TROPICAL PLANTATION

Tropical Plantation Journal. Vol. 1 (2022), No.2 Journal home page: https://jurnal.akpy-stiper.id ISSN : **2828-1551** e-ISSN : **2828-1543** DOI : https://doi.org/10.56125/tpj.v1i2.8

# Food Legume Production Performance in Support of World Food

Amar Ma'ruf<sup>1,2</sup>, Muhammad Fahmi Sidiq<sup>3</sup>, Ni Luh Suriani<sup>4</sup>

<sup>1</sup> Department of Agrotechnology, Faculty of Agriculture, Universitas Asahan, Indonesia

<sup>2</sup> Department of Field Crop, Faculty of Agriculture, Akdeniz University, Antalya, Turkey

<sup>3</sup> Master's Program of Agroecology, Wageningen University, Gelderland, Netherlands

<sup>4</sup> Biology Study Program, Mathematics and Natural Sciences, Udayana University, 80232, Bali, Indonesia

\*Corresponding author: amarsanis92@gmail.com

Article History: Received: 23 Mei 2022, Final Revision: 17 Juni 2022, Accepted: 13 Juli 2022, Online Publication: 30 Juli 2022

## 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 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; Stampt 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 limits agricultural most often 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 (Fover 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 genomicassisted 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 vield 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).

Category	Cron	Nutrient content			
	Clop	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 1.** Composition of energy, protein, carbohydrate, and fiber content in several pulses and cereals (100g cooked)

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

Cluster	Logumos	Nutritional content (%)			
	Legumes	Carbohydrate	Protein	Dietary fiber	Fat
1	Chickpea, lima bean, adzuki bean,	63.78	25.44	9.32	2.58
	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				
2	Soybean, sweet lupin, groundnut,	37.10	36.09	17.72	14.11
	bitter lupin, sword bean				
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 logumon	Production in 2017	Viold in 2017 (Ira ha-1)	The average increase in annual
rood leguilles	(million tons)	$1 \text{ leid in } 2017 \text{ (kg ina ^{\circ})}$	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



**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 griseola), (Phaeoisariopsis spots 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).

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> )	<ul> <li>QTL: BC420 (Pv06), SU91 (Pv08), Xa11.40V1</li> </ul>	• Viteri et al. 2015; Miklas et al. 2017	
Fungi			
<ul> <li>Angular leaf spot (<i>Phaeoisariopsis</i>)</li> <li>Anthracnose (<i>Colletotrichum</i>)</li> </ul>	<ul> <li>QTL: Pv04, Pv10 (ALS10.1) Phg1, Phg2</li> <li>QTL: Pv01, Pv04, Pv10, Co-1, Co-2</li> </ul>	<ul> <li>Oblessuc et al. 2012; 2015; Keller et al. 2015</li> <li>Zuiderveen et al. 2016</li> </ul>	
• Fusarium	• QTL (FRR3.1 <sup>km</sup> ) (Pv03), LGs B2 and B3	<ul><li> Roman-Aviles and Kelly 2005</li><li> Hanson et al. 1993</li></ul>	

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

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

ascocyhta 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 Maroccan 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 Recherce 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 (Keneni et al. 2010). Some of the abiotic stresstolerant genotypes are following in table 5.

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

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

## Peas

Pea (*Pisum sativum* L.) is one of the oldest domesticated crops included in the annual coolseason 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<sup>-1</sup>. 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 rootlesion nematode (Prathylencus 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 oxyporum 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 truncathum (Andrus) (Adebitan 1984; Adetumbi et al. 2019). Studies on European cowpea landraces novel foods and agricultural system for 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 heattolerant 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. acutifolius is resistant to pod borer С. (Mallikarjuna et al. 2007). C. platycarpus is resistant to Phytophtora 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 Asccochyta 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 heattolerant 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 heattolerant 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  $40/30^{\circ}$ 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 M<sub>2</sub> 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). OTLs 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.

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

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

43 Production Performance of World Food - Amar Ma'ruf, et al

	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, Liva, Moldovskava, 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 OTL analysis for vellow 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 leafedlupine) 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/)

## REFERENCES

- Abbes Z, Kharrat M, Delavault P, Simier P, Chaibi
  W (2007) Field evaluation of the resistance of some faba bean (*Vicia faba* L.) genotypes to the parasitic weed *Orobanche foetida* Poiret. Crop protection 26:1777-1784
- Abdelmula AA, Link W, Kittlitz EV, Stelling D (1999) Heterosis and inheritance of drought tolerance in faba bean, *Vicia faba* L. Plant Breeding 118(6):485-490. <u>https://doi.org/10.1046/j.1439-</u> 0523.1999.00411.x
- Abdelmula AA and Abuanja IK (2007) Genotypic responses, yield stability, and association between characters among some of Sudanese Faba bean (*Vicia faba* L.) genotypes under heat stress. In Proceedings of the Tropical German Conference (Utilization of diversity in land use systems: Sustainable and organic approaches to meet human needs). Witzenhausen pp 9-11
- Abid G, M'hamdi M, Mingeot D, Aouida M, Aroua I, Muhovsk Y et al. (2017) Effect of drought stress on chlorophyll fluorescence, antioxidant enzyme activities and gene expression patterns in faba bean (*Vicia faba* L.). Arch Agron Soil Sci 63:536-552. <u>https://doi.org/10.1080/03650340.2016.122</u> <u>4857</u>
- Adebitan A (1984) Studies on the brown blotch disease of cowpea (*Colletotrichum truncatum* Schew). Andrus and More. M.Sc. project, University of Ibadan, Nigeria, p 89
- Adetumbi JA, Solomon TA, Adeola A, Kareem KT, Oduwaye OF et al (2019) Genetic variability in the agronomic traits, inheritance pattern of seed coat colour and response to brown blotch disease among cowpea hybrids. Euphytica 215:142. https://doi.org/10.1007/s10681-019-2466-6
- Ahmed S and Morrall RAA (1996) Field reactions of lentil lines and cultivars to isolates of *Ascochyta fabae* f. sp. *lentis*. Can J Plant Path 18:362-369
- Ahloowalia BS, Maluszynki M, Nichterlein K (2004) Global impact of mutation-derived varieties. Euphytica 135:187-204

