CAB International, Wallingford, UK, pp 373-384.

Bayuelo-Jimenez S, Debouck DG, Lynch JP (2002) Salinity tolerance in *Phaseolus* species during early vegetative growth. Crop Science 42: 2184-2192

Becerra-Velásquez VL, Gepts P (1994) RFLP diversity in common bean (*Phaseolus vulgaris* L.). Genome 37: 256–263.

Beebe S, Gonzalez AV, Rengifo J (2000) Research on trace minerals in the common bean. Food and Nutrition Bulletin 21: 387-391.

Beebe SE, Pastor-Corrales MA (1991) Breeding for disease resistance. In: Common Beans-Research for Crop Improvement (Van Schoonhoven A and Voysest O eds). CAB International, Wallingford, UK, pp. 561-610.

Bellucci E, Bitocchi E, Rau D, Rodriguez M, Biagetti E, Giardini A, Attene G, Nanni L, Papa R (2014) Genomics of origin, domestication and evolution of *Phaseolus vulgaris*. In: Genomics of Plant Genetic Resources- Volume 1 (Tuberosa R, Graner A and Frison E eds). Springer: Dordrecht, The Netherlands, pp. 483–507.

Bennett MD, Leitch IJ (2010) Plant DNA C-values Database (Release 5.0, Dec. 2010).

Bitocchi E, Nanni L, Bellucci E, Rossi M, Giardini A, Zeuli PS, Logozzo G, Stougaard J, McClean P, Attene G, Papa R (2012) Mesoamerican origin of the common bean (*Phaseolus vulgaris* L.) is revealed by sequence data. Proceedings of the National Academy of Sciences of the USA 109 (14): E788–E796.

Brown JWS, Osborn TC, Bliss FA, Hall TC (1982) Bean lectins-Part 1: Relationships between agglutinating activity and electrophoretic variation in the lectin-containing G2/albumin seed protein of French bean (*Phaseolus vulgaris* L.). Theoretical and Applied Genetics 62: 263–271.

Busogoro JP, Jijakli MH, Lepoivre P (1999) Identification of a novel source of resistance to angular leaf spot disease of common bean within the secondary gene pool. Plant Breeding 18: 417–423.

Caixeta ET, Borém A, Niestche S, Moreira MA, Barros EG (2003) Inheritance of angular leaf spot resistance in common bean line BAT 332 and identification of RAPD markers linked to the resistance gene. Euphytica 134: 297–303.

Cardona C, Kornegay J (1999) Bean germplasm resources for insect resistance. In: Global Plant Genetic Resources for Insect-resistant Crops (Clement SL and Quisenberry SS eds). CRC, Boca Raton, Florida, USA, pp. 85–99.

Carvalho GA, Paula-Júnior TJ, Alzate-Marin AL, Nietsche S, Barros EG, Moreira, MA (1998) Herança da resistência da linhagem AND-277 de feijoeiro-comum à raça 63-23 de Phaeoisariopsis griseola e identificação de marcador RAPD ligado ao gene de resistência. Fitopatologia Brasileira 23: 482-485.

Chacon MI, Pickersgill B, Debouck DG, Salvador Arias J (2007) Phylogeographic analysis of the chloroplast DNA variation in wild common bean (*Phaseolus vulgaris* L.) in the Americas. Plant Systematics and Evolution 266: 175–195.

Chacón SMI, Pickersgill B, Debouck DG (2005) Domestication patterns in common bean (*Phaseolus vulgaris* L.) and the origin of the Mesoamerican and Andean cultivated races. Theoretical and Applied Genetics 110: 432–444.

Chataika BYE, Bokosi JM, Chirwa RM, Kwapata MB (2011) Inheritance of halo blight resistance in common bean. African Crop Science Journal 19 (4): 325-333.

Correa RX, Good-God PI, Oliveira MLP, Niestche S, Moreira MA, de Barros EG (2001) Herança da resistência à mancha-angular do feijoeiro e identificação de marcadores moleculares flanqueando o loco de resistência. Fitopatologia Brasileira 26: 27-32.

Debouck DG (1988) *Phaseolus* germplasm exploration. In: Genetic resources of *Phaseolus* beans (Gepts P ed). Kluwer Academic Publishers, Dordrecht, The Netherlands, pp. 3-29.

