Chapter 5
Common Bean (*Phaseolus vulgaris* L.) Breeding

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Abstract The common bean (*Phaseolus vulgaris* L.) is a grain legume species, mostly cultivated in many developing countries of Africa, America and Asia. It is considered a key crop for improving food security of people vulnerable to malnutrition. From the 1930s, common bean genetic improvement has historically been conducted by international programs in coordination with government institutions and following traditional methods. Those efforts have created successful varieties in recent decades. But, current climate change effects and the reduced adoption of adequate technologies for cultivation, have threatened common bean productivity. Probably, challenges for the next decades cannot meet using only traditional breeding. Thus, new techniques and approaches for conducting breeding should be soon adopted to obtain new varieties with broad resistance to varied biotic and abiotic stresses. When planning new breeding programs, it is important to consider the current agro-biotechnology advances in molecular markers, functional genomics, mutagenesis, tissue culture and even genetic engineering, which could improve breeding efficiency. Additionally, the conservation, utilization of genetic resources and the promotion of participatory breeding will be crucial to strengthen the least productive common bean systems. It will be important to provide varieties that respond well to agro-ecological management under an integral ecology approach. Finally, it is evident that there is still an opportunity to improve productivity by improving access and adoption of more resilient technologies. In this particular case, community seed banks can play an important role in the future.

Keywords Agro-biotechnology · Climate change · Food security · Participatory breeding · Traditional breeding

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J. M. Al-Khayri et al. (eds.), *Advances in Plant Breeding Strategies: Legumes*,
https://doi.org/10.1007/978-3-030-23400-3_5

5.1 Introduction

The common bean or dry bean (*Phaseolus vulgaris* L.), chromosome number 2n = 2x = 22, genome size ~637 Mbp (Varshney et al. 2010), is an herbaceous annual plant, cultivated worldwide by millions of small-scale farmers for the purpose of harvesting its seeds and immature pods. Mostly, bean production is for subsistence in developing countries involving farmers with low incomes and problems associated with malnutrition. This edible legume crop is recognized as a pulse crop due to the high protein and fiber content of its seeds and low fat content. Its origins extend back to the development of ancient American civilizations; where in combination with other crops such as maize (*Zea mays*), amaranth (*Amaranthus* spp.), cucurbits (*Cucurbita* spp.), tomato (*Lycopersicum esculentum*) and cacao (*Theobroma cacao*), provided food for people before Spanish colonization of the Americas after 1492 (Bukasov 1931; Dressler 1953). After that period, common bean and its cultivation practices were introduced into African and Asian countries, adapting to new crop conditions and providing important nutrition to people to the present day.

The Natural Resources Conservation Service (NRCS) classifies this species as belonging to the genus *Phaseolus*; family Fabaceae; order Fabales; sub-class Rosidae, and class Magnolipsida (USDA 2018). The genus *Phaseolus* encompasses more than 52 species distributed around the world, including wild and cultivated types (Gepts and Debouck 1991). According to FAOSTAT (2018), Asian countries harvested the greatest area in the world (15,101,109 ha; 49.33%) in 2014, followed by Africa (7,653,580 ha; 25%) and the Americas (7,512,139 ha; 24.54% of the total), respectively (Table 5.1). In the same way, the highest production was obtained from Asia (11,660,529 mt; 43.95%) followed by the Americas (7,942,764 mt; 29.94%) and Africa (6,192,711 mt; 23.34% of the total). However, yield statistics position European countries with the greatest yields (2.25 mt/ha) followed by the Americas (1.06 mt/ha).

Table 5.1 Common bean harvested area, production and yield in Africa, America, Asia, Europe and Oceania

Continent	Harvested area (ha)	Production (mt)	Yield (mt/ha)
Africa	7,653,580	6,192,711	0.81
America	7,512,139	7,942,764	1.06
Asia	15,101,109	11,660,529	0.77
Europe	311,014	701,575	2.25
Oceania	35,000	32,000	0.91
World (Total)	30,612,842	26,529,579	0.86[a]

Source: FAOSTAT (2018)
[a]average data, *mt* metric tons, *ha* hectares

Table 5.2 Common bean: world ranking of the twenty largest country producers ordered by production and indicating yields in 2016

Country	Production (mt)	Yield (mt/ha)
Myanmar	5,189,977	1.68
India	3,897,611	0.41
Brazil	2,615,832	1.01
USA	1,269,916	2.01
Tanzania	1,158,039	1.04
China	1,139,866	1.64
Mexico	1,088,767	0.69
Uganda	1,008,410	1.50
Kenya	728,160	0.62
Ethiopia	483,923	1.66
Rwanda	437,673	0.85
Cameroon	390,816	1.30
Burundi	371,892	1.78
Angola	367,255	0.44
Argentina	366,588	1.02
Korea	320,399	0.88
Belarus	277,755	2.51
Indonesia	277,408	1.16
Canada	249,400	2.26
Guatemala	247,680	0.98

Source: FAOSTAT (2018)

For 2016, statistics tabulated by country indicated that the five largest common bean producers were Myanmar, India, Brazil, USA and Tanzania (Table 5.2). Others positions in ranking of the twenty largest common bean producers are mainly represented by African and American countries. Common bean production in North America is promoted by residents coming from Latin American countries that represent the so-called *nostalgic market*. However, yield data are showed do not match with the greatest production, meaning that while some countries have relatively high production, for instance India and Mexico (3,897,611 and 1,088,767 mt, respectively), but yields are low compared with other countries.

This fact could be ascribed to the high investment of appropriate technology during production such as utilization of high-quality seeds, irrigation systems, and proper pest and diseases control during growth and development stages, appropriate plant nutrition practices, among others. Countries producing above 1 million mt, Myanmar, Brazil, USA, Tanzania, China and Uganda, also registered yields of more than 1 mt/ha. Belarus registered the highest yield (2.51 mt/ha), but its total production is small compared with other industrialized countries.

5.1.1 Importance for Human Nutrition and Food Security

The common bean is cultivated as a staple food mainly by farmers under subsistence conditions in developing countries, where it represents the main source of protein, iron and zinc to people vulnerable to malnutrition. Lareo and Gonzalez (1988) provided a valuable literature compilation of the potential benefits of incorporating beans in the human diet. That review estimates that crude protein in bean seeds is 16–30%. This protein can be divided into five main fractions: phaseolin (36–46% by weight), globulin-2 (5–12%), albumin (12–16%), prolamine (2–4%) and alkali-soluble fraction (20–30%). The same source mentions that iron content is on average 70 mg/kg and in the same way as protein, its concentrations varies depending on environmental and cultivating conditions. Protein intake, in humans, can be improved from 4.54 to 6.26% when combined in a ration 3:7 with cereals such as maize. Indeed, some nutritionists point out that common bean and maize are a perfect food combination due to amino acids complementarity, enhancing their assimilation by humans (Mora-Aviles et al. 2007).

Condensed tannin and anthocyanin content, the first affecting iron absorption and the second with antioxidant properties, have a relationship with seed coat coloration (Díaz et al. 2010a). In this sense, total phenolic content (free, soluble conjugate, insoluble bound fraction) have diverse antioxidant capacities that vary depending upon the variety, some genotypes being an important dietary sources of natural antioxidants for prevention of diseases triggered by oxidative stress (Wang et al. 2016). Recent studies suggest that peptides present in common bean seeds, specifically in non-digestible fractions, have an antiproliferative effect on human colorectal cancer cells by modifying expression of markers associated with cell cycle arrest or mitochondrial activated apoptosis (Luna et al. 2014). Additionally, common bean consumption could have the potential to reduce serum cholesterol concentrations, improving health conditions in diabetic patients and providing, in many aspects, metabolic multiple benefits for weight control as well (Anderson et al. 1999). Also, it is estimated that the consumption of partially-hydrolyzed bean seeds may provide important functional elements to protect cells against inflammation present in injured tissue or chronic disease conditions (Oseguera-Toledo et al. 2011).

Despite the natural high nutritional quality of beans, they are considered a suitable vehicle for iron and zinc biofortification (Petry et al. 2015). Thus, there have been efforts to develop and release biofortified varieties in many developing countries. These varieties have been added to local seed programs aiming to improve iron, zinc and protein intake in rural families (Saltzman et al. 2017). Many seed programs are distributing seeds from those varieties to people vulnerable to malnutrition. The release, production and distribution of common bean varieties with high protein, iron and zinc contents can be traced, following information from the centers and institutes listed in Appendix I.

5.1.2 Climate Change Scenarios and Challenges

Reliable knowledge about the occurrence of different phenomena related to the variability and changes of climate that scientists have projected for the coming decades is essential for the establishment of resilience strategies in agriculture. Here, genetic improvement of key crops including common bean in conjunction with the adoption of new management practices, will be vital to prevent global famine.

Currently, it is difficult to predict with a high level of certainty how the effects of change and climatic variability are going to affect bean production in each part of the world. Therefore, each country must carefully analyze the different projections and take corresponding measures. It is almost a shared consensus that temperatures will increase in magnitude globally with continents experiencing reduction or increase in precipitation rates (Christensen et al. 2013). Model predictions point out that East Africa could experience impacts in common bean yields from −18.1 to +23.7%. Similarly, Southern Brazil could present impacts of up to +45% and for Central America from −4 to −87% (Porter et al. 2014). The range of predictions is quite large and it limits, to an extent, the drafting of general measures per region. More valuable information about global climate change reports can be found at the Intergovernmental Panel on Climate Change's website (http://www.ipcc.ch/).

According to global climate models, CSIRO-Mk3 and MIROC-H, for the years 2050 and 2100 climate conditions are expected to be more favorable for common bean cultivation in the Northern Hemisphere, but unfavorable in the Southern Hemisphere (Ramírez-Cabral et al. 2016). Also, heat and drought stresses are considered among the foremost factors limiting common bean production under present and future projected conditions (Beebe et al. 2011; Beebe 2012; Ramírez-Cabral et al. 2016; Rodríguez and Creamer 2014). Based on those scenarios, considerable parts of Africa and Latin America, where common bean is a crucial staple food, are projected to reduce areas for cultivation because of unfavorable conditions, affecting the food security of millions of people whose survival and nutrition relies on this legume (Wortmann et al. 1998). For South America, projections indicate that in comparison with the historical period (1980–2005), climate change will make drought more recurrent, but less severe across this part of the continent (Heinemann et al. 2017).

For heat and drought conditions, a comprehensive understanding of plant behavior through the application of biophysical crop models is needed. For instance, during field experiments using common bean plants exposed to heat and drought stresses, the Farquhar-Ball-Collatz model (FBC model) was found to be reliable to predict water dynamics, plant growth and stomatal conductance in comparison with the Goudriaan and van Laar model (GvL model) (Seidel et al. 2016). It will be important to continue setting up, calibrating and validating more models to provide useful information to design experiments for plant selection under stressful conditions.

Water scarcity is a limitation for common bean, which requires at least 300–500 mm of rainfall throughout the 60–120 days of growth and developmental stages (Allen et al. 1989; White et al. 1995). In addition, periods of fluctuating rainfall can cause significant losses due to off-season rains that create conditions for the occurrence of fungal and bacterial infections, more so when they coincide with the periods of pre-harvest, harvest and drying of the grain (the latter, many times, are carried out in the open field in semiarid and inter-cropping systems). After more than nine days of heat stress (33 °C days and 27 °C nights) before anthesis, the anthers of the heat-susceptible varieties could experience indehiscent and abnormalities in pollen grains reducing seed formation and yields (Gross and Kigel 1994; Porch and Jahn 2001). It is estimated that a heat stress of 33 °C days and 30 °C nights could reduce yield components; seed number, pod number, mean seed weight and seeds per pod by 83, 63, 47 and 73%, respectively (Rainey and Griffiths 2005). When drought and heat stresses are present together, the effect can be overwhelming, generating total crop loss.