- Amanullah (2016) International year of pulses 2016. EC Agriculture Editor's Column 2016.http://www.fao.org/fsnforum/sites/def ault/files/discussions/contributions/ECAG-01-ECO-IYP2016.pdf. Accessed 5 November 2019
- Annicchiarico P, Romani M, Pecetti L (2018) White lupin (*Lupinus albus*) variation for adaptation to severe drought stress. Plant Breeding 137:782-789. DOI: 10.1111/pbr.12642
- Aryamanesh N, Byrne O, Hardie DC, Khan T, Siddique KHM., Yan G (2012) Large-scale density-based screening for pea weevil resistance in advanced backcross lines derived from cultivated field pea (*Pisum sativum*) and *Pisum fulvum*. Crop Pasture Sci 63:612-618. https://doi.org/10.1071/CP12225
- Assefa T, Mahama AA, Brown AV, Cannon KS et al (2019) A review of breeding objectives, genomic resources, and marker-assisted methods in commong bean (*Phaseolus vulgaris* L.). Mol Breeding 39:20
- Atchison GW, Nevado B, Eastwood RJ et al (2016)
  Lost crops of the Incas: Origins of domestication of the Andean pulse crop tarwi, *Lupinus mutabilis*. Am J Bot 103:1592-1606. Doi: 10.3732/ajb.1600171
- Babayeva S, Akparov Z, Amirov L et al (2018) Genetic relationship among introduced lentil germplasm using agronomic traits and ISSR markers. Genetika 50(2):575-590
- Bagheri A, Paull JG, Rathjen AJ (1994) The response of *Pisum sativum* L. germplasm to high concentrations of soil boron. Euphytica 75:9-17.

https://doi.org/10.1007/BF00024526

- Beebe SE, Corrales M (1991) Breeding for disease resistance. In: Schoonhoven A, Voysest O (eds) Common beans: research for crop improvement. CAB Int, CIAT, Cali Wallingford, pp 561-610
- Bergvinson D. From gene bank to farmer's hand. http://dgblog.icrisat.org/?p=627. Accessed 5 November 2019

- Beyene AT, Derera J, Sibiya J (2018) Genetic variability of faba bean genotypes for chocolate spot (*Botrytis fabae*) resistance and yield. Euphytica 214:132. https://doi.org/10.1007/s10681-018-2210-7
- Blair MW, Muñoz C, Garza R, Cardona C (2006) Molecular mapping of genes for resistance to the bean pod weevil (*Apion godmani* Wagner) in common bean. Theor Appl Genet 112:913-923
- Blair MW, Rodriguez LM, Pedraza F, Morales F,
  Beebe SE (2007) Genetic mapping of the
  bean golden yellow mosaic geminivirus
  resistance gene bgm-1 and linkage with
  potyvirus resistance in common bean
  (*Phaseolus vulgaris* L.). Theor Appl Genet
  114:261-271
- Bressani R, Navarrete D, Elias L (1984) The nutritional value of diets based on starchy foods and common beans. Plant Food Hum Nutr 34:109-115.
- Briache FZ, Ennamil M, Mbasani-Mansi J, Gaboun F, Abdelwahd R, Fatemi ZEA, El-Rodeny W, Amri M, Triqui ZEA, Mentag R (2019)
  Field and controlled conditions screenings of some faba bean (*Vicia faba* L.) genotypes for resistance to the parasitic plant *Orobanche crenata* Forsk. and investigation of involved resistance mechanisms. Jour Plant Dis Prot 126:211-224. <a href="https://doi.org/10.1007/s41348-019-00207-x">https://doi.org/10.1007/s41348-019-00207-x</a>
- Brisco EI (2012) Empoasca leafhopper species resistance in common bean, Phaseolus vulgaris: Field Screening and QTL Identification. Dissertation, Michigan State University, Plant Breeding, Genetics and Biotechnology Program/Crop and Soil Sciences
- Burstin J, Gallardo K, Mir RR, Varshney RK, Duc G (2011) Improving protein content and nutrition quality (Chapter 20). In A. Pratap, & J. Kumar (Eds.), Biology and breeding of food legumes (pp 314-328). New Delhi, India: CABI. <u>https://doi.org/10.1079/9781845937669.00</u> <u>00</u>