Debouck DG (1991) Genetic variation in crop species and their wild relatives: a viewpoint for their conservation. In: Genetic diversity and crop strategies for roots and tubers (Becker B ed). Arbeitsgemeinschaft Tropische und Subtropische Agrarforschung e.V. and International Board for Plant Genetic Resources, Bonn, Germany, pp. 41-51.

Debouck DG (1999) Systematics and morphology. In: Common Beans: Research for Crop Improvement (Van Schoonhoven A and Voysest O eds). Commonwealth Agricultural Bureaux International, Wallingford, UK, pp. 55-118.

Debouck DG, Toro O, Paredes OM, Johnson WC, Gepts P (1993) Genetic diversity and ecological distribution of *Phaseolus vulgaris* in north-western South America. Economic Botany 47: 408–423.

Delgado-Salinas A, Bibler R, Lavin M (2006) Phylogeny of the genus *Phaseolus* (Leguminosae): A recent diversification in an ancient landscape. Systematic Botany 31: 779–791.

Delgado-Salinas, A (1985) Systematics of the genus *Phaseolus* (Leguminosae) in North and Central America. PhD Dissertation, The University of Texas, Austin, USA, pp. 363.

Dobie P, Dendy J, Sherman C, Padgham J, Wood A, Gatehouse AMR (1990) New sources of resistance to *Acanthoscelides obtectus* (Say) and *Zabrotes subfasciatus* Boheman (Coleoptera: Bruchidae) in mature seeds of five species of *Phaseolus*. Journal of Stored Products Research 26: 177–186.

Drijfhout E (1978) Inheritance of temperature-dependent string formation in common bean (*Phaseolus vulgaris* L.). Netherlands Journal of Agricultural Science 26: 99-105.

FAO (2010) The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture. Rome, Italy, pp. 251-252.

FAOSTAT (2012) http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567#ancor (accessed on 28 February 2014).

Federici CT, Ehdaie B, Wanes JAG (1990) Domesticated and wild tepary bean: field performance with and without drought-stress. Agronomy Journal 82: 896-900.

Ferreira JJ, Alvarez E, Fueyo MA, Roca A, Giraldez R (2000) Determination of the outcrossing rate of *Phaseolus vulgaris* L. using protein markers. Euphytica 113: 259–263.

Fourie D, Miklas PN, Ariyarathne HM (2004) Genes conditioning halo blight resistance to races 1, 7, and 9 occur in a tight cluster. Annual Report of the Bean Improvement Cooperative 47: 103-104.

Freytag GF, Debouck DG (2002) Taxonomy, Distribution, and Ecology of the Genus *Phaseolus* (Leguminosae-Papilionoideae) in North America, Mexico and Central America. Botanical Research Institute of Texas, Ft. Worth, Texas, USA.

Geffroy V, Sévignac M, De Oliveira J, Fouilloux G, Skroch P, Thoquet P, Gepts P, Langin T, Dron M (2000) Inheritance of partial resistance against *Colletotrichum lindemuthianum* in *Phaseolus vulgaris* and co-localization of QTL with genes involved in specific resistance. Molecular Plant-Microbe Interactions 13: 287–296.

Genchev D, Kiryakov I (2002) Inheritance of resistance to white mold disease [*Sclerotinia sclerotiorum* (Lib.) de Bary] in A 195 (*Phaseolus vulgaris* L.). Bulgarian Journal of Agricultural Science 8: 181–187.

Gepts P (1998) Origin and evolution of common bean: Past events and recent trends. HortScience 33: 1124-1130.

Gepts P, Bliss FA (1985) F1 hybrid weakness in the common bean: differential geographic origin suggests two gene pools in cultivated bean germplasm. Journal of Heredity 76: 447-450.

Gepts P, Bliss FA (1986) Phaseolin variability among wild and cultivated common beans (*Phaseolus vulgaris*) from Colombia. Economic Botany 40: 469-478.

Gepts P, Kmiecik K, Pereira P, Bliss FA (1988) Dissemination pathways of common bean (*Phaseolus vulgaris*, Fabaceae) deduced from phaseolin electrophoretic variability I. The Americas Economic Botany 42: 73-85.

Gepts P, Osborn TC, Rashka K, Bliss FA (1986) Phaseolin-protein variability in wild forms and landraces of the common bean (*Phaseolus vulgaris*): Evidence for multiple centers of domestication. Economic Botany 40: 451–468.

http://isa.ciat.cgiar.org/urg/beancollection.do

Islam FMA, Basford KE, Jara C, Redden RL, Beebe S (2002) Seed compositional and disease resistance differences among gene pools in cultivated common bean. Genetic Resources and Crop Evolution 49: 285–293.