On the other hand, increased temperatures, elevated CO_2 levels and precipitation variations, conditions projected in various climate scenarios, may trigger significant changes in pathogen and pest population dynamics (Jones 2016). Thus, pest and disease populations could experience changes in population growth rates, number of generations, occurrence, interspecific interactions, virulence, balance of natural enemies and efficacy of crop protection technologies (Macedo et al. 2017; Reddy 2013; Sharma et al. 2010; Taylor et al. 2018). Under those conditions, some secondary or even tertiary pests and diseases could turn into first order, limiting control measures because of the lack of proper practices and experience by farmers and technicians to control them. Also, the dynamics of many insect vectors could become aggressive, spreading new virus strains to other locations (Jones 2016; Jones and Barbetti 2012).

5.1.3 Domestication, Selection and Early Improvements

There is extensive literature on the domestication and origin of the common bean, using different approaches, some posit common bean with a Middle American origin and another Andean. But, most researchers agree that this species was domesticated following two main events, in Middle America and the Andes. According to multiple DNA-based studies, this species was probably domesticated from wild forms around 8000–10,000 years ago (Bitocchi et al. 2012, 2013; Chacon et al. 2005; Gepts and Debouck 1991; Schmutz et al. 2014; Singh 1992). Archaeological records, DNA and morphological differences between domesticated and wild species indicate that ancient civilizations selected from wild types those plants holding more upright growth habits, shorter stem inter-nodes, completely indehiscent pods and larger seeds; ultimately accounting for current cultivated phenotypes (Gepts and Debouck 1991; Schmutz et al. 2014). Likely, the occurrence of spontaneous mutations and natural hybridizations contributed to broaden genetic variability, crucial during human selection.

Voysest (1983, 2000) reported the early improvements of common bean carried out between 1930 and 1999. There is consensus that common bean breeding activities began on 1930s, probably simultaneously in Mexico and Brazil. There is limited historical information about the breeding process for obtaining the first varieties, but it is inferred that breeders started by improving agronomic traits of local landraces. The first varieties were named for their seed coloration and other main attributes. Later in the 1940s, the Rockefeller Foundation sponsored formal common bean breeding programs in Mexico and Colombia. The first initiatives for breeding activities in collaboration among countries were coordinated from Costa Rica, incorporating efforts from Mexico, Guatemala and El Salvador. Later in 1962 the Central American Cooperative Program for Common Bean Breeding (PCCMF, Spanish acronym) was created through the Centro American Cooperative Program for Food Crop Improvement (PCCMCA, Spanish acronym). Between 1950 and 1970, common bean programs operating locally in Mexico, Colombia and Costa Rica, were strengthened through international cooperation which provided training for young researchers from different Latin American countries. The Inter-American Institute of Agricultural Sciences (IICA, Spanish acronym) and Pan-American Agricultural School (Zamorano, Honduras) both played important roles in the development common bean in the region. Around 91 varieties were evaluated during that period. In 1973, the International Center for Tropical Agriculture (CIAT, Spanish acronym) inaugurated its Grain Legume Program through an international symposium entitled: Potential of Grain Legumes. Since then, CIAT has provided a leadership tradition that persists in common bean breeding, with remarkable worldwide achievements to the present.

In 1980, the Bean/Cowpea Collaborative Research Support Program was established for the purpose of improving the nutritional situation of people suffering from food scarcity and enhancing human capacities for bean and cowpea research. Four American universities took part in important projects at that time. The program contributed significant new varieties, improving nitrogen fixation by symbiosis with rhizobia, improving nutritional quality and digestibility of seeds, and conferring resistance to heat, drought and viral infections. Kelly and Cichy (2013) document that there were six public bean breeding programs at major land grant universities, four programs that focused on bean genetics and pathology and five private companies actively working on bean breeding in the USA. Singh et al. (2007) and Teran et al. (2009) reviewed the bean breeding improvements in the western USA over 56 years, documenting 34% genetic gains, increasing seed size and incorporating some degree of resistance to diseases in most varieties. In Brazil, the Brazilian Agricultural Research Corporation (Embrapa, Portuguese acronym) Rice and Beans, has coordinated, since 1974, a program for the genetic improvement of carioca-type common bean for the entire country. According to Faria et al. (2013) and Moreira et al. (2010), between 1984 and 2010 this program released around 50 new varieties (mostly using pedigree method) at an average rate of 1.9 varieties per year, showing significant genetic progress in terms of grain yield (0.72% per year), plant architecture (2%), resistance to lodging (2%) and quality of grains (2.4% per year). At present, Embrapa Rice and Beans continues to provide bean farmers with highly-productive cultivars with high-quality grains.

In Tanzania, the first bean improvement program was initiated at Tengeru Agricultural Research Institute (TARI), near Arusha, in 1959. Subsequent events were summarized by Allen et al. (1989) and Hillocks et al. (2006) in a review of common bean breeding activities in Tanzania 1959–2005. A total of 82 accessions were introduced into the breeding program at TARI from around the world, 1960–1961, which released the first rust (*Uromyces appendiculatus*) resistant varieties, Tengeru 8 and Tengeru 16. In the 1970s the first National Bean Improvement Program in Tanzania began breeding to improve the quality and yield of beans. In 1975 a total of 1046 germplasm lines had been collected at three centers; Uyole Agriculture Center in the south, Ilonga Agricultural Research Institute in the center and Lyamungu Agricultural Research Institute (LARI) in the north. Later, regional networks and international programs played an important role to enhance bean-breeding activities, CIAT in Colombia being an important partner. Today, breeding programs are working collaboratively to overcome common limitations in around 30 African countries. Detailed information is available at web pages shown in Appendix I.

5.2 Cultivation and Traditional Breeding

The genetic improvement of key crops can provide dependable solutions to the problems resulting from climate change only if the varieties created are released in conjunction with the most appropriate forms of sowing and field management to allow exploiting all the attributes that plant breeders have identified throughout the experimental phase.

5.2.1 Current Cultivation Practices

In developing countries, the common bean is cultivated in semiarid and subsistence intercropping systems; small and large monoculture are also present in countries with higher incomes (Singh 1992). Regardless of the diversity of cropping systems, plant breeding can still play an important role to improve productivity, in semiarid and subsistence intercropping systems, which includes poor farmers in the developing countries (Waldman et al. 2014).

It is indisputable that despite the fact that regional breeding programs have released successful varieties, there is still low productivity in relation to the actual potential of the species. This situation is caused in part by the low utilization of high-quality seeds in developing countries. Diverse reports from Africa and Central America point out that typical bean farmers use their own seeds for sowing (Asfaw et al. 2013; Goettsch 2016; IICA 2009; Katungi et al. 2011; Opole et al. 2003; Wortmann et al. 1998). In Central America, for instance, it is estimated that only 14% of common bean farmers use certified seeds for production, the remaining area is sown with self-produced seed of suboptimal quality (IICA 2009).

Some seed programs have implemented a modality called *Community Seed Banks* (CSBs) with the purpose of increasing the availability of adapted seeds at lower costs, compared with certified seeds. According to FAO (2014) Community Seed Banks are farmers' organizations that store and manage seeds, aiming to provide community members with seeds to use, which are obtained from the farmers in the community. Those organizations provide seeds of improved varieties, landraces and old cultivars to the region, receiving in some successful cases, a sort of technical supervision and following quality standards from non-governmental and governmental institutions. The results and positive impacts of these initiatives have been documented, highlighting successful cases around the world (Coomes et al. 2015; FAO 2014; Katungi et al. 2011; Vernooy et al. 2015, 2017). Nevertheless, it is important that CSBs take into account some technical principles of seed production; otherwise this mechanism could be distributing low-quality seed and spreading important seed-borne pathogens (Marcenaro and Valkonen 2016). The use of common bean seeds with low vigor could reduce yield by up to 20% (Mondo et al. 2016); whereas the use of proper plant densities in semiarid and subsistence systems can increase bean yield by 30–70%, also avoiding costs associated with weed management (Dusabumuremyi et al. 2014).

It is known that many agricultural research institutes have published local technical bulletins, guidelines and booklets about appropriate practices for common bean cultivation, as outputs of different regional projects. More detailed information about technical documentation is available at the international institution websites listed in Appendix I. Nonetheless, despite all available documentation, the adoption and implementation of best practices is still too low (Goettsch 2016; Opole et al. 2003). Most common bean production in developing countries is managed using only minimal inputs. That means, farmers after sowing, carry out weed control, fertilization, pests and disease management, pre-harvest, harvest and storage, using scarce resources and family labor, limiting the real potential of varieties developed by international programs which respond best to optimum management practices (Goettsch 2016; Opole et al. 2003). In addition, common bean can be found prospering in mixture systems with other crops (Singh 1992; Woolley and Davis 1991; Woolley et al. 1991). According to Argaw and Muleta (2017) and Taylor et al. (1983) the simple adoption of the best-adapted variety, use of quality seed and the inoculation of the seed with an appropriate rhizobium strain could easily double yields; adoption of complete management packages could improve common bean production even more. On the other hand, in industrialized countries the suitable utilization of technology has prompted high yields and good economic profitability for special markets as in North American, for instance, where common bean systems are based on monoculture with the use of complete technological packages (Kelly and Cichy 2013; Thung 1991).

It is also important to consider the increasing interest in the use of bio-inputs (beneficial biological agents, fungi, bacteria) for fertilization and crop management of pests and diseases. Far from trying to create an economic dependence, bio-inputs could be produced at the laboratory level, as well as at the farm level by artisanal methods, reducing the costs associated with their wide use, all this under an integral ecology approach.

5.2.2 Improvement Strategies, Methods and Limitations

International breeding programs work on a regional framework, centralizing the first stages of breeding at headquarters locations of international centers and institutions and employing specialized expertise. Thereafter, activities are coordinated with national institutes of agriculture research (NIARs) in target countries, to carry out evaluations and yield trials under different environmental conditions until release of a new variety (Fig. 5.1). This approach optimizes economic and human resources. However, it is important to point out that there are some NIARs that have a robust research agenda, developing most common bean breeding activities at the local level.

Since the first formal common bean breeding programs began in the 1930s, most activities have involved phenotypic evaluations and pedigree information. These programs began by making manual crossings between or among elite parents holding desirable characteristics. From 20 to 200 crosses could be performed to obtain a desirable number of individuals at the F_1 generation, but it would depend on economic resources and facilities (Acquaah 2007, 2012). Common bean breeders could improve the success percentage of effective crosses by adopting procedures that reduce minimum damage to floral buds, increase seed setting and confirm successful hybrid F_1 plants by using DNA markers (Jiménez and Korpelainen 2013; Kelly and Cichy 2013).

Individual self-pollinated species are highly homozygous in most of their loci, although heterogeneous when compared among populations. This means that via directed crosses it is possible to reshuffling allelic combinations to search for new promising genotypes, to be fixed in subsequent generations. In this sense, crossing has become a crucial approach for obtaining working populations that permit the greatest possible genetic variability.

