

Food Legume Production Performance in Support of World Food

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ABSTRACT

Over the past 50 years (1970-2020) the world's population has risen by an average of 1.49% per year so that in 2020 it reached 7.79 billion people. This increase automatically increases food needs. While to this day there are still over 820 million undernourished people. Food legumes have enormous potential in supporting food security because they are rich in nutrients, including high energy, protein, carbohydrate, fiber, and other nutrients. Even among them, like chickpeas have higher energy content than some major cereal crops. Food legumes production continues to increase from year to year. Compared to three decades ago, soybean annual production more than tripled with production in 2017 reaching 352.2 million tons, as well as pulses that increased more than 35 million tons with production in 2017 reaching 96 million tons. These improvements are not only supported by field expansion, but also the impact of technological improvements which have effect on increasing yield. This review describes the trends in increasing production and yield of food legumes, as well as the progress of breeding technologies in order to increase diversities have impact on increasing the yields and adaptation against the environment. These explanations are discussed in each food legume species.

Keywords: breeding , food, food legume, pulse,

INTRODUCTION

Over the past 50 years, from 1970 to 2020, the average world population increased by 1.49% per year, from 3.70 billion in 1970 to 7.79 billion in 2020 (UN, 2019). An ever-increasing population automatically increases food needs. But in fact, there is still food insecurity. This is shown by more than 820 million undernourished people to this day. It is targeted that by 2030 food insecurity can be overcome but the challenges faced are increasingly

severe (FAO 2018). These constraints are most often addressed to the declining environmental potential (Godfray et al. 2010; Foley et al. 2011) such as climate change which has serious impacts on food security (Campbell et al. 2016) through impacts on crop yields, impacts on livestock and fisheries no less serious (Lobell et al. 2011; Creighton et al. 2015; Herrero et al. 2015). Crop diversification is also very necessary to support the

sustainability of food production. Three types of cereals, namely corn, wheat, and rice, dominate the agricultural area by 40% (Tilman et al. 2011; Stamp et al. 2012). Optimization of legume crops is projected to be a solution that supports food security. With the 'nutritious seeds for sustainable future' banner, the UN declared 2016 as the International Year of Pulse (Foyer et al. 2016).

Food legume is able to be the main staple food because of its high energy, protein, and carbohydrate content. Some of them even have higher energy content than cereal crops, for example, chickpeas that have higher energy content than corn, barley, white and brown rice (USDA National Nutrient Database 2016). In addition to its high nutritional content, food legume crops are able to correlate with fixing bacteria. This relationship benefits both the legume as host and fixing-bacteria (Oldroyd 2013). Nitrogen fixation has an ecological and economic impact due to the fact that the availability of N fixed is the factor that most often limits agricultural production

worldwide (Smil 2004). With a variety of potential legumes that impact food security, production and yield of legumes over the past 50 years have increased, although they have not exceeded the production of cereal crops (Foyer et al. 2016). Both extensification and intensification continue to be carried out from year to year to increase food legume production (FAOSTAT 2019). Breeding technology in the context of intensification continues to be done in order to increase the yield of food legume crops. Such as the use of genomic-assisted breeding that has the possibility to unlock valuable genes such as heat and drought tolerance in wild species which are then transferred efficiently to cultivated species (Varshney et al. 2015; Varshney 2016). Likewise, mutations that have been proven to have supported the increase in yields (Ahloowalia et al. 2004). In this review, it is explained about the contribution of food legume in supplying world food needs as well as reviewing the progress of breeding technology in food legume crops that support the increase in diversity and yield described in each major food legume.

HEALTH AND NUTRITION OF FOOD LEGUMES

Based on the definitions published by FAO in 1994, variations in the type of legumes can be divided into four categories: pulses, legumes used for oil extraction, pulses used for forages, and legumes that are harvested fresh or before they have dried. Pulses are harvested solely for dry grains, for example, chickpeas, beans (dry), peas (dry), and lentils. Legumes for oil extraction such as soybeans and peanuts. Legumes used for forages such as clover and alfalfa. Freshly harvested legumes before drying are used for green food and are classified as vegetable crops, for example, green/fresh beans and peas.

Legume is the highest source of protein from the crop with a percentage of 18-36% (uncooked). The amount of energy produced by pulses is also relatively high, averaging more than 100 kcal per 100 grams cooked. Even from 100 grams of cooked chickpeas, the energy content reaches 160 kcal. Complete data on the composition of energy, protein, carbohydrates, and fiber undercooked conditions can be seen in Table 1, which presents both pulse and cereal as a

