



ISSN: 0975-833X

Available online at <http://www.journalcra.com>

INTERNATIONAL JOURNAL
OF CURRENT RESEARCH

International Journal of Current Research

Vol. 16, Issue, 05, pp.28531-28565, May, 2024

DOI: <https://doi.org/10.24941/ijcr.47292.05.2024>

REVIEW ARTICLE

ORIGIN, DISTRIBUTION, TAXONOMY, BOTANICAL DESCRIPTION, GENETICS AND CYTOGENETICS, GENETIC DIVERSITY AND BREEDING OF BROAD BEAN (*Vicia faba* L.)

*K.R.M. Swamy

Retd. Principal Scientist & Head, Division of Vegetable Crops, ICAR-Indian institute of Horticultural Research,
Bangalore-560089

ARTICLE INFO

Article History:

Received 20th February, 2024

Received in revised form

25th March, 2024

Accepted 14th April, 2024

Published online 30th May, 2024

Key words:

Broad Bean, Origin, Distribution,
Taxonomy, Botanical Description, Genetic
Diversity, Breeding.

*Corresponding author:

K.R.M. Swamy

ABSTRACT

Broad bean belongs to family Fabaceae, subfamily Faboideae, tribe Fabeae, genus *Vicia* and species *Vicia faba* L. It is also known as broad bean, aba bean, fava bean, field bean, horse bean, tick bean. Bakela (Ethiopia), Boby kurmoujve (former USSR), Faveira (Portugal), Ful masri (Sudan), Feve (French) and Yeshil Bakla (Turkey) are the few names used in different parts of world. In India in Hindi language, it is popularly known as Kala Matar and Bakala as well. In much of the English-speaking world, the name "broad bean" is used for the large-seeded cultivars grown for human food, while "horse bean" and "field bean" refer to cultivars with smaller, harder seeds that are more like the wild species and used for animal feed, though their stronger flavour is preferred in some human food recipes, such as falafel. The term "fava bean" (from Italian: *fava* for the bean) is used in some English-speaking countries such as Canada and the US, and "broad bean" is the most common name in Commonwealth countries like the UK, Australia and New Zealand. Though, its green pod is mainly used as vegetables, dry cotyledons are one of the excellent and cheap sources of lysine rich protein for poor's. Faba bean is also a good source of *levadopa* (*L-dopa*), a precursor of dopamine, can be potentially used as medicine for the treatment of Parkinson's disease. It is one of the best crop that can be used as green manure and one of the best bio factory of nitrogen by fixing 130 to 160 kg N/ha. Broad beans are stiffly erect plant in the Fabaceae family, native to North Africa and Southwest Asia but now widely cultivated elsewhere. Faba bean is an important legume crop because of its high-yield potential and nutrition-dense grains. There have been significant achievements in faba bean improvement in the last four decades, which led to the doubling of the global yield average. Faba bean is cultivated primarily as a human food source in Asia and Africa and as animal feed/silage in the European region. Fresh faba bean seeds are used for a variety of savory dishes, and dry grain are used for paste and snacks, while sprouts for traditional food. The dried fresh stems and leaves of faba beans are good fodder for cattle, sheep and pigs. Faba bean flowers contain a large amount of L-DOPA and can be used to make flower tea. Faba bean is a macronutrient-rich legume known for its great potential for yield and a rich source of proteins, carbohydrates, fiber, vitamins, and minerals. It is one of the most important winter crops for human consumption in the Middle East. Faba bean is grown worldwide under different cropping systems such as a dry grain (pulse), green grains/pods, and a green-manure legume. Fava beans were first grown thousands of years ago in the Middle East and southwest Asia. They can grow in many different places around the world. They are a staple in cooking across cultures, from Chinese to South American dishes. Fava beans, or broad beans, are a type of bean that is eaten around the world. They are high in protein and other important nutrients. Eating fava beans can help with weight loss, aid in your body's immunity, and provide other health benefits. It is grown worldwide and popularly in Morocco, France, Italy, Germany and Egypt. Ethiopia and China are largest producers. In Indian subcontinent, it is important Rabi season crop cultivated popularly in Bihar, Uttar Pradesh and Madhya Pradesh are major producers and minorly produced in localized areas of Punjab, Rajasthan, Haryana, and Karnataka. In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding, Uses, Nutritional Value and Health Benefits of Broad Bean are discussed.

Copyright©2024, Swamy. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Citation: K.R.M. Swamy. 2024. "Origin, distribution, taxonomy, botanical description, genetics and cytogenetics, genetic diversity and breeding of broad bean (*Vicia faba* L.)". *International Journal of Current Research*, 16, (05), 28531-28565.

INTRODUCTION

One of the oldest crops is broad bean (*Vicia faba* L.), belonging to family Fabaceae, order Fabales, class Magnoliopsida, division Magnoliophyta (Kosev and Georgieva, 2023). Broad bean belongs to family Fabaceae, subfamily Faboideae, tribe Fabeae, genus *Vicia* and species *Vicia faba* L. (Wikipedia, 2024). It is also known as broad bean, aba bean, fava bean, field bean, horse bean, tick bean (Petruzzello, 2024). It is also known as bell bean, broad bean, english bean, fava bean, field bean, horse bean, pigeon bean, tick bean and windsor bean (Sylvia, 2017; NCSE, 2024). Faba bean, Fava bean, Broad bean, Horse bean, Windsor bean, Tick beans (small types), Bakela (Ethiopia), Boby kurmoujje (former USSR), Faveira (Portugal), Ful masri (Sudan), Feve (French) and Yeshil Bakla (Turkey) are the few names used in different parts of world. In India in Hindi language, it is popularly known as Kala Matar and Bakala as well (Singh *et al.*, 2013). In much of the English-speaking world, the name "broad bean" is used for the large-seeded cultivars grown for human food, while "horse bean" and "field bean" refer to cultivars with smaller, harder seeds that are more like the wild species and used for animal feed, though their stronger flavour is preferred in some human food recipes, such as falafel (Wikipedia, 2024). The term "fava bean" (from Italian: *fava* for the bean) is used in some English-speaking countries such as Canada and the US, and "broad bean" is the most common name in Commonwealth countries like the UK, Australia and New Zealand (Wikipedia, 2024).

Vicia faba L. (= *Faba vulgaris* Moench), the faba, field, tick, horse or broad bean, is the sixth most important pulse crop in terms of global production, after soyabean, dry (*Phaseolus*) bean, groundnut (*Araehis*), dry (field) pea and chickpea. An important food crop in North Africa, the Middle East and China, it is also well adapted to agriculture in much of Europe, where it has been grown for four millenia or more. It remains a staple of the diet in Arab countries. While there is a surplus of cereal grains in many European countries, vegetable protein for animal feed is in short supply and faba beans and peas are considered to be among the best potential remedies to both problems. Faba bean is among the oldest crops in the world. Globally, it is third most important feedgrain legume. Currently, 58 countries produce this bean on large scale. Probably faba beans are one of the best performing crops under global warming and climate change scenario because of its unique ability to excel under all most all type of climatic conditions coupled with its wide adoptability to range of soil environment. Faba bean being incredible and crop complete food, unfortunately some part of world including India, it is still underutilized crop and not fully exploited so far, though it is seen as an agronomically viable alternative crop to cereal, with a potential of fixing free nitrogen up to 300 kg N ha⁻¹. It is a good source of lysine rich protein and good source of *levadopa* (*L-dopa*), a precursor of dopamine, can be potentially used as medicine for the treatment of Parkinson's disease (Singh *et al.*, 2013). The area under faba bean crop in India is very less and that is why it is still categorized as minor, unutilized, underutilized, less utilized, and still not fully exploited crops. Though, its green pod is mainly used as vegetables, dry cotyledons are one of the excellent and cheap sources of lysine rich protein for poor's. Faba bean is also a good source of *levadopa* (*L-dopa*), a precursor of dopamine, can be potentially used as medicine for the treatment of Parkinson's disease (Singh *et al.*, 2013). It is one of the best crop that can be used as green manure and one of the best bio factory of nitrogen by fixing 130 to 160 kg N/ha (Singh *et al.*, 2013).

The broad bean, *Vicia faba* L., is known as a cultivated plant from the very onset of agriculture and is an important crop until the present. According to the most recent revision, *V. faba* represents a monospecific section in its genus, nearly warranting upgrade to generic rank. Until the present, neither wild representatives of this species nor any closely related species have been found. The absence of a link to the extant wild flora made the broad bean scarcely considered in reconstructions of the origin of plant cultivation and domestication in the Near East. However, the absence of a wild relative of some specific crop may be as such meaningful and indicative (Kosterin, 2014). Absence of extant wild relatives of the broad bean suggests that the wild progenitor was not a common and widespread plant. If so, all its scarce natural populations would be soon converted into primary fields and then, without gene flow from wild relatives, it would undergo rapid domestication, leaving no remnants of the wild ancestor. Wild progenitors of other founder crops were scattered over much larger areas, as they still are at present that would hardly favour the emergence of the idea of cultivation at a restricted field. At the same time presence of other potential crops in the habitat of the broad bean wild progenitor, being converted into primary fields, would lead to their involvement into cultivation as well. Moreover, conversion of the broad bean natural habitats into primary fields would most likely result in mixed species cultivation. Probably this was an initial type of plant cultivation in the Near East where the founder crop set included so many species altogether. In this respect, the set of founder crops could be balanced rather ecologically than nutritionally (Kosterin, 2014).

The broad bean is one of the most food crop cultivated in the world. It is a vegetable whose origin has long been discussed. Today, there are Mediterranean regions which are considered as the origin of this vegetable, its culture represents almost 25% of the total cultivated area (Aouar-sadli *et al.*, 2018). The broad bean is nutritional, economic and environmental interesting vegetable. North Africa is one of the top-producing regions of the broad bean in the world. The average area reserved for this crop is between 23000 and 73000 ha, with an annual production of 137000 to 410000 quintals (Aouar-sadli *et al.*, 2018). Broad bean occupies the first place among the pulses in Algeria because it has high nutritional value and divers' uses. It is mainly cultivated in the plains and sublittoral regions and has an important role in the national economy and agricultural production. In the wilaya of Tizi-Ouzou, this culture extends over large areas. The broad bean has a very important place in the culinary arts of this region (Aouar-sadli *et al.*, 2018). Broad beans are stiffly erect plant in the Fabaceae family, native to North Africa and Southwest Asia but now widely cultivated elsewhere. It is grown for its ovoid shaped seeds. The term bean can refer to the pod or seeds. *Vicia faba* is an annual plant, with the life cycle of one year. It is a cool season crop that is grown in well drained soils. The immature beans are used fresh, as a vegetable, canned or frozen (Sylvia, 2017). Broad beans are the crop which is grown in autumn and the beans are harvested in May and June. The beans are grown for their seeds which are rich in protein, Vitamin B, carbohydrate and fiber. The plants produce the pods as the fruits which contain eight seeds that vary in shape, size and color (Sylvia, 2017). Faba bean is an

important legume crop because of its high-yield potential and nutrition-dense grains. There have been significant achievements in faba bean improvement in the last four decades, which led to the doubling of the global yield average (Maalouf *et al.*, 2018). *Vicia faba* L. (faba bean, named also broad beans or horse bean) is the fourth most widely grown cool season legume after pea (*Pisum sativum*), chickpea (*Cicer arietinum*) and lentil (*Lens culinaris*). Its protein content is higher than other common food legumes. Moreover, the total grain yield of faba bean is positively correlated with high seed protein contents (Maalouf *et al.*, 2018). The cultivation of faba bean traces back to the beginning of agriculture and it remains an important crop today because of its high-yield potential, nutrition-dense grains and its role as forage and cover crop. As other legumes crops, faba bean plays a critical role in improving cereal-based system and it can improve soil fertility (Maalouf *et al.*, 2018). Faba bean (*Vicia faba* L.) is an important cool season legume grown widely in the world due to its palatability as well as its ecological and environmental value in sustainable agriculture and cropping system. As its protein content is higher than other common food legumes, it is mainly harvested in the form of dry seeds for human food and for animal feed worldwide, but its fresh seeds or pods are often used as vegetables in China, India and other countries with rapidly expanding areas. The dry grain, fresh seeds and sprouts of faba bean are a highly nutritional food source for the human diet. Fresh faba bean seeds are used for a variety of savory dishes, and dry grain are used for paste and snacks, while sprouts for traditional food. The dried fresh stems and leaves of faba beans are good fodder for cattle, sheep and pigs. Faba bean flowers contain a large amount of L-DOPA and can be used to make flower tea (Zong *et al.*, 2019).

Faba bean, also known as fava bean, broad bean, horse bean, is among one of the oldest crops in the world. Faba bean is cultivated primarily as a human food source in Asia and Africa and as animal feed/silage in the European region (Dhull *et al.*, 2021). Faba bean is a rich source of proteins, carbohydrates, and dietary fiber, and also contains a variety of bioactive compounds, *e.g.*, total phenolics and flavonoids. There is enormous potential for expanding faba bean use for food and nutritional security (Dhull *et al.*, 2021). *Vicia faba* L. (faba bean) is a main legume species; growing in winter season in the area of North Nile Delta. It has high protein content (24–30%), nutritional value, and high energy, and the faba bean is grown for animal feed and human food. The quality and yield of faba bean seeds are affected by fungal diseases, which are among the biotic factors cause major yield losses in faba beans, by decreasing the growth of plants, in excessive cases leading to wilt and plant death. Some fungal pathogens can cause the closure of seed plantations by epidemic outbreaks (El-Dawy *et al.*, 2021). Faba bean, a member of the Fabaceae family, is one of the important food legumes cultivated in cool temperate regions. It holds great importance for human consumption and livestock feed because of its high protein content, dietary fibre, and nutritional value (Khazaei *et al.*, 2021).

Faba bean, like most other legumes, forms a symbiosis with nodule-forming bacteria that have nitrogen fixing ability, which provides major benefits to cropping systems and the environment and contributes to agricultural sustainability by soil improvement. It is considered an excellent protein crop due to its ability to provide nitrogen inputs into temperate agricultural systems on account of its wide adaptation, as well as its high yield potential and nitrogen-fixing capacity even when nitrogen is present in the soil, compared with other grain legumes. These particular nitrogen-fixing traits in combination with yield potential mean that faba bean can be produced in a sustainable manner, making it particularly well-suited for providing the protein required for the globally expanding plant-based food chain (Khazaei *et al.*, 2021).

Faba bean delivers plant protein products suitable for consumption both by those with soybean (*Glycine max* (L.) Merr.) allergy or intolerance and by those wishing local products. According to Food and Agriculture Organization Corporate Statistical Database, faba bean is the fourth most widely grown cool-season grain legume (pulse) globally after pea (*Pisum sativum* L.), chickpea (*Cicer arietinum* L.), and lentil (*Lens culinaris* Medik.), with annual production of around 4.5 million tonnes from nearly 2.5 Mha (Khazaei *et al.*, 2021). Faba bean (*Vicia faba* L.) is a cool-season grain legume cultivated throughout the world for human consumption and animal feed. Its high protein content (25–37%) makes it a highly valuable grain for both food and feed purposes. Among pulses it occupies sixth place in terms of production (Adhikari *et al.*, 2021).

Faba bean fits well in cereal-based cropping systems as a rotational crop that enhances soil fertility while breaking the cycle of biotic stresses associated with parasitic weeds and other pathogens. Its nitrogen fixation capacity is one of the highest among legumes, fixing nitrogen even in the presence of high levels of nitrogen in the soil and leaving a significant residue that reduces the need for application of inorganic N fertilizer in subsequent crops (Adhikari *et al.*, 2021). No extant wild relative capable of producing fertile progeny when crossed with *V. faba* has been found and thus genetic diversity available for breeding purposes is limited to the cultivated gene pool. Recent archaeological findings suggest pre-domestication ancient form of faba bean existed about 14,000 years ago in el-Wad (Mount Carmel, Israel) (Adhikari *et al.*, 2021).

Faba bean is a macronutrient-rich legume known for its great potential for yield and a rich source of proteins, carbohydrates, fiber, vitamins, and minerals. It is one of the most important winter crops for human consumption in the Middle East. Faba bean is grown worldwide under different cropping systems such as a dry grain (pulse), green grains/pods, and a green-manure legume. It plays an important role as a rotation and mixed crop in improving soil fertility that helps sustainable production of cereal grains and intercrops with vegetables and sugarcane (Chaudhary *et al.*, 2022). Faba bean ranked 5th under pulse crops world average production of the last decade annually. The global production of faba bean increases every year, and China, Ethiopia, the United Kingdom, Australia, and France are the main producers of faba beans (Chaudhary *et al.*, 2022). Faba bean was first domesticated in the Fertile Crescent of the Near East. It ranks fourth among the cool season food legumes and is now grown in more than 66 countries. Faba bean is a versatile crop; besides being an important source of protein for food and feed, it offers many services for the ecosystem. The Mediterranean and East African countries account for nearly 32% of the global Faba bean production (Abou-Khater *et al.*, 2022). While major achievements have been made toward the development of faba bean varieties having desired traits, there is still a lot of work to be done. The high level of genetic diversity in Faba bean accessions and the available molecular

markers will considerably help tighten the gap between the production and the demand in the Mediterranean and East African region (Abou-Khater *et al.*, 2022).

Legumes are the world's primary source of dietary protein and are particularly important for those in developing economies. However, the biofortification potential of legumes, especially that of Faba beans, remains underexploited. Faba bean has been ranked as the third most important grain legume in terms of cultivated areas and production in the world. According to reports, Faba bean contains appreciable amount of proteins, complex carbohydrates, dietary fiber, choline, lecithin, minerals, and secondary metabolites (Abiodun *et al.*, 2022). Micronutrient malnutrition has been a major concern and according to statistics, about two billion people around the world suffer from micronutrient deficiency leading to stunted growth to reduced lifespan. As a result, enhancing Faba bean nutritional composition presents an appealing target for addressing the "hidden hunger" of global micronutrient malnutrition (Abiodun *et al.*, 2022). Biofortification of Faba bean provides a cost effective method of solving the problem of hidden hunger. Increasing the micronutrient availability in Faba beans, for those economies or populations that are undernourished, may probably ameliorate hidden hunger and increase the positive health effects of the consumers (Abiodun *et al.*, 2022).

Faba bean, a cross-pollinated plant with a high natural outcrossing rate of 19–49%, is the only cultivated species of *Vicia* L. The high outcrossing rate makes the breeding of faba bean varieties highly challenging. The outcrossing rates of faba bean are affected by many biotic and abiotic factors, and bees are considered to be one of the important pollinators (Zhang *et al.*, 2023). The Middle East and the Mediterranean are considered to be its primary original center, after which it has spread to Central Asia, Afghanistan, India and subsequently to the European countries. In countries like Great Britain and France, it is mainly used as feed for livestock, and in the Mediterranean countries, the Middle East and China – mainly in culinary industry. Broad bean can be included in different growing systems, contributing to their sustainability through its ability to provide nitrogen via biological fixation; diversification of production, leading to pest reduction; its capacity to reduce energy consumption from fossil fuels; providing food and feed, which are rich in proteins. In addition, the broad bean, along with other legumes, plays an important role in soil revegetation and therefore it is of importance to the modern systems of organic farming (Kosev and Georgieva, 2023). Variety breeding is the key to the development of the seed industry, and germplasm resources can be regarded as the basis for breeding varieties. A comprehensive insight into the genetic diversity of germplasm resources is of great significance for crop genetic improvement. With the development of molecular marker technology, single-nucleotide polymorphism (SNP) has been widely used in the genetic diversity analysis of faba bean due to its numerous genomic loci in the genome, wide distribution, genetic stability, easy genotyping, and high-throughput automated analysis (Zhang *et al.*, 2023).

Some authors used RAPD markers to analyze the genetic diversity of 13 European small-grain faba bean accessions, six European large-grain accessions, and nine Mediterranean accessions, finding that the genetic diversity of the small-grain accessions was relatively high (Zhang *et al.*, 2023). Broad bean is grown in more than 55 countries, as the harvested area is 2.46 million ha, and the total production is 4.84 million tons of dry grains. Over the past 50 years, the areas have been reduced by 34%. On the other hand, grain yields increase from 980 kg/ha (1961-1963) to 1964 kg/ha (2017), mainly due to the replacement of the old cultivars with new ones. Gene banks in the world conserve more than 36000 accessions. As a whole, the total production is dominated by local landraces and cultivars, despite a number of improved cultivars which are developed by different national breeding programs. The main reason for the low yields and insufficient production is the sensitivity of landraces and cultivars to biotic and abiotic stress. The fluctuations in the harvested areas and the negative effects of different biotic and abiotic stress have led to a reduction in genetic diversity (Kosev and Georgieva, 2023). Faba bean is also known by many other names: faba bean, broad bean, horse bean, Windsor bean, and more. By whatever name, it is a productive and nutritious member of the legume family (Fabaceae), grown for its protein-rich seeds and as a forage and cover crop. Faba bean is commonly grown and consumed in Europe, the Middle East, East Asia, Australia, and parts of Africa and Latin America, but is an overlooked crop in the U.S. *V. faba* is an erect, robust plant 30-180 cm tall, adapted to cool, temperate climates. It has white flowers with a characteristic black blotch and fleshy seed pods with up to eight large, flat seeds (Byrne, 2023). Faba bean, one of the oldest cultivated plants, which is also called as field bean, windsor bean, bakla bean, tick bean, horse bean, be one of the 4th premier leguminous crop after pea, beans and chickpea (Brar *et al.*, 2023). Broad bean can be included in different growing systems, contributing to their sustainability through its ability to provide nitrogen via biological fixation; diversification of production, leading to pest reduction; its capacity to reduce energy consumption from fossil fuels; providing food and feed, which are rich in proteins. In addition, the broad bean, along with other legumes, plays an important role in soil revegetation and therefore it is of importance to the modern systems of organic farming (Kosev and Georgieva, 2023). Legumes such as broad beans were called the "slow runners of the Green Revolution", because — unlike staple cereals such as rice, wheat and maize (corn) — legume yields benefited little from changes in breeding and agriculture. Emerging tools for crop breeding, such as genomic selection, are starting to make it possible to unlock the potential of these underused crops, enabling rapid improvement in yields even in the face of climate change and widespread food insecurity. But although whole-genome sequencing and related forms of high-throughput genetic characterization have become routine in crops such as rice, it has been challenging to apply them to species that have big genomes, such as the broad bean (Wettberg and Guerra-Garcia, 2023).