It is important to highlight the limitation of plant breeding processes based mainly on mass selection, since the opportunity to identify new and useful allelic combination is very small compared to the segregating populations obtained from crosses (Jiménez and Korpelainen 2013). Conducting crosses requires expertise and resources, but the benefits are significant since by choosing suitable parents it is possible to create thousands of divergent pure lines. There are four different gene pools for the common bean showing a certain degree of cross incompatibility: primary gene pool comprises both *P. vulgaris* cultivars and wild relatives from that species; secondary gene pool that encompasses *P. coccineus*, *P. dumosus* (=*P.*

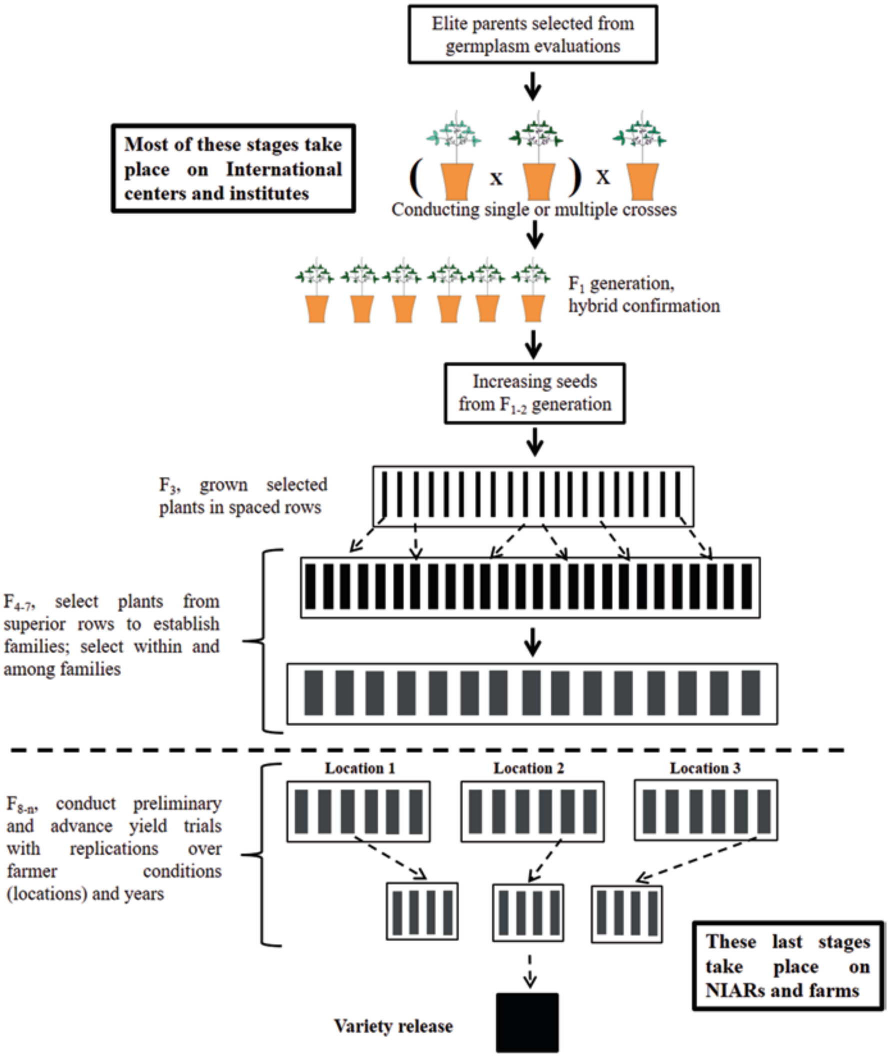

Fig. 5.1 Flowchart showing the basic steps in common bean breeding. The dotted line separate activities carried out in international centers from those on NIARs

polyanthus), and *P. costaricensis*; tertiary gene pool including *P. acutifolius* and *P. parvifolius*; and quaternary gene pool that counts *P. lunatus*, *P. carteri*, *P. filiformis* and *P. angustissimus* (Pathania et al. 2014). For the utilization of genes from different gene pools, specifically for crosses of *P. acutifolius, P. coccineus*, *P. costaricensis* and *P. polyanthus* with the common bean, it is necessary to improve crossing performances by tissue culture techniques for the rescue of embryos in early developmental stages (Andrade-Aguilar and Jackson 1988; Geerts et al. 2002; Ivančič and Šiško 2003; Mbogo 2007; Mejía-Jiménez et al. 1994; Pathania et al. 2014;

Porch et al. 2013). These crosses between different species have allowed incorporating valuable alleles for conferring resistance to biotic and abiotic stresses and nutritious value in important breeding lines. Protoplast fusion techniques have also been used to hybridize different *Phaseolus* species (Geerts et al. 2008). However, the recalcitrant nature of the common bean has limited its use due to the very low regeneration rates as addressed in Sect. 5.5.1. It is important to point out that recent efforts could improve plant regeneration rates in the coming years.

In the F_2 generation, plants are grown in greenhouse to increase the quantity of seeds obtained from each F_1 plant. From F_2 generation onwards, selection could adopt different pathways depending upon the selection method used. Acquaah (2007, 2012) provides a comprehensive description and examples of different selection methods that can be used to perform selection from the F_2 generation until release of a new variety. However, most current common bean varieties have been obtained using the pedigree method (Kelly and Cichy 2013; Moreira et al. 2010). In some cases, breeders may innovate in combining the best attributes of two or more methods as one, obtaining benefits in genetic gains.

Most developing countries receive pure lines or families (F_8–F_{12} generations) from international breeding programs to be incorporated into local research projects in NIARs. Thus, once common bean nurseries are received, the latest stages of selection are focused on comparisons among families and lines and not on selecting individuals within populations. Thus, there is no chance to improve important traits in these genetic materials. These field trials are conducted under farmer field conditions to ensure profitability and acceptability by consumers as well. Unfortunately, each NIAR releases a new variety applying their own nomenclature, causing confusion and making the identification of varieties difficult because the same genetic material can be in more than one country, but holding different names.

It is evident that even under this efficient approach, there is not enough genetic variability in advance genetic materials to confront new challenges, because it derives from a narrow genetic base (Pathania et al. 2014). The wide gamma of genetic diversity documented in various marker-based studies has not been exhausted by all breeding programs (see Sect. 5.3.1 for references). All this germplasm could conserve useful allelic variation to be incorporated into breeding programs. But, this option has been limited by reduced funding, inadequate infrastructure (laboratories, greenhouse) and lack of skilled human resources to conduct those activities in countries of origin.

Most breeding activities have used traditional methods, without actively exploiting all available biotechnological tools to strengthen bean breeding programs and increase efficiency (Aragão et al. 2013; Dwivedi et al. 2006; Ender et al. 2008; Gupta et al. 2010; Kumar et al. 2011; Mahuku et al. 2004; Miklas et al. 2000, 2006; Oliveira et al. 2005; Pasev et al. 2014; Schneider et al. 1997; Varshney et al. 2010; Yu et al. 2000; Zargar et al. 2017). Moreover, breeding activities in a good number of NIARs have not strengthened local breeding activities aiming to complement regional efforts. For instance, it would be practical to incorporate new alleles into old but successful commercial varieties, conserving desirable characteristics by backcrossing. This could be considered a derived variety according to the

International Union for the Protection of New Varieties of Plants (UPOV, Spanish acronym) (UPOV 1991, 2017). Also, it could be important to consider maintenance breeding as an option to overcome loss of adaptation of some old varieties (Peng et al. 2010). As the success of symbiosis of common bean and bio-inputs increases significantly yields (Bennett et al. 2013; Blair 2013; Dall'Agnol et al. 2013; Kawaka et al. 2014; Maougal et al. 2014; Snoeck et al. 2003; Weisany et al. 2016) and it depends on variety and microorganism strain correspondence (Samago et al. 2017), it is important to consider the inclusion of this factor/variable during selection as the response of a variety to management using bio-inputs for fertilization, pest and disease control. All these strategies seem promising because they decrease production costs, increase soil fertility, disrupt the life cycles of pests and diseases and improve resilience under the climate change context.

On the other hand, recently, participatory breeding has risen forcibly in Latin American and African countries in response to the necessity of providing well-adapted varieties to local conditions. Basically, this approach is conducted starting with planning workshops led by breeders, technicians and some well-trained farmers. During these workshops, farmers in coordination with breeders define an ideotype as a target, holding the characteristics depending on environmental conditions and farmers' preferences. Thereafter, farmers collect all the available germplasm from the community or abroad; this collection may include landraces, old cultivars and improved varieties. In practical terms, the initial genetic material as a population is highly heterogeneous, but homozygous at the same time. Most participatory breeding programs are carried out using mass selection on homozygous populations, but there are some experiences where populations obtained from crosses are also used (Almekinders 2011; Asfaw et al. 2012). Because the mass-selection method is not efficient for quantitative traits with low heritability, such as yield, it is possible to improve the performance of participatory breeding at initial stages by adopting other selection methods, for instance, mixed-model selection under augmented block design that has been used in different species with successful results (Aruna and Audilakshmi 2008; Balestre et al. 2013; Gonçalves-Vidigal et al. 2008; Oliveira et al. 2012; Piepho et al. 2008; Upadhyaya et al. 2009). Participatory initiatives are a good source of adapted varieties for farmers when combined with seed multiplication at CSBs. Unfortunately, these kinds of varieties have not found a place in current seed legislations in most countries; consequently, seed production following formal mechanisms is not possible for those varieties, despite their high-resilience potential (Dawson and Goldringer 2012).

5.2.3 Role of Biotechnology

Present advances in plant biotechnology and recent reference genome and genome-wide analysis for common bean have made available different methods with high potential to be used for breeding (Schmutz et al. 2014), refining the incorporation of key traits, the performance of selection programs or for identifying promising parents for crosses. Marker-assisted selection (MAS), genomic selection using single nucleotide polymorphisms (SNPs), genome editing using CRISPR/Cas system, plant transformation, in vitro culture, are some examples of those developments (Aragão et al. 2013; Dwivedi et al. 2006; Ender et al. 2008; Gupta et al. 2010; Kumar et al. 2011; Mahuku et al. 2004; Miklas et al. 2000, 2006; Oliveira et al. 2005; Pasev et al. 2014; Scheben et al. 2017; Schneider et al. 1997; Varshney et al. 2010; Yu et al. 2000; Zargar et al. 2017). But, the use of these approaches have been quite limited in current international programs, because of high costs (Blair et al. 2007; Varshney et al. 2005) and the misconception that biotechnology tools frequently are confused with genetic engineering or transgenics by farmers' organizations. Although Sect. 5.2.2 stressed the importance of exploring and exploiting all the available germplasm, in some cases recruiting novel alleles by phenotypic methods could be too slow, so new traits related to resistance to drought, heat, pests and diseases may be supplied through biotechnology (Svetleva et al. 2003); therefore, it is economically reasonable to balance the time and cost for certain traits that biotechnology could incorporate into new varieties to cope with new future challenges.

5.3 Germplasm Biodiversity and Conservation

Plant breeders evaluate large numbers of accessions looking for new sources of genes from different gene pools that, together with seed bank curators and other experts, can identify and study their potential for genetic improvement. Without genetic variability the work of the breeder is severely limited, since the selection process is a game of numbers whose richness significantly increases the chances of finding something new and useful. This is why ex situ and in situ collections represent a key element of any plant breeding process.

5.3.1 Germplasm Diversity and Phylogeny

The common bean is a species that exhibits high phenotypic variability of most of the 90 traits commonly suggested for phenotypic studies and variety description (Muñoz et al. 1993). Seed characteristics; size, color and shape are the most relevant and visible trait when identifying a variety and it determines in some countries the market value of beans, because of consumer preferences (Fig. 5.2). Singh (1989) in one of the most extended studies, examined 18,000 accessions from the CIAT seed bank at two different locations in Colombia, describing relevant phenotypic diversity in populations collected from different gene pools. That study divided germplasm into a total of six gene pools from Middle American and four gene pools from South American centers of domestication. In a more recent study, Rana et al. (2015) described the characterization of a collection of 4274 accessions originating from

Fig. 5.2 Phenotypic diversity for seed traits in *Phaseolus* collections of Mesoamerican origin. Photos: Rows (**a** and **b**) courtesy of National Institute of Forestry, Agriculture and Livestock Research (INIFAP), Mexico. Rows (**c** and **d**) courtesy of National Center of Genetic Resources (CNRG), INIFAP, Mexico. Scale in centimeters (cm)

58 countries using 22 phenotypic traits measured during two years, finding high phenotypic diversity for traits such as leaf length, leaf width, pod length, pods per plant, seeds per pod and 100-seed weight.