comparison (USDA National Nutrient Database 2016). The clustering of 22 food legumes has been carried out. There are three groups of clusters, cluster 1 represents legume crops with a moderate amount of protein, high carbohydrate, low dietary fiber and fat. Cluster 2 represents a high amount of protein, moderate carbohydrates and fat, and high dietary fiber. Cluster 3 represents low protein and carbohydrate, moderate dietary fiber, and high fat (table 2) (Maphosa and Jideani 2017). In addition to being high in energy, high in protein, carbohydrates, and fiber, pulses are also rich in vitamins, minerals, and rich in antioxidant compounds including polyphenols, flavonoids, phenolic acids, and have a low glycemic index (Kouris and Belski, 2016; Hall et al. 2017). Unlike most types of food crops, which are limited in amount, the protein content in legumes is actually rich in amino acid lysine and sulfur amino acids such as methionine (Bressani et al. 1984). Legumes contribute to reducing the risk of mortality because it has the benefit of preventing several chronic diseases and risk factors such as cancer, diabetes,

obesity, cardiovascular disease, and gut health (Kushi et al. 1999). In addition to its use for food, grain legumes such as cowpeas are also potentially used in the pharmaceutical, cosmetic and even

textile sectors because of their therapeutic properties (Singh and Basu 2012).

Table 1. Composition of energy, protein, carbohydrate, and fiber content in several pulses and cereals (100g cooked)

Category	Crop	Nutrient content			
		Energy (kcal)	Protein (g)	Carbohydrat (g)	Fiber (g)
Pulse	Bean	126	8.86	22.48	7.41
	Chickpea	164	8.86	27.42	7.6
	Pea	120	7.55	22.18	7.5
	Lentil	116	9.02	20.13	7.9
Cereal	Corn	96	3.41	20.98	2.4
	Rice (white)	130	2.69	28.17	0.4
	Rice (brown)	123	2.74	25.58	1.6
	Barley	123	2.26	28.22	3.8

Table 2. Three cluster groups based on the nutritional content of 22 legumes using K-means cluster

Cluster	Legumes	Nutritional content (%)			
		Carbohydrate	Protein	Dietary fiber	Fat
1	Chickpea, lima bean, adzuki bean, green gram, kidney bean, cowpea, mung bean, pinto, black gram, pigeon pea, broad bean, African yam bean, hyacinth, white velvet bean, sword bean, black velvet bean, bambara groundnut, lentil	63.78	25.44	9.32	2.58
2	Soybean, sweet lupin, groundnut, bitter lupin, sword bean	37.10	36.09	17.72	14.11
3	Groundnut, hyacinth	19.33	18.73	13.28	55.03

IMPROVEMENT TECHNOLOGIES ON FOOD LEGUMES

Authors retrieve the latest data from FAOSTAT for total trends in production and harvested areas of pulses and soybeans in the world presented in Figure 1. Pulses production is obtained by combining crop production that is included in the category of pulses including beans (dry), broad beans, peas (dry), chickpeas, cowpeas, pigeon peas, lentils, bambara beans, vetches, lupins, and pulses nes (FAO 1994).

Production trends were obtained from 1990 to 2017. Both pulses and soybeans,

production trends increased. Certainly, an increase in field area is a big support in increasing production. Pulses production in 1990 was 59.2 million tons produced from the 68.8 million ha harvested area, in 2017 pulses produced 96 million tons from the harvested area of 95.2 million ha. For soybeans, in 1990 a total production of 108.5 million tons was produced from the harvested area of 5.2 million ha, in 2017 soybean production was 352.2 million tons from the harvested area of 123.6 million ha. Intensification also supports increased

production. Although the yields fluctuate annually, overall from 1990 to 2017 both pulses and soybean yields have increased. The average increase in pulses and soybean yields per year was 0.67% and 1.68% respectively (Table 3) (FAOSTAT 2019).

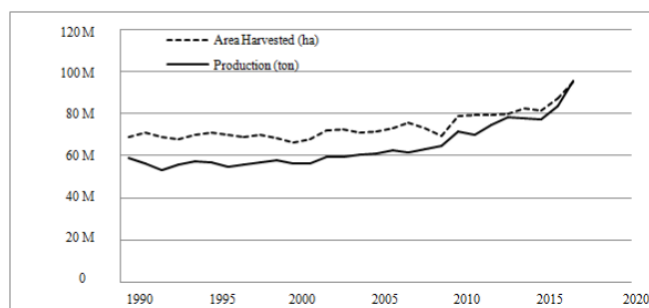
Grain legume is a vital part of the response at the 2009 Declaration of the World Summit on Food Security with the need for an increase in agricultural output of 70% in 2050 as a step to face an increase in population, while optimizing the sustainable use of genetic sources for adaptation to climate change (Foyer et al. 2016). The relatively

low yield of pulses is an important part of the production challenge, which is caused by the low number of high-yielding varieties, poorly adapted varieties, biotic and abiotic stress (Bergvinson; Sabbaghpour 2006). For this reason, high-yielding and biotic/abiotic stress tolerance varieties need to be developed (Amanullah 2016). The production trends of each crop and the progress of the breeding technology are discussed in detail based on the type of each species of grain legumes.