Broad bean, species of legume (family Fabaceae) widely cultivated for its edible seeds. The broad bean is the principal bean of Europe, though it is generally less well known in the United States. As with other vetches, broad beans are frequently planted as cover crops and green manures, as they add nitrogen to the soil by means of nitrogen-fixing bacteria. The plant is also used as livestock and poultry fodder, where it is sometimes called field, or tick, bean (Petruzzello, 2024). *Vicia faba*, commonly known as the broad bean, fava bean, or faba bean, is a species of vetch, a flowering plant in the pea and bean family Fabaceae. It is widely cultivated as a crop for human consumption, and also as a cover crop.

Varieties with smaller, harder seeds that are fed to horses or other animals are called field bean, tic bean or tick bean. Horse bean, *Vicia faba* var. *equina* Pers., is a variety recognized as an accepted name. This legume is very common in Southern European, Northern European, East Asian, Latin American and North African cuisines (Wikipedia, 2024). Some people suffer from favism, a hemolytic response to the consumption of broad beans, a condition linked to a metabolism disorder known as G6PDD. Otherwise the beans, with the outer seed coat removed, can be eaten raw or cooked. In young plants, the outer seed coat can be eaten, and in very young plants, the seed pod can be eaten (Wikipedia, 2024). Broad beans are still often grown as a cover crop to prevent erosion because they can overwinter and, as a legume, they fix nitrogen in the soil. The broad bean has high plant hardiness; it can withstand harsh and cold climates. Unlike most legumes, the broad bean can be grown in soils with high salinity, as well as in clay soil. However, it prefers rich loams (Wikipedia, 2024). Fava beans are a type of legume. Legumes (also known as pulses) are vegetables that grow inside pods, although you may not always eat the pod. Common legumes include peanuts, kidney beans, and lentils. Fava beans were first grown thousands of years ago in the Middle East and southwest Asia. They can grow in many different places around the world. They're a staple in cooking across cultures, from Chinese to South American dishes. Fava beans, or broad beans, are a type of bean that's eaten around the world. They're high in protein and other important nutrients. Eating fava beans can help with weight loss, aid in your body's immunity, and provide other health benefits (WMDEC, 2024).

Area and Production

Fava bean is grown over a wide geographical range, with significant production zones from 50° N to 40° S and at an altitude of up to 3000m above sea level, and minor production beyond these ranges. It is grown as an autumn/winter crop in regions with a mild winter such as the Middle East, north Africa, the Mediterranean Region, maritime Europe, southern China and Australia, or a spring sown crop where winters are severe such as continental Europe, northern China and Canada. It is grown under either rainfed or irrigated conditions. The crop is harvested as dry seed which is used for food, particularly in the Middle East and north Africa where it is a staple component of the diet, or as a protein component in feed diets (Redden *et al.*, 2014). The average world production of faba bean for 2009-2011 was 4.1 million metric tonnes (mmt) and the major producing countries were; China 1.53 mmt, Ethiopia 0.67 mmt, France 0.42 mmt, Australia 0.26 mmt, Egypt 0.24 mmt, U.K. 0.16 mmt, Morocco 0.15 mmt and Sudan 0.13 mmt, (FAOSTAT 2013). Correspondingly the mean percentages of the crop area were; 36% for China, 20% for Ethiopia, 7% for Morocco, 6% for Australia and below 5% for the other major producers. About 25% of world faba bean production is internationally traded, with Egypt being the major importer and France, U.K. and Australia the major exporters (Redden *et al.*, 2014). China is the world's dominant producer of faba beans, and it is useful to appreciate its production environments. Fava bean production in China is mainly located in the paddy field of southern China after harvest of rice, as an irrigated winter legume crop for fresh green seeds and for dry grain. The major biotic limiting factors are chocolate spot, rust, aphids and leaf minors. The major abiotic limiting factors for winter faba bean are frost damage during both flowering and podding stages, as well maturity stresses of terminal drought, or of water logging (Redden *et al.*, 2014). China is the leading producer, followed currently by Ethiopia, Australia, France, Egypt, Morocco, Sudan, and the UK (O'Sullivan and Angra, 2016). The global faba bean-harvested area was 2.4 million ha in 2016, covering wide latitudinal range from approximately 50°N to 40°S and from the sea level up to 3,000 m' altitude. The total production in 2016 was 4.46 million tons of dry grains. The global area of faba bean cultivation has been declining, especially in China and countries in North Africa and West Asia. This reflects a general trend, observed since the 1960s, of increasing reliance by farmers on N fertilizers as a source of N input. The global average yield has increased from 0.9 tons/ha between 1961 and 1964 to 1.86 tons/ha in 2016, thanks to the significant achievement in genetic improvement (Maalouf *et al.*, 2018). Broad bean is grown in more than 55 countries, as the harvested area is 2.46 million ha, and the total production is 4.84 million tons of dry grains. Over the past 50 years, the areas have been reduced by 34%. On the other hand, grain yields increase from 980 kg/ha (1961-1963) to 1964 kg/ha (2017), mainly due to the replacement of the old cultivars with new ones (Kosev and Georgieva, 2023). Being a cool-adapted crop, fava beans are grown in temperate regions such as northern Europe, or in highland areas or as a winter crop in the tropics. China is the largest producer, followed by Ethiopia and Australia (Byrne, 2023). It is grown worldwide and popularly in Morocco, France, Italy, Germany and Egypt. Ethiopia and China are largest producers. In Indian subcontinent, it is important Rabi season crop cultivated popularly in Bihar, Uttar Pradesh and Madhya Pradesh are major producers and minorly produced in localized areas of Punjab, Rajasthan, Haryana, and Karnataka (Brar *et al.*, 2023).

Cultivation: Broad bean is a cool-season crop and should be grown in early Spring or late summer to avoid high summer temperatures. Broad beans will grow best at soil temperatures between 15.5 and 18.3°C (60–65°F) and will not grow well at temperature below 4.4°C (40°F) or above 23.8°C (75°F). Broad bean is particularly susceptible to high temperatures during the summer which make the plants unproductive. Broad beans will grow best in a fertile, well-draining soil with a pH between 6.0 and 6.75 positioned in full sunlight. Sowing seeds Broad beans should be direct seeded in the garden in Spring as soon as the soil is workable and temperature is above 4.4°C (40°F) with the optimum temperature for germination being between 10 and 21°C (50–70°F). A second planting can be made in early Fall in areas with moderate winters. Seeds should be planted 2.5–5.0 (1–2 in) deep allowing 7.5–15 cm (3–6 in between plants and approximately 0.6 m (2 ft) between rows (PV, 2024). Broad bean plants are bush-like but can grow quite tall and will benefit from staking to provide some support and keep them from flopping over due to the weight of the pods. Keep soil moist during flowering to ensure optimum pod development and soak ground thoroughly if plants come into flower during a dry spell. As they are legumes, broad beans generally do not require additional fertilization as long as they have sufficient root nodules. Nodulation can be promoted by inoculating seeds with additional *Rhizobacteria* prior to planting. Broad beans are ready to harvest when the pods are fat and full and beginning to droop from the plant due to the weight of the seeds inside. Seeds can be dried either by leaving pods on the plant until they begin to shrivel or by picking and hanging up to dry out (Fig. 1) (PV, 2024).



Fig.1. Broad beans will benefit from staking to support the weight of the pods

Harvesting and Yield: Pods are harvest at 90-120 days thereafter sowing. Tender green and immature pods should be harvested by hands at short and regular intervals. The harvesting should be done before seeds become hard, stinky, and tough and seed became large enough to cause pods bulge around seed. The marketable length of pod is 12-15 cm long and 1.8-2 cm thick. If harvest delay, pod maturity is occurred, yield may increase quality may decrease due to increase in fiber content. 7 to 10 t/ha tender green pods are harvested and 1.8-2.0 tonnes of green bean is harvested per hectare. Seed yield of broad bean can be achieved by pure line selection or mass selection of indigenous and exotic genetic resources. About 10-15 q/ha of seed of broad bean can be produced. For seed production broad beans are cultivated as in same way of cultivation of green pods. For foundation seed production of broad bean, isolation distance is 50 m and for certified seed production distance is 25 m apart (Brar *et al.*, 2023).

Post-Harvest Handling: The harvest is sorted in different grades to fetch good return. 3 grades are considered *i.e.*, Super, fancy and commercial. In super grade, pods of good size, tender, shaped and glossy are arranged which attract good market price. Medium sized pod with good texture and color, bulging with full developed seed arranged in fancy grade. Dull color pods and uneven shape and sized, without any deformity are arranged under commercial grade to increase marketing. In order to maintain freshness and quality of produce for longer period, edible pods are packed in basket cardboard boxes, fiber board boxes, wire bound boxes for distant marketing. For vegetable purpose, pods are packed in gunny bags or bamboo chips round basket for local market provided with cushioning materials like paddy straw or dry grass, paper cuttings stitched properly so that quality should not get reduced or compromised. In ordinary room conditions pods are easily kept for 2-3 days. For 10-14 days pods can be stored at 4.4-7.2 °C with 90-95 % RH (Brar *et al.*, 2023).

Physiological Disorders

Damage by Hail: white streaks and markings appear on leaves when hail hit the plant. Leaves became torn and pods are smashed opened and seeds discoloured rapidly. Sometimes the stem got damage and top part of plant are broken off due to hail.

Damage due to water logging: problem severely occur during rainy season and poor drainage conditions black colour appear on the leaf tip, die back of leaf tips, new leaves became necrotic, rupturing of apical cells of new leaflets (Brar *et al.*, 2023).

Diseases: Diseases caused with fungi are amongst the biotic factors responsible for decreasing in faba bean yields. In this work, *Cladosporium* isolates were recorded in cultivated faba bean leaves and pods collected from markets in Qena, Upper Egypt; morphological features and molecular characterization based on actin gene were performed. The ability of the pathogens to cause disease in faba bean seedlings and the biocontrol method to avoid the pathogenic effect of *Cladosporium* were determined. Results showed that *Cladosporium* is the main genera isolated from faba beans, and the morphological criteria showed presence of three species complex groups of *Cladosporium* (*C. cladosporioides*, *C. herbarum* and *C. sphaerospermum*) and the confirmation with molecular characterization revealed the existence of four species in the three groups. All the 26 tested strains of *Cladosporium* were able to cause leaf lesions on *Vicia faba* seedlings with different levels. *Chaetomium globosum* is a biocontrol agent could inhibit the growth of the majority strains of *Cladosporium* (El-Dawy *et al.*, 2021).

In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding, Uses, Nutritional Value and Health Benefits of Broad Bean are discussed.

ORIGIN AND DISTRIBUTION

The wild progenitor and the exact origin of Faba bean still remains unknown. However, it is generally accepted that *V. faba* L. is one of the earliest domesticated food legumes in the world; probably cultivated since Neolithic Period. Most authors agree that the subspecies *V. faba paucijuga*, presently found in the region extended from Afghanistan to India, is the primitive form. Large seeded types (*V. faba major*) were developed in Iraq. Small seeded types (*V. faba minor*) are found in Ethiopian area and have been favoured by North European agriculture. Medium seeded types (*V. faba equina*) were developed throughout Middle East and North Africa with major concentration in Egypt. Over the long period of its cultivation, the crop has undergone large natural selection and selection by man and therefore ecotypes and cultivars specifically adapted to different sets of environmental combinations have developed (Ali Oujii *et al.*, 2011).

Faba bean is assigned to the Central Asian, Mediterranean, and South American centers of Diversity and believe to be a native to North Africa and southwest Asia, and extensively cultivated elsewhere. It was postulated a Near Eastern center of origin, with four radii to Europe along the North African coast to Spain, along the Nile to Ethiopia, and from Mesopotamia to India. Secondary centers of diversity are postulated in Afghanistan and Ethiopia. However, it was reported the origin to be Central Asia. The Chinese used them for food almost 5,000 years ago, and they were cultivated by the Egyptians 3,000 years ago, by the Hebrews in biblical times, and a little later by the Greeks and Romans. Probably, it was introduced by Europeans as a garden crop into India during the Sultan period (1206–1555), during which its cultivation has been mentioned. The wild progenitor and the exact origin of faba bean remain unknown (Singh *et al.*, 2013). Broad bean (*Vicia faba* L.), an ancient crop species that originated in the Near East, is mainly grown in Europe, North Africa, the Middle East and China (Li and Yang, 2014).

Faba bean is a grain legume of great importance in world agriculture due to its high yield potential compared to alternative grain legumes, its ability to fix nitrogen through symbiosis with *Rhizobium leguminosarum* in its root nodules, but most crucially for its role as a staple dietary protein source in North African and Middle Eastern cultures. The species is thought to have been domesticated in the Eastern Mediterranean region, perhaps somewhere between Afghanistan and the Eastern Mediterranean, but no extant wild relative has yet been found although new species closely related to Faba bean have been found in recent decades. Nonetheless, there is great variability within the domesticated genepool, with the major center of diversity centered around the Mediterranean basin and secondary centers of diversity in the Nile Valley, South America, and Central and Eastern Asia, providing much untapped potential to breeders. This diversity of forms is exemplified by the botanical classification of “major”(large-seeded or “broad” bean), “equine”(mid-sized or “horse” bean), and “minor”(small, rounded seed) types. Faba bean is one of the earliest domesticated Old World agricultural crops, with credible archaeobotanical evidence linking it to the pre-pottery Neolithic period around 10,000 BP in a site in North-West Syria. However, again in keeping with its great diversity and adaptability, it has a long history of utilization outside the center of origin in diverse agro-ecological settings from the Boreal and Atlantic Maritime climates to arid and sub-tropical regions (O’Sullivan and Angra, 2016). Before it spread to Western Europe, it was cultivated for 8000 years in the Middle East. The cultivation of broad bean was started from 6,800 to 6,500 years BC. Today, broad bean is cultivated all over the world, being native to North Africa and Southwest Asia (Sylvia, 2017).

Faba bean is one of the first domesticated food legumes and has a long history of cultivation; seeds as old as 14,000 years were identified in the southern Levant. Faba beans are widely grown for food and feed as a generous source of high-quality protein, dietary fibre and other valuable nutrients. The protein content of Faba bean seeds is about 29% of the dry matter, which makes it one of the main sources of affordable protein for people in the Middle East, Latin America and Africa, and for livestock feed in many developed countries (Khazaei *et al.*, 2021). The primary center of origin of Faba bean is likely to be the Mediterranean basin from where it spread to the Nile Valley, Central and Eastern Asia, and much later South America. Faba bean is grown as a staple food crop in low rainfall areas in northern Africa (Morocco, Algeria and Tunisia), high rainfall areas in Ethiopia and Eritrea and under irrigation in Sudan and Egypt (North-east Africa) and in the highlands of the South American Andes. These are traditionally faba bean growing areas, but the farming systems have now shifted to monoculture of cereals, resulting in poor soil health, land degradation, increasing greenhouse gases through the use of chemical fertilizer, emergence of new pests and diseases, declining response to farm inputs and yield stagnation (Adhikari *et al.*, 2021).

Faba bean was domesticated in the near East more than 10,000 years BP and its broad adaptability, value as a restorative crop in rotations and high nutritional density have propelled it to the status of a global crop grown on all continents except Antarctica. Despite its global importance, no extant wild progenitor has been found. Nonetheless, the finding of Neolithic charred wild faba bean seeds points to pre-domestication use of this species by hunter-gatherers and possible domestication in the Levant. The presence of several closely related species (*Vicia narbonensis*, *Vicia palaestina* and *Vicia kalakhensis*) in the same region gives hope that a wild progenitor may yet be found (Jayakodi *et al.*, 2023). Fava bean is believed to have originated in the eastern Mediterranean region, but its exact place of origin is unknown. It is considered one of the oldest cultivated plants, with the earliest archaeological evidence for domestication of this species dating to over 10,000 years BP. Before 1492 when beans from the Americas began to arrive in Europe, this crop was the only edible bean grown on the continent. Faba bean became an important food crop in China after 1200 CE (Byrne, 2023).

It is one of the oldest crops cultivated since pre-historic time, wild ancestor is unknown. Its probable site of origin is from south-western Asian or Mediterranean region. Its secondary region of diversity is in Ethiopia and Afghanistan, raised and produced by ancient Hebrews, Greeks, Egyptians and Romans. It is popularly grown in temperate and subtropical regions and well adapted to cool climate. It was only edible bean known in Europe up to pre-Columbian times and later came to new world after 1492. ICARDA (International Center for Agricultural Research in the Dry Area) of Syria has the world-wide collection of germplasm of Broad Bean. In Mediterranean region the germplasm is preserved by Ethiopian Genetic Resource Center, Ethiopia and The Germplasm Institute, CNR, Bari, Italy (Brar *et al.*, 2023). The Middle East and the Mediterranean

are considered to be its primary original center, after which it has spread to Central Asia, Afghanistan, India and subsequently to the European countries. In countries like Great Britain and France, it is mainly used as feed for livestock, and in the Mediterranean countries, the Middle East and China – mainly in culinary industry (Kosev and Georgieva, 2023).

Broad beans have a long tradition of cultivation in Old World agriculture, being among the most ancient plants in cultivation and also among the easiest to grow. However, their wild ancestor has not been identified and their origin is unknown. Charred faba bean remains were discovered at three adjacent Neolithic sites in Israel's Lower Galilee (Yiftah'el, Ahi'hud and Nahal Zippori). Based on the radiocarbon dating of these remains, scientists now believe that the domestication of the crop may have begun as early as 8,250 BCE (Wikipedia, 2024).

TAXONOMY

One of the oldest crops is broad bean (*Vicia faba* L.), belonging to family Fabaceae, order Fabales, class Magnoliopsida, division Magnoliophyta (Kosev and Georgieva, 2023). Broad bean belongs to family Fabaceae, subfamily Faboideae, tribe Fabeae, genus *Vicia* and species *Vicia faba* L. (Wikipedia, 2024). It is also known as broad bean, aba bean, fava bean, field bean, horse bean, tick bean (Petruzzello, 2024). It is also known as bell bean, broad bean, english bean, fava bean, field bean, horse bean, pidgeon bean, tick bean and windsor bean (Sylvia, 2017; NCSE, 2024). Faba bean, Fava bean, Broad bean, Horse bean, Windsor bean, Tick beans (small types), Bakela (Ethiopia), Boby kurmoujje (former USSR), Faveira (Portugal), Ful masri (Sudan), Feve (French) and Yeshil Bakla (Turkey) are the few names used in different parts of world. In India in Hindi language, it is popularly known as Kala Matar and Bakala as well (Singh *et al.*, 2013). In much of the English-speaking world, the name "broad bean" is used for the large-seeded cultivars grown for human food, while "horse bean" and "field bean" refer to cultivars with smaller, harder seeds that are more like the wild species and used for animal feed, though their stronger flavour is preferred in some human food recipes, such as falafel (Wikipedia, 2024). The term "fava bean" (from Italian: *fava* for the bean) is used in some English-speaking countries such as Canada and the US, and "broad bean" is the most common name in Commonwealth countries like the UK, Australia and New Zealand (Wikipedia, 2024).

Vicia can be divided into three different types according to the morphology of the floral peduncle: *ervum*, with a small number of tiny flowers in gracile peduncles (e.g. *V. tetrasperma*); *cracca*, with a high number of flowers in long racemes (e.g. *V. cracca*, *V. villosa*); and *euvicia*, with sessile flowers (e.g. *V. sativa*, *V. narbonensis*), or flowers in small numbers in very short racemes (*V. faba*, *V. roelanops*) (Cubero, 1984). Faba bean has a very wide range in seed size, which is usually regarded as seed type groups; *major* (large flattened or broad bean, 100-200 g/100 seed), *equina* (horse bean, 60-100g/100 seed), *minor* (tic bean with ellipsoidal seed, 40-60 g/100 seed) and *paucijuga* (regarded as primitive, 31-40g/100 seed). It was recognised 4 seed types but classified *paucijuga* as a sub species. *V. faba* var. *paucijuga* has dehiscent pods as do the other groups but to a much lesser extent, it is self-fertile with short stature and strong tillering, and closest to a wild type in traits, occurring in the Afghan-north Indian subcontinent region. The small seed / pod features are dominant over that of the larger more recent seed types. Fossil remains of faba bean date to 8,500 BP in Israel, and to 9,300 BP in Syria or even 11,200 BP in Iraq, with seed small flat to wedge shape at the hilum end, distinct from the more globular seed of wild *V. narbonensis* and *V. johannis* which still occur in the vicinity of the Israeli site. Medium size seed were found in Iberia and central Europe from 5,000 BP and larger more flattened seed are not known before 1,500 BP. There is archaeological evidence that indicates faba bean arrived in China/Japan around 4,000 – 5,000 BP and it has developed into a very distinct genepool, as discussed below (Redden *et al.*, 2014).

Faba bean has chromosome number $n=6$, with twice the DNA content of the nearest wild relatives (*Vicia* species; *narbonensis*, *johannis*, and *galilea*) in the subgenus *Vicia* of the family *Viceae*, which have $n=7$ and appear to be only distantly related although morphologically similar. *V. faba* is cross incompatible with these and other *Vicia* relatives, and also differs from them in mitochondrial and nuclear DNA. Thus no wild relative is known for *V. faba*, and no genetic divergence accompanied its geographic dispersal. Possibly *V.faba* had lateral multiplicity in the number of lateral chromosome strands to result in disjunct karyotype groups with DNA content per chromosome in 1: 2: 4 ratios with one chromosome being very large, possibly with segmental duplications. There is high cross compatibility between the different seed groups of *V. faba*, indicating that they belong to one species. The greatest morphological diversity in *V. faba* is found in the Fertile Crescent region of SW Asia, which may have been the centre of origin for this species. It is not clear whether the *paucijuga* group located in the region from Afghanistan to north India, derived from the main *V. faba* diversity in SW Asia or could have been independently domesticated. Wild *V. faba* was reported in Algeria as *V. pliniana* and in Morocco in the 19th century, but is apparently extinct today (Redden *et al.*, 2014).