Johnson WC, Gepts P (1999) Segregation for performance in recombinant inbred populations resulting from inter-gene pool crosses of common bean (*Phaseolus vulgaris* L.). Euphytica 106: 45-56.

Johnson WC, Guzman P, Mandala D, Mkandawire ABC, Temple S, Gilbertson RL, Gepts P (1997) Molecular tagging of the bc-3 gene for introgression into Andean common bean. Crop Science 37: 248-254.

Jung G, Skroch PW, Coyne DP, Nienhuis J, Arnaud-Santana E, Ariyarathne HM, Kaeppler SM, Basset MJ (1997) Molecular-marker-based genetic analysis of tepary bean-derived common bacterial blight resistance in different developmental stages of common bean. Journal of the American Society for Horticultural Science 122: 329-337.

Kami J, Velásquez VB, Debouck DG, Gepts P (1995) Identification of presumed ancestral DNA sequences of phaseolin in *Phaseolus vulgaris*. Proceeding of the National Academy of Sciences of the USA 92: 1101–1104.

Karel AK, Autrique A (1989) Insects and other pests in Africa. In: Bean Production Problems in the Tropics (Schwartz HF and Pastor-Corrales MA eds.). 2nd edition, CIAT, Cali, Colombia pp. 455-504.

Kelly JD (2004) Advances in common bean improvement: some case histories with broader applications. Acta Horticulturae 637: 99–122.

Kelly JD, Kolkman JM, Schneider K (1998) Breeding for yield in dry bean (*Phaseolus vulgaris* L.). Euphytica 102: 343–356.

Kelly JD, Msuku WAB, Saettler AW (1985) Genetics of resistance to Malawian halo blight isolates. Annual Report of the Bean Improvement Cooperative 28: 80-81.

Kelly JD, Gepts P, Miklas PN, Coyne DP (2003) Tagging and mapping of genes and QTL and molecular marker-assisted selection for traits of economic importance in bean and cowpea. Field Crops Research 82: 135–154

Kiryakov I (2000) Race variability of *Colletotrichum lindemuthianum* in Bulgaria. Plant Science 37: 248–251.

Kiryakov I, Genchev D (1996) Sourses of resistance to common blight in *Phaseolus* germplacm. 2nd Balkan Symposium of Field Crops, Novi Sad, Yugoslavia, 1: 537–540.

Kiryakov I, Genchev D (2000) Resistance of bean cultivars and lines to *Xanthomonas campestris* pv. *phaseoli* (Smith) Dye. Bulgarian Journal of Agricultural Science 6: 525–528.

Kiryakov I, Genchev D (2002) Sources of resistance to the main diseases in Bulgaria on dry bean (*Phaseolus vulgaris* L.) in the collection of Dobroudja Agricultural Insütute. In: Breeding and agrotechnics of field crops- 50 years of

Dobroudja Agricultural Institute (Tsenov *et al.* eds). Dobroudja Agricultural Institute, General Toshevo, Bulgaria, pp. 251–260.

Kiryakov I, Genchev D (2004a) New anthracnose races of bean in Bulgaria. Field Crops Studies 1(4): 336–341.

Kiryakov I, Genchev D (2004b) New sources of resistance to bean rust in the collection of Dobroudja Agricultural Institute. Research Communication of USB Branch Dobrich, 6(1): 72–77.

Kiryakov I, Genchev D (2009) Resistance of *Phaseolus vulgaris* L. and *Phaseolus coccineus* L. landraces to *Colletotrichum lindeuthianum* races distributed in Rhodoppi Mountains, Bulgaria. Plant Science 46: 335–341.

Kmiecik K, Nienhuis J (1998) Recent notes and observations on standardization of popping and evaluations of nuña germplasm. Annual Report of the Bean Improvement Cooperative 41: 220.

Koenig R, Gepts P (1989) Allozyme diversity in wild *Phaseolus vulgaris*: Further evidence for two major centers of genetic diversity. Theoretical and Applied Genetics 78: 809–817.

Koenig R, Singh SP, Gepts P (1990) Novel phaseolin types in wild and cultivated common bean (*Phaseolus vulgaris*, Fabaceae). Economic Botany 44: 50–60.

Kolkman JM, Kelly JD (2003) QTL conferring resistance and avoidance to white mold in common bean. Crop Science 43: 539–548.