- Cakmakci S , Aydinoglu B, Karaca M, Bilgen M (2006) Heritability of yield components in common vetch (*Viciasativa* L.), Acta Agri Sca Sec B-Soil Pl Sci 56(1):154-59. DOI: 10.1080/09064710510008531
- Campbell BM, Vermeulen SJ, Anggarwal PK, Corner-Dollof C et al (2016) Reducing risks to food security from climate change. Global Food Security 11:34-43. http://dx.doi.org/10.1016/j.gfs.2016.06.002
- Carter TE, Nelson RL, Sneller CH, Cui Z (2004) Genetic diversity in soybean. In: Boerma HR, Specht JE (eds) Soybeans: improvement, production, and uses, 3rd edn. ASA, CSSA, and SSSA, Madison, pp 301-416
- Carvalho M, Bebeli PJ, Pereira et al (2017) European cowpea ladraces for a more sustainable agriculture system and novel foods. J Sci Food Agric 97:4399-4407. DOI 10.1002/jsfa.8378
- Carvalho M, Matos M, Castro I et al (2019) Screening of worldwide cowpea collection to drought tolerant at a germination stage. Scientia Horticulturae 247:107-115. <u>https://doi.org/10.1016/j.scienta.2018.11.08</u> <u>2</u>
- Chen C, Berger J, Fletcher A, Lawes R, Robertson M (2016) Genotype x environment interactions for phonological adaptation in narrow-leafed lupin: A simulation study with a parameter optimized model. Field Crop Res 197:28-38. http://dx.doi.org/10.1016/j.fcr.2016.08.002
- Clement SL, Hardie DC, Elberson LR (2002) Variation among accessions of *Pisum fulvum* for resistance to pea weevil. Crop Sci 42:2167-2173.

https://doi.org/10.2135/cropsci2002.2167

- Clement SL, McPhee KE, Elberson LR, Evans MA (2009) Pea weevil, *Bruchus pisorum* L. (Coleoptera: Bruchidae), resistance in *Pisum sativum* x *Pisum fulvum* interspecific crosses. Plant Breed 128:478-485. <u>https://doi.org/10.1111/j.1439-</u> 0523.2008.01603.x
- Collard BCY, Ades PK, Pang ECK, Brouwer JB, Taylor PWJ (2001) Prospecting for sources

of resistance to *ascochyta* blight in wild *Cicer* species. Australas Plant Pathol 30:271-276

- Creighton C, Hobday AJ, Lockwood M, Pecl GT (2015) Adapting management of marine environments to a changing climate: A checklist to guide reform and assess progress. Ecosystems 1-33. <u>http://dx.doi.org/10.1007/s10021-015-</u> 9925-2
- Das A, Parihar AK, Saxena D et al (2019) Deciphering genotype-by-environment interaction for targeting test environments rust resistant genotypes in pea (*Pisum sativum* L.). Front in Plant Sci 10:825. <u>https://doi.org/10.3389/fpls.2019.00825</u>
- De Ron AM, Rodiño AP, Santalla M, González AM, Lema MJ, Martín I et al (2016) Seedling emergence and phenotypic response of common bean germplasm to different temperatures under controlled conditions and in open field. Front Plant Sci 7:1087.

https://doi.org/10.3389/fpls.2016.01087

- Diaz LM, Ricaurte J, Tovar E, Cajiao C, Teran H, Grajales M, et al (2018) QTL analyses for tolerance to abiotic stresses in a common bean (*Phaseolus vulgaris* L.) population. PLoS ONE 13(8):e0202342. <u>https://doi.org/10.1371/journal.pone.02023</u> <u>42</u>
- Di Vito M, Singh KB, Greco N, Saxena MC (1996) Sources of resistance to cyst nematode in cultivated and wild *Cicer* species. Genet Resour Crop Evol 43:103-110
- Duc G, Agrama H, Bao S, Berger J, Bourion V, De Ron AM et al (2015) Breeding annual grain legumes for sustainable agriculture: new methods to approach complex traits and target new cultivar ideotypes. Crit Rev Plant Sci 34:381-411. <u>https://doi.org/10.1080/07352689.2014.898</u> 469
- EPPO (2012) Standards pea. <u>https://www.eppo.int/</u>. Accessed 15 November 2019.

FAOSTAT (2019) Crops visualize data. Food and Agriculture Organization of The United Nations. <u>http://www.fao.org/faostat/en/#data/QC/vis</u>