Broad bean is an important crop worldwide. An increase in seed yield would increase both the grain reserve and the profit for farmers. Previous studies on increasing broad bean seed yield have focused mainly on increases at the whole population level. Few studies have focused on the differences in plant type within populations. In this study, we classified broad bean plants into four categories based on pod type and then evaluated the ratio of each category in field-grown broad bean populations. We analysed the seed and pod characteristics of each category and their contributions to total seed yield. The number of seeds per pod and the number of pods or seeds per plant differed among the four plant categories, but the seed weight was relatively uniform. There were significant differences in seed yield per plant among the four plant categories. We calculated the effects of increasing the proportion of each plant category by 10% or to 100% on seed yield and found that seed yield could be improved by increasing the ratio of plants with the highest seed production rate. This study provides a novel perspective on estimating the seed yield of broad bean (Li and Yang, 2014).

We have cultivated broad bean in southwest China for a long time. In our continuing observation, we noticed that broad bean plants produce three types of full pods. These have been designated as Pod I (containing one seed), Pod II (two seeds) and Pod III (three seeds) (Fig. 2A). Based on the pod types, the broad bean plants can be classified into four categories: Category I, all pods are Pod I (Fig. 2B); Category II, all pods are Pod II (Fig. 2C); Category III, pods are either Pod I or Pod II (Fig. 2D); and Category IV, at least one Pod III is among the pods (Fig. 2E). Because the four categories of plants produce different numbers of seeds and seed size is relatively stable within a species, we hypothesized that plants producing different numbers of seeds as a result of their pod characteristics might affect the seed yield of a broad bean population (Li and Yang, 2014).

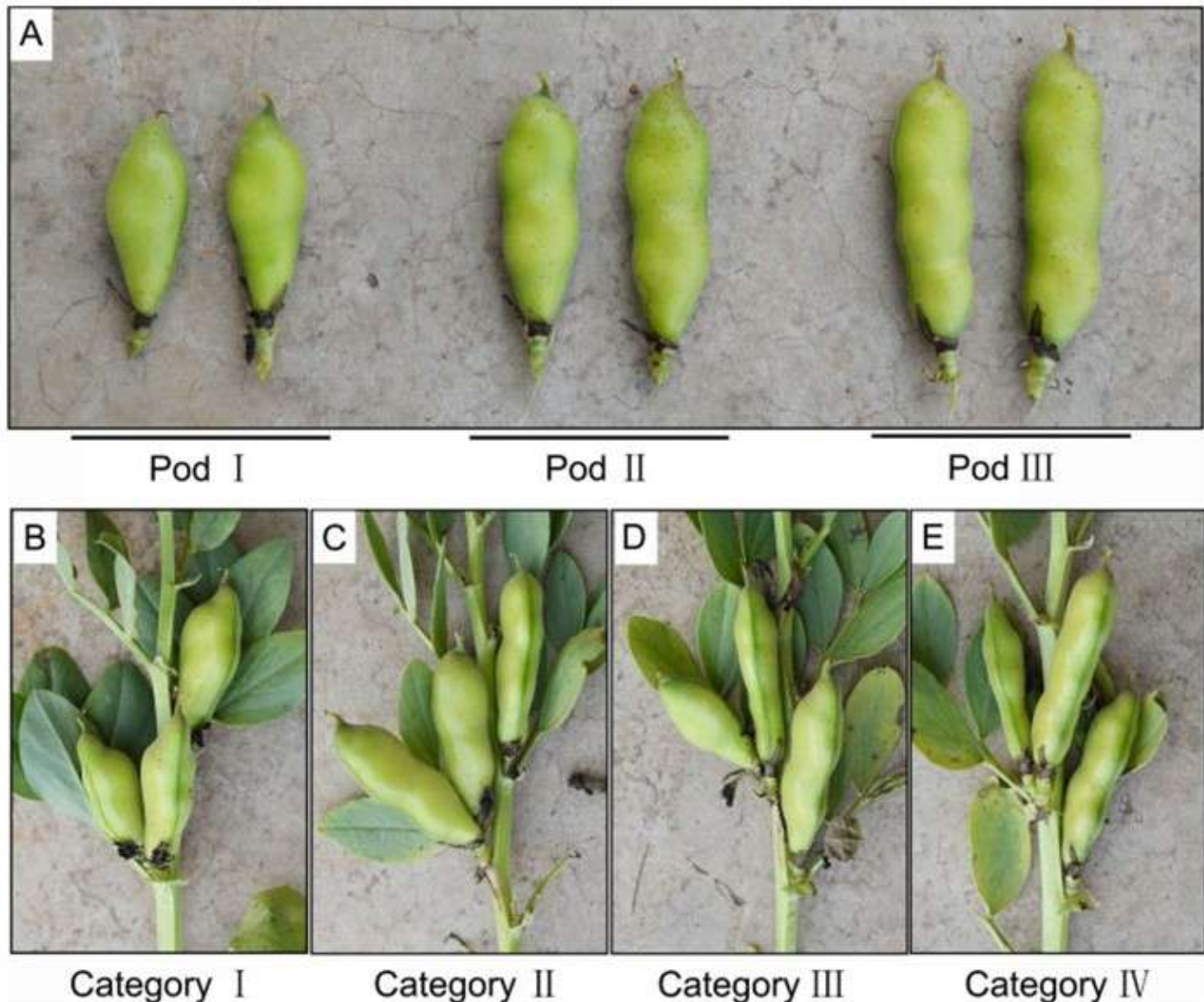


Fig. 2. Morphology of three pod types and four plant categories of broad bean. Morphology of Pod I, Pod II and Pod III. Morphology of plants in Category I (B), Category II (C), Category III (D) and Category IV (E)

One of the oldest crops is broad bean belonging to family Fabaceae, order Fabales, class Magnoliopsida, division Magnoliophyta (Kosev and Georgieva, 2023). Faba bean exhibits such extreme variation in seed size that some taxonomists defined the primitive, small-seeded 'paucijuga' forms or small-seeded 'minor' forms as separate subspecies from the medium-large 'faba' types. However, the absence of reproductive barriers between any of these forms means that 'major', 'minor', 'equina' and 'paucijuga' forms are now regarded as botanical types resulting from sustained human selection on growth habit and seed size over many thousands of years (Jayakodi *et al.*, 2023). Faba bean continues to be relevant in the twenty-first century as humanity strives to lower agricultural greenhouse gas emissions by replacing meat or milk protein with plant-based alternatives. It is the highest yielding of all grain legumes and has a favourable protein content (approximately 29%) compared with other cool-season pulses such as pea, lentil and chickpea, making it a suitable candidate to meet challenging projected future protein demands. Furthermore, the high biological nitrogen fixation rates of faba bean and the long duration of nectar-rich, pollinator-friendly flowers provide important ecosystem services, which means that cultivation of faba bean is increasingly seen as key for sustainable intensification strategies (Jayakodi *et al.*, 2023).

BOTANICAL DESCRIPTION

Numerous attempts to cross the wild species to cultivate faba bean have failed. Although, usually classified in the same genus *Vicia* as the vetches, some botanists treat it in a separate monotypic genus as *Faba sativa* Moench. *V. faba* is an annual herb with
















coarse and upright stems, unbranched 0.3 to 2 m tall, with 1 or hollow stems from the base. The leaves are alternate, pinnate and consist of 2 to 6 leaflets each up to 8 cm long and unlike most other members of the Genus; it is without tendrils or with rudimentary tendrils. The plant flowers profusely but only a small proportion of the flowers produce pods. Flowers are large, white with dark purple markings, borne on short pedicels in clusters of 1-5 on each axillary raceme usually between the 5 and 10th node; 1-4 pods develop from each flower cluster, and growth is indeterminate though determinate mutants are available (Singh *et al.*, 2013). Broad bean is an annual stiffly erect herb up to 3-4 ft. (90-120cm) tall. The stems are tetragonous, glabrous, thick, bluish green, 6 ft. high and square shape at cross section. The plant bears bluish grey- green leaves about 10-25 cm long in a triangular to ovate shape. The leaflets are 4-10 cm long, 1-4 cm wide having the oval-elliptic shape. The flowers are white with black dots, about 1–2.5 cm long and they give pods as a fruit. The white flowers give way to pods 5-10 cm long and 1 cm diameter. Pods are thick, broad and leathery. These may be light green when young and blackish-brown when mature, each containing 3 to 8 seeds. The seeds are ovoid to oblong shaped, 1-3 cm as a diameter ranges from white, yellow, green, pinkish-red in color. Broad beans possess sweet, tender and succulent taste with mild flavour (Sylvia, 2017).

In Algeria, the broad bean is sown in autumn and blooming between February and April. The flowering lasts 30 days and runs from bottom to the top of the stem. A broad bean's stalk produces 50 to 80 flowers grouped in clusters of 2 to 9 flowers. The broad bean is an annual plant with a cycle effected in 24 to 28 weeks. The maturation phase of pods and the flowering overlapped with each other. We can find pods at widely varying from bottom to top of the plant: pods were being filled and pods in terminal stage, with a few flowers at the vertices of the stems. The formation of pods occurred in March-April, the maturity period was noted in May. The autopollens guarantee less fertilization of all ova. The more number of pollen grains is important on the stigma, the more rate of fructification is higher (Aouar-sadli *et al.*, 2018). Broad bean or Faba bean, is a member of the Fabaceae family. This cool-season, annual legume is characterized by its upright growth habit, typically reaching heights of 2 to 4 feet. The plant features a central stem with compound leaves that consist of several leaflets. The leaves of *Vicia faba* are alternate, with an odd number of leaflets ranging from one to seven. Each leaflet is ovate or lanceolate, showcasing a vibrant green color. The leaf arrangement contributes to the overall aesthetic appeal of the plant. The flowering stage of *Vicia faba* is visually striking. The plant produces large, white to pinkish-purple flowers that are held in clusters. These conspicuous flowers play a crucial role in the pollination process, attracting bees and other pollinators. As the flowers are pollinated, they give rise to pods that house the developing seeds. The pods of *Vicia faba* are distinctive, elongated, and typically contain 3 to 8 seeds, depending on the variety. The pods mature from green to a pale yellow or brown color. *Vicia faba* develops a well-branched root system that aids in anchoring the plant in the soil. This root structure also facilitates the absorption of water and nutrients essential for the plant's growth. Broad beans exhibit a relatively short growth cycle, making them well-suited for cultivation in various climates. They are often grown as a winter cover crop or a spring-sown crop, depending on the region and climate (Agric4Profits, 2023). Faba Bean is an annual, erect and glabrous herb. Plants are 40 to 190cm in length, with both dwarf and tall varieties, with tap root system of root length up to 90 cm or more bearing small nitrogen fixing lobbed nodules. Stem bearing 1-7 branches, erect, hollow. Leaves are broad, pinnate and large, short axillary inflorescence 1-6 fragrant flowered with length of 2.4-3.5 cm with short stamens and terminal stigma, 2-6 leaflets, pods are upright, leaflets are alternate and pods are glossy green borne in leaf axils, flattened or sub cylindrical pods containing 5-7 large seeds with length of 6-10 cm long in field cvs up to 28-30 cm in garden cultivars, fleshy when young and hard at maturity. Seeds are 0.8-1.8 cm long, 100 seeds weighted 50-180 g approximately. The small seed types are used for animal feed known as field bean. *Vicia faba* var *paucijuga* is another Broad bean which is not generally grown (Brar *et al.*, 2023).

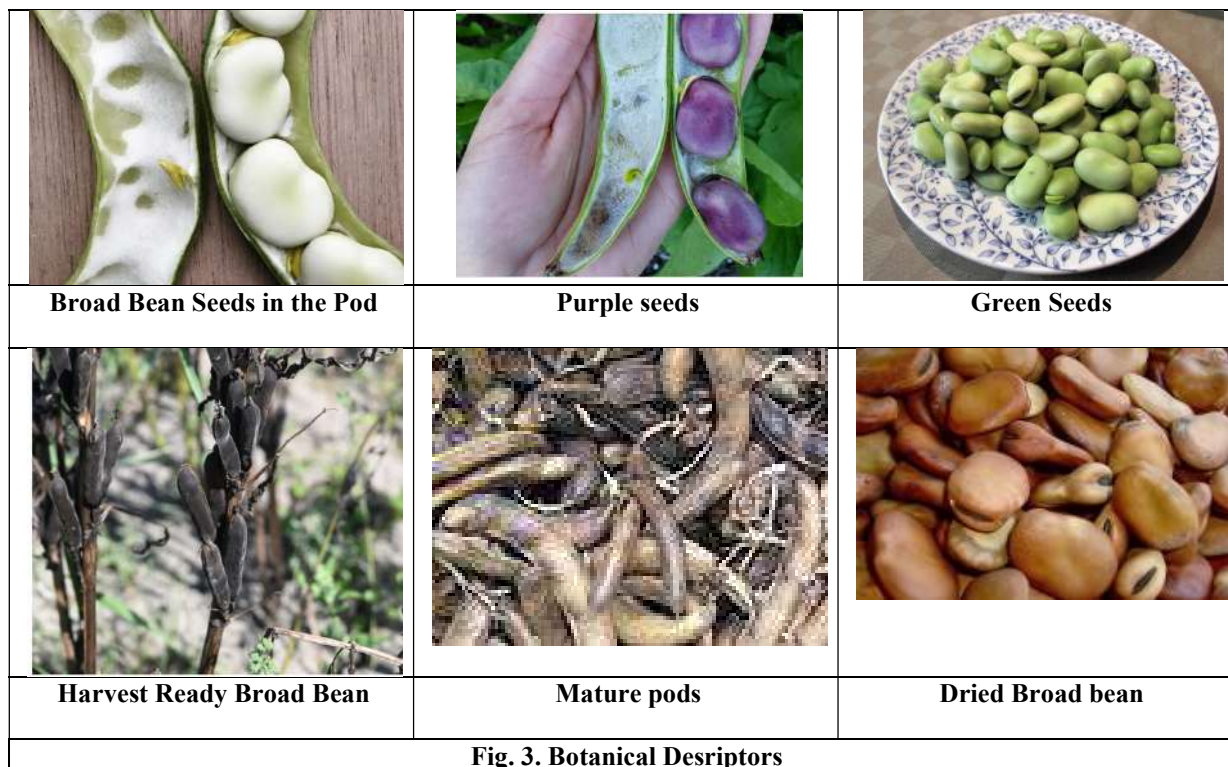
The plant is erect, from 60 to 150 cm tall (2 to 5 feet), and bears few branches. The stem and branches are crowded with short-petioled compound leaves. The pods are nearly erect in clusters in the axils of the leaves, and the seeds are large and irregularly flattened. The broad bean will not tolerate hot weather; it is grown in summer only in the cool parts of the temperate zone and during the winter in the warmer parts. Unlike many other beans, it tolerates slight freezing (Petruzzello, 2024). *Vicia faba* is a stiffly erect, annual plant 0.5 to 1.8 metres (1 ft 8 in to 5 ft 11 in) tall, with two to four stems that are square in cross-section. The leaves are 10 to 25 centimetres (4 to 10 in) long, pinnate with 2–7 leaflets, and glaucous (grey-green). Unlike most other vetches, the leaves do not have tendrils for climbing over other vegetation. The flowers are 1 to 2.5 centimetres ($\frac{1}{2}$ to 1 in) long with five petals; the standard petals are white, the wing petals are white with a black spot (true black, not deep purple or blue as is the case in many "black" colorings) and the keel petals are white. Crimson-flowered broad beans also exist, which were recently saved from extinction. The flowers have a strong sweet scent which is attractive to bees and other pollinators. https://en.wikipedia.org/wiki/Vicia_faba#cite_note-4The fruit is a broad, leathery pod that is green, but matures to a dark blackish-brown, with a densely downy surface; the wild species has pods that are 5 to 10 cm (2 to 4 in) long and 1 cm diameter, but many modern cultivars developed for food use have pods 15 to 25 cm (6 to 10 in) long and 2–3 cm thick. Each bean pod contains 3–8 seeds. They are round to oval and have a 5–10 mm diameter in the wild plant, but are usually flattened and up to 20–25 mm long, 15 mm broad and 5–10 mm thick in food cultivars (Wikipedia, 2024).

Faba bean or broad bean is a self-fertile, widely cultivated annual legume in the Fabaceae (bean) family. Grown primarily for its nutritious seeds and pods which are high in protein and consumed by millions of people throughout the world. Legumes also have the ability to fix nitrogen from the air and are often used as a cover crop. It is a stiffly erect plant that grows 2-6 feet tall and prefers moist loams but is tolerant of clay and saline soils and once established, drought. Four to five months are needed between sowing seed and harvesting. This cool season crop can be grown in most climates, however, temperatures in the 60's are ideal. In locations where the daytime temperatures exceed the mid 70's may result in poor yield unless planted at a time when temperatures are milder. In areas that experience dry, hot weather, this plant may not be a good choice. Two subspecies are grown. *Vicia faba* var. *major* (broad beans) has large seeds, and is grown as a vegetable for human consumption. It can be used in soups, stews, salads and side dishes. *Vicia faba* var. *minor* (horse beans or field beans) is grown for feeding livestock (NCSE, 2024). Broad bean, *Vicia faba*, is a leguminous plant in the family Fabaceae primarily grown for its edible beans. Broad bean is a

an annual vetch reaching between 0.5–1.8 m (1.6–6 ft) tall. There are often multiple stems originating from the base of the plant and the compound leaves are often broad, oval shaped, and come groups of 6 leaflets to a stem. The flowers are white with purple markings. Between 1 and 4 pods develop from each flower cluster. The beans can be greenish black, brown or black in color. *Vicia faba* may also be referred to as bell-bean, fava bean or horsebean and originates from the Mediterranean or in South-West Asia (PV, 2024). Fig.3 gives the botanical description of broad bean.

| | | |
|---|--|---|
|  |  |  |
| Seed Sowing | Young Leaves | Young Leaves |
|  |  |  |
| Young Seedlings | Young Seedlings | Field |
|  |  |  |
| Plants | Flowers | Purple Flowers |
|  |  |  |
| Crimson flowers | Flower | Foliage |
|  |  |  |
| Plants | Green pods | Green pods |

Continue



Floral biology: Racemes of 3-8 flowers, exceptionally as many as 25 or as few as one, are borne in the leaf axils, and within each raceme the flowers develop acropetally (i.e. successively away from the axis so that the youngest arise at the apex). The flowers (Fig.4) are of the usual papilionoid form, with an erect standard petal. Each of the two wing petals typically bears a large dark spot and they clasp the keel petal by infoldings and protuberances. The keel encloses the ten stamens and single pistil. Nine of the staminal filaments are united in a sheath which surrounds the ovary and the tenth is free. In each flower, the ovules usually number three or four, exceptionally 1-11. The style, ovarian cavity and micropyle are hollow so the stigmatic surface presents the only physical barrier between any deposited pollen and the interior of the ovule. The style is at a right angle to the distal end of the ovary and bears a brush of long hairs just below the stigma. About 0.5-0.9 mg of nectar is held at the base of the corolla tube, and rates of secretion of nectar are highest in the early morning and late evening. The scent is very attractive to bees. Flowers usually reach anthesis (flower-bud opening) between 13.00 and 16.00 h and close again at dusk. They reopen about 11.00 h on the second day and about 09.00 h on the third and subsequent days. The flowers fail to reopen under two conditions: either 2-3 days after pollination, probably when all of the ovules have been fertilized, or 6-7 days after anthesis. Flowers which are pollinated when up to six days old are capable of developing into pods. Pollen remains capable of fertilizing ovules for five days and alive for seven. The anthers dehisce in such a way that the plug of sticky pollen is contained within a pocket in the keel petal and held above the stigma. The filaments then contract, the empty anther locules being left near the neck of the style. When a bee alights on the wing petal and opens the flower, the wing petal/keel petal complex is forced downward while the pistil stays in place and the flower is said to be 'tripped'. Some of the pollen is thereby forced on to the stigmatic surface and is pushed ahead of the stigma through the opening at the top of the keel petal and into contact with the bee. The brush of stylar hairs increases the surface area against which the pollen is forced. The self-pollen (i.e. pollen from the plant being visited) is rubbed on to the body of the bee while it pushes into the flower toward the nectar. Then the stigma itself is rubbed by the bee so the stigmatic cuticle is broken and an exudate, which is essential for pollen germination, is released. Pollen already present on the body of the bee contacts the stigma and thus cross-pollination is functionally favoured, although the total quantity of self pollen present in the flower and on the bee (from flowers on the same plant) usually far exceeds that of foreign pollen brought by the bee. The 'scrabbling' activity of honeybees collecting pollen looks as if it should favour self-pollination. A weak self-incompatibility system, hindering pollen tube growth in the style, has been postulated but not confirmed. Inbred embryos, however, may be more likely to abort than hybrid ones, due to mitotic irregularities. Some seeds resulting from self-pollination are, of course, set from flowers that remain unvisited (Stoddard and Bond, 1987).

Pollination: Floral biology in faba bean is intermediate between allo- and auto-gamous. However, some differences may exist within types (spring types are more allogamous than winter types) or within regions (southern have often more autogamous types than northern ones). *V.faba* is partially insect-cross pollinated crop. Indeed, in Mediterranean region, it is especially pollinated by diverse solitary bees which trip the flowers and cause either self or cross fertilization. According to literature, faba bean out-crossing rate varies widely depending on the genotype and environmental conditions and it is ranged from 10 to 60%. Differences in out-crossing among botanical groups have been mentioned. However, there is not a general agreement if there is more out-crossing rate within *major*, within *equina* or *minor*. Differences in self-fertility between the botanical groups *major*, *equina*, and *minor* have also been reported (Ali Oujji *et al.*, 2011). It is naturally cross pollinated (20-40 %) crop done by honeybees and bumble bees. It is not highly autogamous. The breeding procedures include like mass selection, recurrent selection, pure line

selection and for pedigree selection, hybridization and population improvement in backcrossing, developing synthetic varieties, segregating progenies and single seed decent.