Kuksal RP, Seth JN (1981) A note on interlocular cavitations inheritance studies in dwarf French bean (*Phaseolus vulgaris* L.). Progressive Horticulture 13(3/4): 37–39.

Kwapata K, Nguyen T, Sticklen M (2012) Genetic transformation of common bean (*Phaseolus vulgaris* L.) with the Gus color marker, the Bar herbicide resistance, and the barley (*Hordeum vulgare*) HVA1 drought tolerance genes. International Journal of Agronomy Vol. 2012: 1–8.

Leakey CLA (1988) Genotypic and phenotypic markers in common bean. In: Genetic Resources of *Phaseolus* Beans (Gepts P ed). Kluwer Academic Publishers, Boston, USA, pp. 245–327.

Lopez-Bucio J, Cruiz-Ramirez A, Herrera-Estrella L (2003) The role of nutrient availability in regulating root architecture. Current Opinion in Plant Biology 6: 280–287.

Mahuku G, Montonya C, Henriquez MA, Jara C, Teran H, Beebe S (2004) Inheritance and characterization of angular leaf spot resistance gene presence in common bean accession G 10474 and identification of an ALFP marker linked to the resistance gene. Crop Science 44: 1817–1824.

Mahuku GS, Henríquez MA, Muñoz J, Buruchara RA (2002) Molecular markers dispute the existence of the Afro-Andean group of the bean angular leaf spot pathogen, *Phaeoisariopsis griseola*. Phytopathology 92: 580–589.

Mahuku GS, Jara C, Cajijo C, Beebe S (2003) Sources of resistance to angular leaf spot (*Phaeoisariopsis griseola*) in common bean core collection, wild *Phaseolus vulgaris* and secondary gene pool. Euphytica 130: 300–313.

Markhart AH (1985) Comparative water relations of *Phaseolus vulgaris* and *Phaseolus acutifolius*. Plant Physiology 77: 113-117.

Melotto M, Afanador L, Kelly JD (1996) Development of a SCAR marker linked to the I gene in common bean. Genome 39: 1216–1219.

Mendez-Vigo B, Rodríguez-Suárez C, Pañeda A, Ferreira JJ, Giraldez R (2005) Molecular markers and allelic relationships of anthracnose resistance gene cluster B4 in common bean. Euphytica 141: 237–245.

Mihov A, Manuelyan H, Kovachev A, Poryazov I (1975) Breeding of garden bean cultivars for processing and suitable for mechanized harvesting. Horticultural and Viticulture Science 7: 76–81.

Miklas PN (2005) DNA markers (SCARS) linked with disease resistance traits in bean (*Phaseolus vulgaris* L.). http://www.ars.usda.gov/sp2UserFiles/Place/53540000/Miklas/SCARtable.pdf (accessed on 10.09.2014).

Miklas PN, Delorme R, Riley RH (2003) Identification of QTL conditioning resistance to white mold in a snap bean population. Journal of the American Society for Horticultural Science 128: 564–570.

Miklas PN, Kelly JD, Beebe SE, Blair MW (2006) Common bean breeding for resistance against biotic and abiotic stresses: from classical to MAS breeding. Euphytica 147: 106–131.

Miklas PN, Larsen R, Victry K, Delorme R, Marma C, Riley RH, Kelly JD (2000a) Marker- assisted selection for the bc-12 gene for resistance to BCMV and BCMNV in common bean. Euphytica 116: 211–219.

Miklas PN, Stone V, Daly MJ, Stavely JR, Steadman JR, Bassett MJ, Delorme R, Beaver JS (2000b) Bacterial, fungal, and viral disease resistance loci mapped in a recombinant inbred common bean population ('Dorado'/XAN 176). Journal of the American Society for Horticultural Science 125: 476–481.

Msuku WAB (1984) Pathogenic variation in Malawian isolates of *Pseudomonas syringe* pv. *phaseolicola* [(Burk) Kong, Dye, and Wilkie] and implications for breeding disease resistant beans. PhD dissertation, Michigan State University, East Lansing, Michigan, USA.

Mukeshimana G, Paneda A, Rodriguez C, Ferreira JJ, Giraldez R, Kelly JD (2005) Markers inked to the bc-3 gene conditioning resistance to bean common mosaic potyviruses in common bean. Euphytica 144: 291–299.