Blair et al. (2009) analyzed the level of genotypic diversity in a collection composed of 604 accessions collected from different countries and continents, indicating on average 18.4 alleles per locus. In primary and even secondary centers of origin in Africa, America, Asia and Europe, analysis using different kind of markers revealed a high level of genetic diversity, suggesting spontaneous hybridizations among gene pools and mutations playing a relevant role in fixing new allele variants after introduction from America (Angioi et al. 2010; Asfaw et al. 2009; Ávila et al. 2012; Blair et al. 2006, 2009, 2012; Burle et al. 2010; Cabral et al. 2011; Díaz et al. 2010b; Fisseha et al. 2016; Gómez et al. 2004; Jiménez and Korpelainen 2012; Kwak and Gepts 2009; McClean et al. 2012; Nemli et al. 2017; Raggi et al. 2013; Santalla et al. 2010; Sharma et al. 2012; Tiwari et al. 2005; Xu et al. 2014; Zhang et al. 2008).

5.3.2 Genetic Resources Conservation Approaches

Common bean genetic resources are conserved ex situ, in seed banks and in situ on farms around the world. The first strategy allows conserving (intact) representative seed samples in cold rooms at low or ultra-low temperatures (from −20 to +4 °C) for long time periods, until physiological quality declines by natural aging. On the other hand, in situ conservation is conducted on farms following normal production systems and allowing the varieties to continue to evolve and change. There is consensus that the best approach is to combine efficiently both strategies, taking advantage of both in situ and ex situ systems as an integrated approach.

The Seed Bank of CIAT located in Palmira, Colombia holds the biggest common bean collection in the world (Johnson et al. 2003). This collection consists of around 37,390 accessions, with 441,225 samples distributed for breeding and research purposes to 105 countries. About 71.6% of the distributed samples have been used actively in breeding programs conducted by CIAT, 15.5% have been requested by the National Agricultural Research System, USA (NARS), 10.4% by various universities and the remaining 2.5% has been distributed to private companies and other applicants (CIAT 2018). It is estimated that over 70% of the value of increased common bean production is due to the use of imported varieties derived from breeding programs using the CIAT bean collection (Johnson et al. 2003). There are also important *Phaseolus* collections in international centers and research institutes elsewhere in the world.

On the other hand, in situ conservation of the common bean germplasm has relevance as a policy for improving crop resilience under climate change conditions in different countries (Coomes et al. 2015; FAO 2014; Katungi et al. 2011; Vernooy et al. 2015, 2017). In addition to producing seeds, CSBs also contribute to the conservation of genetic diversity on farms and ensure continuity. Under on-farm conservation, biotic and abiotic factors, in combination with the systematic processes underlying phenotypes, creating genetic divergence at the subpopulation level with significant implications for conservation (Thomas et al. 2015; Tiranti and Negri 2007). Studies in Uganda point out that the production of several landraces and improved varieties in mixed cropping systems is important for pest and disease management (Mulumba et al. 2012; Ssekandi et al. 2016).

5.3.3 Cytogenetics

The common bean is a diploid species with chromosome number $2n = 2x = 22$ (Fig. 5.3) and genome size ~ 637 Mbp (Varshney et al. 2010). There are 52 species in the genus *Phaseolus*, most have the same chromosome number with the exception of *P. leptostachyus* ($2n = 20$) (Delgado-Salinas et al. 2006; McClean et al. 2008). Some minor variations between *P. vulgaris* and *P. lunatus* genomes are

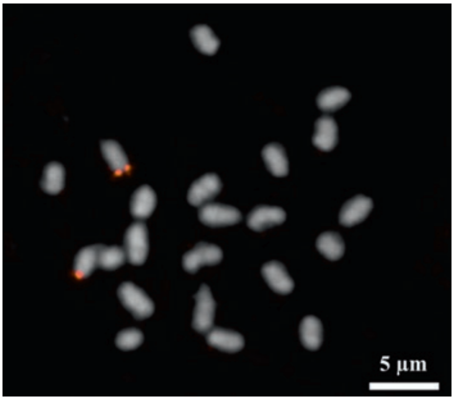

Fig. 5.3 Common bean chromosomes showing in situ localization of the single-copy BAC (Bacterial Artificial Chromosome) 224I16 (red) on chromosome pair 9 of *Phaseolus vulgaris*, cultivar BAT93. Chromosomes are counter-stained with DAPI (4′-6-diamidino-2-phenylindole) and visualized in gray. Photo: Courtesy of Andrea Pedrosa Harand and Artur Fonseca, Federal University of Pernambuco, Brazil

ascribed to pericentric inversions on chromosomes 2, 9 and 10 during evolution of the genus (Bonifácio et al. 2012). Aneuploidy probably has been important during the evolution of the karyotype (Mercado-Ruano and Delgado-Salinas 1998). The common bean genome is composed of 52% euchromatin, 31% pericentromeric heterochromatin, 5% ribosomal DNA (rDNA) and 12% centromeric heterochromatin (Fonseca et al. 2010). In comparison with other legumes, with the exception of soybean, the common bean shares same or similar chromosome number with cowpea (*Vigna unguiculata*), mung bean (*Vigna radiata*), rice bean (*Vigna umbellata*), pigeon pea (*Cajanus cajan*) and hyacinth bean (*Lablab purpureus*) (McClean et al. 2008).

5.4 Molecular Breeding

The molecular breeding of economically-important crops has attained great relevance in the last decade. Although the common bean is a crop which has had fewer efforts and resources applied to it in recent years, several research groups have made important discoveries. These have revealed the potential of marker-assisted selection and the opportunity to influence genetic improvement via genetic expression and metabolic processes which are involved in yield formation under stress conditions. As well, advances in bioinformatics and the development of platforms in cyberspace have made it possible to share applications and databases within the scientific community.

5.4.1 Molecular Marker-Assisted Breeding

Molecular markers and molecular genetic linkage maps are needed to conduct MAS (Acquaah 2007, 2012; Varshney et al. 2005). The first linkage maps for common bean were constructed using few linkage groups and included only genes controlling seed coloration and patterns (Basset 1991). Subsequently, advances in DNA markers such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), SSRs and SNPs provided more information for fine mapping of divergent inbred populations (Bassi et al. 2017; Blair et al. 2011; Briñez et al. 2017; Chen et al. 2017; Cordoba et al. 2010; Cortes et al. 2011; Ferreira et al. 2010; Galeano et al. 2011; Gonzalez et al. 2017; Goretti et al. 2013; Gujaria-Verma et al. 2016; Hanai et al. 2010; Kelly et al. 2003; Song et al. 2015; Valdisser et al. 2017; Vidak et al. 2017). The integration of an intra-gene pool linkage map towards a consensus linkage map is an important task to fill in gaps and also to strengthen synteny studies (Galeano et al. 2011; Song et al. 2015; Yuste-Lisbona et al. 2012). Today, there are a significant number of available markers for this species; for instance, more than 2000 SSRs markers derived from genomic and genes sequences are available for common bean (Müller et al. 2014).

Nonetheless, the use of MAS has been limited for common bean in comparison with other legumes. Most experiments have focused on improving resistance to fungal, bacterial and virus diseases (Beaver and Osorno 2009; Blair et al. 2007; Jiménez 2014; Kumar et al. 2011; Mukeshimana et al. 2005; O'Boyle et al. 2007; Oliveira et al. 2005; Rocha et al. 2012; Souza et al. 2014; Yu et al. 2000) and for selection of genotypes under drought conditions (Schneider et al. 1997) with successful results in terms of genetic gains. However, despite experimental advances, the practical use of MAS and genomic-assisted selection in international and regional breeding programs is low because of the high costs associated with the screening of large numbers of individuals at each generation (Blair et al. 2007; Varshney et al. 2005). But, considering their evident advantages, compared with traditional selection and the efforts to reduce costs and to obtain new varieties possessing novel traits, these techniques should be adopted in the future. As participatory breeding is increasing in many developing countries, with promising results, it will be important to make efforts to incorporate marker-based tools into participatory breeding to strengthen the emergence of that approach. Figure 5.4 illustrates the practical utilization of molecular markers to identify alleles for virus resistance in F_{3-4} plants.

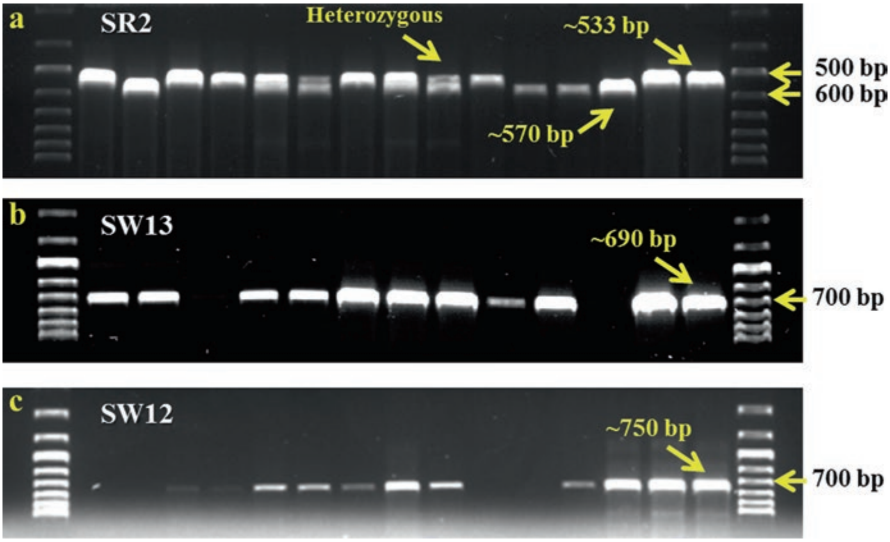

Fig. 5.4 Plant screening in F_{3-4} generation to confirm resistance to viruses. (**a**) The 533-base pairs (bp) DNA fragment at codominant SCAR marker SR2 suggests linkage to gene *bgm-1*(resistance) and the 570-bp fragment to susceptibility (Jiménez 2014), (**b**) DNA fragment 690-bp confirms the presence of gene *I* dominant for resistance to bean common mosaic virus (BCMV), (**c**) Allele 750-bp for locus SW12 confirms a variant resistance to BGYMV ascribed to major QTL obtained from variety DOR364

5.4.2 Functional Genomics

Further genetic improvement of the common bean will need a more fundamental understanding of the genetic principles of how this species responds to biotic and abiotic stresses (Schmutz et al. 2014). Despite the very incipient advances in common bean functional genomics, there have been some recent studies focused on providing insights into common bean response to drought, virus infections, aluminum toxicity, phosphorus (P-) starvation and symbiosis with nitrogen-fixing bacteria (Aparicio-Fabre et al. 2013; Formey et al. 2016; Martin et al. 2016; Mendoza-Soto et al. 2015; Nova-Franco et al. 2015; Ramírez et al. 2013; Wu et al. 2016).