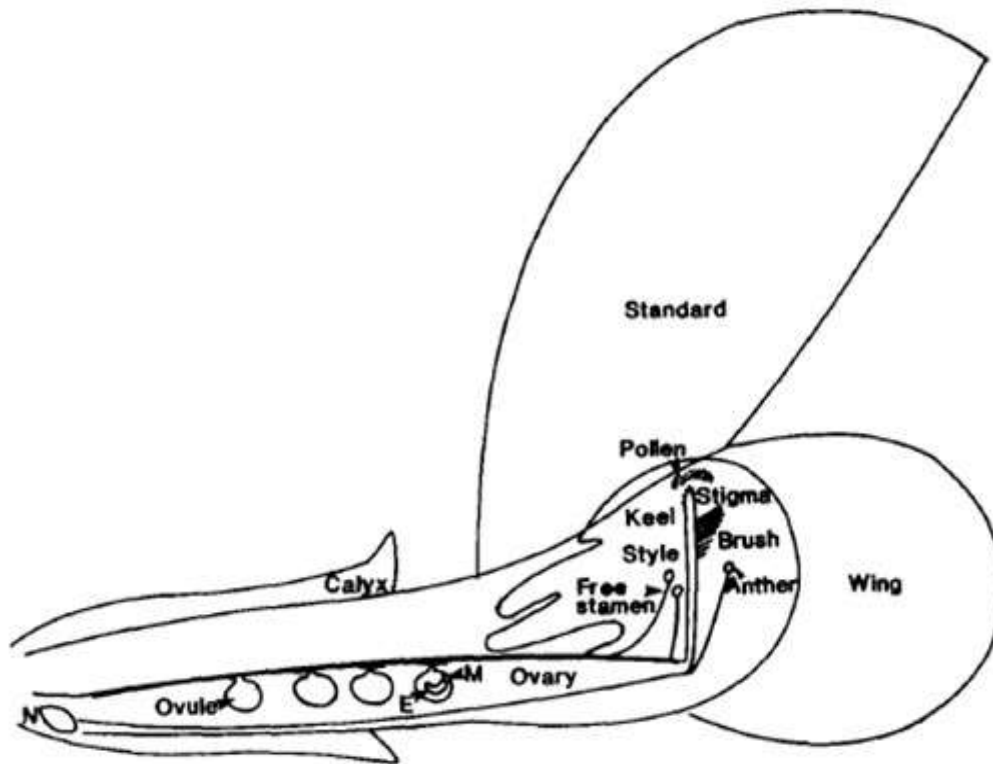


Fig. 4. A longitudinally split flower of *Vicia faba*. For clarity, only three of the ten stamens are shown. E, embryo sac; M, micropyle; N, nectary

The breeding of Broad Bean is limited for vegetable purpose. Fabaceae is one of the 3rd large family of angiosperms. It is Zygomorphic, Bisexual, Calyx- 5 sepals, Gamosepalous (united), Corolla- 5 petals, Polypetalous, Androecium- 10 stamens, Diadelphous, Gynoecium- monocarpellary, Superior ovary. Seeds are Nonedospermic and with two cotyledons. Pollination is mainly by insects (entomophilous). Roots nodules containing N fixing Rhizobium, which is the characteristic property of the family (Brar *et al.*, 2023).

An experiment conducted with caged plots confirmed the large seed yield of *Vicia faba* L. in the presence of pollinating insects during the flowering season of the year 2003. The plants that were accessible to pollinators provided more pods per plant, more seeds per pods; the pods were longer and the seeds were heavier than the encaged plants. Among the pollinating insects of *Vicia faba*, in the Tizi Ouzou area (Algeria), the wild bee *Eucera pulveracea* Dours was the most abundant and seemed to be the most effective pollinator. His visits were all able to fertilize the flowers. On the contrary, several floral visits of the honey bee *Apis mellifera* L. and all visits of *Xylocopa violacea* were “nectar robbery” through the holes made by the bumblebees at the base of the corolla. The floral visits of *Eucera pulveracea* L. were also faster (10 visits per minute) (Aouar-sadli *et al.*, 2018). An investigation was carried out at Garag village of Dharwad district to study the diversity of pollinators visiting broad bean during rabi 2019. The pollinator fauna of broad bean comprised of a total of nine insect species belonging to three insect orders viz., Hymenoptera, Lepidoptera and Diptera. Among these, Hymenoptera was the most dominant pollinator group with a maximum of 62.27 per cent proportion followed by Lepidoptera (25.16) and Diptera (12.57). The most abundant pollinator among the hymenopterans was the little bee, *Apis florea* Fabricius which recorded 31.14 per cent proportion followed by *Apis dorsata* Fabricius, *Apis cerana* Fabricius and *Megachilae* sp. with 15.23, 10.60 and 5.30 per cent proportion, respectively.

Two species of lepidopterans viz., *Phoebis sennae* Linnaeus and *Lampides boeticus* Linnaeus, among depterans, *Musca* sp., *Episyrphus* sp., and *Lucilia* sp were also found visiting broad bean flowers (Kambrekar *et al.*, 2019). About 30% of the plants in a population are cross-fertilized and the main insect pollinators are bumblebees. There is a robust tap root with profusely branched secondary roots. *V. faba* is a partially allogamous species (Self-fertile with about equal amount of self and cross-pollination occurring depending on the presence of insect pollinators). The Apoides play a decisive role in the pollination of allogames lines. The importance of bees in cross-pollination of this plant and the improvement of its production has been demonstrated and recognized by several authors. Inadequate pollination is considered as a major obstacle to achieve the potential yield and improved seed quality of faba bean. Insects appear to be the major pollinators of faba bean. Numerous studies have shown the value of honey bees as pollinators of faba beans in Australia and overseas (Singh *et al.*, 2013). It is predominately self-pollinated, but its flowers are visited by bees and therefore, considerable cross-pollination occurs. Fava bean does not produce fertile offspring in crosses with other species in the genus; however, variation within *V. faba* is considered ample for genetic improvement (Byrne, 2023).

GENETICS AND CYTOGENETICS

V. faba has a diploid ($2n$) chromosome number of 12, meaning that each cell in the plant has 12 chromosomes (6 homologous pairs). Five pairs are acrocentric chromosomes and 1 pair is metacentric (Singh et al., 2013). Several wild species are taxonomically closely related to the cultivated crop, but they contain $2n = 14$ chromosomes, whereas cultivated faba bean has $2n = 12$ chromosomes (Singh et al., 2013). Classical Genetic Analysis: The period 1930–1993 was the era of molecular marker-free genetic analysis. During this period and beyond, useful foundations were laid showing simple inheritance patterns for a variety of heritable traits. As mentioned already, it was found single dominant or semi-dominant genes explaining flower, seed, and hilum color as well as plant height, though there was no well-developed locus nomenclature in this early work. Faba bean received much attention in the 1960s to the early 1990s as a model for cytogenetics due to its uncommonly large haploid genome size of 13Gb and modest haploid chromosome number ($n = 6$), which made for large, readily observable chromosomes. For a time, the study of chromosome breakage response to arrangement of physical and chemical agents became quite fashionable and faba bean was one of the early crop species whose chromosomes were found to be amenable to flow sorting. The more direct relevance of cytogenetics to modern molecular genetics was the identification of asynaptic mutants, on which a series of trisomic stocks were founded. Genetic analyses of crosses involving trisomic parents allowed genetic markers to be assigned to physical chromosomes (O’Sullivan and Angra, 2016).

Genetic modification represents both a research tool, permitting testing of hypotheses on gene function by over-expression, mis-expression or knockdown/knockout studies and an outlet for genetic research in generation of targeted phenotypic modifications based on knowledge of gene function. Stable germline transformation of faba bean using *in vitro* regeneration of *Agrobacterium*-infiltrated (non-meristematic) internode stem segments was first reported. Adopting a somewhat different strategy, it was reported that infiltrated excised (meristematic) embryo axes with *Agrobacterium* and successfully recovered stable transgenic lines. Both methods, however, reported low primary transformation efficiencies and relied on micro-grafting of putative transgenic shoot material onto non-transgenic roots, a slow and highly manual process. It was later reported abiotic stress resistance phenotypes of faba bean, transgenic lines over expressing potato PR10a using their previous methods. This remains to our knowledge the sole successful demonstration to date of the feasibility of a biotechnological approach to faba bean improvement. In the absence of a robust and efficient transformation method, some attention has been devoted to the task of decreasing generation time using tissue-culture based embryo rescue, with some success. The prospects afforded by new insights into the phenotypic effects of allelic variation and the more refined biotechnological possibilities afforded by rapidly maturing genome editing technologies could potentially stimulate renewed interest in genetic transformation. An example of a game-changing product which could readily be generated using even a medium efficiency transformation system would be herbicide resistance obtained by directed mutagenesis of endogenous herbicide target genes *e.g.*, introduction of heterologous glyphosate resistance of bacterial origin (O’Sullivan and Angra, 2016). Much progress has been made in the power and possibilities of genetic analysis in faba bean on inheritance of color, size, and form of seeds and other traits. Mendelian inheritance of genes controlling readily observable (but nonetheless important) characters including hilum color, seed, and flower color and height. However, many years were to pass before the genes underlying these or any other traits have been identified. Between then and now, faba bean genetics has passed through distinct phases which will be described below in chronological order (O’Sullivan and Angra, 2016).

Vicia faba L. ($2n = 12$) is a close relative of *Narbonensis* ($2N = 14$) within subgenus *Vicia*, even though they have different chromosome numbers and nuclear DNA content (Maalouf et al., 2018).

Faba bean improvement is currently impeded by development of rich genomic resources having not kept pace with those of other cool-season grain legumes. Faba bean is a partially allogamous diploid species with six pairs of remarkably large chromosomes. Its genome is one of the largest of any diploid field crop, about 13 Gbp in the haploid complement and contains more than 85% repetitive DNA. The large genome of faba bean is 2.9, 3.0 and 15.9 times larger than pea, lentil and chickpea, respectively. Assembly of the faba bean genome and map-based cloning was delayed both due to its genome complexity (*e.g.* abundance of transposable elements) and the lower investment in its study compared with, for example, soybean. In the absence of a reference genome assembly for this species, high-throughput approaches such as transcriptome analysis have been efficient tools for enrichment of genomic resources. However, from these reported transcriptome datasets, only limited DNA sequence data are available in public databases (Khazaei et al., 2021). Genomic research in faba bean lags behind other major grain legumes, hampered by its gigantic genome size of 13.1 Gb and lack of investment in underpinning research compared to other crops. Pulses may be considered as research-neglected orphan crops and amongst pulses, faba bean has received comparatively less attention compared to pea, common bean, chickpea, lentil or even cowpea; it is an orphan of the orphans. There is a need to tap on the discoveries made in genetics and genomics research to make significant improvement of this crop (Adhikari et al., 2021). Gene editing is developing as a new breeding approach in many crops, thus, assisting to accelerate genetic gains. No CRISPR/Cas9 system has been reported for faba bean yet. The absence of an annotated reference genome for this crop poses challenges for the application of CRISPR/Cas gene editing, particularly with the design of specific gRNA-targeted genes of interest. However, with recent gene discoveries for quality traits such as vicine-convicine (v-c) and seed coat tannins, this technology may be used to advance our understanding of gene function and accelerate development of new cultivars with reduced anti-nutritional factors (Adhikari et al., 2021).

Faba bean is a high-protein grain legume crop with great potential for sustainable protein production. However, little is known about the genetics underlying trait diversity. In this study, we used 21,345 high-quality SNP markers to genetically characterize 2678 faba bean genotypes. We performed genome-wide association studies of key agronomic traits using a seven-parent-MAGIC population and detected 238 significant marker-trait associations linked to 12 traits of agronomic importance. Sixty-five of these

were stable across multiple environments. Using a non-redundant diversity panel of 685 accessions from 52 countries, we identified three subpopulations differentiated by geographical origin and 33 genomic regions subjected to strong diversifying selection between subpopulations. We found that SNP markers associated with the differentiation of northern and southern accessions explained a significant proportion of agronomic trait variance in the seven-parent-MAGIC population, suggesting that some of these traits were targets of selection during breeding. Our findings point to genomic regions associated with important agronomic traits and selection, facilitating faba bean genomics-based breeding (Kovbjerg *et al.*, 2023). Faba bean has a high yield potential and is well suited for cultivation in temperate regions, but genomic resources are scarce. Here, we report a high-quality chromosome-scale assembly of the faba bean genome and show that it has expanded to a massive 13 Gb in size through an imbalance between the rates of amplification and elimination of retrotransposons and satellite repeats. Genes and recombination events are evenly dispersed across chromosomes and the gene space is remarkably compact considering the genome size, although with substantial copy number variation driven by tandem duplication. Demonstrating practical application of the genome sequence, we develop a targeted genotyping assay and use high-resolution genome-wide association analysis to dissect the genetic basis of seed size and hilum colour. The resources presented constitute a genomics-based breeding platform for faba bean, enabling breeders and geneticists to accelerate the improvement of sustainable protein production across the Mediterranean, subtropical and northern temperate agroecological zones (Jayakodi *et al.*, 2023).

Faba bean is one of the most important legumes in the world. However, there is relatively little genomic information available for this species owing to its large genome. The lack of data impedes the discovery of molecular markers and subsequent genetic research in faba bean. Faba bean varieties with different phenotype were used in transcriptome analysis. The functions of the unigenes were analyzed using various database. SSR markers were developed and the polymorphic markers were selected to conduct genetic diversity analysis (Hou *et al.*, 2023). Substantial progress has been made in faba bean genomics and pre-breeding research. The mining of the first faba bean transcriptomes and development of single-nucleotide polymorphism (SNP)-based genetic maps, which showed strong collinearity with model legumes, set the scene for the identification of the WD40 transcription factor underlying the *Zero Tannin1* locus, whereas a combination of high-resolution mapping, transcriptomic and metabolomic approaches led to the cloning of the *VCI* gene, which controls seed content of the antinutrients vicine and convicine, paving the way for safer exploitation of the crop in the human food chain. However, the lack of a reference genome sequence greatly complicated these studies, and improved faba bean genomic resources are urgently needed to accelerate crop improvement (Hou *et al.*, 2023). *V. faba* is a diploid species with six pairs of chromosomes and a massive genome size estimated at 13 Gb of DNA (Byrne, 2023). *V. faba* has a diploid (2n) chromosome number of 12 (six homologous pairs). Five pairs are acrocentric chromosomes and one pair is metacentric (Wikipedia, 2024). The diploid genome of *Vicia faba* contains 13 GB of DNA, mostly obtained through amplification of retrotransposons and satellite repeats. The genome is one of the largest diploid field crops and contains a predicted 34,221 protein-coding genes (Wikipedia, 2024).

GENETIC DIVERSITY

De Angelis *et al.* (2020) reported faba bean seeds with different seed color and size *viz.*, (A) small-seeds; (B) medium-seeds; (C) large-seeds; (D) green seeds; (E) brown seeds; (F) purple seeds (Fig. 5).



Fig. 5. Faba bean seeds with different seed color and size. (A) small-seeds; (B) medium-seeds; (C) large-seeds; (D) green seeds; (E) brown seeds; (F) purple seeds

Induced mutagenesis is one of the most widely used breeding methods for rapidly increasing genetic diversity in many crops. This study used gamma radiation and diethyl sulfate (DES) to increase the genetic diversity in two faba bean genotypes. The genetic diversity assessment was based on 12 qualitative traits. The purpose of this study was to assess the genetic diversity in the M₂ faba bean mutant populations and to select promising mutant. A total of 5271 M₂ seeds generated from the M₁ generation of two genotypes—Hassawi 2 and ILB4347—were used in this study. The seeds of M₁ were obtained by gamma-ray exposure (25 and 50 Gy) and treatment of 0.01, 0.02, and 0.05% DES. A total of 4333 (82.2%) seeds germinated, of which 4102 plants survived and were screened for morphological diversity. A total of 36 mutant types are presented in this study. Determinate plant type, white flower color, white hilum, and black seed coat color were some of desirable traits that were considered for further generations. Multivariate-based principal component analyses showed that high genetic diversity was induced by gamma radiation and DES in faba bean mutant populations. This study revealed the potency of gamma radiation and DES on increasing genetic diversity and demonstrated the successful program of induced mutagenesis in the faba bean (Fig. 6,7,8,9,10, 11) (Nurmansyah *et al.*, 2020).

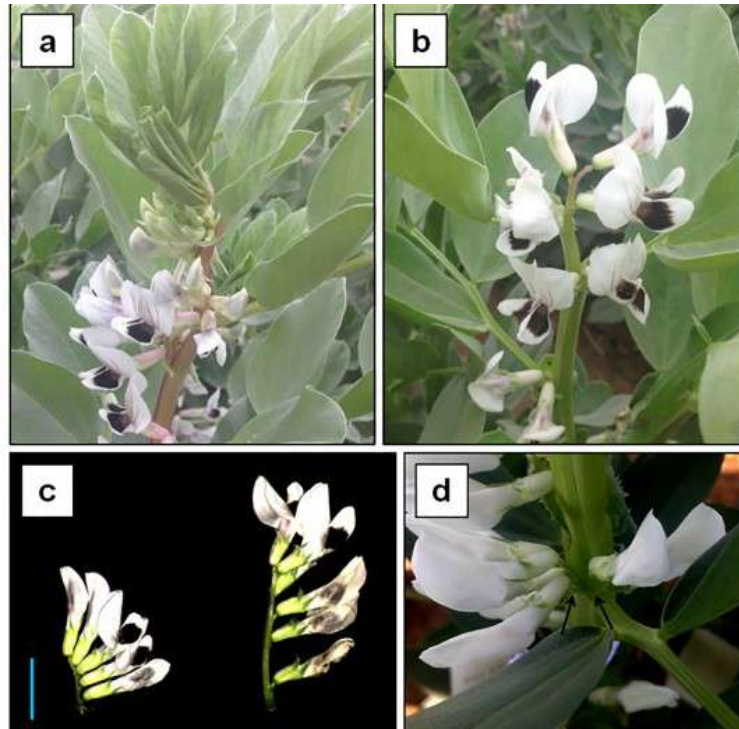


Fig. 6: Inflorescence variations a control indeterminate type without terminal inflorescence. b mutant determinate type with terminal inflorescence. c comparison between control (left) and mutant long peduncle (right), blue bar = 2 cm. d double peduncle mutant

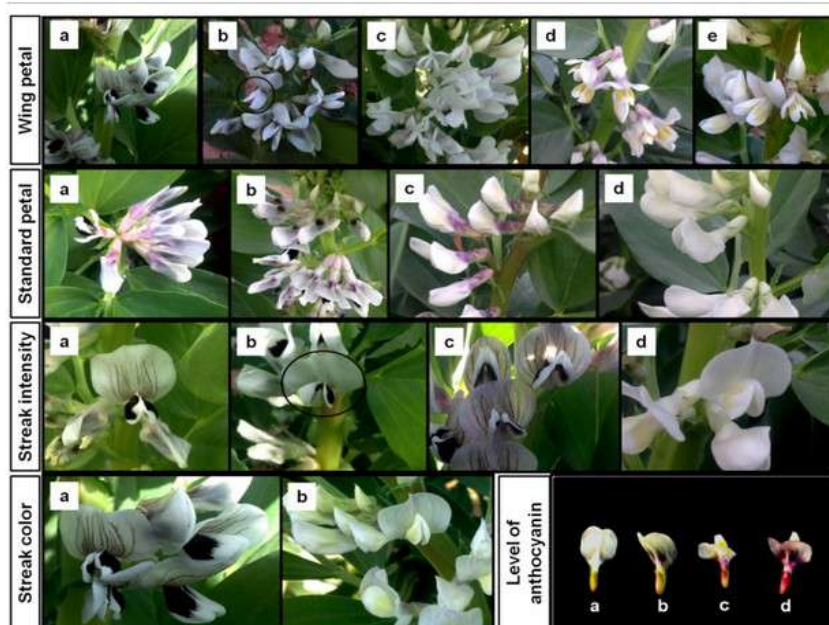


Fig. 7. Flower characters variation. Wing petal color variations, a black spotted (control), b faded black, c white, d yellow spotted, e light yellow spotted. Standard petal color variations, a purple spotted (control), b brown spotted, c violet spotted, d white. Intensity of streak variations, a medium intensity (control), b slight, c intense, d absence or without streak. Streak color variations, a brown (control), b purple. Level of anthocyanin coloration variations, a absence or without anthocyanin coloration, b small coloration (control), c medium coloration, d intense coloration

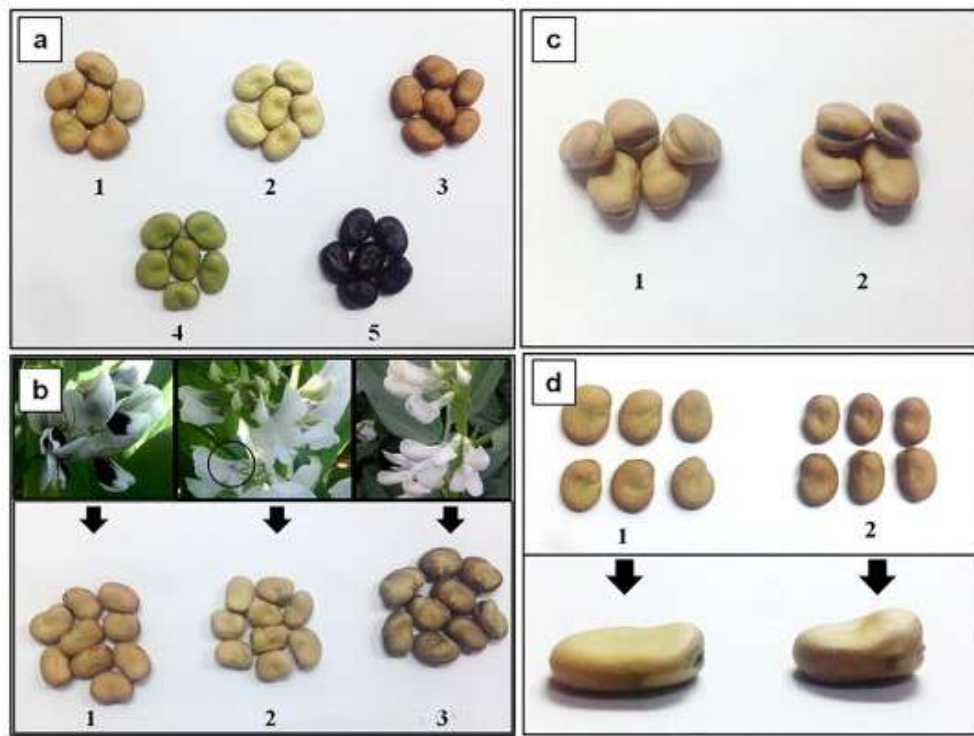


Fig. 8. Seed characters variation a seed coat color variations, 1: beige (control), 2: yellow, 3: brown, 4: green, 5: black. b Comparison of flower colors and their seed colors. 1: black spotted control flower has beige seed, 2: white flower with anthocyanin coloration (black circle) has beige seed, 3: white flower has darken-beige in seed color. c hilum color variations, 1: white, 2: black (control). d Seed shape variations, 1: flattened, 2: angular (control)