Mutlu N, Miklas P, Reiser J, Coyne D (2005) Backcross breeding for improved resistance to common bacterial blight in pinto bean (*Phaseolus vulgaris* L.). Plant Breeding 124: 282–287.

Myers JR, Baggett JR (1999) Improvement of snap bean. In: Common Bean Improvement in the Twenty-first Century (Singh SP ed). Kluwer Academic Press, Dordrecht, The Netherlands, pp. 289–329.

Nene YL (1988) Multiple disease resistance in grain legumes. Annual Review of Phytopathology 26: 203–217.

Nietsche S, Borém A, Carvalho GA, Rocha R C, Paula-Júnior TJ, Barros EG, Moreira MA (2000) RAPD and SCAR markers linked to a gene conferring resistance to angular leaf spot in common bean. Journal of Phytopathology 148: 117–121.

Ockendon DJ (1983) Pre-breeding in *Phaseolus* beans. Genetica 15: 273–285.

Osorno, JM, Beaver JS, Ferwerda F, Miklas PN (2003) Two genes from *Phaseolus coccineus* L. confer resistance to

bean golden yellow mosaic virus. Annual Report of the Bean Improvement Cooperative 46: 147–148.

Paredes M, Gepts P (1995) Extensive introgression of Middle American germplasm into Chilean common bean cultivars. Genetic Resources and Crop Evolution 42: 29–41.

Parsons L, Howe T (1984) Effect of water stress on the water relations of *Phaseolus vulgaris* and drought resistance *Phaseolus actifolius*. Physiologia Plantarum 60: 197–202.

Poryazov I (1990) Breeding green beans resistant to halo blight, common bacterial blight and BCMV in Bulgaria, Tag.-Ber. Akademy Landwirtsch.-Wiss., Berlin, Germany, 297, S.83–85.

Poryazov I, Mihov A, Kovachev A, Manuelyan H, Velev S (1984) Cultivar Zarya-new garden bean cultivar for mechanized harvesting. Horticultural and Viticulture Science 8: 58–62.

Prakken R (1934) Inheritance of colors and pod characters in *Phaseolus vulgaris* L. Genetica 16: 177–294.

Queiroz VT, Sousa CS, Souza TLPO, Costa MR, Sanglad DA, Ragagnin VA, Barros EG, Moreira MA (2004) SCAR marker linked to the common bean rust resistance gene Ur-11. Annual Report of the Bean Improvement Cooperative 47: 271–272.

Ragagnin VA, Sanglard DA, de Souza TLPO, Moreira MA, de Barros EG (2003) Simultaneous transfer of resistance genes for rust, anthracnose and angular leaf spot to cultivar Perola assisted by molecular markers. Annual Report of the Bean Improvement Cooperative 46: 159–160.

Ram HH (2005) Vegetable breeding: principle and practices. 2nd Revision, Kalyani Publishers, Ludhiana, India, pp 256–273.

Santana G, Blair M, Morales F, Mahuku G, Jaray C, Castaño N (2004) Selección de genotipos de frijol resistentes a antracnosis y mosaico común utilizandotécnicas convencionales y avanzadas de mejoramientogenético. Fitotecnia Colombiana 4(1): 44–54.

Sartorato A, Nietsche S, Barros EG, Moreira MA (2000) RAPD and SCAR markers linked to resistance gene to angular leaf spot in common beans. Fitopatologia Brasileira 25: 637–642.

Schmit V, Baudoin JP (1992) Screening for resistance to *Ascochyta* blight in populations of *Phaseolus coccineus* L. and *P. polyanthus* Greenman. Field Crops Research 30: 155–165.

Schmit V, Jardin P, Baudoin JP, Debouck DG (1993) Use of chloroplast DNA polymorphisms or the phylogenetic study of seven *Phaseolus* taxa including *P. vulgaris* and *P. coccineus*. Theoretical and Applied Genetics 87: 506–516.

Schuster ML, Coyne DP (1981) Biology, epidemiology, genetics and breeding for resistance to bacterial pathogens of *Phaseolus vulgaris* L. Horticultural Reviews 3: 28-58.

Schwartz HF, Brick MA, Nuland DS, Franc GD (2001) Dry bean production and pest management, Regional Bulletin No. 562A. Colorado State University Extension and Agricultural Experiment Station, Fort Collins, Colorado.

Schwartz HF, Peairs FB (1999) Integrated pest management. In: Common bean improvement in the twenty-first century (Singh SP ed). Kluwer Academic Press, Dordrecht, The Netherlands, pp 371–388.