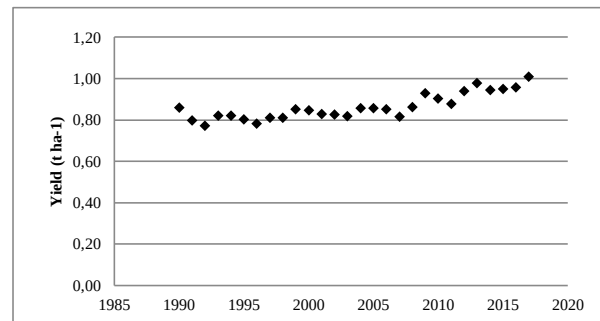
Table 3. Production and yields in 2017 and the average percentage increase in annual yields from 1990 to 2017 of several major food legumes

Food legumes	Production in 2017 (million tons)	Yield in 2017 (kg ha ⁻¹)	The average increase in annual yield from 1990 to 2017 (%)
Beans	31.41	861	1.1
Broad beans	4.84	1,964	1.18
Peas	16.21	1,991	0.61
Chickpeas	14.78	1,015	1.78
Cowpeas	7.41	589	2.99
Pigeon peas	6.81	969	1.79
Lentils	7.59	1,153	1.65
Bambara beans	0.18	715	1.74
Vetches	0.92	1,644	1.95
Lupins	1.61	1,730	5.33
Soybeans	352.64	2,854	1.68

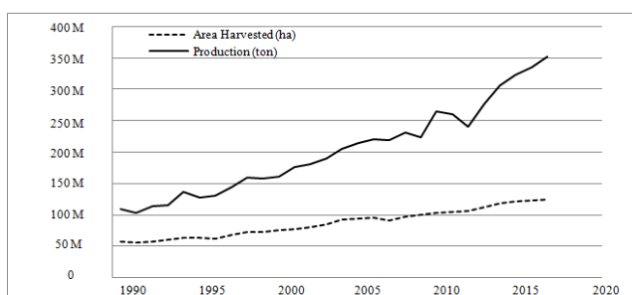
a.



c.



b.



d.

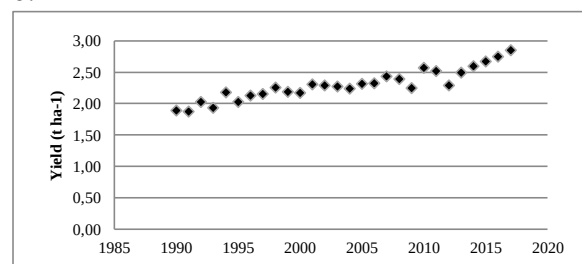


Figure 1. Production of pulses and soybean throughout the world from 1990 to 2017. Total production (tons) and harvested area (ha) in units of million, pulses (a), soybean (b). Figure c and d are the trends of the yield of pulses (c) and soybean (d) from 1990 to 2017.

Beans

When viewed from its production, bean is the most important pulse crop in the world today. Bean production in 2017 of 31.4 million tons worldwide was produced from a harvested area of 36.5 million ha. Compared to three decades ago, bean production clearly surged by more than 10 million tons. For example, the 1990 production of 17.5 million tons produced from 26.5 million ha (FAOSTAT 2019).

A significant increase in production, apart from the expansion of the field, is inseparable from the continuous improvement technology in increasing yield. In common beans, breeding objects are addressed in diseases, abiotic stress, agronomic, quality, and environment (Assefa et al. 2019). In the context of markers development, from the Pulse Crop Database so far more than 500 quantitative trait loci (QTL) in the bean have been identified (Pulse Crop Database 2019). Among them reported stable yield QTL on the Pv04 chromosome. Still in the same study, it was subsequently identified on the Pv01 and Pv08 chromosomes as the most stable QTL for maturity traits (Diaz et al. 2018).

Some of the main biotic constraints on common beans include anthracnose (*Colletotrichum lindemuthianum*), angular leaf spots (*Phaeoisariopsis griseola*), common bacterial blight, bean common mosaic virus, and bean golden mosaic virus (Beebe and Corrales 1991; Duc et al. 2015; Miklas et al. 2017). Summary of the resistance gene in several common bean diseases is reviewed in table 4 (Assefa et al. 2019). Drought and heat stress are major abiotic constraints in common bean (Rao 2014; De Ron et al. 2016). To add the insight of the adaptation of common bean to the environment, it is necessary to know the physiological character. For the analysis of abiotic stress, in general, the physiological characters evaluated include shoot structure, grain yield, water potential, osmotic adjustment, and gas exchange (Lanna et al. 2018). Analysis of traits in drought stress is directed at yield components, biomass, partitioning, phenology, and water relations (Ramirez-Vallejo and Kelly 1998). Schneider et al. (1997) identified QTLs using Random Amplified Polymorphic DNA (RAPD) markers to be drought. By using five RAPD markers, under drought conditions improve yield by 11% while under normal conditions improve yield by 8% (Schneider et al. 1997). The other identification of QTL in drought was reported by Trapp et al. (2015) which detects Pv01 and Pv02 as two major QTLs for seed yield on drought tolerance and several abiotic stress conditions (Trapp et al. 2015).