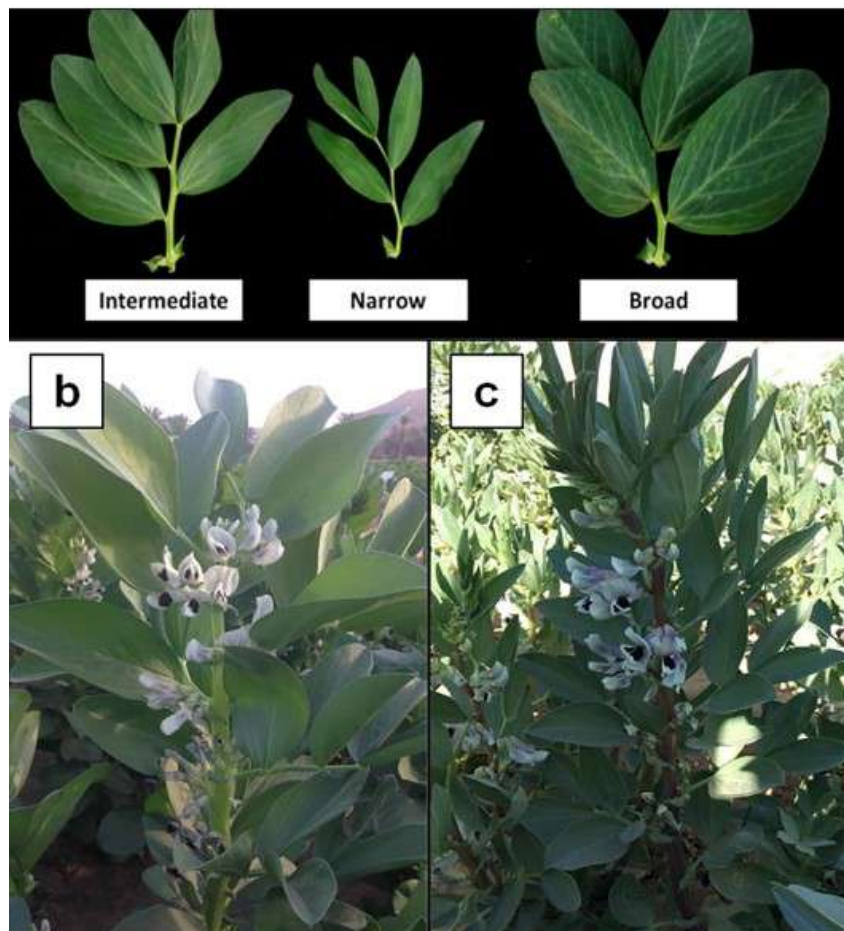


Fig. 9. Leaf shape and stem pigmentation variations a three different leaf shape. b stem without pigmentation (absence). c stem with intense pigmentation

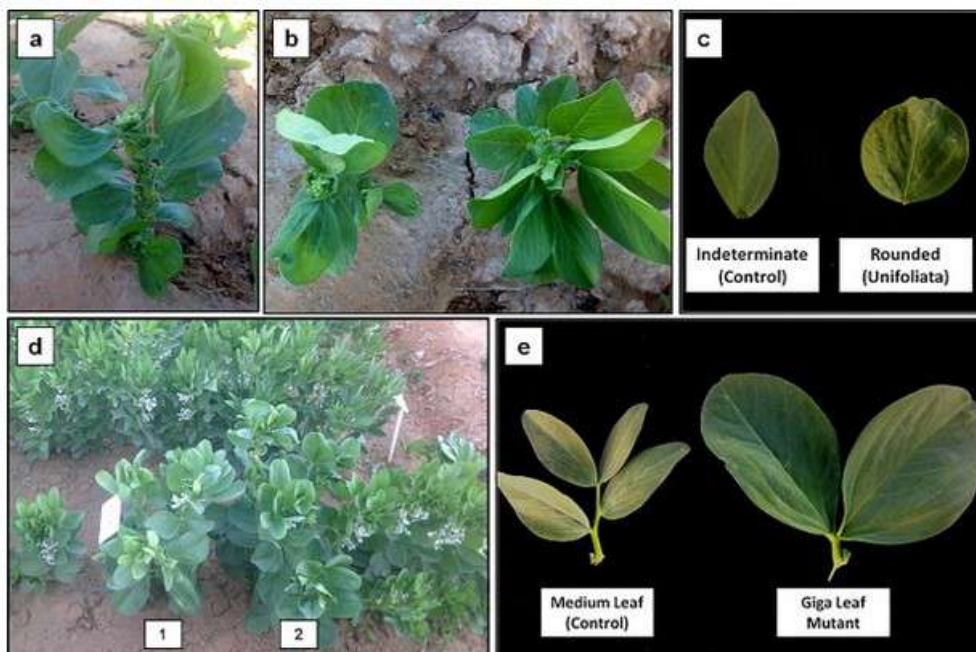


Fig.10. Unifoliolate and giga mutant characters.

a unifoliolate plant structure. b comparison between unifoliolate (left) and control plant (right) from above. c comparison between control and unifoliolate leaf. d two giga plants in the field. e comparison between control and giga mutant leaf (taken from node number 8).

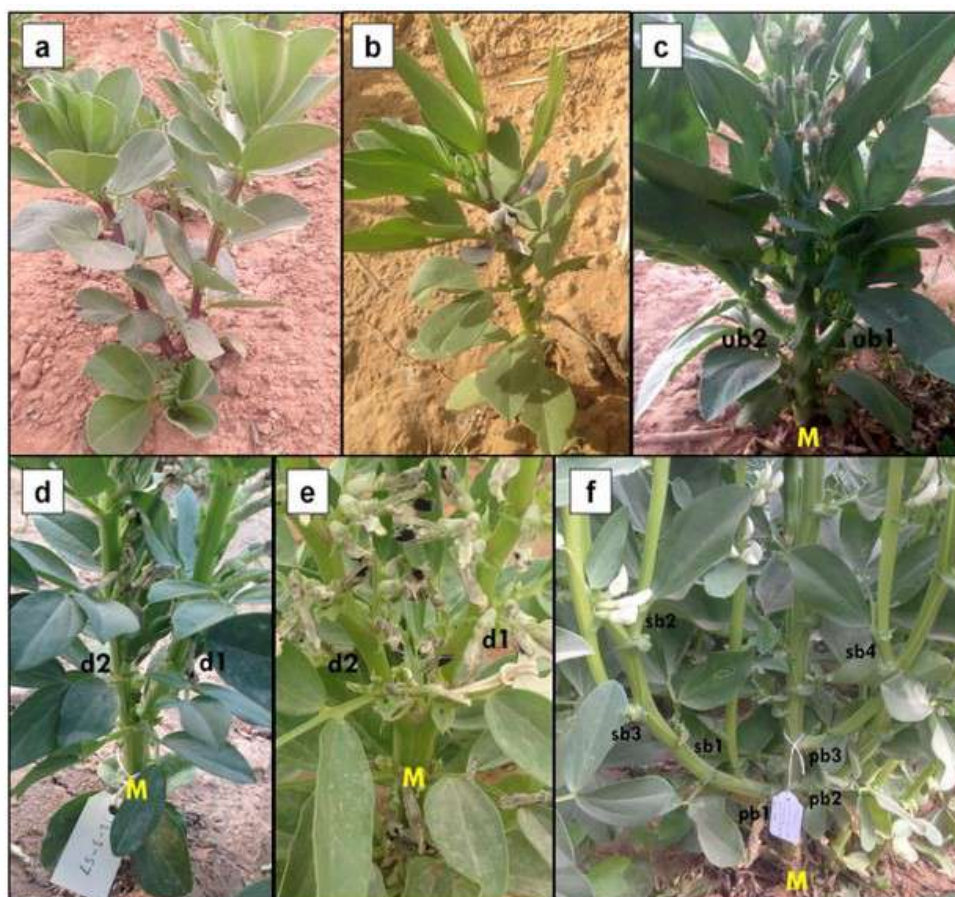


Fig. 11: Branching pattern variations.

a control lower axillary branch pattern, b homeostatis pattern, c upper axillary branch pattern, d-e dichotomous branch pattern, f multi-branch pattern. M: main stem, ub: upper branch, d: dichotomous branch, pb: primary axillary branch, sb: secondary axillary branch.

Zhu et al. (2021) reported differences in plant morphology, flowers, stem, roots, pods, and seeds between Lingxiyicun (LX, left panel of each subfigure) and Cixidabaican (CX, right panel of each subfigure). (A) Plant morphology at flowering stage, (B) flowers and stems, (C) roots at flowering stage, and (D) whole plant morphology at mature stage. (E) Fresh pods and (F) dried seeds (Fig. 12).



Fig. 12: Differences in plant morphology, flowers, stem, roots, pods, and seeds between Lingxiyicun (LX, left panel of each subfigure) and Cixidabaican (CX, right panel of each subfigure).

(A) Plant morphology at flowering stage, (B) flowers and stems, (C) roots at flowering stage, and (D) whole plant morphology at mature stage. (E) Fresh pods and (F) dried seeds.

39 local faba bean genotypes differing in seed shape, size and color were collected from different areas of Kashmir valley were evaluated during three successive rabi growing seasons of 2019–20, 2020–21 and 2021–22. Data were recorded on ten agro-morphological traits *viz.*, plant height, number of branches/plant, days to 50% flowering, days to 80% maturity, pod length, pod width, number of seeds/pod, pod yield/plant, seed yield/plant and 100-seed weight. Average plant height ranged from 55.8 to 91.3 cm, pod length 5.2 to 9.7 cm, pod width 1.1 to 1.8 cm, seed yield/plant 18.748 to 42.050 g and 100-seed weight 41.118 to 89.966 g. Pod yield/plant evaluated during one year of 2021–22 only ranged from 43.633 to 199.930 g with a mean value of 99.981 g. The results have indicated significant variability in most of these traits. Flattened, medium-sized, beige seeds were more common traits in these faba bean genotypes. Lower mean plant height, number of branches/plant, pod length and seed yield/plant were recorded in 2021–22 than the other two experimental years due to lower rainfall and higher mean temperatures during the active vegetative, flowering and pod filling stages. Principal component and cluster analysis revealed three distinct clusters mainly on the basis of greater agro-morphological similarity. Interestingly, 8 genotypes with the highest individual 100-seed weight were clustered in a separate group with an average 100-seed weight of 83.997 g. Besides, this cluster recorded highest average plant height, pod length, pod width and seed yield/plant as well; all these traits showed significant positive correlations with each other. Therefore, these traits should be considered when selecting faba bean genotypes to improve the region's crop performance (Fig. 13) (Sultan *et al.*, 2023). There is wide genetic variability which has been collected, characterized, and sometimes induced through mutagenesis in *Vicia faba* L. (Duc, 1997). This work use isozyme markers for studying genetic diversity within and among 9 populations of *V. faba* belonging to the three botanical varieties (*major*, *equina* and *minor*) (Table 1). It aims to analyse population structure, gene flow between *major*, *equina* and *minor* varieties and to compare them (Table 1).

Table 1. Common name, origin/pedigree, and botanical class of *Vicia faba* L. populations.

| Populations common name | Origins/pedigree | Botanical class |
|-------------------------|--|-----------------|
| Malti | Local population | <i>Major</i> |
| Batata | Local big seeded landrace collected from Bousalem (Tunisia) | <i>Major</i> |
| Chahbi | S83182-22/New Mammoth x Local Tunisian faba bean variety | <i>Major</i> |
| Super aguadulce | Commercial variety | <i>Equina</i> |
| Aguadulce | Commercial variety | <i>Equina</i> |
| Chemlali | Local population | <i>Equina</i> |
| Badi | Bulk selection from Tunisian POL3 (Tunisian faba bean variety) | <i>Minor</i> |
| Bachaar | FLIP84-59FB (cross S82166) (Tunisian faba bean variety) | <i>Minor</i> |
| Massri | Local small seeded landrace collected from Bousalem (Tunisia) | <i>Minor</i> |



Fig. 13. Representative faba bean (*V. faba*) inflorescences of 39 local genotypes with flowers showing anthocyanin coloration and striations. Note also variability in seed shape, size and color in these genotype

These populations were assayed and scored for nine isozymes loci. 36 seeds from each population were used to study genetic diversity inter and intra-populations. Seven isozyme systems (Sod, 6-Pgd, Me, Est, Skdh, Fdh and Gdh) representing nine loci were used to study the genetic diversity of nine faba bean populations. Seven loci revealed polymorphic bands and showed the same quaternary structure as that found in several species. They revealed a high number of phenotypes. Indeed, from 3 to 9 phenotypes per locus were investigated in this study. The percentage of polymorphic loci ($P = 59.3\%$) was higher than that mentioned in the autogamous species ($P = 20.3\%$) and less than the optimum ($P=96\%$) indicated for allogamous plants. Total genetic diversity (HT) and within population genetic diversity (HS) were estimated with the isozyme markers. The contribution of among population genetic diversity (DST) to total genetic diversity was 22%. Enzyme markers pointed out an average inbreeding level for whole population (FIT) and within population (FIS). Within population genetic diversity represents 78% of total diversity. Intra-population genetic diversity ($HS = 0.206$) was ranged with the respect of allogamous species and was clearly higher than that of among population genetic diversity ($DST = 0.057$) indicating an out-crossing predominance in the studied populations. The expected heterozygosity was higher than that observed heterozygosity at the allogamous species was confirmed in this study. Although, the mean estimated gene flow was less than 1 ($Nm=0.814$), the dendrogram based on Nei's genetic distance of the 9 populations using UPGMA method showed some genetic drift between populations (Ali Ouji *et al.*, 2011). Fortunately, genetic variability of the species is quite large. Based on differences in seed weight, shape, and size, most researchers refer to four botanical varieties: *V. faba paucijuga* (particular shape), *V. faba major* (more than 2.0 g per seed), *V. faba equina* (0.45-1.1 g per seed) and *V. faba minor* (0.2-0.5 g per seed) (Ali Ouji *et al.*, 2011).

Faba beans require long days to flower and mature, with temperatures below 20°C for germination and below 30°C for optimal growth. Although indeterminate in habit, a radiation induced mutation has provided a gene for a determinate growth habit used in the ICARDA and other breeding programs for the 'major' seed types. The seed type classification as described under 'History' is widely accepted as a description of the range in seed size and associated end-use as food or feed. At ICARDA one representative plant per landrace was inbred for at least five generations as a bean pure line (BPL) for much of the faba bean collection. Compared to the initial landrace accessions, the pure lines provided the advantages of ease of maintenance, screening could be undertaken on several plants of the same genotype, the possibility of genetic drift due to inter-crossing among accessions was reduced, specific genotypes could be maintained even if a destructive screening method was used and recessive genes that were hidden by heterozygosity were uncovered. A BPL collection of 840 accessions was field evaluated for 22 discretely scored vegetative, phenologic and seed traits according to IBPGR/ICARDA descriptor lists. All accessions were indeterminate and over 98% had stipule spot pigmentation and no secondary branching. Although 72% were susceptible to lodging, 7.3% were rated as partially resistant due to stiffer straw and with similar height. Leaf size ranged from small (38%), to medium (51%) to large

(11%). There was little variation in flower colour (99.8% white with 99.5% of the wings spotted), with the uniform white colour significant as an indicator of low or zero tannin content which confers higher digestibility for monogastrics. The flower standard was moderately streaked for the majority with variation from no streaks (0.4%) to intensely streaked (12%). Pods were non-shattering for 90% of BPLs and 97% had a matte surface, with mostly (93%) uniform distribution on the stem but 6% with basal distribution. For ease of harvest 43% of BPLs had erect pods, in contrast to 17% pendant. Over 60% of BPLs had dark coloured mature pods, and almost all had plain testa with black hilum (94%). There was variation amongst BPLs in levels of autofertility. The seed was 28% major type, with a range through to the *paucijuga* type, reflecting the preponderance of origins from the Fertile Crescent, North Africa, Ethiopia and Afghanistan. Patterns of trait combinations were associated with BPL origins; low stem pigmentation in Sudan and the Nile valley, a high frequency of small leaves in North Europe which also had the least lodging, erect pods in the Indian subcontinent but pendant in south Europe, and both dark pods and severe lodging in Ethiopia (Redden *et al.*, 2014).

The largest genetic diversity study of faba bean landraces was of 802 landraces and varieties from China, North Africa, Europe and Asia, using ISSR markers. The Chinese landraces were widely separated from a combined grouping of African, European and Asian (outside of China) germplasms which were closely similar though still distinct. Within China there was a major separation of the spring and winter grown landraces which corresponded with northern and southern regions respectively. Spring landraces from the northern group of Shanxi, Hebei, Inner Mongolia and Xinjiang provinces/regions were the most diverse, followed by the European group, and then spring landraces from north west China (Qinghai, Ningxia and Gansu provinces), while a winter group from central China (Hubei, Hunan, Anhui and Jiangsu provinces) was the least diverse. Two of the Chinese winter groups (Sichuan and Guizho provinces) and (Jiangxi and Zhejiang provinces) respectively from medium-low elevation (200 – 1,000m) regions in SW China and SE China, were widely separated from a) the central China group (mainly low (0 – 400m) elevation including the lower reaches of the Yangtze river), and b) from the Yunnan group above 1,500m. These various groupings in China reflect in part selection for adaptation to different crop ecologies. Faba bean landraces/varieties from outside of China were clustered in groups for; north Africa with the Egypt and Sudan accessions the most related; Europe from Turkey to Germany with distinct separation of those from Portugal; Asia from Syria to Afghanistan with distinct separation of those from Japan. Again this is a general eco-geographical separation, indicating a trend for a crop with medium to high levels of out-crossing to evolve a dynamic population in equilibrium with local seasonal conditions provided that sufficient genetic variation is available, thus a degree of local adaptation. An association of diversity across a wide range of geographic origins was also found by Kwon *et al.* (2010), who evaluated a world collection of 151 faba bean landraces and varieties with ‘target region amplified’ (TRAP) markers. Five major groups were identified with a dendrogram I with single entries from France and Nepal II with 13/15 accessions from Afghanistan III with four accessions from China plus one from Afghanistan, IV with 25 European accessions plus three from Nepal and China and two commercial varieties, and V with 101 accessions from China. Wider variation was found in landraces than the advanced breeding line included for comparison in this analysis. Within relatively small geographic regions and relatively small numbers of landraces, associations of genetic diversity with geographic distance of origins may not be found or are weak, with morphology being an unreliable guide to genetic diversity. However when studies include cross-continental sources of landraces and varieties, associations of genetic diversity with geographic diversity tend to be found, especially with spring and winter habits of landraces reflecting the agriculture practices in respective diverse environments and geographic origins (Redden *et al.*, 2014).

The long history of cultivation, the wide distribution across diverse environments, the mating system and responses to human selection have led faba bean to become one of the most variable species, possessing a wide spectrum of variation in plant architecture, leaf size and shape, seed colour, seed shape and size. There is more than 10-fold range of seed sizes among the faba bean accessions (20–250 g/100 seeds). Trait analyses have separated them into three groups: (a) faba bean small-seeded forms in south-western Asia, (b) large-seeded forms in the west and (c) the third group, medium-seeded type is very ancient and can be traced back to Neolithic agriculture. This group is found over a large area, from Spain to the Himalayas. Archaeological findings at Tell El-Kerkh, north-west Syria, indicate a date of origin for faba bean domestication during the late 10th millennium BC. In addition, the 14,000-year-old specimens, discovered in the Mount Carmel region, as the lost ancestor of faba bean. After examining the seed size variation, it was proposed to divide *V. faba* into four sub-species based on seed size: *major* large-seeded type), *equine* (medium-seeded type), *minor* (small-seeded type) and *paucijuga* (small-seeded type). It is considered that the larger seed of faba bean is a result of human selection. The medium-sized type was found in the Iberian Peninsula—both in Portugal and in Spain—as well as Central Europe 5,000 before present (BP). The flattened larger types were not known before 1,500 BP. The first scientific study on genetic variability in faba bean began in 1976 when the natural variability and selection in some local and exotic populations of faba beans were reported. Since then studies on genetic diversity were based on morphological characteristics, isozyme markers of the variation of selected traits in the context of cultivar diversification. The application of DNA-based markers since the mid-1990s offered great opportunity to assess the genetic diversity in faba bean germplasm. Moreover, a global composite collection of 996 accessions established from ICARDA-Aleppo-Syria (499 accessions), INRA-Dijon France (245 accessions) and CSIC-Cordoba-Spain (252 accessions) were evaluated at ICARDA in the spring of 2007 at Tel Hadya as part of the Generation Challenge Program (GCP). Thirty-five polymorphic SSR markers were identified, and 20 were used for diversity analysis. The cluster analysis (Figure 1) indicated two major clusters separating European and African genotypes in two different clusters. Mediterranean genotypes were divided between these two major clusters. ICARDA breeding lines clustered together close to North African, Asian and Mediterranean genotypes. According to the cluster analysis, a subset of 135 faba bean genotypes representing the diversity observed in the total set of 996 accessions was identified. Thus, the major outcomes of this research are the identification of this subset as high diverse reference set and refocusing the ICARDA breeding programme with the development of wider crosses using germplasm from different origins (ICARDA, unpublished results) (Maalouf *et al.*, 2018).