ualize. Accessed 2 November 2019

- Foley JA, Ramankutty N, Brauman KA, et al (2011) Solution for a cultivated planet. Nature 478(7369):337-342
- Food and Agricultural Organization of the United Nations (1994) Definition and classification of commodities (draft): 4. Pulses and derived products. <u>http://www.fao.org/waicent/faoinfo/econom</u> <u>ic/faodef/fdef04e.htm</u>. Accessed 2 November 2019
- Food and Agriculture Organization of the United Nations (FAO) (2018) The State of Food Security and Nutrition in The World. FAO, Rome
- Foyer CH, Lam HM, Nguyen HT et al (2016) Neglecting legumes has compromised human health and sustainable food production. Nature Plants 16112:1-10. DOI: 10.1038/NPLANTS.2016.112
- Freytag GF and Debouck DG (2002) Review of taxonomy, distribution, and ecology of the genus *Phaseolus* (Leguminosae Papilionoideae) in North America, Mexico, and Central America. Sida Bot Misc 23:1-300
- Gan YT, Siddique KHM, MacLeod WJ, Jayakumar
  P (2006) Management options for minimizing the damage by Ascochyta blight (Ascochyta rabiei) in chickpea (Cicer arietinum L.). Field Crops Research 97:121-134
- Georgieva N, Nikolova I, Kosev V (2015) Stability analysis for seed yield in vetch. Em Jour Food Agri 27(12):903-910. doi:10.9755/ejfa.2015-04-172
- Ghanem ME, Kibbou FE, Guiguitant J, Sinclair TR
  (2017) Opportunities to improve the seasonal dynamics of water use in lentil
  (*Lens culinaris* Medik.) to enhance yield increase in water-limited environments. Chem Biol Technol Agric 4:22.
- Girma F and Haile D (2014) Effects of supplemental irrigation on physiological

parameters and yield of faba bean (*Vicia faba* L.) varieties in the highlands of Bale, Ethiopia. J Agron 13:29-34.

- Godfray HCJ, Beddington JR, Crute IR et al (2010) Food security: The Challenge of feeding 9 billion people. Science 327:812-818.
- Gresta F, Wink M, Prins U, Abberton M, Capraro J, Scarafoni A et al (2017) Lupins in European cropping systems. In: Legumes in Cropping System. CABI, pp 88-108.
- Griffiths DW and Lawes D A (1978) Variation in the crude protein content of field beans (*Vicia faba* L.) in relation to the possible improvement of the protein content of the crop. Euphytica 27(2):487-495 https://doi.org/10.1007/BF00043174
- Gulisano A, Alves S, Martins JN, Trindade LM (2019) Genetics and Breeding of *Lupinus mutabilis*: An Emerging Protein Crop. Front Plant Sci 10:1385.
- Hall AE (2004) Breeding for adaptation to drought and heat in cowpea. Eurp J Agronomy 21:447-454. doi:10.1016/j.eja.2004.07.005
- Hall C, Hillen C, Robinson JG (2017) Composition, nutritional value and health benefits of pulses. Cereal Chem 94:11-31.
- Hanocq E, Jeuffroy MH, Lejeune-Hénaut I, Munier-Jolain N (2009) Construire des idéotypes pour des systèmes de culture varies en pois d'hiver. Innov Agron 7:14-28
- Hanounik SB and Robertson, LD (1989) Resistance in *Vicia faba* germplasm to blight caused by *Ascochyta fabae*. Plant Disease 73(3):202-205. <u>https://doi.org/10.1094/PD-73-0202</u>
- Hanson PM, Pastor-Corrales MA, Kornegay JL (1993) Heritability and sources of Ascochyta blight resistance in common bean. Plant Dis 77:711-711
- Haware MP (1990) Fusarium wilt and other important diseases chickpea in the Mediterranean area. In Present Status and Future Prospects of Chickpea Crop Production and Improvement in the Mediterranean Countries; Saxena MC, Cubero JI, Wery J. Eds CIHEAM, Zaragoza, Spain, pp 61-64

- Herrero M, Wirsenus S, Henderson B, Rigolot C (2015) Livestock and the environment: what have we learned in the past decade? Annu Rev Environ Resour 40:177-202. <u>http://dx.doi.org/10.1146/annurev-environ-031113-093503</u>
- Hurtado-Gonzales OP, Valentini G, Gilio TS, Martins AM, Song Q, Pastor-Corrales MA (2017) Fine mapping of Ur-3, a historically important rust resistance locus in common bean. G3 7:557-569
- Hymowitz T (1970) On the domestication of the soybean. Econ Bot 24:408-421
- Imtiaz M, Malhotra RS, Yadav SS (2011) Genetic adjustment to changing climates: chickpea.
  In: Yadav SS, Redden R, Hatfield JL, Lotze-Campen H, Hall A (eds) Crop adaptation to climate change. Wiley, Oxford, pp 251-268
- Infantino A, Porta-Puglia A, Singh KB (1996) Screening wild *Cicer* species for resistance to fusarium wilt. Plant Dis 80:42-44
- Iqbal MM, Huynh M, Udall JA, Kilian A, Adhikari KN et al (2019) The first genetic map for yellow lupin enables genetic dissection of adaptation traits in an orphan grain legume crop. BMC Genetics 20:68. https://doi.org/10.1186/s12863-019-0767-3
- Jacob I, Feuerstein U, Heinz M, Michael S (2017) Evaluation of new breeding lines of white lupin with improved resistance to anthracnose. Euphytica 213:236. DOI 10.1007/s10681-017-2011-4
- Jimenez-Fernandez D, Navas-Cortes JA, Montes-Borrego M, Jimenez-Diaz RM, Landa BB (2011) Molecular and Pathogenic Characterization of Fusarium redolens, a New Causal Agent of Fusarium Yellows in Chickpea. Plant Dis 95:860-870
- Johnson WC, Guzmán P, Mandala D, Mkandawire AC, Temple S, Gilbertson RL et al (1997) Molecular tagging of the bc-3 gene for introgression into Andean common bean. Crop Sci 37:248-254
- Jung G, Ariyarathne HM, Coyne DP, Nienhuis J (2003) Mapping QTL for bacterial brown spot resistance under natural infection in field and seedling stem inoculation in