Table 4. Summary of several resistance genes against biotic constraints in common bean

Constraint	Resistance gene	Reference
Bacteria		
• Bacterial brown spot (<i>Pseudomonas</i>)	• LG02	• Jung et al. 2003; Muedi et al. 2015
• Common blight (<i>Xanthomonas</i>)	• QTL: BC420 (Pv06), SU91 (Pv08), Xa11.40V1	• Viteri et al. 2015; Miklas et al. 2017
Fungi		
• Angular leaf spot (<i>Phaeoisariopsis</i>)	• QTL: Pv04, Pv10 (ALS10.1) Phg1, Phg2	• Oblessuc et al. 2012; 2015; Keller et al. 2015
• Anthracnose (<i>Colletotrichum</i>)	• QTL: Pv01, Pv04, Pv10, Co-1, Co-2	• Zuiderveen et al. 2016
• Fusarium	• QTL (FRR3.1 ^{km}) (Pv03), LGs B2 and B3	• Roman-Aviles and Kelly 2005 • Hanson et al. 1993

• Leafspot (<i>Ascochyta</i>)	• Quantitative (<i>P. polyanthus</i>)	
• Rust (<i>Uromyces</i>)	• KASP SS68 marker associated with Pv11	• Hanson et al. 1993; Hurtado-Gonzales 2017
Insects		
• Bean stem maggot (<i>Ophiomyia phaseoli</i> Tryon)	• Qualitative and quantitative	• Miklas et al. 2006
• Bean pod weevil (<i>Apion godmani</i>)	• Quantitative: Chr2, (b01) Chr3 (b08), Chr4 (b07), Chr6 (b11)	
• Leaf hopper (<i>Empoasca fabae</i> , <i>E. kraemeri</i>)	• QTL: Pv01, Pv02, Pv03, Pv06, Pv07, Pv08, Pv09	• Blair et al. 2006b
		• Murray et al. 2004; Brisco 2012
Viruses		
• Mosaic virus and mosaic necrosis virus	• Qualitative: <i>bc-1</i> , <i>bc-2</i> , <i>bc-3</i>	• Johnson et al. 1997;
• Golden yellow mosaic	• Qualitative, quantitative, Bgm-1, RNAi	Strausbaugh et al. 1999
		• Blair et al. 2007

Broad beans

Broad beans (*Vicia faba* L.) named also faba bean or horse bean have higher protein content than other common food legumes (Griffiths and Lawes 1978; Burstin et al. 2011). From 1990 to 2017 broad beans yield increased by an average of 1.18% per year. In 2017 there was 2.5 million ha of the harvested area of broad bean area with a production of 4.8 million tons (FAOSTAT 2019).

High genetic diversity among broad beans is useful for increasing yield potential in plants. This potential is used to improve plant adaptation to the environment, biotic stress, and abiotic stress. Biotic stress includes foliar diseases, pests, insects, viruses, and parasitic diseases. Major foliar diseases include ascochyta blight (*Ascochyta fabae*), chocolate spot (*Botrytis fabae*), gall disease (*Olpidium viciae* Gusano), and rust (*Uromyces viciae-fabae*), (Maalouf et al. 2019). Insect pests include cowpea aphid (*Aphis cracivora* Koch), black bean aphid (*A. fabae* Scopoll), and sitona weevil (*Sitona lineatus* L.) (Mwanauta et al. 2015). For the virus category, faba bean necrotic yellow virus (FBNYV) disease causes up to 90% loss of faba bean in Egypt (Kumari and Makkouk 2007). *Orobanche crenata* Forsk. is parasitic weed as a serious constraint for legumes crop in the Mediterranean area. Case in Morocco reported severe level *O. crenata* infestation in many faba bean fields (Briache et al. 2019). ICARDA has identified the first effective source of resistance for

ascochyta blight and chocolate spots (Robertson 1984; Hanounik and Robertson 1989). Kaur et al. (2014) have reported the identification of QTLs for ascochyta blight resistance. ILB 4726, ILB 938, and BPL 710 are lines found in ICARDA that are high-level resistant to chocolate spots (Beyene et al. 2018). The results of the study in Morocco, Giza 843 genotype (selected in Egypt that is resistant to *O. crenata*) was chosen as a source of genotyping for resistant to *O. crenata* so that it was introduced as Moroccan faba bean breeding program (Briache et al. 2019), while the Tunisian line experiment XBJ90.03-16-1-1-1 produced by the National Institute de la Recherche Agronomique de Tunisie (INRAT) has a high resistance to *O. crenata* (Abbes et al. 2007).