There is a high degree of genetic diversity in the current gene pool. Despite having a close genetic similarity within eco-geographical regions, differences exist across wide geographical regions. For example, accessions from China are markedly different from African, European and Asian counterparts. Within China, the spring sown faba beans were different from the winter sown types and they also differed from other Asian accessions which were close to the African and European accessions. It was later found the Chinese spring accessions resembled more to the African and European accessions than the Chinese winter types. Although four types of faba bean—major, minor, equina and paucijuga, there is no reproductive barrier among them. The paucijuga type is considered as the most primitive extant faba bean lineage (Adhikari *et al.*, 2021). In order to evaluate the level of genetic diversity in a collection of broad bean accessions for the needs of the combinative breeding, a field experiment was carried out during the period 2016-2018, at the Institute of forage crops (Pleven). The studied 17 accessions had different origin: Portugal, Spain, Bulgaria. It was used a randomized block method. Plants were grown under conditions of organic farming, without using fertilizers and pesticides. The results showed considerable differences between the accessions regarding the main quantitative traits. The impact of environmental conditions was well expressed and exceeded the impact of the factor of genotype. The level of genetic variance was lower for the traits of seed weight (6.84%), pods number (9.49%) and 1st pod height (9.77%). The coefficient of genetic variance was higher than the coefficient of phenotypic variance for pod length. In terms of the traits of pod length (84.32%, 1.33), 100 seeds mass (69.08%, 7.87) and 1st pod height (52.76%, 1.26) was found high heritability, coupled with medium to high genetic advance, which is a prerequisite for increasing the productive potential of the broad bean in these traits. Positive correlations were established between seed productivity and all quantitative traits, especially 100 seeds mass ($r = 0.574$), pod length ($r = 0.568$) and plant height ($r = 0.411$). From the breeding point of view, accessions BGE 041470 and Fb 2486, which were distinguished by high values of pods number, seeds number and 100 seeds mass, were of interest. Also, attention deserves to be paid to FbH 14, which formed a large number of pods and seeds per plant, as well as FbH 16, which was characterized by a good balance between the traits of seeds number, seed weight, and 100 seeds mass. These accessions are definitely of interest for hybridization programs and can be recommended as parent components in selection for increased productivity (Kosev and Georgieva, 2023).

A total of 92.43 Gb of sequencing data was obtained in this study, and 133,487 unigene sequences with a total length of 178,152,541 bp were assembled. A total of 5,200 SSR markers were developed on the basis of RNA-Seq analysis. Then, 200 SSR markers were used to evaluate polymorphisms. In total, 103 (51.5%) SSR markers showed significant and repeatable bands between different faba bean varieties. Clustering analysis revealed that 226 faba bean materials were divided into five groups. Genetic diversity analysis revealed that the relationship between different faba beans in China was related, especially in the same region. These results provided a valuable data resource for annotating genes to different categories and developing SSR markers (Hou *et al.*, 2023).

Windsor type beans: Gaint Four seeded green Windsor, Imperial green Windsor and Imperial White Windsor.

Long Pod Type beans: Red Epicure, Masterpiece green long pod, Imperial Whitelong pod, Aquadule Claudin, Imperial Green Long pod.

Local Type beans: Bakla local (selection from local population grown in North Uttar Pradesh).

Synthetic Varieties: these varieties are artificially produced by breeders and are an advanced generation of seed mixture of selected Geno-type, maintained by hybridization in all combinations (Brar *et al.*, 2023).

In order to evaluate the level of genetic diversity in a collection of broad bean accessions for the needs of the combinative breeding, a field experiment was carried out during the period 2016-2018, at the Institute of forage crops (Pleven). The studied 17 accessions had different origin: Portugal, Spain, Bulgaria. It was used a randomized block method. Plants were grown under conditions of organic farming, without using fertilizers and pesticides. The results showed considerable differences between the accessions regarding the main quantitative traits. The impact of environmental conditions was well expressed and exceeded the impact of the factor of genotype. The level of genetic variance was lower for the traits of seed weight (6.84%), pods number (9.49%) and 1st pod height (9.77%). The coefficient of genetic variance was higher than the coefficient of phenotypic variance for pod length. In terms of the traits of pod length (84.32%, 1.33), 100 seeds mass (69.08%, 7.87) and 1st pod height (52.76%, 1.26) was found high heritability, coupled with medium to high genetic advance, which is a prerequisite for increasing the productive potential of the broad bean in these traits. Positive correlations were established between seed productivity and all quantitative traits, especially 100 seeds mass ($r = 0.574$), pod length ($r = 0.568$) and plant height ($r = 0.411$). From the breeding point of view, accessions BGE 041470 and Fb 2486, which were distinguished by high values of pods number, seeds number and 100 seeds mass, were of interest. Also, attention deserves to be paid to FbH 14, which formed a large number of pods and seeds per plant, as well as FbH 16, which was characterized by a good balance between the traits of seeds number, seed weight, and 100 seeds mass. These accessions are definitely of interest for hybridization programs and can be recommended as parent components in selection for increased productivity (Kosev and Georgieva, 2023).

BREEDING

Germplasm: Seed is the basic unit for any agricultural production system without quality seed no one can even think of good harvest. Production of high quality seed of improved varieties having high analytical quality, coupled with high germination capacity, vigour and uniformly large size, is need of hours for improving faba bean culture in this country (Loss, 2006). Greater insight into the pattern and dynamics of genetic resources of Faba bean (*V. faba* L.) is needed in order to understanding and

establishing the relationship among collected germplasm from Bihar region. Plant exploration and collection of germplasm is quickest way to collect modest variability. At present, global collection of faba bean germplasm kept in various seed/field gene bank of respective country is more than 30000 accessions. Characterization and preliminary evaluation is the one of the important technique which helps in to elucidate the extent and pattern of agro-morphological as well as molecular diversity in this crop. The breeding objectives for this crop are grain yield and grain yield stability and lodging resistance, and furthermore resistances against drought (winter frost in case of winter bean breeding), and against fungi and further pathogens and pests, with additional objective of underground root dynamic and grain quality (Singh *et al.*, 2013).

Faba bean germplasm accessions (500) were evaluated for morphologic traits, disease resistance and abiotic stress tolerances. Some accessions from the Chinese provinces Zhejiang, Fujian, Gansu and Sha'anxi were salinity tolerant, consistent with another screening of 504 diverse sources of germplasm in which there were 16 tolerant lines especially from Greece and China, including Zhejiang. In southern China, faba beans sown prior to winter are known as winter types. They are adapted to short mild winters and tolerate temperatures to -5°C , whereas in northern China where there is snow cover through a long winter, only spring types which tolerate temperatures of only $3-5^{\circ}\text{C}$ as seedlings are sown. The differences between these two ecotypes can be characterised by responses to both photoperiod and to temperature which operate independently, with a lower base temperature for growth in the winter types which may have a higher optimum temperature for rate of progress towards flowering. Though both ecotypes require 1,000 degree days for flowering at sub-optimal temperatures, varietal differences in base temperature and in sensitivity to temperature range characterise the geographic range in adaptation of different Chinese faba bean landraces to their respective local environments. In Ethiopia faba landrace variation showed accessions from the north to be closely related with small seed and lower yield, plant height and greater susceptibility to chocolate spot disease, whereas in the south the diversity of morphologies and seed types was greatest and included those with large seed, superior yield and disease resistance. Thus the clustering of land races in Ethiopia did not correspond to geographic diversity of their origins (Redden *et al.*, 2014). Faba bean germplasm of over 38,000 accessions of landraces and varieties is conserved worldwide in at least 43 national genebanks as well as at ICARDA. The size of the collections range from below 100 to 9,000 at ICARDA, exceeding 1,000 in China, Australia, France, Germany, Italy, Russia, Spain, Poland, Morocco and Ethiopia. Although 52% of accessions originated in Europe, the range of habitats may be wider in Ethiopia and China, with cultivation up to 3,000 m altitude (Redden *et al.*, 2014).

Novel germplasm resources are the key to crop breeding, with their genetic diversity and population structure analysis being highly significant for future faba bean breeding. We genotyped 410 global faba bean accessions using the 130K targeted next-generation sequencing (TNGS) genotyping platform, resulting in a total of 38,111 high-quality SNP loci by high-standard filtering. We found the polymorphism information content (PIC) and Nei's gene diversity were 0.0905–0.3750 and 0.0950–0.5000, with averages of 0.2471 and 0.3035, respectively. After evaluating the genetic diversity of 410 accessions using Nei's gene diversity and PIC, on the basis of their geographical origin (continent) and structure-analysis-inferred subpopulations, we found that the faba bean accessions from Asia (except China) and Europe had rich genetic diversity, while those from the winter sowing area of China were low. The 410 faba bean accessions were divided into four subpopulations according to population structure analysis and clustering analysis. However, the same subpopulation contained materials from different geographical origins, thereby indicating that the gene flow or introgression occurred among the accessions. Results from clustering based on shared allele genetic distance indicated that the 410 accessions were divided into three groups according to their dissemination routes. The genetic diversity analysis results demonstrated that the genetic relationships among the faba bean groups with similar ecological environments and geographic origins in neighboring regions or countries were closer and frequently found within the same group, while genetic variation among individuals was the main source of their total genetic variation (Zhang *et al.*, 2023). Gene banks in the world conserve more than 36000 accessions. As a whole, the total production is dominated by local landraces and cultivars, despite a number of improved cultivars which are developed by different national breeding programs. The main reason for the low yields and insufficient production is the sensitivity of landraces and cultivars to biotic and abiotic stress. The fluctuations in the harvested areas and the negative effects of different biotic and abiotic stress have led to a reduction in genetic diversity (Kosev and Georgieva, 2023).

Breeding Objectives: The key breeding objectives in faba bean include improved resistance to biotic and abiotic stress and enhanced seed quality traits. Regarding quality traits, major progress on reduction of vicine-convicine and seed coat tannins, the main anti-nutritional factors limiting faba bean seed usage, have been recently achieved through gene discovery. Genomic resources are relatively less advanced compared with other grain legume species, but significant improvements are underway due to a recent increase in research activities. A number of bi-parental populations have been constructed and mapped for targeted traits in the last decade. Faba bean now benefits from saturated synteny-based genetic maps, along with next-generation sequencing and high-throughput genotyping technologies that are paving the way for marker-assisted selection. Developing a reference genome, and ultimately a pan-genome, will provide a foundational resource for molecular breeding (Khazaei *et al.*, 2021). Fava bean is subject to a long list of biotic stresses, including fungal, bacterial, and viral pathogens, black bean aphid, and the parasitic plant *Orobanche crenata*. Several of these are the targets of resistance breeding programs, as explained by Maalouf *et al.* The most important abiotic stresses of fava bean are heat, drought, waterlogging, salinity, and frost; genetic variation for tolerance to these stresses has been reported. Low levels of vicine and convicine (see 'FAVISM' below), better balance of amino acids for human nutritional needs, and reduced concentrations of seed phytate and protease inhibitors for improved nutrient bioavailability (Byrne, 2023).

The Breeding System: A consequence of the floral biology is that the faba bean is partially inbreeding and partially outbreeding. The more vigorous and high yielding individuals in a population are usually the products of outcrossing.

Outcrossed individuals tend to be more capable of spontaneous autogamy (self-fertilization) than inbreds, which in turn are more reliant on bee visitation for their pollination and which are therefore more likely to produce outcrossed offspring in an open-pollinated (random-mating) population. The mixed breeding system is thus self-perpetuating and tends to be balanced around a level of 35% outcrossed individuals (*see* Bond and Poulsen). The available heterozygosity buffers the population against changing environments while the homozygosity preserves immediate adaptation. The ability of individual flowers to self-fertilize in the absence of tripping is called autofertility. The autofertility of F1 hybrids is said to be the result of hybrid vigour and may partly be due to the increase in number of pollen grains over that found in inbred flowers. The additional mass of pollen overfills the cavity in the keel petal and thus is forced on to the stigma. In contrast, additively inherited autofertility is unchanged by further inbreeding and can be fixed in an inbred line. Its mechanism may involve subtle changes to petal and style morphology together with early release of the stigmatic exudates. The recessive allele of the closed-flower gene (*cf*) is associated with the absence of unfurling of the standard petal and with no production of scent and nectar; these characters largely exclude bees from the flowers--which hence must rely on autofertility. As a result, outcrossing is substantially reduced but not prevented. Either the number of seeds per pod or the number of pods per plant, or both, may be increased by tripping the flowers of partially autofertile genotypes. Within a plant, later flowers are usually more autofertile than their predecessors. Direct evidence showing an increase during a season from 3% to 35% autofertility was obtained in a single inbred line, and there is much supporting circumstantial evidence. The percentage of seeds formed as a consequence of outcrossing declines up the plant. The pattern of this decline probably depends on the pattern of increase in autofertility, which has been shown in conditions of enforced reliance on autofertility to be heritable. In most closed-flower genotypes, and many others with poor autofertility, setting of pods reaches a maximum towards the middle of the plant. The usual interpretation is that autofertility has increased until further pod retention is suppressed by previously set pods. Bee visitation also declines late in the flowering season as the floral display is reduced. Experiments are needed to investigate the contributions of genotype and environment to the changes in autofertility. Drought has recently been found to depress autofertility and, indeed, to cause it to decline with Time (Stoddard and Bond, 1987).

Breeding Methods

Vicia faba L. is a partial allogamous species with outcrossing rates varying from 4% to 84%. The level of cross-fertilization potentially determines the amount of realized heterosis, which increase yield and yield stability and resistance to abiotic stresses. The elevated level of cross-fertilization in faba bean (>0.5) is essential to developing synthetic varieties and improved open population. The suitable option is to develop synthetic varieties using autofertile lines to ensure minimum yield in the absence of insect pollinators and to take advantage of their presence by exploring heterosis to increase yield and yield stability. Some authors have proposed transforming the mating system of faba beans (partial allogamy) towards autogamy and developing inbred lines especially for organic agriculture uniformity and specific adaptability. Selection for high self-fertility degree might represent an important advantage for simplifying the breeding and facilitating the seed production technology. However, it has been difficult to fix a low level of allogamy in faba bean as single plant selection with lower outcrossing rate (*t*) than the average of original population tended to express a higher *t* in the offspring, or vice versa. Faba bean pure lines obtained by pedigree methodology, bulk lines by recurrent selection and synthetic varieties were evaluated at ICARDA from 2013 to 2017 to assess the performance of the different breeding methodologies. Genetic gains per year (%) for grain yield and biological yield were higher in the synthetics (9.3) and recurrent lines (4.3) than the inbred lines (0.5; Figure 2). The yield increase in open pollinated population is mainly due to the exploitation of heterosis. The maximum heterosis is achievable in faba bean hybrids but this is not yet possible at commercial level as stable Cytoplasmic Male Sterility (CMS) systems have not been yet identified as in the case of other legume crops such as mung bean. Hybrid-enabled line profiling (HELP) for self-pollinated crops would help to exploit maximum heterosis and reduce breeding cycles in faba bean (Maalouf *et al.*, 2018).

The principal methods used in the development of virtually all modern faba bean cultivars include mass selection, sophisticated methods of recurrent selection, and conventional methods of cultivar development such as phenotype-based pedigree selection, single-seed descent line breeding, or development of synthetic cultivars (Fig. 14) (Adhikari *et al.*, 2021). For these methods, parental lines are chosen on the basis of their pedigree and their phenotypic attributes.

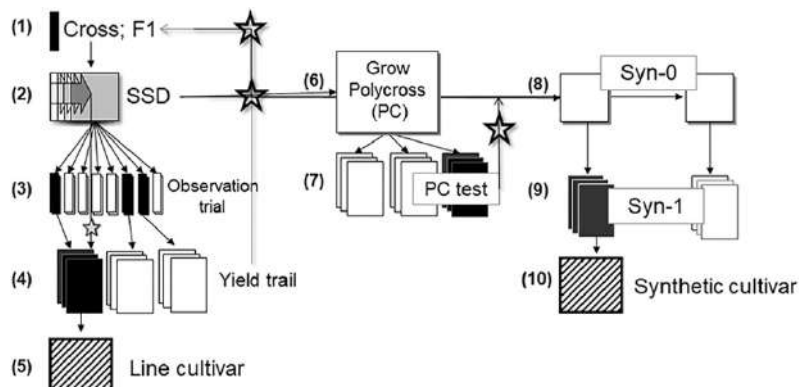


Fig. 14: Phenotypic-based breeding scheme in faba bean. (1) Making crosses, (2) Run SSD (single seed descent) until about F7, (3) Multiply SSD F8 individuals in open field and apply phenotypic selection on *per se* performance, (4) Test open pollinated offspring in replicated yield trials and identify best SSD lines as new crossing parental lines, (5) Identify and multiply the best SSD line(s) and release as a line cultivar or take the best lines as parents for a polycross, (6) Grow a polycross from selected SSD lines, (7) Run yield trial (PC test) and identify offspring of best SSD lines, (8) Grow best-predicted Syn-0 from best SSD lines, (9) Grow and test Syn-1, (10) Identify and multiply best synthetic cultivars. Star symbol indicates that information stems from field trials, seed from maintenance of SSD lines is taken for new crosses, for polycross and for Syn-0, respectively.

Faba bean is a partially allogamous species, and in principle, is amenable to line breeding, population breeding, and hybrid breeding. The degree of outcrossing of faba bean varies widely among genotypes (10–70%) and is highly affected by the environment, including the degree of heat stress (Bishop et al., 2016b), which is one of the major challenges of breeding the crop. Outcrossing is a poorly heritable character and is markedly influenced by the inbreeding coefficient of a genotype and by the type of insect pollinators. Moreover, faba bean genotypes markedly differ in their ability to spontaneously self-fertilize, spontaneous meaning without access of their pollinators, which are primarily honeybees (*Apis mellifera*) and bumblebees (*Bombus hortorum* and other *Bombus* spp.). Thus, a calamity occurs if breeders multiply pure lines under insect-proof enclosures. These genotypes fully depend upon insect pollinators and do not set seed in their absence without mechanical tripping of flowers. Auto fertility is defined as the ability of a plant to self-fertilize and hence set seed without being tripped. Genetic variability for auto fertility has been reported in faba bean, and higher levels of auto fertility were reported in F1 hybrids than in inbred lines. Australian bred cultivars are highly auto fertile as their original genetic resources trace back to ICARDA germplasm that were mostly auto fertile. Furthermore, they are initially grown and selected under insect-proof enclosures. Depending on the level of outcrossing, faba bean breeding may be performed under conditions of controlled selfing in insect-proof cages or, with less control and in case of little outcrossing, based on developing lines under open field conditions (Adhikari et al., 2021).

Hybrid Breeding: Heterozygous F1-hybrids exceed the yield of their homozygous parents by 40 to 70%. Early approaches to hybrid breeding using cytoplasmic male sterility (CMS) system in faba bean trace back to David Bond in Cambridge, UK in 1957 and Pierre Berthelem in Rennes, France in 1967. To date, hybrid breeding is not established in this crop due to instability of the available CMS systems. An alternative to hybrid breeding is developing synthetic cultivars (i.e., a population breeding method). Breeding line cultivars and synthetic cultivars (or composite cultivars) are widely used products for faba bean improvement (Adhikari et al., 2021). There are three major obstacles to faba bean hybrid breeding. First, an operational CMS system must be available. The available CMS systems in faba bean have shown an insufficient level of male sterility. The pollen sterility is not very “deep” and not reliable, and frequent, spontaneous reversion to fertility occur. The second obstacle is the availability of appropriate pollinators. Pollinators often “steal” nectar, removing it without placing pollen on the stigma of the flowers. Pollinator insects, if gathering pollen, learn to avoid the pollen-free mother plants, thus limiting seed set in hybrid seed production. Lastly, the low propagation coefficient of faba bean requires three or more generations of seed increase from the manually tended, single row level of propagation to reach the seed quantity required for certified seed production. Thus, all operational steps and tools for hybrid seed production, including the reliability of the CMS system, must be flawlessly conducted to be successful. Given the lack of CMS and gametocides, breeders have employed monogenic traits to support or realize hybrid seed production. These traits include recessive and dominant nuclear-genetic pollen sterility, testa color, hilum color, cotyledon color, flower color, and other plant morphological characteristics as markers. In addition, even seed size was used, although this is a multigenic trait. Breeders have shown high levels of creativity over the decades for faba bean hybrid breeding but a breakthrough has yet to occur (Adhikari et al., 2021).

Line Breeding: Cultivars released via line breeding undergo strict selection intensity. One (the best) single line is developed into a cultivar, compared to two lines required to produce a hybrid, or more than three lines to develop a synthetic cultivar. Line cultivars can be developed faster than synthetic cultivars, since the latter need lines as components. Line cultivars are more widely accepted based on rules of distinctiveness, uniformity, and stability than synthetic cultivars. The single seed descent (SSD) procedure as proposed in Fig. 1 may be substituted by using F₂-derived lines (i.e., partial bulks) at F₃ or advanced generations to test, select and hence release new cultivars, however, such cultivars can be relatively heterogeneous. This approach is focused on short breeding cycles and relies on high seed multiplication rates. Oftentimes, F₅-derived or F₆-derived lines are chosen as the basis for a new line cultivar and its maintenance breeding. Whichever approach is used for making lines, there is a need to multiply them under controlled self-fertilization or isolation: whether it is to initiate the multiplication as a line cultivar or to enter into the polycross or into a Syn-0 (Fig. 1). The observation trial may be, focusing on synthetic cultivar breeding (see below), arranged as a soft version of a polycross, with several rather than one plant per label and hence a reduced number of replicates; or, as top cross, with few replicates, and with half or less of the area devoted to a joint, constant pollinator genotype. The low propagation coefficient of faba bean limits the breeding and especially the yield testing, compared to other crops. For example, one faba bean plant produces just enough seed for planting a 1 m² of a field plot (about 20–40 seeds). Hence, one individual plant of an SSD pipeline, after controlled self-fertilization, gives just enough seed for a small observation trial; harvesting that plot would give enough seed for a test in about 20 to 40 m² plot. This could be a trial in one location with two replicates; or two locations with one replicate including some checks in an augmented *p*-rep design. A further point in conventional faba bean breeding is to optimize choice of parents. Focusing on line cultivars, basically half of the genetic variance of the breeding germplasm resides between the lines that result from the crosses that—potentially—can be made. The other half of the genetic variance lingers between these crosses, highlighting the importance of choice of parents and therefore, it is of high importance to eliminate entire crosses that promise poorer performing lines than other crosses before investing too much in testing their offspring. Even if several crosses could be rejected as late as the observation trials in step 3, then more plots of the more promising crosses could be tested in step 4. If a pedigree-type of selection is installed, then as early as in generation F₃ and F₄, an observation trial or yield trial would allow to judge the yield potential of the entire cross (i.e., the entire family) and, as described above, eliminate inferior crosses (families). A corresponding marker investment should be made to select between crosses, before making them and after having made them (Adhikari et al., 2021).