growth chamber in common bean. Crop Sci 43:350-357

- Kabir AH, Paltridge NG, Able AJ, Paull JG, Stangoulis JCR (2012) Natural variation for Fe-efficiency is associated with upregulation of Strategy I mechanisms and enhanced citrate and ethylene synthesis in *Pisum sativum* L. Planta 235:1409-1419. <u>https://doi.org/10.1007/s00425-011-1583-9</u>
- Kachare DP, Satbhai RD, Rathod DB, Naik RM (2018) Evaluation of Pigeon pea (*Cajanus Cajan* L.) Genotypes for Nutritional Quality. Leg Res Inter Jour 42:485-489
- Kaur S, Kimber RBE, Cogan NOI, Materne M, Forster JW, Paul JG (2014) SNP discovery and high-density genetic mapping in faba bean (*Vicia faba* L.) permits identification of QTLs for ascochyta blight resistance. Plant Science 217-218:47-55
- Keller B, Manzanares C, Jara C, Lobaton JD, Studer B, Raatz B (2015) Fine-mapping of a major QTL controlling angular leaf spot resistance in common bean (*Phaseolus vulgaris* L.). Theor Appl Genet 128(5):813-826
- Keneni A, Assefa F, Prabu PC (2010) Characterization of acid and salt tolerant rhizobial strains isolated from faba bean fields of Wollo, Northern Ethiopia. Jour of Agri Sci Tech 12:365-376
- Kimurto PK, Towett BK, Mulwa RS (2013) Evaluation of chickpea genotypes for resistance to Ascochyta blight (*Ascochyta rabiei*) disease in the dry highland of Kenya. Phytopathologia Mediterranea 52(1):212-221
- Klein A, Houtin H, Rond Celine et al (2014) QTL analysis of frost damage in pea suggests different mechanisms involved in frost tolerance. Theor Appl Genet 127:1319-1330 https://doi.org/10.1007/s00122-014-2299-6
- Knights EJ and Siddique KHM (2002) Chickpea status and production constraints in Australia. In: Abstract of Proceedings: Integrated Management of Botrytis Grey Mould of Chickpea in Bangladesh and Australia. 1-2 June 2002, Bangladesh

Agricultural Research Institute, Joydebpur, Bangladesh, pp 33-41

- Kouris BA and Belski R (2016) Health benefts of legumes and pulses with a focus on Australian sweet lupins. Asia Pac J Clin Nutr 25:1-17
- Kumar J, Gupta S, Gupta DS, Singh NP (2018) Identification of QTLs for agronomic traits using association mapping in lentil. Euphytica 214:75. https://doi.org/10.1007/s10681-018-2155-x
- Kumari SG and Makkouk KHM (2007) Virus diseases of faba bean (*Vicia faba* L.) in Asia and Africa. Plant Viruses 1:93–105
- Kushi LH, Meyer KA, Jacobs DR (1999) Jr Cereals, legumes, and chronic disease risk reduction: evidence from epidemiologic studies. Am J Clin Nutr 70:451-458
- Landry EJ, Coyne CJ, McGee RJ, Hu J (2016) Adaptation of autumn-sown faba bean germplasm to southeastern Washington. Agronomy Journal 108(1):301-308. https://doi.org/10.2134/agronj2015.0028
- Lanna AC, Silva RA, Ferraresi TM, Mendonca JA et al (2018) Physiological characterization of common bean (*Phaseolus vulgaris* L.) under abiotic stresses for breeding purposes. Env Sci Poll Res 25:31149-31164. https://doi.org/10.1007/s11356-018-3012-0
- Laskar RA, Laskar AA, Raina A, Khan S, Younus H (2018) Induced mutation analysis with biochemical and molecular characterization of high yielding lentil mutant lines. Int Jour Bio Macro 109: 167-179. https://doi.org/10.1016/j.ijbiomac.2017.12. 067
- Leonforte A, Sudheesh S, Cogan NO et al (2013) SNP marker discovery, linkage map construction and identification of QTLs for enhanced salinity tolerance in field pea (*Pisum sativum* L.). Plant Biology 13:161
- Lobell DB, Schlenker W, Costa-Roberts J (2011) Climate trends and global crop production since 1980. Science 333(6042):616-620. http://dx.doi.org/10.1126/science.1204531
- Maalouf F, Hu J, O'Sullivan DM, Zong X, Hamwieh A, Kumar S, Baum M (2019) Breeding and genomics in faba bean (*Vicia*

*faba*). Plant Breeding 138:465-473. https://doi.org/10.1111/pbr.12644

- Mallikarjuna N, Sharma HC, Upadhyaya HD (2007) Exploitation of wild relatives of pigeonpea and chickpea for resistance to Helicoverpa armigera. J. SAT Agricult. Res. 3(1):4
- Mallikarjuna N, Saxena KB, Jadhav DR (2011) Cajanus. In: Kole C (Ed.) Wild Crop Relatives: Genomic and Breeding Resources, Legume Crops and Forages. Springer-Verlag, Berlin, Heidelberg, pp 21-33

10.1080/00288233.2013.845231.