In common bean-*Rhizobium* symbiosis, it was recently revealed that posttranscriptional regulator miR172c (miRNA172) plays an important role in silencing transcription factor AP2–1 (APETALA2), inducing positive effects such as improved root growth, increased rhizobia infection, increased expression of early nodulation, autoregulation of nodulation genes, improved nodulation and nitrogen fixation in common bean plants (Nova-Franco et al. 2015). As well, the study of six miRNAs, including novel miR-RH82, involved in regulation of nodulation factors for early nodulation events in common bean roots, provided a better understanding of the role of miRNAs in rhizobia-common bean symbiosis (Formey et al. 2016). Nanjareddy et al. (2016a) discovered the role of TOR (the target of rapamycin) protein kinase during the common bean-*Rhizobium tropici* symbiotic interaction by means of posttranscriptional gene silencing of TOR using RNA interference, demonstrating that these genes are involved in lateral-root elongation and root-cell organization and also alters the density, size and number of root hairs. Improved expression of TOR ATG genes (in TOR-RNAi roots) indicated that TOR plays a role as well in even the recognition of *Rhizobium* as a symbiont. In a recent study, Arthikala et al. (2018) demonstrated through analyses using PvBPS1-RNAi transgenic roots that PvBPS1 genes (responsible of rooting and meristem formation) are critical in the induction of meristematic activity in root-cortical cells and in the establishment of nodule primordia during common bean-*Rhizobium* symbiosis.

For plant nutrition, the regulatory mechanisms of root response to aluminum toxicity (under acid soils) involve 14 up-regulated miRNAs along other regulators, suggesting that the participation of miR164/NAC1 (NAM/ATAF/CUC transcription factor) and miR393/TIR1 (TRANSPORT INHIBITOR RESPONSE 1-like protein) in auxin and of miR170/SCL (SCARECROW-like protein transcription factor) in gibberellin signaling are key for response and adaptation to this abiotic stress (Mendoza-Soto et al. 2015). Similarly, it has been inferred that the jasmonate-signaling pathway involving PvTIFY genes might be relevant in regulating common bean response and adaptation to phosphorus starvation (P-starvation) stress (Aparicio-Fabre et al. 2013). In this sense, changes in three bases of the binding site of PvPHO2 one, a negative regulator of PvPHR1 transcription factor signaling pathway that encodes an ubiquitin E2 conjugase (that promotes degradation of P-responsive proteins), are responsible for tolerance to P-starvation in some genotypes (Ramírez et al. 2013).

For drought stress, Wu et al. (2016) studied the plant-specific transcription factors CUC2 (NAC) genes that constitute with NAM and ATAF1/2 the largest families of plant transcription factors. They identified a nonredundant set of 86 NAC genes related to drought response in common bean, displaying phylogenetic relationships, conserved motifs, gene structure and expression profiles. These findings will accelerate functional genomics studies and molecular breeding programs, providing a new resource for molecular breeding even in other crops.

For plant defense, Martin et al. (2016) experimented with the transcriptional responses of a widely susceptible variety of common bean to two bean common mosaic virus (BCMV) strains (with moderate and severe symptoms) finding different transcriptome responses and large differences in splicing forms, and pathway specific expression patterns. There have been numerous studies and reviews aiming to reveal and make available useful information about the gene expression related to different stresses, suggesting the possibility of strengthening breeding programs and solving future challenges using transcriptomics and proteomics-based strategies (Iñiguez et al. 2017; Jha et al. 2017; O'Rourke et al. 2014; Schmutz et al. 2014; Vlasova et al. 2016; Zargar et al. 2017).

5.4.3 *Bioinformatics*

There are various websites with valuable information concerning functional genomics freely available to the common bean community. For example, the *Phaseolus vulgaris* Gene Expression Atlas (PvGEA) (http://plantgrn.noble.org/PvGEA/). There, researchers can query gene expression profiles of a gene of interest, search for genes expressed in different tissue, or download the dataset in a tabular form (O'Rourke et al. 2014). Also, the database PvTFDB (https://www.multiomics.in/PvTFDB/) contains 2370 putative transcription factors gene models in 49 transcription factor families, including sequence data, functional annotation, SSRs with their primer sets, protein physical properties, chromosomal location, phylogeny, tissue-specific gene expression data, orthologues, cis-regulatory elements and gene ontology assignment. The *Phaselusgenes* is another database developed by University of California Davis (http://phaseolusgenes.bioinformatics.ucdavis.edu/) identifies and explores markers, quantitative trait loci (QTLs), and SSRs region information for common bean. Finally, there are many other resources in international institutions, not developed exclusively for common bean, but that provide useful information for breeding purposes.

5.5 Genetic Engineering

Genetic engineering, although much debated in some countries, has provided important achievements to increase yields in important crop species such as maize, soybean (*Glycine max*) and cotton (*Gossypium* spp.). Research teams worldwide have made advances in the modification of traits of great importance in response to different stresses linked to climate change. In particular, the genomic correspondence of soybean with common bean opens the possibility of taking advantages of those advances in the future.

5.5.1 *Transformation and Regeneration Methods*

The *Agrobacterium tumefaciens*-mediated transformation has been employed in many studies and using different common bean tissue (epicotyl containing seedling, mature seed embryos, cotyledonary node and embryonic axis explants, primary leaf explants, stem sections) obtaining genotype-dependent results (Amugune et al. 2011; Collado et al. 2016; Mukeshimana et al. 2013; Singh 2016). Five common bean varieties were transformed via the biolistic bombardment of the apical shoot meristem primordium in order to incorporate selectable markers and genes for HVA1 protein which confers drought resistance by increasing root lengths in transgenic plants (Kwapata et al. 2012). Electroporation method (single pulse of 260 ms at field strength of 225 $V.cm^{-1}$) was applied to intact embryonic axes, confirming good results in different varieties through the β-glucuronidase (GUS) reporter gene (Dillen et al. 1995). Rech et al. (2008) designed a protocol by combining resistance to the herbicide Imazapyr [IUPAC name = 2-(4-Methyl-5-oxo-4-propan-2-yl-1H-imidazol-2-yl)pyridine-3-carboxylic acid] as a selectable marker, multiple shoot induction from embryonic axes of mature seeds and biolistic techniques, obtaining average frequencies (the total number of fertile transgenic plants divided by the total number of bombarded embryonic axes) of producing germ-line transgenic bean plants of 2.7%, employing 7–10 months. In a recent study, Singh (2016) tested infecting with *Agrobacterium tumefaciens* (strain EHA 101, harboring GUS intron plasmid) cotyledonary node and embryonic axis explants, without any successful results. But, using primary leaf explants under Murashige and Skoog (MS), B5 vitamin and different growth hormones concentrations it was possible to recover full transgenic callus and transformed roots from this tissue with a transformation frequency of 7.5%. Nanjareddy et al. (2016b) isolated protoplasts from different tissues and transformed them using a polyethylene glycol-mannitol magnesium (PEG-MMG)-mediated transformation method with results reported by GUS assays and RT-qPCR analysis of protoplasts. Interestingly, sonication-assisted *Agrobacterium*-mediated transformation, for the leaf disc infiltration of common bean transformed 60–85% of the cells in a given area of the leaf surface, resulting in 90% of transformation efficiency.

The common bean is considered a recalcitrant species, but it is not known if it is really resistant to regeneration or transformation due to an absence of indigenous competition or if the best technique has not yet been found (Hnatuszko-Konka et al. 2014; Veltcheva et al. 2005). However, most experiments have established that the plant regeneration protocol for this species is genotype-dependent (García et al. 2012; Martínez-Castillo et al. 2015; Mukeshimana et al. 2013). Direct-shoot regeneration (without intermediate callus) using the transverse thin cell layer method with special culture conditions achieved 100% well-developed shoots and the regeneration of complete and fertile common bean plants (Cruz de Carvalho et al. 2000; Veltcheva et al. 2005). Also, the use of somatic embryogenesis based upon the use of benzyl-amino-purine (BAP) and adenine (A) coupled with osmotic stress (sucrose 12% w/v, 0.5 M) adaptation, instead of somatic embryogenesis response, that is induced by auxins, induced up to 25% complete and fertile plants in a non-genotype-dependent protocol (Cabrera-Ponce et al. 2015). Shoot induction of embryonic axes using MS culture media with B5 vitamin and BAP or Thidiazuron provided differentiated results with two varieties (Martínez-Castillo et al. 2015). Regeneration capacity of different tissues were tested on 30 media, each containing MS medium and different combinations of hormones, confirming the recalcitrance of common bean. But, better results were reported when using embryo axis explants, although optimal protocol was genotype-dependent (Mukeshimana et al. 2013).

Also, embryonic axes were cultured in MS medium containing different BAP and A concentrations, resulting in full plant regeneration up to 83% with variety identity confirmed using AFLP markers (Delgado-Sánchez et al. 2006). Embryos extracted from sterilized mature seeds and cultured in Gamborg media, containing BAP and A, showed a good differentiation of cells like bud clusters at the internodal segment of the embryo axes with up to 93% full plant regeneration (Quintero-Jiménez et al. 2010). Kwapata et al. (2010) evaluated 63 different media combinations of cytokinins and auxins for in vitro regeneration of multiple shoots and somatic embryos for ten varieties, reporting promising results for a specific media combination. It is evident that a specific protocol has to be fine-tuned in order to improve the plant regeneration for a specific variety.

5.5.2 Enhanced Traits and Transgenic Varieties

According to the International Service for the Acquisition of Agri-biotech Applications (ISAAA 2018) only one transgenic event for common bean is recorded with the name Embrapa 5.1, whereas for soybean there are 37 events. Embrapa 5.1 was engineered using an RNA interference constructed to silence the sequence region of the AC1-viral gene of bean golden mosaic virus (BGMV), generating a highly-resistant transgenic common bean variety (Aragão et al. 2013; Bonfim et al. 2007). During the experimental phase, 18 transgenic common bean lines were obtained with an intron-hairpin construction that induces posttranscriptional gene silencing against the AC1 gene. As result of that phase, approximately 93% of plants from line 5.1 were free of symptoms upon inoculation at high whiteflies pressure at a very early stage of plant development (Bonfim et al. 2007). After that this variety was subject to characterization in order to confirm the transgene insert, its stability for at least eight self-pollinated generations and backcrosses with nontransgenic commercial cultivar and absence of siRNA signals on seeds after cooking (Aragão et al. 2013). Although the ISAAA (2016) stated that there are still no GMO common bean areas under cultivation, there are expectations of future commercial initiatives. Figure 5.5 shows transgenic common bean plants, without virus affections even growing under high whitefly pressure. Similarly, the same ISAAA report mentions the advances of INIFAP Mexico in order to obtain transgenic common bean cultivars, possessing the biotech event FMA pdf1.2-INIFAP that confers wide resistance to fungal diseases, very critical in many tropical and subtropical countries.

Because common bean is a strategic crop for food security in many developing countries, much of its production is promoted by international programs, farmers' organizations and governments that in some cases distance themselves from GMO technology, because of the associated controversy. Nonetheless, GMO technology should be considered when available genetic diversity fails to provide novel traits to confront biotic and abiotic stresses. Transgenic technology could provide valuable methods to strengthen breeding programs. Perhaps the perception of GMOs that has led to overregulation will change in future years in light of the discovery of sponta-

Fig. 5.5 Common bean field showing on the left a plot with transgenic variety (AC1-viral gene silenced) showing immunity to BGMV and on the right a commercial variety severely affected (yellowish plants). (Photo: Courtesy of Francisco J.L. Aragão, Embrapa, Brazil, 2018)

neous transgenic organisms prospering in nature (Chiba et al. 2011; Kreuze and Valkonen 2017; Kyndt et al. 2015) and also the safe production of common bean events monitored by Embrapa (Faria et al. 2010; Pinheiro et al. 2014).

5.6 Mutation Breeding

Although common bean holds a considerable amount of genetic diversity, not all the targeted traits can be found by traditional methods during the breeding process. Mutagenesis is a feasible approach considering the advantages over other approaches, such as transgenesis that is overregulated and still causes polemics in some countries. Nevertheless, due to the high costs of equipment and qualified personal, it is important to strengthen international cooperation among laboratories in order to design more robust regional programs.