Synthetic Breeding: In synthetic breeding, usually four or more founder lines serve as components of a cultivar. The cultivar can, hence, be “re-synthesized” from these lines at any time. Selecting these inbred lines based on their *per se* performance is probably suboptimal because the synthetic population will not be as highly inbred as its components. The purpose of choosing synthetic breeding instead of line breeding is indeed to exploit heterosis as much as possible for agronomic performance, i.e., to

decrease inbreeding. Inbred lines as synthetic components should hence be selected mainly for their so-called varietal ability. This parameter is associated with general combining ability and breeding value. The varietal ability of a candidate line is approximately realized by the performance of its polycross-progeny or top-cross progeny. To assess, in addition to this, the line's *per se* performance, and even more to assess their degree of cross-fertilization and their paternal success, this all might allow to better predict the performance of the potential synthetics. Yet these additional parameters might not be worthwhile; assessing them might not be the optimum allocation of breeders' budget. *Per se* yield of lines and yield of their polycross progenies were correlated and had a genetic correlation coefficient (r_G) = 0.51. It was reported that a slightly higher correlation (r_G = 0.63) between inbred lines and their polycross progenies for yield performance. Due to this, and because only slight corrections can be realized if *per se* performance is available in addition to polycross-progeny data, yield-testing of the lines may not be adequate. Yield testing of the lines themselves is expensive, since seed has to be multiplied under conditions of controlled selfing, whereas seed production for yield testing of progenies (from polycross or from top cross) is cheaper. The terms polycross and top cross need not be taken literally. First, both options may serve a very similar purpose. A top cross may be easier to be conducted than a polycross. The pollinator (tester) of a top cross might be sown in strips, such as with 50% or less of the field area, the candidates would mainly cross-pollinate with the common pollinator, according to their individual extent of outcrossing. The discrepancy between the line's *per se* performance and the performance of their open pollinated offspring (polycross-progenies; top cross-progenies) is caused by several reasons (beyond the deviations of randomness in the outcrossing that may come from compromises in the experimental and field lay-out; from pollinator behavior; from differences in paternal outcrossing success of the lines. The major source of this discrepancy is General combining ability, which is a component of the polycross/top cross progenies' performance, and this is line-specific. The same applies for the degree of self-fertilization of the candidate lines and the paternal outcrossing success. Consequently, the level of inbreeding and actual composition of the progenies is line-specific. Yet, and moreover, the seed for inbred lines is produced in cages, seed for open-pollinated progenies is produced in open field, hence in different environmental conditions. Thus, when comparing performance of lines with that of their open-field derived progenies, seed size and seed quality and thus the resulting cropstands are expected to differ for non-genetic reasons (Adhikari *et al.*, 2021).

Mutagenesis: Novel mutations on certain faba bean genes will enrich its diversity for breeding. Such mutants may be induced by chemical mutagenesis or irradiation. Physical (*e.g.*, gamma-ray) and chemical (*e.g.*, ethyl methane sulphonate-EMS) mutagens have demonstrated their usefulness in faba bean mutation induction. Ion beam irradiation has also been reported as an effective and unique technique for inducing mutations in faba bean. The first mutagenesis on faba bean was reported with the description of determinate mutants, *ti1* and *ti2* which significantly reduced the number of flowering nodes giving the plant type as "topless." A dwarf mutant was reported, *dw1*, which reduced the internode length by almost 50%. A gene for reduced vicine-convicine content, *ver*, and five nodulation mutants through EMS mutagen where one of them was a super modulating mutant (*f32*) giving 3-5 times more nodules than the normal type. A detailed description of 265 varieties developed through induced mutation on grain legumes including 13 in faba bean genotypes was reported. A number of imazapyr resistance mutations through EMS were identified in South Australia that resulted in the development of the first imidazolinone herbicide resistant variety, PBA Bendoc in Australia. Recently morphological diversity of faba bean mutant populations was explored. A number of mutation breeding projects across the world have proven the efficiency of mutagenesis in grain legumes to broadening the genetic variation. Seeking mutants that increase resistance against the root parasitic weeds broomrape and stem parasitic dodders, both being increasingly a problem in the Mediterranean basin, will promote faba bean production in this region; resistance of faba bean against herbicides that control these weeds would especially be useful and is a sought-for trait. Similarly, mutants that decrease pod wall thickness will increase grain yield. Inbred lines harboring new diversity such as increased resistance or improved quality, accruing from recombination-fueled transgression or from mutagenesis may be used. Currently 20 faba bean mutant varieties have been developed from various countries which are listed at IAEA mutant variety database that might be used in breeding programs. Mutagenesis combined with biotechnology tools may accelerate releasing novel faba bean germplasm and improved cultivars (Adhikari *et al.*, 2021).

Speed Breeding: Speed breeding to shorten breeding cycles is a must have tool in any breeding programs for the purpose of increasing genetic gains per year. Significant progress has been made toward shortening the reproductive cycle and hence the overall process of cultivar development (see below) as a tool for accelerating the breeding of pulse crops. Up to seven generations/year can be obtained in chickpea without applications of chemical treatment. Recently an *in vivo* speed breeding protocol, for the first time, for faba bean has been reported. This can be a valuable tool for developing diverse germplasm and improved cultivars in a relatively short time span. They reported that application of cytokinin or cold treatment could increase pollen viability and seed setting, thus consequently decreasing the length of the breeding cycle in faba bean by 22 days from seed to seed. Additional reduction in faba bean generation time as part of a reliable speed breeding protocol may be obtained by implementing accelerated faba bean development to the flowering stage by regulating light and temperature. Recently, this has been achieved in Australia where five generations per year can be obtained. Speed breeding can accelerate development of faba bean lines and may be integrated with other cutting-edge breeding tools such as marker assisted breeding and genomic selection based on estimated breeding values. However, due to the tiny amount of seed produced on a typical speed-bred plant and the expense of maintaining controlled environments, speed breeding protocols are only suited to the primary cross/backcross and inbreeding generations of a breeding scheme, pending further research to extend the applications of speed breeding. All steps toward phenotyping of agronomic performance rely on considerable seed increase, probably in open pollination conditions. Phenotypic evaluations must eventually be carried out under "natural" conditions (Adhikari *et al.*, 2021).

Molecular Markers Biotechnology: Faba bean suffers from several major biotic and abiotic factors that constrain productivity. Although significant genetic gain to overcome these constraints has been made through conventional selection and breeding efforts, progress through the use of genomics and associated biotechnologies is limited. This is due mainly to the large genome size (13GB), which is approximately 25 times larger than that of the model legume *Medicago truncatula*, and 2.5 times larger than

Pisum sativum, together with a lack of financial investment in this crop species. Most recently, a library with 125,559 putative SSR sequences was constructed and characterized for repeat type and length from a mixed genome of 247 spring and winter sown faba bean genotypes using the Roche 454 GS FLX Titanium Platform sequencing. A suite of 28,503 available primer pair sequences were designed and 150 were randomly selected for validation. Of these, 94 produced reproducible amplicons that were polymorphic among 32 faba bean genotypes selected from diverse geographical locations. The validation by UPGMA cluster analysis of 32 genotypes based on Nei's genetic distance, showed high quality and effectiveness of those novel SSR markers developed via next generation sequencing technology. Large scale SSR marker development was successfully achieved using next generation sequencing of the *V. faba* genome. These novel markers are valuable for constructing genetic linkage maps, future QTL mapping, and marker-assisted trait selection in faba bean breeding efforts (Redden *et al.*, 2014).

Breeding for Abiotic Stresses: Heat, drought, frost and water logging are major abiotic stresses affecting the faba bean productivity. While the first two factors affect the crop globally, the latter two are ecologically and geographically specific to local environments. Water logging is a problem in limited geographical areas such as the high rainfall regions that are dominated by vertisols in Ethiopia, and the irrigated Nile River basin in Egypt. The effect of frost on vegetative growth has been widely studied in Europe. Research on the effect of frost on the reproductive structures is not reported, as the crop in that region flowers when frost does not occur. However, this could be a future problem as the crop expands to northern latitude in continental climates. Furthermore, tolerance to seedling frost is not related to frost after flowering. Several accessions with superior frost tolerance were identified, such as Côte d'Or, Hiverna, ILB3187, ILB2999, ILB14, ILB345. Heat stress in faba bean during the vegetative period can retard plant growth and development, but it is particularly harmful at the reproductive stage, causing reduction in pollen growth and viability that results in significant yield loss. Extreme heat is the major threat to faba bean production in southern Egypt, Sudan, the Ethiopian lowlands, and in northern New South Wales and southern Queensland in Australia. Research conducted under high temperatures (above 35°C) have identified some heat tolerant genotypes, but wider testing for confirmation is still needed. Low rainfall and variable soil moisture in dry areas are the major reasons for low and unstable grain yield of faba bean, especially where the crop is grown under rain fed conditions in the Mediterranean basin, East and North Africa, West Asia and Australia. Drought reduces pollen viability and germination, but recent findings showed the female reproductive tissue was more sensitive to drought than the male part. Development of early maturing cultivars has been a breeding strategy to escape terminal drought. Although genotypic variation for drought tolerance has been documented underlying mechanisms and selection methods for screening germplasm are not fully developed, thereby slowing the progress toward drought-tolerant cultivars. However, some characteristics, such as leaf-level carbon isotope discrimination, stomatal conductance and canopy temperature can be used as selection criteria for drought tolerance in faba bean and can be used for screening large sets of germplasm for drought tolerance under field trials. Soil acidity is among the common problems limiting faba bean production in Ethiopia. It is associated with toxicities of hydrogen ion, aluminum, and manganese, and deficiency of calcium, molybdenum and phosphorus in the soil. Soil acidity also adversely affects survival, growth and nitrogen-fixation efficiency of *Rhizobia*. Generally, *Rhizobium* strains vary markedly in their acid tolerance and ability to modulate on acid soils and some acid tolerant *Rhizobium* strains have been identified, but a higher acid tolerance of the bacteria does not mean a better symbiotic performance under acidic conditions. Therefore, both acid tolerance and symbiotic effectiveness are needed to improve nitrogen fixation, but these traits are not necessarily linked (Adhikari *et al.*, 2021). Faba bean has the highest yield potential among cool season pulse crops, but yield stability is low compared to other winter crops. Much of the low yield stability can be attributed to abiotic constraints such as cold, heat and drought at any stage of plant development, but the flowering stage is particularly vulnerable to adverse conditions (Redden *et al.*, 2014).

Heat stress: Faba beans produce an abundance of flowers and the number that is retained and develops into pods is influenced by a number of environmental factors. These include partitioning of assimilates between the shoot tip and flowers, with cold and overcast conditions at the time of flowering resulting in reduced photosynthesis and reduced pod set, moisture stress. Faba bean is sensitive to high temperature during the reproductive stage and temperature above 23 °C can lead to the termination of flowering (Redden *et al.*, 2014).

Drought stress: Faba bean is relatively intolerant of drought, and temporary moisture stress can occur at any stage of development while terminal drought occurs during the reproductive stage of development. Physiological responses to moisture stress include stomatal closure which enables the plants water status to be maintained. Genetic variation in stomatal conductance among eight faba bean genotypes was reported, with drought avoiding accessions having lower $\Delta^{13}\text{C}$ than a drought-sensitive line. Leaf temperature, as measured by infrared thermometer, was positively correlated with transpiration efficiency and negatively correlated with stomatal conductance and $\Delta^{13}\text{C}$, indicating that leaf temperature might be simple parameter to measure as an indicator of water use. The impact of terminal drought can be minimised via drought escape by developing early flowering faba bean varieties with the reproductive stage completed prior to the onset of drought. However, drought escape is not suitable for managing transient drought during earlier stages of development (Redden *et al.*, 2014).

Winter hardiness : Faba bean is sown in winter in areas of Europe where winters are mild and young plants are able to survive the winter. Crops sown at this time utilise moisture in winter, flower and mature earlier than spring sown crops, thereby reducing exposure to summer drought, and have higher yield potential. An increase in level of winter hardiness to reduce the likelihood of winter kill would increase the potential extent of this type of variety. At present there are limited sources of tolerance to winter hardiness, with the old variety Côte 'Or being the most tolerant line identified, while several other genotypes that can withstand temperatures to -14 °C or lower were reported by Olszewski . Several physiological processes are involved in determining winter hardiness, including (i) vernalisation to ensure plants do not flower until they have been exposed to a sufficiently long period of cold and thereby avoid flowering during winter, and (ii) hardening which occurs as plants are exposed to a prolonged period of low

but non-freezing temperatures prior to extreme cold. Hardening involves changes in the plant cell membrane such as changes in lipid composition and accumulation of proline that protect the cell against freezing. Breeding for winter hardiness requires combining of both processes, and also tolerance to excess moisture that might occur during winter and fungal diseases such as Ascochyta blight that infect winter beans to a greater extent than spring beans (Redden *et al.*, 2014).

Water logging: Faba bean is adapted to heavy texture, often poorly drained soils, sometimes with irrigation, and these situations can result in waterlogging or soil oxygen deficiency. While management of water application and drainage can reduce waterlogging in irrigated situations, identification of varieties tolerant to waterlogging would have wide application. In a comparison of seven grain legume species, faba bean to be more tolerant to waterlogging than six other species on the basis of root and shoot growth in comparison to a control. Variation was also identified among six faba bean genotypes and Acc794 (origin Afghanistan) was significantly more tolerant than the other genotypes and was the only genotype capable of maintaining root growth after the waterlogged treatment (Redden *et al.*, 2014). The comprehensive knowledge collected in the scientific community during the last 30 years has permitted major advances in faba bean breeding. These include control of major biotic and abiotic stresses, and diverse seed quality aspects. Biotechnology approaches have been developed with this species and complex breeding schemes that employ male sterility to increase outcrossing have been proposed (Duc, 1997).

Varieties

There are three main varieties of Broad beans such as Longpod, Windsor varieties and Dwarf varieties (Sylvia, 2017). Several exotic varieties are introduced from abroad in India which are as follow (Brar *et al.*, 2023):

Throw's MS: first synthetic Broad bean grown in UK.

Maris Beagle: another synthetic UK based variety released in 1974 composed of five inbred lines.

Soravi and Avrisso: Synthetic varieties were released in France by international cooperation between National Institute for Agricultural Research (INRA-France) and Plant Breeding Institute of Cambridge (UK). Now most of the North European Broad beans are synthetic variety.

Pusa Sumeet: plant are tall bearing 70-80 cm height and branches approx. 8-10 branches per plant, bearing 90-100 pods. The pod thickness and length are 1.3 cm and 6 cm respectively. They are grown in cluster and it has attractive dark green colour with average potential yield of 170-180 q/ha. Other varieties like Selection BR-1 and Selection BR-2, black-coloured and yellow-coloured seeded varieties developed in Bihar state. "Jawahar Vicia 73-81" variety also reported from Madhya Pradesh.

USES

Cultivated faba bean is used as human food in developing countries and as animal feed, mainly for pigs, horses, poultry and pigeons in industrialized countries. It can be used as a vegetable, green or dried, fresh or canned. It is a common breakfast food in the Middle East, Mediterranean region, China and Ethiopia. The most popular dishes of faba bean are Medamis (stewed beans), Falafel (deep fried cotyledon paste with some vegetables and spices), Bissara (cotyledon paste poured onto plates) and Nabet soup (boiled germinated beans). Feeding value of faba bean is high, and is considered in some areas to be superior to field peas or other legumes. It is one of the most important winter crops for human consumption in the Middle East. Faba bean has been considered as a meat extender or substitute and as a skim-milk substitute. Sometimes grown for green manure, but more generally for stock feed. Large-seeded cultivars are used as vegetable. Roasted seeds are eaten like peanuts in India. Straw from faba bean harvest fetches a premium in Egypt and Sudan and is considered as a cash crop. The straw can also be used for brick making and as a fuel in parts of Sudan and Ethiopia. *V. faba* has a diploid (2n) chromosome number of 12, meaning that each cell in the plant has 12 chromosomes (6 homologous pairs). Five pairs are acrocentric chromosomes and 1 pair is metacentric (Singh *et al.*, 2013).

In ancient Greece and Rome, beans were used in voting; a white bean being used to cast a *yes* vote, and a black bean for *no*. Pythagoras called on his disciples to abstain from beans. It is, however, uncertain whether they were meant to abstain from eating beans or from involving themselves in politics. In Ubykh culture, throwing beans on the ground and interpreting the pattern in which they fall was a common method of divination (favomancy), and the word for "bean-thrower" in that language has become a generic term for seers and soothsayers in general. In Italy, broad beans are traditionally sown on November 2, All Souls Day. Small cakes made in the shape of broad beans (though not of them) are known as *fave dei morti* or "beans of the dead". According to tradition, Sicily once experienced a failure of all crops other than the beans; the beans kept the population from starvation, and thanks were given to Saint Joseph. In ancient Greece and Rome, beans were used as a food for the dead, such as during the annual Lemuria festival. *V. faba* has a diploid (2n) chromosome number of 12, meaning that each cell in the plant has 12 chromosomes (6 homologous pairs). Five pairs are acrocentric chromosomes and 1 pair is metacentric (Singh *et al.*, 2013).

Potential use of fava bean is in the treatment of Parkinson's disease being a good source of levadopa (*L*-dopa) a precursor of dopamine, as a result of Parkinson's disease affected persons unable to synthesize dopamine which regulate motor cells. *L*-dopa is also a natriuretic agent, which might help in controlling hypertension. Some also use fava beans as a natural alternative to drugs like Viagra, citing a link between *L*-dopa production and the human libido. The elders generally restrict the young children from eating them raw (when unmaturing) because they can cause constipation and jaundice-like symptoms. There are epidemiological and *in vitro* studies which suggest that the hemolysis resulting from *favism* acts as protection from malaria, because certain species

of malarial protozoa such as *Plasmodium falciparum* are very sensitive to oxidative damage due to deficiency of *glucose 6-phosphate dehydrogenase* enzyme, which would otherwise protect from oxidative damage via production of glutathione reductase (Singh *et al.*, 2013). The fresh beans are taken boiled or steamed. The leafy top shoots can be steamed. The small beans are consumed whole in the pods. It can be used fresh, canned, dried or substitute for skim-milk and meat. The large beans are added to soups, stews and dishes of poultry, lamb and seafood. Fresh broad beans can be served as appetizers and blended into spreads (Sylvia, 2017). The seeds are eaten at all stages, from small, tender green beans to mature dried seeds. Pods and all can be eaten at the very youngest stage. Some authors recommend removing the outer seed coat from fresh beans, but others say that is an unnecessary step. However, the seed coats should be removed from dried beans after soaking overnight. Fava beans are prepared in a variety of ways: steamed, boiled, pureed, roasted, and in soups, tofu, and Egyptian-style falafel. In addition to culinary uses, the species is grown for animal feed and forage and as a cover crop to reduce erosion and add nitrogen to the soil (Byrne, 2023).

Broad beans are generally eaten while still young and tender, enabling harvesting to begin as early as the middle of spring for plants started under glass or overwintered in a protected location, but even the main crop sown in early spring will be ready from mid to late summer. Horse beans, left to mature fully, are usually harvested in the late autumn, and are then eaten as a pulse. The immature pods are also cooked and eaten, and the young leaves of the plant can also be eaten, either raw or cooked as a pot herb (like spinach). Preparing broad beans involves first removing the beans from their pods, then steaming or boiling the beans, either whole or after parboiling them to loosen their exterior coating, which is then removed. The beans can be fried, causing the skin to split open, and then salted and/or spiced to produce a savory, crunchy snack. In India, fava beans are eaten in the Northeastern state of Manipur. They are locally known as *hawai-amubi* and are ingredients in the dish *eromba* (Wikipedia, 2024).

Broad bean is cultivated for both animal and human consumption, soil development, and medicinal uses. It can be served fresh, dried, canned, or as a substitute for meat and skim-milk. Broad bean is often used as either forage (leaves, plant material) or silage (fermented, high-moisture fodder) for animals. Using broad bean as a spring cover crop allows for protection against erosion, and can be tilled back into the soil as green manure. The taproot also has the added benefit of being able to break-up hard compacted soil (PV, 2024).

Toxicity: Beans generally contain phytohaemagglutinin, a lectin that occurs naturally in plants, animals, and humans. Most of the relatively low toxin concentrations found in *V. faba* can be destroyed by boiling the beans for 10 minutes. Broad beans are rich in levodopa, and should thus be avoided by those taking irreversible monoamine oxidase inhibitors to prevent a pressor response (Wikipedia, 2024).

Genetic predisposition: Sufferers of favism must avoid broad beans, as they contain the alkaloid glycoside vicine which may initiate a hemolytic crisis. A low-content vicine-convicine faba bean line was identified in the 1980s and the trait has been introduced into several modern cultivars. Low vicine-convicine faba beans are safe for consumption by G6PD-deficient individuals. As of 2019, a molecular marker may be used for marker-assisted breeding to reduce levels of vicine-convicine in fava beans (Wikipedia, 2024).