Terminal heat stress can significantly reduce broad bean yield and component yields (Abdelmula and Abuanja 2007). Likewise, terminal drought stress is an important constraint of broad bean production in semi-arid areas under rainfall conditions. Abdelmula et al. (1999) have reported genetic variations in the response of faba bean to drought. In North America and North Europe, frost tolerance is an important breeding focus to improve yield stability (Landry et al. 2016). In Ethiopia waterlogging and soil acidity are common constraints of broad bean production (Kenenen et al. 2010). Some of the abiotic stress-tolerant genotypes are following in table 5.

Table 5. The genotypes of *Vicia faba* that are tolerant to abiotic stress

Genotypes	Type of abiotic stress	References
Zafar 1	Drought stress	Siddiqui et al. 2015
C5	Drought stress	Siddiqui et al. 2015
Hara	Drought stress	Abid et al. 2017
CS20-DK and NC-58	Drought stress	Girma and Haile 2014
Boxer	Heat stress	Zhou et al. 2018
FAB7024	Cold stress	Zhou et al. 2018
NGB8639	Cold stress	Zhou et al. 2018
S_145, S_004, S_081, S_151, S_299	Frost stress	Sallam et al. 2017
Acc 1487/7, Acc 1512/2, Fiesta VF	Salt stress	Tavakkoli et al. 2012

Peas

Pea (*Pisum sativum* L.) is one of the oldest domesticated crops included in the annual cool-season legume. Pea is a high protein food source, dry seed pea contains 22-25% protein (Tayeh et al. 2015). The latest data, in 2017 the harvested area of pea reaches 8.1 million ha with a total production of 16.2 million tons worldwide. In the period 1990 to 2017 pea yield increased an average of 0.61% per year (FAOSTAT 2019).

Pea yield increase is focused on biotic and abiotic stress. Fungal diseases are major constraints for biotic stress, followed by attacks of insects, viruses, and plant parasites. Drought and heat stress are the main abiotic stresses in the flowering phase. Early season flooding, frost, and salinity stress are important whose impacts vary in each phase of growth (Tayeh et al. 2015). Field pea rust caused by the pathogen *Uromyces* spp. is a pea disease that is the main focus in North and South America, Europe, Australia, China, India, and New Zealand (EPPO 2012). Recently, the results of research in India that IPF 2014-16, KPMR 936, and IPF 2014-13 are ideal genotypes and are recommended to be released and exploited as field pea rust resistance (Das et al. 2019). Through backcrossing transferred to cultivated peas, the secondary gene pool (*P. fulvum*) was identified to be resistant to pea weevil (*Bruchus pisorum* L.) (Clement et al. 2002, 2009; Aryamanesh et al. 2012). Has been developed and deployed in the north-west USA and Europe cultivated adapted peas for winter showing which have a longer growing season, earlier maturity to avoid late-season drought and heat

stress, and have higher biomass production, thus potentially giving better yields (Hanocq et al. 2009). Pea semi-leafless cultivars with upright habit have a cooler canopy and seed yield greater than normal leafed vining cultivars in heat stress conditions (Tafesse et al. 2019). To support breeding in frost tolerance, QTL analysis of frost damage has been carried out by Klein et al. (2014). QTL has also been identified in pea to increase salinity tolerance with SNP markers. This is an important set of tools for marker-assisted selection (MAS) to increase resistance to this abiotic stress (Leonforte et al. 2013). The use of landrace accessions has been identified to increase stress tolerance including salinity (Leonforte et al. 2013), iron deficiency (Kabir et al. 2012), boron toxicity (Bagheri et al. 1994), and heat tolerance during flowering (Petkova et al. 2009).

Chickpeas

The average yield of chickpeas in the period 1990 to 2017 was 0.82 ton ha⁻¹. In 1990 and 2017 the total harvested area of chickpea in the world was 9.9 million ha with a production of 6.8 million tons, and 14.6 million ha with a production of 14.8 million tons respectively. During this period the chickpea yield increased with an average percentage of 1.78% per year. (FAOSTAT 2019). As an effort to characterize allelic variation, to date, more than 1200 QTLs have been identified in the *Cicer arietinum* species (Pulse Crop Database 2019).

Major biotic constraints on chickpeas including ascochyta blight, botrytis gray mold, crenata broomrape, plant-parasitic nematodes, and

fusarium wilt. Ascochyta blight (AB) is a necrotrophic fungus caused by *Ascochyta rabiei* (Pass.) (Kimurto et al. 2013). AB is the most important yield-limiting factor for chickpeas. Cases in Canada and Australia AB have the potential to affect 95% of chickpea yield (Knight and Siddique 2002; Gan et al. 2006). Botrytis gray mold (BGM) due to *Botrytis cinerea* Press. Ex. Fr. (Pande et al. 2006a). BGM can damage chickpeas which result in loss of all yields in years of high humidity and extensive winter rains (Reddy et al. 1988; Pande et al. 2002). Nematodes that cause damage to chickpea plants focus on three types of nematodes, namely: cyst nematode (*Heterodera ciceri*), root-knot nematodes (*Meloidogyne artiella*, *M. javanica*, *M. incognita*), and root-lesion nematode (*Prathylenus thornei*) (Zwart et al. 2019). Globally, plant-parasitic nematodes attack results in a 14% loss in chickpea yield (Sasser and Freckman 1987). The pathogen that causes fusarium wilt in chickpeas is *Fusarium oxysporum* f. sp. *Ciceris* Schlechtend: Fr. fSp. *Ciceris* (Padwick) T. Matuo and K. Sato (Jimenez-Fernandez et al. 2006; Haware MP 1990). Each chickpea genotype has varying sensitivity to heat stress. Variation in yield loss of 10-15% for each degree increase in temperature above the optimum temperature (Upadhaya et al. 2011). Generally, heat stress decreases ultimately seed weight and grain filling rate (Munier-Jolain and Ney 1998).