- Miklas PN, Kelly JD, Beebe SE, Blair WM (2006) Common bean breeding for resistance against biotic and abiotic stresses: from classical to MAS breeding. Euphytica 147:106-131
- Miklas PN, Fourie D, Chaves B, Chirembe C (2017) Common bacterial blight resistance QTL BC420 and SU91 effect on seed yield, seed weight, and canning quality in dry bean. Crop Sci 57:802-811
- Miles C and Wayne M (2008) Quantitative trait locus (QTL) analysis. Nature Education 1(1):208
- Muchero W, Roberts PA, Diop NN, Drabo I, Cisse N, et al (2013) Genetic Architecture of Delayed Senescence, Biomass, and Grain Yield under Drought Stress in Cowpea. PLoS ONE 8(7):e70041. doi:10.1371/journal.pone.0070041
- Muedi HH, Fourie D, McLaren NW (2015) Distribution and severity of bacterial brown spot on dry beans in South Africa: an update. South African J Sci 111:1-6
- Muehlbauer FJ, Kaiser WJ, Simon CJ (1994) Potential for wild species in cool season

food legume breeding. Euphytica. 73:109-114

- Munier-Jolain NG, Ney B (1998) Seed growth rate in grain legumes II. Seed growth rate depends on cotyledon cell number. J. Exp. Bot. 49:1971-1976
- Murray JD, Michaels TE, Cardona C, Schaafsma AW, Pauls KP (2004) Quantitative trait loci for leafhopper (*Empoasca fabae* and *Empoasca kraemeri*) resistance and seed weight in the common bean. Plant Breed 123:474-479
- Mwanauta RW, Mtei KM, Ndakidemi PA (2015) Potential of controlling common bean insect pests (Bean Stem Maggot (*Ophiomyia phaseoli*), ootheca (*Ootheca bennigseni*) and aphids (*Aphis fabae*) using agronomic, biological and botanical practices in field. Agricultural Sciences 6:489-497. https://doi.org/10.4236/as.2015.65048
- Oblessuc PR, Baroni RM, Garcia AF, Chioratto AF, Carbonell SM, Camargo LA et al (2012) Mapping of angular leaf spot resistance QTL in common bean (*Phaseolus vulgaris* L.) under different environments. BMC Genet 13:50
- Oldroyd GED (2013) Speak, friend, and enter: signalling systems that promote beneficial symbiotic associations in plants. Nature Rev Microbiol 11:252–263
- Omoigui LO, Kamara AY, Hakeem AA et al (2017) Performance of cowpea varieties under *Striga gesnerioides* (Willd.) Vatke infestation using biplot analysis. Euphytica 213:244. DOI 10.1007/s10681-017-2034-x
- Osorio CE, Udall JA, Salvo-Garrido H, Maureira-Butler IJ (2018) Development and characterization of InDel markers for *Lupinus luteus* L. (Fabaceae) and crossspecies amplification in other Lupin species. Electron J Biotechnol 31:44-47. doi: 10.1016/j.ejbt.2017.11.002
- Pande S, Singh G, Rao JN, Bakr MA, ChaurasiaPCP, Joshi S, Johansen C, Singh SD, KumarJ, Rahman MM, Gowda CLL (2002)Integrated management of botrytis graymold of chickpea. Information Bulletin No.

61, ICRISAT, Andhra Pradesh, India

- Pande S, Ramgopal D, Kishore GK, Mallikarjuna N, Sharma M, Pathak M, Narayana Rao J (2006a) Evaluation of wild *Cicer* species for resistance to ascochyta blight and botrytis gray mold in controlled environment at ICRISAT, Patancheru, India. Int Chickpea Pigeonpea Newslett 13:25-26
- Pande S, Galloway J, Gaur PM et al (2006b) Botrytis grey mould of chickpea: a review of biology, epidomology, and disease management. Aus J Agri Res 57:1137-1150
- Parra-Gonzales LB, Aravena-Abarzua GA, Navarro-Navarro CS (2012) Yellow lupin (*Lupinus luteus* L.) transcriptome sequencing: molecular marker development and comparative studies. BMC Genomics 13:425. Doi: 10.1186/1471-2164-13-425
- Petkova V, Nikolova V, Kalapchieva SH, Stoeva V, Topalova E, Angelova S (2009) Physiological response and pollen viability of *Pisum sativum* genotypes under high temperature influence. Iv Balkan Symp Veg Potato 830:665-671. <u>https://doi.org/10.17660/ActaHortic.2009.8</u> <u>30.96</u>
- Pulse Crop Database (2019) QTL Search. PCD. https://www.pulsedb.org/find/qtl. Accessed 20 December 2019
- Ramirez-Vallejo P and Kelly JD (1998) Traits related to drought resistance in common bean. Euphytica 99:127-136
- Rao IM (2014) Advances in improving adaptation of common bean and Brachiaria forage grasses to abiotic stress in the tropics. In: Pessarakli M (ed) Handbook of plant and crop physiology. FL pp, Boca Raton, pp 847-889
- Reddy MV, Singh O, Bharati MP, Sah RP, Joshi S (1988) Botrytis grey mold epiphytotic of chickpea in Nepal. International Chickpea Newsletter 19, 15
- Robertson LD (1984) A note on the ILB source of Botrytis fabae resistance. In G. P. Chapman,
  & S. A. Tarawali (Eds.), Systems for cytogenetic analysis in Vicia faba L.