5.6.1 *Conventional Mutagenesis*

Among mutation induction methods, the use of ethyl methanesulfonate (EMS, $CH_3SO_3C_2H_5$) has been preferred in common bean with 43.1%, followed by X and gamma rays with 37.2 and 15.6%, respectively. The remaining 4.1% were in minor usage N-nitroso-N-methyl urea ($C_2H_5N_3O$) and ethyleneimine (C_2H_5N) (IAEA

2018). The range of effectiveness for gamma ray treatment (frequency of mutations induced by a unit dose of mutagen) is calculated to be 0.09–0.099 and for EMS treatment 6.86–9.8, and in cases of combination treatment the range is 0.12–0.34, the combination of lower dose of gamma ray and EMS could be more effective (More and Borkar 2016). The use of 40 mM EMS was adequate for generating mutants in common bean, higher concentrations of EMS induced survival rates of less than 10% and lower concentrations reduced the number of mutants (Porch et al. 2009). For gamma rays, 303.17–318.22 Gy are considered proper doses for inducing mutations in common bean varieties (Ulukapi and Ozmen 2017). In a minor way, sodium azide (NaN_3) has been used to induce mutations, proving to be able to broaden the genetic diversity of an improved variety (Chen et al. 2011).

5.6.2 *Enhanced Traits and Improved Cultivars*

According to the International Atomic Energy Agency (IAEA 2018), 59 mutant common bean varieties were registered (1950–2007), of these 44% were generated in the USA and 20.3% in Canada. In contrast, there were 173 varieties registered for soybean. The main improved attributes of mutant varieties are early maturity, high yield, resistance to different pathogen strains, particular seed colorations and patterns, flower colorations, bush growth habit, high protein content and cooking quality. As the same register shows, most induced mutant varieties also serve as parents for crosses and backcrosses to incorporate novel alleles into the base germplasm.

5.7 Conclusions and Prospects

5.7.1 *An Overview of Current Status*

It is estimated that the world population will continue to increase in the coming decades and that climate change will make food production more complex, creating food insecurity in many vulnerable countries (Porter et al. 2014). Under these unpredictable scenarios, the common bean is going to play an important role in providing cheap protein and other essential nutrients for human consumption. Common bean breeding activities, from 1930s until today, have been crucial in improving yields, creating resistance to biotic and abiotic stresses and adding nutritional value. Nonetheless, after reviewing breeding history and its achievements, and being aware of current challenges, it is evident that future breeding projects must be strengthened in order to achieve ambitious goals within a short period of time.

The contemporary production and yield gaps among continents and countries suggest that there are opportunities for significant improvements, with subsequent benefits to farmers, consumers and even the environment. However, current traditional methods of genetic improvement are not sufficient to achieve varieties with high quality in a short period of time. Although many publications indicate advances to better understand molecular processes related to yield formation under stressful conditions, present common bean breeding programs are still based on traditional methods, without incorporating modern methods. Only in a minor cases are some of the modern biotechnology tools being used to incorporate new traits.

International institutes, research centers and NIARs have joined forces to develop regional breeding projects that have achieved important results. However, as most NIARs receive nursery stock of advanced genetic material for evaluation and validation, the development of advanced technical skills among breeders and technicians in the target countries is limited, reducing opportunities for breeding projects relying on local germplasm and expertise. In this sense, the participatory breeding approach has risen in importance in the last decade, providing significant achievements in many countries, but facing limitations in terms of seed systems. Nevertheless, there exist a considerable number of new varieties with high yield potential (Appendix II); but, the use of high-quality seeds and adoption of proper sowing and management practices remains low, reducing the impact of genetic improvement on common bean production.

5.7.2 Current Research Initiatives to Combat Global Climate Change

Section 5.1.2 discussed predicted climate change scenarios based on different models and how common bean production could be affected. In addition to global initiatives to ameliorate the impact of climate change in a broad sense, carrying out common bean breeding has to take into account variables related to resilience to climate change. Multiple programs and projects led by CIAT in Africa, Asia, Latin America and Caribbean can combat climate change affecting the cultivation of common bean by means of genetic improvement on a world scale. The CIAT program aims to release varieties that are high-yielding, tolerant to drought, heat and low-soil fertility, resistant to pest and diseases, nutritionally improved and with market potential. The websites of CIAT (http://ciat.cgiar.org/what-we-do/breeding-better-crops/beans/) and PABRA (Pan-Africa Research Alliance, http://www.pabra-africa.org/) can be consulted to track upcoming information.

5.7.3 Recommendations of Future Research and Utilization

It is very important to recognize that there is great genetic richness among *Phaseolus* species conserved in situ and ex situ, which has not been screened for novel traits. In this respect, and considering the climatic events of the last decade, in situ common bean genetic resources represent a valuable source of novel alleles present in populations prospering under adverse biotic and abiotic conditions. Common bean breeding programs should adopt modern biotechnology tools to conduct germplasm screening and to assist in the selection process. Albeit this approach was not possible before, because of high costs, today new advances have reduced costs significantly (Barabaschi et al. 2016), opening new possibilities for common bean breeders.

We must be aware that some target variants will not be present in germplasm in natural conditions. Thus, interspecific hybridization and mutagenesis could provide important alleles to be incorporated into breeding lines as well. Likewise, as long as functional genomics is advancing for the common bean, we will better understand the processes and dynamics of the genetic expression in response to biotic and abiotic stresses, being able to propose new ways of counteracting the negative effects of climate change on production. It will be important to continue deepening this understanding. Genetic engineering could help to design novel genotypes with special characteristics in the short term, but overregulation of these technologies and the questionable perceptions of both society in general and the political class, currently limit the extent to which these advantages can be brought to bear on future challenges.

Participatory breeding should be strengthened in the coming years focusing on those cropping systems exposed to climate change effects, adopting modern forms to conduct breeding and at the same time considering the conservation of valuable genetic diversity. It will be necessary to expand the variety ideotype to the whole agroecosystems, aiming for varieties that demand fewer inputs and respond better to ecological management using bio-inputs. Finally, although it is not the responsibility of breeders, in addition to releasing a new variety, it is important to promote the use of high-quality seeds and the adoption of proper practices for crop management in order to positively impact common bean production. In this sense, CSBs seem to be a very innovative option for distributing high-quality seeds, but the quality must be ensured by following proper technical practices. CSBs should also be considered as vital spaces for the transfer of technologies that allow educating farmers about new types of cultivation for each variety and in correspondence with climate change, such as the use of bio-inputs and agroecological management.

Appendices

Appendix I: Research Institutes and Online Resources Available for Common Bean Breeding

Institute	Area of specialization and research activities	Contact information
Bioversity International	Plant genetic resources, conservation of common bean genetic resources in situ and ex situ; support to community seed banks for high-quality seed production; plant breeding using participatory approaches	Via dei Tre Denari, 472/a 00054 Maccarese (Fiumicino), Italy https://www.bioversityinternational.org
Brazilian Agricultural Research Corporation (Embrapa)	Plant breeding, agro-biotechnology, crop management, plant breeding for high yield, resistance to biotic and abiotic stresses; tissue culture; genetic engineering	Rodovia GO-462, Km 12, Fazenda Capivara, Zona Rural Caixa Postal: 179 CEP: 75375-000 – Santo Antônio de Goiás GO, Brasil https://www.embrapa.br/en/arroz-e-feijao/
International Center for Tropical Agriculture (CIAT)	Plant breeding, crop management, seed production, phenotypic and molecular characterization of germplasm; plant breeding for high yield, resistance to biotic and abiotic stresses, high grain iron and zinc concentration; pre-breeding; conservation of genetic resources in situ and ex situ; support to community seed banks for high-quality seed production	Km 17 Recta Calí-Palmira CP 763537 Apartado Aéreo 6713, Calí, Colombia Dr. Stephen Beebe (s.beebe@cgiar.org) http://ciat.cgiar.org/what-we-do/breeding-better-crops/beans/
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	Plant breeding, agro-biotechnology, crop management, genetic improvement using modern genomics, molecular biology and breeding approaches	Patancheru 502324 Telangana, India Dr. Rajeev K. Vashney (r.k.varshney@cgiar.org) http://www.icrisat.org/research-development/
Michigan State University	Plant breeding, crop management, breeding and genetics for drought tolerance and disease resistance; support to community seed banks for high-quality seed production	220 Trowbridge Rd., East Lansing, MI 48824, USA Dr. James D. Kelly (kellyj@msu.edu), http://www.canr.msu.edu/psm/research
Misión Biológica de Galicia	Crop biodiversity, plant breeding, phenotypic and molecular characterization of germplasm; breeding for resistance to biotic and abiotic stresses	Pazo de Salcedo. Carballeira, 8. Salcedo. 36143 Pontevedra, España Dr. Marta Santalla (msantalla@mbg.csic.es) http://www.mbg.csic.es

(continued)

Institute	Area of specialization and research activities	Contact information
National Institute of Forestry, Agriculture and Livestock Research (INIFAP México)	Plant breeding, plant genetic resources conservation, crop management, plant breeding for resistance to biotic and abiotic stresses; conservation of genetic resources in situ and ex situ; plant breeding using participatory approaches; support to community seed banks for high-quality seed production	Avenida Progreso No. 5, Col. Barrio de Santa Catarina, Delegación Coyoacan C.P. 0401, México, D.F. www.inifap.gob.mx
United States Department of Agriculture / Agricultural Research Service	Plant breeding for high yields, resistance to biotic and abiotic stresses and to improve cooking time and nutritional value of harvested seeds	Jamie L. Whitten Building, Room 302A, 1400 Independence Ave., S.W. Washington DC 20250, USA https://www.ars.usda.gov/office-of-international-research-programs/ftf-grain-legumes/
University of California (Davis)	Crop biodiversity, plant breeding, study of evolutionary factors that affect crop biodiversity, plant factors such as gene flow and gene diversification, environmental correlations with crop biodiversity, and human effects on the maintenance and generation of diversity	1 Shields Ave, Davis, CA 95616, USA Dr. Paul Gepts (plgepts@ucdavis.edu) https://biology.ucdavis.edu/ https://biology.ucdavis.edu/people/paul-gepts
University of Puerto Rico	Plant breeding, seed production, plant breeding for high yield, resistance to biotic and abiotic stresses. High-quality seed production	Universidad de Puerto Rico, Mayagüez, Puerto Rico 00681-9000 Dr. James S. Beaver (james.beaver@upr.edu) http://www.upr.edu/
Zamorano University	Plant breeding, crop management, plant breeding for high yield, high grain iron and zinc concentration and resistance to biotic and abiotic stresses. Research on *Phaseolus*-rhizobia interaction, high quality seed production	PO Box 93, Km 30 road from Tegucigalpa to Danlí, Yeguare Valley, Municipality of San Antonio de Oriente. Francisco Morazán, Honduras Dr. Juan Carlos Rosas (jcrosas@zamorano.edu) https://www.zamorano.edu/

Note: These institutions have the most significant role at a global level. Nonetheless, there are a significant number of NIARs, universities and international institutes that also contribute to common bean breeding activities in the world

Appendix II: Genetic Resources of Common Bean

Most Popular Common Bean Varieties in African Countries, Their Characteristics and Site of Cultivation