Cowpeas

Cowpea (*Vigna unguiculata* L. Walp.) is a warm-season food legume that is very important in the Africa, Americas, India, and other semi-arid regions (Timko and Singh 2008). Compared to three decades ago, current cowpea production worldwide has more than tripled. In 1990 cowpea production was 2.1 million tons, in 2017 7.4 million tons. During this period the average yield increase was 3% per year (FAOSTAT 2019).

Striga gesnerioides (Willd) Vatke is the main parasitic weed that attacks cowpeas in West and Central Africa which causes a substantial yield reduction. As an effort to control the biotic constraint, research in Nigeria, analysis of genotype x environment (GGE) biplots identified UAM09 1046-6-1 and UAM09 1046-6-2 suggest

as ideal genotypes that have a good adaptation to *S. gesnerioides* relatively (Omoigui et al. 2017). Several improving for other biotic stress-resistant, including flower bud thrips (*Megalurothrips sjostedti* Trybom) (Togola et al. 2019), brown blotch disease due to the pathogen *Colletotrichum truncatum* (Andrus) (Adebitan 1984; Adetumbi et al. 2019). Studies on European cowpea landraces for novel foods and agricultural system sustainability, two accessions from Spain, BGE038477 and BGE038478, and two from Portugal, Cp5553 and Vg60, are ready to be included in the breeding cowpea program (Carvalho et al. 2017). Another study of cowpea landraces by Carvalho et al. (2019) through genotype screening of cowpea worldwide to drought-tolerant at the germination stage. The results of the study showed six landrace genotypes and one cultivated genotype from the entire collections was identified as tolerant to drought stress at the germination stage. These genotypes are the best suitable parents used for further breeding programs (Carvalho et al. 2019). Some breeding to improve drought tolerance is directed to a diallel analysis (Rodrigues et al. 2018) and genetic architecture for grain yield, biomass, and delayed senescence (Muchero et al. 2013). Hall (2004) based on the results of their studies of cowpea breeding to heat stress reviewed that breeding for heat stress adaptation directed on crop phenology, heat tolerance during reproductive development, and interactions between heat-tolerant during reproductive development and other traits.

Pigeon peas

In order to improve the nutritional quality of pigeon pea (*Cajanus cajan* L.), research in India analyzed the content of moisture, protein, fat, carbohydrates, and limiting amino acids tryptophan and methionine. The genotypes of PT-012-9, PT-012-16, and PT 012-23 have good results for breeding to improve nutritional quality (Kachare et al. 2018). For improve resistance to biotic and abiotic constraints, Singh et al. (2016) reported genetics of the Fusarium wilt (FW) resistance disease associated with simple sequence repeat (SSR) markers. Four resistant FW genotypes

were used, namely BDN-2001-9, BDN-2004-1, BWR-133, and IPA-234. The results of the study reported ASSR-1, ASSR-23, and ASSR-148 markers will be used for the FW-resistant pigeon pea-resistant parental screening program. The use of pigeon pea crop wild relatives (CWR) is confirmed to have resistance to biotic and abiotic stress so that it can be used for breeding programs. *C. acutifolius* is resistant to pod borer (Mallikarjuna et al. 2007). *C. platycarpus* is resistant to *Phytophthora* blight (Saxena et al. 2005). *C. scarabaeoides* is resistant to pod borer and sterility mosaic disease (Mallikarjuna et al. 2007, 2011). Tolerance gene has been identified for waterlogging in pigeon pea. Segregation pattern was observed in two crosses derived from the tolerant parent (ICPL 84023) and two susceptible parents (DA 11 and MA 98 PTH 1). Based on that study shown that waterlogging tolerance is influenced by a single gene and as a dominant trait (Sarode et al. 2007).