Schwartz HF, Singh SP (2013) Breeding common bean for resistance to white mold: A review. Crop Science 53 (5): 1832–1844.

Scott ME, Michaels TE (1992) *Xanthomonas* resistance of *Phaseolus* interspecific cross selection confirmed by field performance. HortScience 27: 348–350.

Sharma PP, Joshi AK (1993) Improvement of French bean. In: Advances in Horticulture Vol. 5-Vegetable Crops: Part 1 (Chadha KL and Kalloo G eds). Malhotra Publication House, New Delhi, India, pp. 235–254.

Sicard D, Michalakis Y, Dron M, Neema C (1997) Genetic diversity and pathogenic variation of *Colletotrichum lindemuthianum* in the three centers of diversity of its host, *Phaseolus vulgaris*. Phytopathology 87: 807–813.

Silbernagel MJ (1986) Snap bean breeding. In: Breeding Vegetable Crops (Bassett MJ ed). AVI Publication Co., Westport, Connecticut, USA, pp. 243–282.

Silbernagel MJ, Hannan RM (1992) Use of plant introductions to develop U.S. cultivars. In: Use of plant introductions in developing new cultivars (Shands HL and Wiesner LE eds). American Society of Agronomy, Madison, Wisconsin, USA, pp. 1–9.

Singh BK (2007) Studies on variability and heterosis of important economic and nutritive traits in cabbage (*Brassica oleracea* var. *capitata* L). PhD Thesis, Div. of Vegetable Science, IARI, Pusa, New Delhi.

Singh BK (2014) VRFBB-91: A French bean (*Phaseolus vulgaris*) germplasm for earliness. Vegetable Newsletter 1 (1): 5.

Singh BK, Deka BC, Ramakrishna Y (2014) Genetic variability, heritability and interrelationships in pole-type French bean (*Phaseolus vulgaris* L.). Proceedings of the National Academy of Sciences, India Section B: Biological Sciences 84 (3): 587–592.

Singh BK, Pathak KA, Ramakrishna Y, Verma VK, Deka BC (2011) Purple-podded French bean with high antioxidant content. ICAR News: A Science and Technology Newsletter 17 (3): 9.

Singh BK, Ramakrishna Y, Verma VK, Singh SB (2013) Vegetable cultivation in Mizoram: status, issues and sustainable approaches. Indian Journal of Hill Farming 26 (1): 1–7.

Singh BK, Sharma SR, Singh B (2009) Combining ability for superoxide dismutase, peroxidase and catalase enzymes in cabbage head (*Brassica oleracea* var. *capitata* L). Scientia Horticulturae 122 (2): 195–199.

Singh BK, Sharma SR, Singh B (2010a) Antioxidant enzymes in cabbage: variability and inheritance of superoxide dismutase, peroxidase and catalase. Scientia Horticulturae 124 (1): 9–13.

Singh BK, Sharma SR, Singh B (2010b) Heterosis for superoxide dismutase, peroxidase and catalase enzymes in the heads of cabbage (*Brassica oleracea* var. *capitata* L). Journal of Genetics 89 (2): 217–221.

Singh SP (1989) Patterns of variation in cultivated common bean (*Phaseolus vulgaris*, Fabaceae). Economic Botany 43: 39–57.

Singh SP (1999) Integrated genetic improvement. In: Common bean improvement in the twenty-first century (Singh SP ed). Kluwer Academic Publication, Dordrecht, The Netherlands, pp. 133–165.

Singh SP (2001) Broadening genetic base of common bean cultivars: A review. Crop Science 41: 1659–1675.

Singh SP, Cardona C, Morales FJ, Pastor-Corrales MA, Voysest O (1998) Gamete selection for upright carioca bean with resistance to five diseases and a leaf hopper. Crop Science 38: 666–672.

Singh SP, Gepts P, Debouck DG (1991a) Races of common bean (*Phaseolus vulgaris*, Fabaceae). Economic Botany 45: 379–396.

Singh SP, Gutiérrez JA (1984) Geographical distribution of DL1 and DL2 genes causing hybrid dwarfism in *Phaseolus vulgaris* L., their association with seed size, and their significance to breeding. Euphytica 33: 337–345.

Singh SP, Gutierrez JA, Molina A, Urrea C, Gepts P (1991b) Genetic diversity in cultivated common bean. II. Marker-based analysis of morphological and agronomic traits. Crop Science. 31: 23–29.