Country	Variety name	Characteristics	Site of cultivation
Tanzania	Lyamungu 85	Tolerant to drought and diseases. Yield 2–2.5 mt/ha. Large red/brown Calima type seeds	Northern and Western zone
	Lyamungu 90	Tolerant to drought and diseases. Yield 2–2.7 mt/ha. Large red mottle, Calima type seeds	Northern and Western zone
	Uyole 90	Tolerant to ALS and R. Yield 2–2.5 mt/ha. Medium cream/brown stripe seeds	Southern highlands
	SUA 90	Tolerant to ALS and R. Yield 2–2.5 mt/ha. Small beige seeds	Eastern zone
	Selian 94	Tolerant to A and storage pests. Yield 2–2.5 mt/ha. Medium pink with red spots seeds	Northern and Western zone
	Uyole 94	Tolerant to ALS, R. Yield 2–3 mt/ha. Large cream/dark red seeds	Southern highlands
	Njano-Uyole	Tolerant to ALS and R. Yield 2–3 mt/ha. Medium yellow seeds	Southern highlands, Western and Northern zones
	Uyole 96	Tolerant to R and ALS. Yield 2–2.5 mt/ha. Large dark red kidney seeds	Southern highlands
	JESCA	Drought tolerant, early maturing variety. Yield 2–2.5 mt/ha. Large purple rounded seeds	Northern and Western zone
	Selian 97	Tolerant to ALS and R. Yield 2–2.5 mt/ha. Large dark red kidney seeds	Northern and Western zone
	Uyole 03	Tolerant to A, ALS and HB. Yield 2–2.5 mt/ha. Large sugar/red specked seeds	Southern highlands
	Wanja	Tolerant to drought due to its early maturing nature. Yield 1.5–2 mt/ha. Large khaki seeds	Southern highlands
	Uyole 04	Tolerant to A, ALS and HB. Yield 2.5–3 mt/ha. Medium cream seeds	Southern highlands
	Calima-Uyole	Tolerant to A and ALS. Yield 2–3 mt/ha. Red mottled (Cranberry) medium seed size seeds	Southern highlands, Western and Northern zone
	Cheupe	Tolerant to A, ALS and HB. Yield 4–6.5 mt/ha. Medium white seeds	Northern and Western zone

(continued)

Country	Variety name	Characteristics	Site of cultivation
	Selian 06	Tolerant to A, ALS and HB. Yield 4.6–7.5 mt/ha. Medium purple seeds	Northern and Western zone
Ethiopia	Lehode	Tolerant to foliar diseases	Northeastern
	Loko	Tolerant/Resistant to ALS, HB, A, BCMNV	Western
	Batu	Tolerant/Resistant to ALS and BCMNV	In areas with short season
	Deme	Tolerant/Resistant to ALS and BCMNV	In all bean growing areas
	Kufanzik	Tolerant/Resistant to ALS, HB, A, BCMNV	Eastern (Hararghe highlands)
	Dursitu	Tolerant/Resistant to ALS and BCMNV	Eastern (Hararghe highlands)
	Hawassa Dume	Tolerant/Resistant to ALS, HB, A, BCMV	Southern region (Wolaita, Sidama, Gamu Gofa)
	CRANSCOPE	Tolerant/Resistant to ALS and BCMNV	Central Rift Valley
	ACOS RED	Tolerant/Resistant to ALS and BCMNV	Central Rift Valley and southern region
	GABISA	Resistant to CBB	Western bean growing region
	Chercher	Tolerant/Resistant to ALS, HB, A, BCMV	Eastern (Hararghe highland)
	Haramaya	Tolerant/Resistant to ALS and BCMNV	Eastern (Hararghe highland)
	Chore	Tolerant/Resistant to ALS and BCMNV	Central Rift Valley and Eastern
	Dinkinesh	Tolerant to CBB	All bean growing areas
	Melkadima	Tolerant/Resistant to ALS and BCMV	Southern and Southwest
	Batagonia	Tolerant/Resistant to ALS and BCMNV	Southern
	Anger	Tolerant/Resistant to ALS and BCMNV	Western
	Tibe	Tolerant/Resistant to ALS, HB, A, BCMNV	Western
	Wedo	Tolerant/Resistant to ALS and BCMV	Northwest
	Ibado	Tolerant/Resistant to ALS and BCMNV	Southern
	Omo-95	Tolerant/Resistant to ALS	Southern
	Nasir	Tolerant/Resistant to ALS and BCMV	Across all bean growing regions
	Dimtu	Resistant to BGMV	Across all bean growing regions

(continued)

Country	Variety name	Characteristics	Site of cultivation
	Tabor	Tolerant/Resistant to ALS and BCMNV	Central Rift Valley and Southern
	Zebra	Tolerant/Resistant to ALS, HB, A, BCMNV	Across all bean growing regions
	Gobe Rasha-1	Tolerant/Resistant to ALS and BCMNV	Southern and Southwest
	Red Woliata	Tolerant/Resistant to ALS and BCMNV	Southern
	Awash Melka	Tolerant/Resistant to ALS, HB, A and BCMV	All bean growing regions
	Roba	Tolerant/Resistant to ALS, HB, A and BCMNV	All bean growing regions
	Awash 1	Tolerant/Resistant to ALS, HB, A and BCMNV	All bean growing regions
	Mexican 142	Resistant to ALS	All bean growing regions
Kenya	New Rose Coco	Moderate resistance to R, CBB, ALS, A, BCMV and BCMNV. Yield 1.3–2.3 mt/ha. Large/ calima type seeds	Eastern, Western and Rift valley
	Miezi mbili	Resistance to R, CBB, ALS, A, BCMV and HB. Yield 1.2–2.3 mt/ha. Large seeds	Central, and Rift valley
	Kenya Early	Moderate resistance to R, CBB, ALS, A and BCMV. Yield 1.1–2.2 mt/ha. Large seeds	Eastern, Nyanza, Central, Western and Rift valley
	Kenya Red Kidney	Moderately resistance to R, CBB, ALS, A, BCMV and BCMNV. Yield 1.1–2.8 mt/ha. Large seeds	Eastern, Nyanza, Central, Western
	Kenya Wonder	Moderate resistance to HB, CBB, ALS, A and BCMV. Yield 1.1–2 mt/ha. Large seeds	Eastern, Nyanza, Central, Western and Rift valley
	Kenya Sugar Bean	Moderate resistance to HB, CBB, ALS, A and BCMV. Yield 1.1–1.8. mt/ha. Large seeds	Eastern, Nyanza, Central, Western and Rift valley
	Tasha	Resistant to ALS, A and RR. Yield 1.1–2.1. mt/ha. Large/calima type seeds	Eastern and Rift valley
	Kenya Afya	High grain iron and zinc concentration, medium and brownish yellow seeds. Yield 2.2–3.2 mt/ha. Calima type seeds	Eastern, Nyanza, Central, Western and Rift valley
	Kenya Majano	High grain iron and zinc concentration. Yield 2.2–3 mt/ha. Medium and yellow seeds	Eastern, Nyanza, Central, Western and Rift valley
	Kenya Madini	High grain iron and zinc concentration. Yield 2.2–2.5 mt/ha. Calima type seeds	Eastern, Nyanza, Central, Western and Rift valley

(continued)

Country	Variety name	Characteristics	Site of cultivation
	Kenya mavuno	Resistant to A and CBB. Yield 2–3 mt/ha. Medium/Calima type seeds	Eastern, Nyanza and Central,
	Kenya Safi	Resistant to A. Yield 1.2–1.5 mt/ha. Medium grains/Calima type seeds	Eastern, Nyanza, Central, Western and Rift valley
	Mwitemania	Drought tolerant. Yield 1.2–1.5 mt/ha. Medium size/pinto seeds	Eastern, Nyanza, Central, and Rift valley
	Katheka (KATB 1)	Early maturity, heat and drought tolerant, cooks fast. Yield 1.2–1.5 mt/ha. Medium round yellow seeds	Nyanza, Central, Western and Rift valley
	KATB 9	Tolerant to heat, high yielding, drought tolerant, early maturing, cooks fast. Yield 1–1.8 mt/ha. Medium round red seeds	Eastern, Nyanza, Central, Western and Rift valley
Malawi	Namajengo	High yielding. Yield 2.5 mt/ha	Livingstonia, Viphya, Dedza
	Kanzama	High yielding and wide adaptation. Yield 2.5 mt/ha	Chitipa, Livingstonia, Viphya
	Kalima	Tolerant to ALS and A. 2 mt/ha. Large seeds	Chitipa, Livingstonia, Viphya, Dedza
	Bunda 3	Resistant to BCMV. Yield 2 mt/ha	Lake Basin, Phalombe
	Kambidzi	High yielding, tolerant to ALS. Yield 2.5 mt/ha	Lake Basin, Phalombe
	Nagaga	Tolerant to low soil fertility, resistant to BCMV. Yield 2 mt/ha	Mzimba, Lilongwe, Dowa, Nmawera, Shire
	Kabalabala	Tolerant to ALS and CBW. Yield 2.5 mt/ha	Lake Basin, Phalombe
	NUA 59	Early maturing, high grain iron and zinc concentration. Yield 1.7 mt/ha	Mzimba, Lilongwe, Dowa, Nmawera, Shire
	Iris	Drought tolerant, early maturing. Yield 3.5 mt/ha. Carioca type seeds	Guruve, Gokwe south and Nyanga
	Cardinal	Wide adaptation. Yield 4 mt/ha. Calima type seeds	Kwekwe, Marondera, Chipinge and Lupane
	Speckled Ice	Wide adaptation. Yield 3.5 mt/ha. Sugar type seeds	Chimanimani, Shrugwi, Binga and Chirumanzu
	NUA 45	Good taste, high grain iron and zinc concentration, quick to cook. Yield 2.4 mt/ha. Calima type seeds	Guruve, Gokwe south and Nyanga

(continued)

Country	Variety name	Characteristics	Site of cultivation
	Gloria	Attractive seed color (local market). Yield 2.4 mt/ha	Chimanimani, Shrugwi, Binga and Chirumanzu
	Bounty	Yield 2 mt/ha. Sugar type seeds	Chimanimani, Shrugwi, Binga and Chirumanzu
	PAN148	Widely adapted, resistant to BCMV. Yield 2.1 mt/ha. Sugar type seeds	Kwekwe, Marondera, Chipinge and Lupane
	PAN127	Moderately tolerant to rust and resistant to BCMV. Yield 1.6 mt/ha. Sugar type seeds	Kwekwe, Marondera, Chipinge and Lupane
Uganda	NABE 1	Tolerant to ALS, A and BCMV. Medium/large/sugar/red mottled/yellow seeds	Western and Eastern Tall grass
	Kanyebwa	Tolerant to ALS, A and BCMV. Medium/large/sugar/red mottled/Yellow seeds	Western and Eastern Tall grass
	Nambale	Tolerant to ALS, A and BCMV. Medium/large/sugar/red mottled/Yellow seeds	Western and Eastern Tall grass
	NABE 4	Tolerant to ALS, A and BCMV. Medium/large/sugar/red mottled/Yellow seeds	Western and Eastern Tall grass
	K132, Kanyebwa, Otawa, NABE13, NABE 12C and Kamwanyi	Tolerant to ALS, CBW, wide adaptation. Sugar, medium to large red mottled, small to medium red and brown seeds	Eastern tall grass and Mt. Elgon regions
Burundi	Magorori	Tolerant to BCMV, A, BR and R; intermediate reaction to ALS. Yield 1.2–2 mt/ha. Medium grains/calima seeds	All high-altitude areas in Burundi
	Murengeti	Tolerant to ALS, BCMV, R, BR and A; intermediate reaction to HB. Yield 1.5–2 mt/ha. Large grains/kablanket seeds	All high-altitude areas in Burundi
	Kinure	Tolerant to ALS, BCMV, A, BR and R. Yield 1.5–2 mt/ha. Medium/purple seeds	All high-altitude areas in Burundi
	Mbunduguru	Tolerant to BCMV, A and BR; resistant to ALS; Intermediate reaction to R. Yield 1–1.3 mt/ha. Medium round yellow seeds	Low to medium altitudes
	Inakayoba	Tolerant to BCMV, ALS and R; resistant to A and BR.	Low to medium altitudes

(continued)