Lentils

The foliar disease is the most serious biotic stress for lentils (*Lens culinaris* Medik.). In all the growing regions of the world, Ascochyta blight caused by *Ascochyta lentil* is a problem with various levels (Ahmed and Morral 1996). Many Ascochyta blight resistant cultivars/lines lentils have been released in various countries. Some of these are presented in table 7 (Ye et al. 2002). Abiotic stresses that affect lentils include heat, cold, drought, nutrient deficiency, nutrient toxicity, and salinity. Of these stresses, heat and drought are the most important stresses worldwide (Turner et al. 2001). Previous researches have produced heat-tolerant genotypes including IG2507, IG3263, IG3745, IG4258, and FLIP2009. The study was

conducted to compare the five heat-tolerant genotypes with heat-sensitive genotypes (IG2821, IG2849, IG4242, IG3973, and IG3964). The heat-tolerant genotype has higher pollen germination, pollen viability, stigmatic function, ovular viability, pod set, and growth of pollen tube through the style. Heat-tolerant genotypes result in less damage to membranes, cellular oxidizing abilities, and lower photosynthetic functions. Temperatures up to 40/30°C is able to tolerated by heat-tolerant genotype to produce fewer pods (Sita et al. 2017). For improved tolerance to drought in lentils, there are two traits that are important for research: faster stomatal closure under soil drying, and limitation of transpiration under high atmospheric vapor pressure deficits (Ghanem et al. 2017).

In order to improve lentils, desirable mutants have been identified in quantitative traits in lentils at early M₂ generation (Tabti et al. 2018). Induced mutation analysis is also carried out with molecular characterization and biochemical of high yielding lentils mutant lines. The biochemical and molecular profiles of induced mutant lines can form the basis of future conservation and utilization strategies to broaden the genetic base of current breeding populations (Laskar et al. 2018). Babayeva et al. (2018) identified genetic relationships among introduced lentil germplasm using agronomic traits and inter sequence repeat (ISSR). The ISSR dendrogram is able to clearly distinguish all lentil accessions. (Babayeva et al. 2018). QTLs have been identified for agronomic traits in lentils using association mapping by Kumar et al. (2018). The future lentil breeding program can use these markers as functional markers.

Table 6. Ascochyta blight-resistant cultivars lines on cultivated lentils

Country	Cultivars/lines
India	L442, L448, ILL179, ILL195, ILL201, LG169, LG170, LG171, LG172, LG173, LG174, LG176, LG209, LG217, LG218, LG219, LG221, LG223, LG225, LG231, LG232, LG236, HPL5, Piant 4, Pant L406 ILL 358, ILL 4605, ILL 5588, ILL 5684, ILL6024, FLIP84-27L, FLIP84-43L, FLIP84-55L, FLIP84-85L, FLIP86-9L, FLIP86-12L, 78 S 26018, 78 S 26052,
Pakistan	88518, 88527, 88547, Masoor-93 ILL 857, ILL 2439, ILL 4605, ILL 5244, ILL 5588, ILL 5562, ILL 5590, ILL 5593, ILL5684, ILL 5725

	ILL 857, ILL 2439, ILL 4605, ILL 5244, ILL 5588, ILL 5562, ILL 5590, ILL 5593, ILL 5684, ILL 5725
Syria	ILL 5698, ILL 5700, ILL 5883, ILL 6212
	ILL 358, ILL 5588, ILL 5684, Laird
Morocco	ILL 5684, ILL 5588, ILL 5714, Rajah
Canada	ILL 358, ILL 4605
New Zealand	ILL 358, ILL 857
Chile	
Ethiopia	

Vetches

Studies in Bulgaria to analyze the stability of seed yield in vetch (*Vicia sativa*) cultivars, the formation, and variability of seed yield and its components (plant height, pod per plant, seed per plant, 1000 seed weight) are highly significantly affected by genotype, environment, and their interaction. As a result, Liya, Moldovskaya, and Obrazets 666 cultivars are suitable for inclusion in breeding programs and developing new lines with stable yields (Georgieva et al. 2015). Cakmakci et al. (2006) revealed the heritability of component yields in common vetch. Heritability estimates help determine the right strategy in breeding and are used to determine the level of relationship between relatives and predict the effectiveness of phenotypic selection. A study in Turkey by analyzing 150 accessions and two common vetch cultivars from various agro-ecological regions and countries revealed that seed yields from common vetch could be imported through bulk selection based on 1000-seed weight, number of podding nodes, harvest index, and number of days to flowering by choosing promising accessions (Cakmakci et al. 2006). While research in Serbia identified agronomic characteristics associated with grain yield and crude protein content in common vetch accessions from various geographic origins. Of the 14 accessions, VIC 006 produced the highest grain yield. Topaze produces the highest crude protein dry matter grain. Based on branching relationships, there are 4 clusters and two quite distinct accessions (Mikić et al. 2013).