Dordrecht, the Netherlands,SpringerNetherlands,pp79.https://doi.org/10.1007/978-94-009-6210-1

- Robertson LD, Singh KB, Ocampo B (1995) A catalog of annual *Cicer* species. ICARDA, Aleppo, Syria
- Rodrigues EV, Damasceno-Silva KJ, Rocha MDM, Bastos EA, Santos AD (2018) Diallel analysis of tolerance to drought in cowpea genotypes. Rev Caatinga 31:40-47. <u>http://dx.doi.org/10.1590/1983-</u> 21252018v31n105rc
- Román-Avilés B, Kelly JD (2005) Identification of quantitative trait loci conditioning resistance to Fusarium root rot in common bean. Crop Sci 45:1881-1890
- Rubiales D, Alcantara C, Sillero JC (2004) Variation in resistance to *Orobanche crenata* in species of *Cicer*. Weed Res 44:27-32
- Sabaghpour SH (2006) Prospects and problems for enhancing grian yield of food legume on dryland in Iran. Iranian J Crop Sci 2(30):15-54
- Saeed A, Darvishzadeh R, Hovsepyan H, Asatryan A (2010) Tolerance to freezing stress in *Cicer* accessions under controlled and field conditions. Afr J Biotechnol 18:2618-2626
- Sallam A, Ghanbari M, Martsch R (2017) Genetic analysis of winter hardiness and effect of sowing date on yield traits in winter faba bean. Sci Hortic 224:296-301. <u>https://doi.org/10.1016/j.scienta.2017.04.01</u> <u>5</u>
- Sarode SB, Singh MN, Singh UP (2007) Genetics of waterlogging tolerance in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Ind J Genet Plant Breed 67:264-265
- Sasser JN and Freckman DW (1987) A world perspective on nematology: The role of the society. Vistas on Nematology eds Veech JA and Dickson DW (Hyattsville, MD: Society of Nematologists), pp 7-14
- Saxena KB (2005) Pigeonpea [*Cajanus cajan* (L.) Millsp.]. In: Singh RJ, Jauhar PP (Eds) Genetic Resources, Chromosome Engineering, and Crop Improvement:

Volume 1, Grain Legumes. CRC Press, Boca Raton, pp 86-110

Schneider KA, Rosales-Serna R, Ibarra-Perez F, Cazares-Enriquez B, Acosta-Gallegos JA, Ramirez-Vallejo P, Wassimi N, Kelly JD (1997) Improving common bean performance under drought stress. Crop Sci 37:43-50.

https://doi.org/10.2135/cropsci1997.001118 3X003700010007x

- Shah TM, Hassan M, Haq MA, Atta BM, Alam SS, Ali H (2005) Evaluation of *Cicer* species for resistance to *ascochyta* blight. Pak J Bot 37:431-438
- Siddiqui MH, Al-Khaishany MY, Al-Qutami MA, Al-Whaibi MH, Grover A, Ali HM et al. (2015) Response of different genotypes of faba bean plant to drought stress. Int J Mol Sci 16:10214-10227. https://doi.org/10.3390/ijms160510214
- Singh D, Sinha B, Rai VP, Singh MN, Singh DK, Kumar R, Singh AK (2016) Genetics of Fusarium Wilt Resistance in Pigeonpea (*Cajanus cajan*) and Efficacy of Associated SSR Markers. Plant Pathol J 32(2):95-101. <u>http://dx.doi.org/10.5423/PPJ.OA.09.2015.</u> 0182
- Singh J and Basu PS (2012) Non-nutritive bioactive compounds in pulses and their impact on human health: an overview. Food Nutr Sci 3:1664-1672.
- Singh KB, Malhotra RS, Saxena MC (1990) Sources for tolerance to cold in *Cicer* species. Crop Sci 30:1136-1138
- Singh KB, Malhotra RS, Halila MH, Knights EJ, Verma MM (1994) Current status and future strategy in breeding chickpea for resistance to biotic and abiotic stresses. Euphytica 73:137-149.
- Singh KB, Malhotra RS, Saxena MC (1995) Additional sources of tolerance to cold in cultivated and wild *Cicer* species. Crop Sci 35:1491-1497
- Singh KB, Ocampo B, Robertson LD (1998) Diversity for abiotic and biotic stress resistance in the wild annual *Cicer* species. Genet Resour Crop Evol 45:9-17