Country	Variety name	Characteristics	Site of cultivation
	Inamunihire	Tolerant to A, ALS, BCMV; intermediate reaction to BR. Yield 1.2–2 mt/ha. Large/yellow seeds	Medium altitudes
	Mubogora	Tolerant to A, ALS, BCMV. Yield 1–1.5 t/ha. Large/red kidney seeds	Medium to high altitudes
	Bishaza	Resistant to ALS; tolerant to BCMV and CBB; intermediate reaction to A. Yield 1 mt/ha. Medium/Sugar seeds	Medium to high altitudes
	Bisera	Tolerant to BCMV, ALS, A, BR and RR. Yield 1–1.5 mt/ha. Large/red mottled seeds	Medium altitudes

Sources: Monyo Emmanuel and Laxmipathi Gowda (2014); Mukankusi et al. (2018); Katungi et al. (2017). Papias H. Binagwa is acknowledged for contributing to this table design

Key: *A* Anthracnose, *ALS* Angular Leaf Spot, *BCMNV* Bean Common Mosaic Necrosis Virus, *BCMV* Bean Common Mosaic Virus, *BGMV* Bean Golden Mosaic Virus, *BR* Black Root, *CBB* Common Bacterial Blight, *CBW* Common Bacterial Wilt, *HB* Halo Blight, *R* Rust, *RR* Root Rot

Most Popular Common Bean Varieties in Central American Countries, Their Characteristics and Site of Cultivation

Country	Variety name	Characteristics	Site of cultivation
Costa Rica	Suru	Days to harvest 74–80 days. Yield 1.9 mt/ha. 100-SW of 22 g. White seeds	Whole country, recommended in Brunca region
	Tonjibe	Days to harvest 75–80 days. Resistant to BCMV. Yield 1.5 mt/ha. 100-SW of 23 g. Red seeds	Whole country, recommended in Brunca region
	Chánguena	Days to harvest average 75 days. Resistant to BCMV. Yield 2.3 mt/ha. 100-SW of 21 g. Red seeds	Whole country, recommended in Central region
	Curré	Days to harvest 74–79 days. Resistant to BCMV. Yield 1.8 mt/ha. 100-SW of 21.5 g. Red seeds	Whole country, recommended in Central region
	Gibre	Days to harvest 65–70 days. Resistant to BCMV. Yield potential until 2.5 mt/ha. Red seeds	Whole country, recommended in Central region
	Telire	Days to harvest 72–80 days. Resistant to BCMV and BGMV. Yield 1.8 mt/ha. 100-SW of 23 g. Small red seeds	Whole country, recommended in Brunca region

(continued)

Country	Variety name	Characteristics	Site of cultivation
	Cabécar	Days to harvest 72–75 days. Resistant to BCMV and BGMV. Yield 1.9 mt/ha. 100-SW of 24 g. Small red seeds	Whole country, recommended in north Huetar region
	UCR 55	Days to harvest between 80 and 104 days. Yield 2.3 mt/ha. Black seeds	Whole country, recommended in sites above 840 m under sea level
	Bríbrí	Days to harvest 76–80 days. Resistant to BCMV. Yield 1.7 mt/ha. 100-SW of 18–20 g. Small red seeds	Whole country, recommended in Chorotega region
El Salvador	CENTA Ferromás	Resistant to BCMV and BGYMV. Yield 1.5 mt/ha. High grain iron and zinc concentration. Small red seeds	Most regions
	CENTA Nahuat	Resistant to BCMV and BGYMV. Yield 1.6 mt/ha. Small red seeds	Most regions
	CENTA CPC	Resistant to BCMV and BGYMV. Tolerant to heat and drought. Yield 1.4 mt/ha. Small red seeds	Most regions
	CENTA Pipil	Resistant to BCMV and BGMV. Tolerant to heat and drought. Small red (semi-dark) seeds	Most regions
	CENTA San Andrés	Resistant to BCMV and BGMV. Tolerant to heat and drought. Small red (light) seeds	Most regions
	CENTA 2000	Resistant to BCMV and BGMV. Tolerant to R. Tolerant to heat and drought. Small red (semi-dark) seeds	Most regions
Guatemala	ICTA Chortí	Days to harvest in average 78 days. Tolerant to R, BGMV, ALS and drought. High grain iron and zinc concentration. Yield 1.9 mt/ha. Opaque black seeds	Regions close to the conditions of Jutiapa, Jalapa and Chiquimula
	ICTA Peten	Days to harvest in average of 78 days. Tolerant to R and BGMV. High grain iron concentration. Yield 2.2 mt/ha. Black seeds	Regions close to the conditions of Peten
	ICTA Sayaxche	Days to harvest in average of 88 days. Tolerant to R and BGMV. Yield 2.5 mt/ha. Black seeds	Regions close to the conditions of Peten
	ICTA Superchiva	Days to harvest 120–135 days. High grain iron and zinc concentration. Tolerant to fungus diseases. Yield 1.6 mt/ha. Black seeds	Highland regions
	Hunapú	Days to harvest 120–135 days. Purple pods, Tolerant to R. Yield 1.9 mt/ha. Black seeds	Central and Western Altiplano region
	Altanse	Days to harvest 120–135 days. White pods, Tolerant to R. Yield 1.9 mt/ha. Black seeds	Central and Western Altiplano region
	Texel	Days to harvest 100–110 days. Yield 0.9 mt/ha. Black seeds	Central and Western Altiplano region

(continued)

Country	Variety name	Characteristics	Site of cultivation
Honduras	Honduras Nutritivo	Resistant to BCMV and tolerant to BGYMV. Intermediate tolerance to CBB and R. High grain iron concentration. Small red seeds	Most regions
	Azavache 40	Days to harvest 76–80 days. Resistant to BCMV and BCMNV. Intermediate tolerance to BGYMV, CBB, WB and R. Yield 2.5 mt/ha. Black seeds	Most regions
	Lenca Precoz	Days to harvest 60–70 days. Resistant to BCMV, BCMNV and BGYMV. Tolerant to CBB, WB and R. Yield 2.2 mt/ha. Small black seeds	Most regions
	Cardenal	Days to harvest 65–70 days. Resistant to BCMV and BGYMV. Tolerant to WB and R. Yield 1.8 mt/ha. Small red seeds	Most regions
	Deorho	Days to harvest 70–80 days. Resistant to BCMV and BGYMV. Tolerant to ALS, WB, R, drought, heat and low soil fertility. Yield 2 mt/ha. Small red seeds	Most regions
	Paraisito Mejorado 2	Days to harvest 70–75 days. Resistant to BCMV. Intermediate tolerant to BGYMV, CBB and R. Yield 1.7 mt/ha. Small light-red seeds	Most regions
	Tío Canela 75	Days to harvest 70–80 days. Resistant to BCMV and BGYMV Intermediate tolerance to A and R. Yield 1.7 mt/ha. Small red seeds	Most regions
	Amadeus 77	Days to harvest 70–75 days. Resistant to BCMV and BGYMV. Tolerant to drought. Yield 1.7 mt/ha. Small red seeds	Most regions
	Carrizalito	Days to harvest 70–75 days. Resistant to BCMV and BGYMV. Tolerant to drought. Yield 2.3 mt/ha. Small red seeds	Most regions
Nicaragua	INTA Fuerte Sequía	Days to harvest 72–75 days. Resistant to BCMV and BGYMV. Tolerant to drought and heat. Yield 1.6 mt/ha. Dark red seeds	Most regions
	INTA Precoz	Days to harvest 68–70 days. Resistant to BCMV and BGYMV. Tolerant to drought. Yield 1.3 mt/ha. Small red seeds	Most regions
	INTA Rojo	Days to harvest 75–78 days. Resistant to BCMV and BGMV. Yield 1.6 mt/ha. Light red seeds	Most regions
	INTA Cárdenas	Days to harvest 78–80 days. Resistant to BCMV and BGMV. Yield 1.6 mt/ha. Black seeds	Most regions
	INTA Ferroso	Days to harvest 72–74 days. Resistant to BCMV and BGMV. High grain iron concentration. Yield 1.2 mt/ha. Small red seeds	Most regions

(continued)

Country	Variety name	Characteristics	Site of cultivation
	INTA Nutritivo	Days to harvest 68–72 days. Resistant to BCMV. Yield 1.6 mt/ha. High grain iron concentration. Red (light) seeds	Most regions
	DOR364	Days to harvest 80–85 days. Resistant to BCMV and BGMV. Yield 2.3 mt/ha. Deep dark red seeds	Most regions

Sources: Araya and Hernández (2007); CENTA (2018); DICTA (2018); ICTA (2018); INTA (2018); INTA (2013); Reyes (2012)

Key: *100-SW* average 100-seeds weight, *A* Anthracnose, *ALS* Angular Leaf Spot, *BCMNV* Bean Common Mosaic Necrosis Virus, *BCMV* Bean Common Mosaic Virus, *BGMV* Bean Golden Mosaic Virus, *BGYMV* Bean Golden Yellow Mosaic Virus, *CBB* Common Bacterial Blight, *R* Rust, *WB* Web Blight

Most Popular Common Bean Varieties in South America, Their Characteristics and Site of Cultivation

Country	Variety name	Characteristics	Site of cultivation
Brazil	BRS Ametista	Tolerant to A, CBB and R. Moderate resistance to *Fusarium* wilt. 100-SW of 30 g	East and central regions
	BRS Notável	Resistant to CBB and moderately resistant to A, R, *Fusarium* wilt and *Curtobacterium*. 100-SW of 26 g	East and central regions
	BRSMG Madreperola	Moderate potential resistance to A and ALS. 100-SW of 24.5 g	South-east regions
	BRS Estilo	Adapted to mechanical harvest. Moderately resistant to A and R. 100-SW of 26 g	South and central regions
	BRSMG Realce	High productive potential and excellent culinary properties. Tolerant to A, CBB, R, *Fusarium* wilt and *Curtobacterium*. 100-SW of 43 g	South-east regions
	BRS Radiante	Good culinary quality. Tolerant to A, R, ALS, *Fusarium* wilt and *Curtobacterium*. 100-SW of 44 g	South-east and central regions
	BRS Agreste	Adapted to direct mechanized harvesting. Moderate resistant to A and *Fusarium* wilt. 100-SW of 25 g	East regions
	BRS Vereda	Uniform coloring and excellent culinary properties. Moderately resistant to A, ALS and *Fusarium* wilt. 100-SW of 26 g	South regions
	BRS Pitanga	Excellent culinary properties. Moderate resistance to A, R, ALS and *Fusarium* wilt. 100-SW of 20 g. Red seeds.	West and central regions
	BRS Executivo	It is an option for producers interested in *Sugar Bean* type beans. 100-SW of 76 g	South regions

(continued)

Country	Variety name	Characteristics	Site of cultivation
	BRS Embaixador	Moderate resistance to A and *Fusarium* wilt. Grains favored for the national market, providing price advantages and with potential for export. 100-SW of 63 g. Red seeds	South regions
	Jalo Precoce	Early maturing and tolerant to CBB, R and *Fusarium* wilt. 100-SW of 35 g. Cream seeds	South-east and central regions
	BRS Esplendor	Adapted to direct mechanical harvesting. Resistant to CBB and tolerant to A, R and *Fusarium* wilt and *Curtobacterium*. 100-SW of 22 g. Black seeds	South-east and central regions
	BRS Campeiro	Excellent culinary qualities. Adapted to direct mechanized harvest. Tolerant to A, R and *Fusarium* wilt. 100-SW of 25 g. Black seeds	South-east and central regions

Source: Embrapa (2013)

Note: Due to the special condition explained in Sect. 5.2.2, this appendix contains information about only particular varieties from some African countries, Brazil and Central America illustrating the high genetic diversity available for cultivation and breeding. Furthermore, there are a considerable number of varieties from participatory breeding and thousands of landraces and old cultivars with significant relevance to the food security in the developing world

Key: *A* Anthracnose, *ALS* Angular Leaf Spot, *CBB* Common Bacterial Blight, *R* Rust, *100-SW* Average 100-seeds weight

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