Lupins

The genus lupines consist of nearly 300 species, four of which play an important role in

agriculture: *Lupinus albus* L., *L. angustifolius* L., *L. luteus* L., and *L. mutabilis* L. (Gresta et al. 2017). Drought stress reduced grain yield by 79%. Recently, the breeding program on *L. albus* L. (white lupine) against drought stress by also testing 21 landraces originating from the major historical cropping region, one variety, and two breeding lines. Early flowering is an important stress relief mechanism. Various out-yielded germplasm landraces that are better under stressful and favorable conditions (Annicchiarico et al. 2018). As for biotic stress, anthracnose fungal disease caused by *Colletotrichum lupine* since the mid-1990s caused a rapid decline in white lupine cultivation in Germany and other countries in Central Europe. The testing of new breeding lines in five different locations in Germany showed improved resistance performance against *C. lupine* compared to reference varieties. Increased resistance is favorable for grain yield (Jacob et al. 2017). In an effort to improve *L. luteus* L. (yellow lupine), Iqbal et al. (2019) developed the first linkage map and conducted a QTL analysis for yellow lupine under well-watered and water-deficit conditions. These genetic resources and QTL information offer significant potential for use in MAS in yellow lupine (Iqbal et al., 2019). For *L. mutabilis* L., currently, the species' molecular resources are still rare. The majority of molecular studies so far have focused on understanding phylogeny (Gulisano et al. 2019). Recently, the emergence of nextRADseq technology has explained the timing and domestication area of *L. mutabilis* L. (Atchison et al. 2016). A total of 118 InDel polymorphisms and 113 SSR primers from *L. luteus* L. have been used successfully to characterize *L. mutabilis* L. genetically (Parra-Gonzales et al. 2012; Osorio et al. 2018). A study

in Australia identified genotype x environment interaction in *L. angustifolius* (narrow leafed-lupine) for phonological adaptation which was explored using the Agricultural Production System Simulator (APSIM). Simulation results show that narrow leafed-lupine yield is significantly affected by water availability and temperature. Therefore, narrow leafed-lupine breeding in Australia must focus on rainfall gradients and temperature regimes (Chen et al. 2016)

Soybean

When viewed from its production, soybean is the most important food legume crop in the world. From 1990 to 2017 soybean yield increased by an average of 1.68% per year. During this period the harvested area more than doubled. In 1990 the harvested area of soybean was 57.2 million ha with a production of 108.5 million tons, in 2017 the harvested area was 123.6 million ha with production of 352.6 million tons worldwide (FAOSTAT 2019).

Species (*Glycine max* [L.] Merr.) or cultivated soybean have been domesticated thousands of years ago is believed from wild soybean (*Glycine soja*) (Carter et al. 2004; Hymowitz 1970). It is estimated that there are more than 47,000 accessions of *Glycine max* among

germplasm throughout the world. More than 1,000 of them have been used for cultivar development programs (Carter et al. 2004). While the USDA Soybean Germplasm Collection has more than 22,000 accessions of *Glycine max* (U.S. National Germplasm System, 2019). The genetic source is the result of previous development programs and is useful for expanding the genetic diversity needed to improve genetic gain in the future development of soybean cultivars.

QTL studies can provide functional genomics information so they can characterize allelic variations and how they affect the fitness and function of all organisms (Miles and Wayne 2008). Updates to the QTL soybean collection can be accessed through SoyBase Integrating Genetics and Genomics to Advance Soybean Research (<https://www.soybase.org/>). The database is very complete as supporting material to improve soybean. Starting from soybean cultivation tutorials, genetic maps, genome browsers, genome sequences, mutants, to information on soybean activist communities. The database was developed by the USDA-Agricultural Research Service (ARS) SoyBase and Legume Clade Database group at the Iowa State University and funded by the USDA-ARS (Fig. 2).

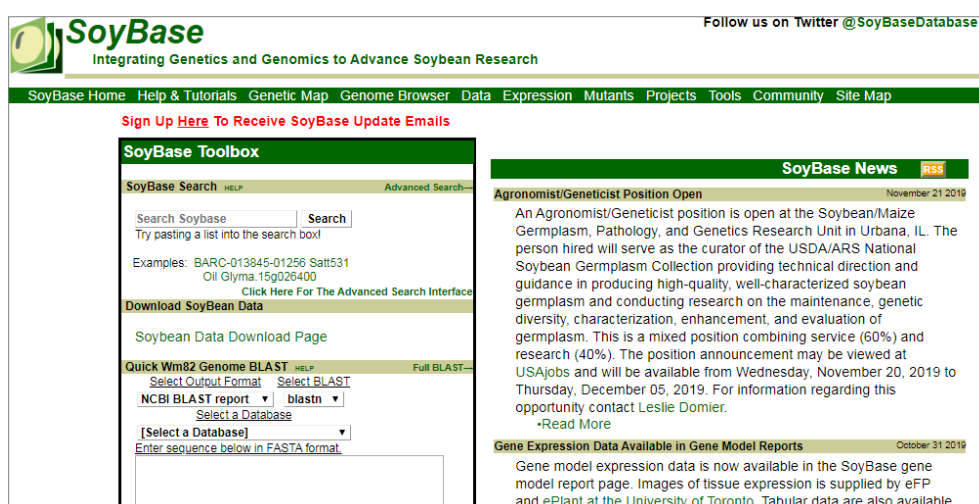


Figure 2. Display of the SoyBase Integrating Genetics and Genomics to Advance Soybean Research page (<https://www.soybase.org/>)

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