Singh SP, Muñoz CG (1999) Resistance to common bacterial blight among *Phaseolus* species and common bean improvement. Crop Science 39: 80–89.

Singh SP, Nodari R, Gepts P (1991c) Genetic diversity in cultivated common bean. I. Allozymes. Crop Science 31: 19–23.

Singh SP, Schwartz HF (2011) Review: Breeding common bean for resistance to insect pests and nematodes. Canadian Journal of Plant Science 91: 239–250.

Skroch PW, dos Santos JB, Nienhuis J (1992) Genetic relationship among *Phaseolus vulgaris* genotypes based on RAPD marker data. Annual Report of the Bean Improvement Cooperative 35: 23–24.

Skroch PW, Nienhuis J (1995) Qualitative and quantitative characterization of RAPD variation among snap bean genotypes (*Phaseolus vulgaris* L.). Theoretical and Applied Genetics 91: 1078–1085.

Sofkova S, Poryazov I, Kiryakov I (2010) Breeding green beans (*Phaseolus vulgaris* L.) for complex disease resistance. Genetics and Breeding 38 (3): 77–88.

Souza TLPO, Alzate-Marin AL, Dessaune SN, Nunes ES, Queiroz VT, Moreira MA, Barros EG (2007a) Inheritance studyand validation of SCAR molecular marker for rust resistance in common bean. Crop Breeding and Applied Biotechnology 7: 11–15.

Souza TLPO, Dessaune SN, Sanglard DA, Moreira MA, Barros EG (2007b) Rust resistance gene present in common bean cultivar Ouro Negro (Ur-ON) does not correspond to Ur-3^{+}. Annual Report of the Bean Improvement Cooperative 50: 119–120.

Souza TLPO, Faleiro FG, Dessaune SN, Paula-Junior TJ, Moreira MA, Barros EG (2013) Breeding for common bean (*Phaseolus vulgaris* L.) rust resistance in Brazil. Tropical Plant Pathology 38: 61–374.

Sparvoli F, Bollini R (1998) Arcelin in wild bean (*Phaseolus vulgaris* L.) seeds: sequence of arcelin 6 shows it is a member of the arcelins 1 and 2 subfamily. Genetic Resources and Crop Evolution 45: 383–388.

Strausbaugh CA, Myers JR, Forster RL, McClean PE (1999) Bc-1 and Bc-u–Two loci controlling bean common mosaic virus resistance in common bean are linked. Journal of the American Society for Horticultural Science 124: 644–648.

Taylor JD, Teverson DM, Allen DJ, Pastor-Corrales MA (1996a) Identification and origin of races of *Pseudomonas syringae* pv. *phaseolicola* from Africa and other bean growing areas. Plant Pathology 45: 469–478.

Taylor JD, Teverson DM, Davis JHC (1996b) Sources of resistance to *Pseudomonas syringae* pv. *phaseolicola* races in *Phaseolus vulgaris*. Plant Pathology 45: 479–485.

Thomas CV, Waines JG (1984) Fertile backcross and allotetraploid plants from crosses between tepary beans and common beans. Journal of Heredity 75: 93–98.

Welsh W, Bushuk W, Roca W, Singh SP (1995) Characterization of agronomic traits and markers of recombinant inbred lines from intra- and inter-racial populations of *Phaseolus vulgaris* L. Theoretical and Applied Genetics 91: 169–177.

White JW, Kornegay J, Cajiao C (1996) Inheritance of temperature sensitivity of the photoperiod response in common bean (*Phaseolus vulgaris* L.). Euphytica 91 (1): 5-8.

Yu K, Chun S, Zhang BL (2012) Development and application of molecular markers to breed common bean (*Phaseolus vulgaris* L.) for resistance to common bacterial blight (CBB)–current status and future directions. In: Applied Photosynthesis (Najafpour M ed). Shanghai, China, pp 365-388. http://cdn.intechopen.com/pdfs-wm/30614.pdf.

Yu K, Park SJ, Poysa V, Gepts P (2000) Integration of simple sequence repeat (SSR) markers into a molecular linkage map of common bean (*Phaseolus vulgaris* L.). Journal of Heredity 91: 429–434.

Zapata M, Beaver JS, Porch TG (2010) Dominant gene for common bean resistance to common bacterial blight caused by *Xanthomonas axonopodis* pv. *phaseoli*. Euphytica 179: 373–382.