- Sita K, Sehgal A, Kumar J, Kumar S, Singh S, Siddique KHM, Nayyar H (2017) Identification of High-Temperature Tolerant Lentil (*Lens culinaris* Medik.) Genotypes through Leaf and Pollen Traits. Front Plant Sci 8:744. doi:10.3389/fpls.2017.00744
- Smil V (2004) Enriching the earth: Fritz Haber, Carl Bosch, and the transformation of world food production. MIT Press, Cambridge.
- Stamp P, Messmer R, Walter A (2012) Competitive underutilized crops will depend on the state funding of breeding programmes: An opinion on the example of Europe. Plant Breed 131:461-464.
- Strausbaugh CA, Myers JR, Forster RL, McClean PE (1999) Bc-1 and Bc-u-two loci controlling bean common mosaic virus resistance in common bean are linked. J Amer Soc Hort Sci 124:644-648
- Tabti D, Laouar M, Rajendran K, Kumar S, Abdelguerfi A (2018) Identification of desirable mutants in quantitative traits of lentil at early (M<sub>2</sub>) generation. Jour Envir Bio 39:137-142.
  http://doi.org/10.22438/jeb/39/2/MRN\_476

http://doi.org/10.22438/jeb/39/2/MRN-476

Tafesse EG, Warkentin TD, Bueckert RA (2019) Canopy architecture and leaf type as traits of heat resistance in pea. Field Crop Reasearch 241:107561.

https://doi.org/10.1016/j.fcr.2019.107561

- Tavakkoli E, Paull J, Rengasamy P, McDonald GK (2012) Comparing genotypic variation in faba bean (*Vicia faba* L.) in response to salinity in hydroponic and field experiments. Field Crops Res 127:99-108.
- Tayeh N, Aubert G, Pilet-Nayel ML, Lejeune-Henaut I, Warkentin TD, Burstin J (2015) Genomics tools in pea breeding programs: Status and perspective. Front in Plant Sci 6:1037.

https://doi.org/10.3389/fpls.2015.01037

- Tilman D, Balzer C, Hill J, Befort BL (2011) Global food demand and the sustainable intensification of agriculture. Proc Natl Acad Sci 108:20260-20264
- Timko MP and Singh BB (2008) Cowpea, a<br/>multifunctional legume. In:<br/>Genomics of Tropical Crop Plants. Plant

Genetics and Genomics: Crops and Models (eds) Moore PH and Ming R. Springer, New York

- Togola A, Boukar O, Chamarthi S et al (2019) Evaluation of cowpea mini core accessions for resistance to flower bud thrips *Megalurothrips sjostedti* Trybom (Thysanoptera: Thripidae). J Appl Entomol 143:683-692. DOI: 10.1111/jen.12637
- Trapp JJ, Urrea CA, Cregan PB, Miklas PN (2015) Quantitative trait loci for yield under multiple stress and drought conditions in a dry bean population. Crop Sci 55:1596-1607
- Turner NC, Wright GC and Siddique KHM (2001) Adaptation of grain legumes (Pulses) to water-limited environments. Adv Agron 71:193-231.
- United Nation (UN) (2017) World Population Prospects 2019. United Nation-New York, USA. https://population.un.org/wpp/. Accessed 1 November 2019
- Upadhaya HD, Dronavalli N, Gowda CLL, Singh S (2011) Identification and evaluation of chickpea germplasam for tolerance to heat stress. Crop Sci 51:2079-2094
- U.S. National Plant Germplasm System (2019) Accessions by Site. <u>https://npgsweb.ars-grin.gov/gringlobal/query/accessionsbysite.</u> aspx. Accessed 11 December 2019
- US Department of Agriculture (2016) USDA National Nutrient Database for Standard Reference: Release 28. <u>https://www.ars.usda.gov/northeast-</u> <u>area/beltsville-md-bhnrc/beltsville-human-</u> <u>nutrition-research-center/methods-and-</u> <u>application-offood-composition-</u> <u>laboratory/mafcl-site-pages/sr17-sr28/</u>. Accessed 11 November 2019

- Varshney RK et al (2015) Analytical and decision support tools for genomics-assisted breeding. Trends Plant Sci. <u>http://dx.doi.org/10.1016/j.tplants.2015.10.</u> 018
- Varshney R K (2016) Exciting journey of 10 years from genomes to felds and markets: some success stories of genomics-assisted breeding in chickpea, pigeonpea and groundnut. Plant Sci 242:98-107
- Viteri DM, Cregan PB, Trapp JJ, Miklas P, Singh SP (2014) A new common bacterial blight resistance QTL in VAX 1 common bean and interaction of the new QTL, SAP6, and SU91 with bacterial strains. Crop Sci 54:1598-1608
- Ye G, McNeil DL, Hill GD (2002) Breeding for resistance to lentil Ascochyta blight. Plant Breeding 121(3):185-191.
- Zhou R, Hyldgaard B, Yu X, Rosenqvist E, Ugarte RM, Yu S et al. (2018) Phenotyping of faba beans (*Vicia faba* L.) under cold and heat stresses using chlorophyll fluorescence. Euphytica 214:68. https://doi.org/10.1007/s10681-018-2154-y
- Zuiderveen GH, Padder BA, Kamfwa K, Song Q, Kelly JD (2016) Genome-wide association study of anthracnose resistance in Andean beans (*Phaseolus vulgaris*). PLoS One 11:e0156391.

https://doi.org/10.1371/journal.pone.01563 91

Zwart RS, Thudi M, Channale S, Manchikatla PK, Varshney RK, Thompson JP (2019) Resistance to plant-parasitic nematodes in chickpea: Current status and future perspective. Front Plant Sci 10:966. doi:10.3389/fpls.2019.00966