Precautions (Sylvia, 2017):

- Those having G6PD should avoid raw Broad beans which causes favism which is harmful. Others should consume the raw Broad beans in small amounts.
- Those who intake monoamine oxidase (MAO) inhibitors should also avoid Broad beans it contains high tyramine content.
- The symptoms which might be experienced with an intake of Broad beans are dizziness, bloody urine, jaundice and vomiting.
- Its green pods and pollens cause some time allergy to people and also some time illness causes fatal, known as "Favism".

NUTRITION VALUE

Broad bean is an important leguminous crop worldwide because of its nutrient-rich seeds. It is extensively used as a legume, a vegetable and as fodder. In China, broad bean is widely cultivated in Sichuan, Yunnan, Guizhou, Hunan, Hubei, Jiangsu, Zhejiang and Qinghai provinces and the planting area and total production account for 53% and 61% of those worldwide, respectively. Therefore, increases in the seed yield of broad bean will result in greater economic profits and a larger food supply (Li and Yang, 2014). Apart from their taste, it is rich in protein and fiber content. In 100 grams, Broad beans supply 62 calories and are 7.77% carbohydrates, 1.43% total fat and 9.60% protein. Broad beans are exceptional source of nutrients, providing in a 100 gram serving dietary fiber (9.47%), iron (18.75%), manganese (11.35%), phosphorus (10.43%), and vitamins such as folate (14.50%) (Sylvia, 2017). Nutritional value of broad beans is given in Table 2 (Sylvia, 2017).

Fava beans are a very nutritious food, containing 18-35% protein, high levels of folate, iron, manganese, magnesium, and phosphorus and a variety of other health-promoting compounds (Byrne, 2023). Fava bean is rich in minerals, vitamins, carbohydrate and protein.

**Table 2: Nutritional value of Broad beans Serving Size: 1 Cup, 100 g
Calories 62 Kcal. Calories from Fat 4.5 Kcal**

| Proximity | Amount | % DV |
|---------------------|---------------|-------------|
| Water | 83.7 g | N/D |
| Energy | 62 Kcal | N/D |
| Energy | 259 kJ | N/D |
| Protein | 4.8 g | 9.60% |
| Total Fat (lipid) | 0.5 g | 1.43% |
| Ash | 0.9 g | N/D |
| Carbohydrate | 10.1 g | 7.77% |
| Total dietary Fiber | 3.6 g | 9.47% |
| Minerals | Amount | % DV |
| Iron, Fe | 1.5 mg | 18.75% |
| Manganese, Mn | 0.261 mg | 11.35% |
| Phosphorus, P | 73 mg | 10.43% |
| Magnesium, Mg | 31 mg | 7.38% |
| Copper, Cu | 0.06 mg | 6.67% |
| Zinc, Zn | 0.47 mg | 4.27% |
| Potassium, K | 193 mg | 4.11% |
| Sodium, Na | 41 mg | 2.73% |
| Selenium, Se | 1 µg | 1.82% |
| Calcium, Ca | 18 mg | 1.80% |

| Vitamins | Amount | % DV |
|---|---------------|-------------|
| Water soluble Vitamins | | |
| Vitamin B9 (Folate, Folic acid) | 58 µg | 14.50% |
| Vitamin B1 (Thiamin) | 0.128 mg | 10.67% |
| Vitamin B3 (Niacin) | 1.2 mg | 7.50% |
| Vitamin B2 (Riboflavin) | 0.09 mg | 6.92% |
| Vitamin B6 (Pyridoxine) | 0.029 mg | 2.23% |
| Vitamin B5 (Pantothenic acid) | 0.066 mg | 1.32% |
| Vitamin C (Ascorbic acid) | 19.8 mg | 22.00% |
| Fat soluble Vitamins | | |
| Vitamin A | 14 µg | 2.00% |
| Lipids | Amount | % DV |
| Fatty acids, total saturated | 0.142 g | 0.22% |
| Fatty acids, total polyunsaturated | 0.303 g | 1.78% |
| Palmitic acid 16:00 (Hexadecanoic acid) | 0.121 g | N/D |
| Stearic acid 18:00 (Octadecanoic acid) | 0.02 g | N/D |
| Fatty acids, total monounsaturated | 0.02 g | N/D |
| Oleic acid 18:1 (octadecenoic acid) | 0.02 g | N/D |
| Linoleic acid 18:2 (octadecadienoic acid) | 0.121 g | N/D |
| Linolenic acid 18:3 (Octadecatrienoic acid) | 0.182 g | N/D |

| Lipids | Amount | % DV |
|---------------|---------|--------|
| Isoleucine | 0.215 g | 12.86% |
| Valine | 0.235 g | 11.13% |
| Tryptophan | 0.048 g | 10.91% |
| Threonine | 0.178 g | 10.11% |
| Leucine | 0.37 g | 10.01% |
| Lysine | 0.313 g | 9.36% |
| Histidine | 0.115 g | 9.33% |
| Phenylalanine | 0.195 g | 6.71% |
| Methionine | 0.037 g | 2.21% |
| Cystine | 0.066 g | N/D |
| Tyrosine | 0.168 g | N/D |
| Arginine | 0.397 g | N/D |
| Alanine | 0.195 g | N/D |
| Aspartic acid | 0.541 g | N/D |
| Glutamic acid | 0.733 g | N/D |
| Glycine | 0.197 g | N/D |
| Proline | 0.216 g | N/D |
| Serine | 0.21 g | N/D |

| Flavonoids | Amount | % DV |
|----------------------|--------|------|
| Flavan-3-ols | | |
| (+)-Catechin | 8.2 mg | N/D |
| (-)-Epigallocatechin | 4.6 mg | N/D |
| (-)-Epicatechin | 7.8 mg | N/D |

*Above mentioned Percent Daily Values (%DVs) are based on 2,000 calorie diet intake. Daily values (DVs) may be different depending upon your daily calorie needs. Mentioned values are recommended by a U.S. Department of Agriculture. They are not healthbenefitstimes.com recommendations. Calculations are based on average age of 19 to 50 years and weighs 194 lbs (Sylvia, 2017).

Due to member of Leguminosae, are able to fix atmospheric nitrogen (Brar *et al.*, 2023). Pods are generally gluten free food, green and tender, shelled green beans are consumed singly or mixed with potatoes, mixed pickles and even boiled seeds are also consumed by sprinkling salt and black pepper powder. Edible part of Broad Bean contains calories 48, moisture 85.4 g, calcium 50 mg, ascorbic acid 12 mg, carbohydrate 7.2 g, protein 4.5 g, iron 1.4 mg, fat 0.1 g, thiamine 0.08 mg, vitaminA 14 I.U. per 100 g (Brar *et al.*, 2023).

Nutritional value of *Vicia faba* (Agric 4 Profits, 2023).

- **Nutritional Content:** *Vicia faba* is valued for its rich nutritional profile. The seeds, in particular, are an excellent source of protein, fiber, and essential vitamins and minerals. They contribute to a well-rounded and nutritious diet.
- **Protein Content:** One of the standout features of *Vicia faba* is its high protein content. The seeds contain a significant amount of plant-based protein, making them a valuable protein source for vegetarians and vegans.
- **Carbohydrates and Dietary Fiber:** Broad beans are also rich in carbohydrates, providing a sustainable energy source. Additionally, the dietary fiber content supports digestive health and helps regulate blood sugar levels.
- **Vitamins:** *Vicia faba* contains essential vitamins, including B vitamins such as folate, thiamine, and vitamin B6. These vitamins play key roles in energy metabolism and overall well-being.
- **Minerals:** The seeds of *Vicia faba* are a good source of minerals such as iron, magnesium, phosphorus, and zinc. These minerals contribute to various physiological functions, including bone health and immune system support.
- **Antioxidant Compounds:** Broad beans contain antioxidant compounds, including flavonoids and polyphenols. These antioxidants help neutralize free radicals in the body, offering potential health benefits.
- **Phytochemicals:** *Vicia faba* contains various phytochemicals, including saponins and lectins. These compounds may have protective effects and are of interest in ongoing research into their potential health-promoting properties.
- **Nutrient Density:** The overall nutrient density of *Vicia faba* makes it a valuable addition to a balanced diet. Incorporating broad beans provides an array of essential nutrients that contribute to overall health and well-being.
- **Culinary Uses:** The chemical composition of *Vicia faba* extends to its culinary versatility. Broad beans are used in various dishes, including soups, stews, salads, and spreads. They add both nutritional value and a distinct flavor to recipes.
- **Potential Health Benefits:** While enjoying *Vicia faba* as a part of a balanced diet, individuals may experience various health benefits. These may include improved protein intake, enhanced digestive health, and the intake of essential vitamins and minerals. Additionally, the antioxidant and anti-inflammatory properties found in the chemical composition of *Vicia faba* contribute to its potential positive impact on overall health.

Table 3. Fava beans, mature seeds, raw (Wikipedia, 2024)

| Nutritional value per 100 g (3.5 oz) | |
|--------------------------------------|----------------------------------|
| Energy | 340 kcal (1,400 kJ) |
| Carbohydrates | 58.29 g |
| Dietary fiber | 25 g |
| Fat | 1.53 g |
| Protein | 26.12 g |
| Vitamins | Quantity; %DV[†] |
| Thiamine (B1) | 46%; 0.555 mg |
| Riboflavin (B2) | 26%; 0.333 mg |
| Niacin (B3) | 18%; 2.832 mg |
| Vitamin B6 | 22%; 0.366 mg |
| Folate (B9) | 106%; 423 µg |
| Vitamin C | 2%; 1.4 mg |
| Vitamin K | 8%; 9 µg |
| Minerals | Quantity; %DV[†] |
| Calcium | 8%; 103 mg |
| Copper | 92%; 0.824 mg |
| Iron | 37%; 6.7 mg |
| Magnesium | 46%; 192 mg |
| Manganese | 71%; 1.626 mg |
| Phosphorus | 34%; 421 mg |
| Potassium | 35%; 1062 mg |
| Selenium | 15%; 8.2 µg |
| Sodium | 1%; 13 mg |
| Zinc | 29%; 3.14 mg |
| Other constituents | Quantity |
| Water | 11 g |

As with other beans, broad beans are rich in protein and provide moderate amounts of iron, thiamin, and riboflavin. Ingestion of broad beans can cause acute hemolytic anemia in people with favism, a genetic disorder (Petruzzello, 2024). Nutritional value of fava beans, mature seeds, raw is given in Table 3 (Wikipedia, 2024). Raw mature fava beans are 11% water, 58% carbohydrates, 26% protein, and 2% fat. A 100-gram reference amount supplies 1,425 kJ (341 kcal; 341 Cal) of food energy and numerous essential nutrients in high content (20% or more of the Daily Value, DV). Folate (106% DV), and dietary minerals, such as manganese, phosphorus, magnesium, and iron (range of 52 to 77% DV), have considerable content. B vitamins have moderate to rich content (19 to 48% DV).

Fava beans present the highest protein-to-carbohydrate ratio among other popular pulse crops, such as chickpea, pea and lentil. Moreover, their consumption is recommended along with cereals as both foods are complementary in supplying all essential amino acids (Wikipedia, 2024).

HEALTH BENEFITS

Broad beans are loaded with nutrition which provides enormous health benefits. They possess high amount of fiber and protein. Broad beans possess an amino acid known as L-dopa that enhances brain to make dopamine which is a chemical substance used to treat Parkinson's disease. The cholesterol is absent in Broad beans with low fat and calories (Sylvia, 2017):

Enhance immunity: Vitamin C promotes the white blood cells production and assists in the functioning of these immune cells. Vitamin C is an antioxidant which prevents the oxidative damage and helps in the functioning of white blood cells. It is also believed that Vitamin C enhances the immune system, assist to counteract the colds and prevent illness.

Anemia prevention: Anemia is the result of the low hemoglobin and red blood cells. It results to the poor functioning of the brain to reduce immunity due to the low energy levels. It is estimated that half of the anemia cases is caused due to the low presence of iron and others are caused by the genetic factors. Broad beans provide 1.5 mg of iron which helps to treat as well as prevent anemia.

Prevents cancer: The damage of DNA is the cause of cancer. As Vitamin B9 helps in the reproduction of DNA, it forbids the damage of DNA and helps to replicate the damaged cells. The low presence of Vitamin B9 is related to the high chances of breast, brain, cervical, colon and lung cancer. Since Broad beans provide an adequate amount of Vitamin B9, it should be added to the diet.

Eliminates free radicals: Manganese provides an antioxidant properties which helps to remove the free radicals from the human body. The free radicals results in cells damage that leads to cancer and other diseases. So addition of manganese rich foods such as Broad beans helps to prevent the chances of health ailments.

Prevents osteoporosis: Manganese helps to cure osteoarthritis syndrome and osteoporosis as it adds density to the minerals and bones. It is an essential element for the development and repair of bones. Further research is still needed on the mechanisms and roles of manganese on the human body.

Improves sleep: The evidence shows that tryptophan provides the sedative effect that helps to provide the sound sleep. It also assists to promote overall health. Lack of sleep is the cause for reduction in memory, concentration, depression, weight gain, muscle aches and others. Tryptophan is an aid for the problems related to insomnia or sleep apnea without side effects.

Eye health: The research shows that thiamine has the ability to prevent the eye ailments such as glaucoma and cataracts. This is possible as it influence the signals of nerves and muscles which are essential in transmitting the information from eyes to brain.

Prevents tooth decay: Phosphorus helps to maintain the health of the gums and teeth. Vitamin D, Calcium and Phosphorus is essential to maintain the dental health. It supports the tooth enamel, holds the teeth, mineral density of jaw-bone. These vitamins and minerals assist to treat the tooth decay. Vitamin D with phosphorus is essential to balance the calcium in the body and enhance its absorption during the formation of tooth. Vitamin D reduces the gum inflammation related to periodontal gum disease.

Reduce stroke: The study shows that the people having high amount of Vitamin C in the blood, their risk of stroke was reduced by 42%. The addition of fruits and vegetables rich in Vitamin C reduce the chances of having stroke.

Brain health: The function of brain relies upon the oxygen. The absence of iron results to the low productivity, poor memory and apathy. The people with low levels of iron experience the symptoms such as restlessness, irritable and inattentive which could be eliminated by restoring the iron levels.

Health Benefits (Agric4Profits, 2023).

Nutrient-Rich Composition: *Vicia faba*, commonly known as broad beans, is packed with essential nutrients, including vitamins, minerals, and antioxidants, contributing to overall health.

Cardiovascular Support: Regular consumption of *Vicia faba* is associated with cardiovascular benefits, such as improved heart health and the regulation of blood pressure levels.

Anti-Inflammatory Properties: The plant's compounds exhibit anti-inflammatory effects, potentially alleviating inflammation associated with conditions like arthritis.

Weight Management: *Vicia faba* can be beneficial in weight management, offering a combination of fiber and nutrients that promote a sense of fullness.

Digestive Health: The fiber content in *Vicia faba* supports digestive health by aiding in regular bowel movements and preventing constipation.

Blood Sugar Regulation: Studies suggest that *Vicia faba* may assist in stabilizing blood sugar levels, making it a potential dietary addition for individuals with diabetes.

Antioxidant Defense: Rich in antioxidants, *Vicia faba* helps combat oxidative stress, reducing the risk of chronic diseases linked to free radical damage.

Protein Source: As a plant-based protein source, *Vicia faba* contributes to muscle health, making it an excellent option for vegetarians and vegans.

Respiratory Health: Certain compounds in *Vicia faba* may support respiratory health, potentially alleviating symptoms associated with respiratory conditions.

Skin Health: Antioxidants present in *Vicia faba* contribute to skin health by combating free radicals, supporting a youthful complexion.

Hormonal Balance: Some studies suggest that *Vicia faba* may play a role in hormonal balance, particularly in women, offering potential benefits for menstrual health.

Cognitive Function: The nutrients in *Vicia faba* may contribute to cognitive function, supporting brain health and potentially reducing the risk of cognitive decline.

Immune System Support: Components in *Vicia faba* may enhance immune function, helping the body defend against infections and illnesses.

Anti-Cancer Potential: Preliminary research hints at the potential anti-cancer properties of *Vicia faba*, though more studies are needed to establish its efficacy.

Joint Health: Compounds in *Vicia faba* may contribute to joint health, offering potential relief for individuals with arthritis or joint-related issues.

Health Benefits (WMDEC, 2024).

Protein: One cup of cooked fava beans contains almost a third of your daily protein needs. Protein is one of the most important nutrients in your diet. Eating high-protein foods can help you feel fuller for longer. Protein also helps grow and maintain your muscles. If you don't eat animal-based foods that are high in protein, like meat, cheese, or eggs, adding fava beans and other plant sources to your diet can help make sure you're getting enough protein.

Folate: One cup of fava beans meets almost half of your daily folate needs. Folate is a type of vitamin that helps your body create DNA and make new cells. Folate is especially important for pregnant women. Getting enough folate can lower the risk of brain-related birth defects like spina bifida and anencephaly. You can get folate from over-the-counter vitamins and supplements. Combining supplements with high-folate foods like fava beans is an easy way to get enough into your diet.

Manganese: Fava beans are high in the mineral manganese. Your body uses manganese to maintain bone structure and strength. Getting enough manganese in your diet may help prevent osteoporosis and other bone problems. One cup of fava beans has about 1.5 mg of manganese, which is about a third of your daily manganese needs. Manganese also helps your body digest glucose, a key nutrient that provides energy. Your body has trouble turning glucose into energy or can't digest it at all if you have diabetes. Getting enough manganese in your diet may lower your chances of getting diabetes.

Fiber: Fava beans are rich in fiber. Fiber is a nutrient that helps with digestion, maintaining healthy glucose levels, and preventing cholesterol buildup. Cholesterol is a chemical that occurs naturally in your body and in other foods. Too much cholesterol from oils or animal products can build up in your arteries (tubes that your blood flows through). This can lead to heart attacks, strokes, and other problems. Eating enough fiber can help prevent cholesterol from blocking your arteries.

Iron: Fava beans are a good source of iron. Iron is an element your body uses to get energy from oxygen when you breathe. Not getting enough iron in your diet can lead to anemia. Anemia is when your body doesn't get enough oxygen. It can lead to extreme tiredness, weakened immunity, and stomach problems. Eating fava beans can help you reach your daily recommended amount of iron.

Risks

Digestive upset: Legumes and beans often cause bloating and gas. This is normal and happens because of the way your body digests them. These digestive problems can be uncomfortable. To avoid bloating, try to introduce fava beans into your diet gradually instead of eating a lot at once. This can reduce passing gas and bloating.

Favism. Fava beans can cause shortness of breath, raise heart rate, and other symptoms for people with the genetic disorder G6PD. This reaction is called favism and usually isn't life-threatening. Children are at higher risk for severe symptoms of favism. Many people with G6PD don't know they have it. If you're unsure whether you'll get favism from eating fava beans, talk to your doctor. You can get a test to see if you have G6PD.

Side Effects (Agric4Profits, 2023)

Gastrointestinal Issues: Excessive consumption may lead to digestive discomfort, gas, or bloating for some individuals.

Allergic Reactions: Individuals with allergies to legumes should exercise caution, as *Vicia faba* belongs to the legume family.

Interactions with Medications: *Vicia faba* may interact with certain medications, and individuals on medication should consult with healthcare professionals before regular consumption.

Oxalate Content: Individuals prone to kidney stones may need to monitor their intake due to the oxalate content in *Vicia faba*.

Antinutrient Presence: *Vicia faba* contains antinutrients, and while they are generally in low levels, excessive consumption may lead to nutrient absorption issues.

Purine Content: Individuals with gout or high uric acid levels may need to moderate their intake due to the purine content in *Vicia faba*.

Hemagglutinin Concerns: Raw *Vicia faba* contains hemagglutinins, which can be harmful in large quantities. Cooking eliminates this concern.

Potential for Hypotension: Due to its blood pressure-lowering effects, individuals with low blood pressure should monitor their intake.

Interaction with Blood Thinners: *Vicia faba* may have mild anticoagulant effects, and individuals on blood thinners should be cautious and consult with healthcare professionals.

Pregnancy Concerns: Pregnant women should consult with healthcare professionals before including *Vicia faba* in their diet due to potential effects on pregnancy.

Influence on Thyroid Function: Individuals with thyroid issues should be aware of *Vicia faba*'s potential influence on thyroid function and consult with healthcare professionals.

Respiratory Sensitivity: Individuals with respiratory conditions may experience sensitivity to certain compounds in *Vicia faba*, and caution is advised, particularly when inhaling vapors or dust from the plant.

REFERENCES

- Abiodun, O., Dauda, A.O., Fabiyi, O.A. and Akintayo, F.M. 2022. Biofortification: Quality Improvement of Faba Bean. In book: Faba Bean: Chemistry, Properties and Functionality. pp 275–299
- Abou-Khater, L., Fouad Maalouf and Diego Rubiales. 2022. Status of Faba Bean (*Vicia faba* L.) in the Mediterranean and East African Countries. In: Developing Climate Resilient Grain and Forage Legumes. pp 297–327
- Adhikari, K.N., Hamid Khazaei, Lamiae Ghaouti, Fouad Maalouf, Albert Vandenberg, Wolfgang Link and Donal M. O'Sullivan. 2021. Conventional and Molecular Breeding Tools for Accelerating Genetic Gain in Faba Bean (*ViciaFaba* L.). *Frontiers in Plant Science*, 12: 744259
- Agric4Profits. 2023. 15 Medicinal Health Benefits Of *Vicia faba* (Broad Bean). <https://agric4profits.com/benefits-of-vicia-faba-broad-bean/>
- Ali Ouji, Maria José Suso, Mustapha Rouaïssi, Raoudha Abdellaoui and Mohamed El Gazzah. 2011. Genetic diversity of nine faba bean (*Vicia faba* L.) populations revealed by isozyme markers. *Genes & Genomics*, 33: 31-38. DOI 10.1007/s13258-010-0070-1
- Aouar-sadli1, M., Louadi, K. and Doumandji, S.E. 2018. Pollination of the broad bean (*Vicia faba* L.var. *major*) (Fabaceae) by wild bees and honey bees (Hymenoptera: Apoidea) and its impact on the seed production in the Tizi-Ouzou area (Algeria). *Global Journal of Food and Agribusiness Management* Vol. 2 (9), pp. 001-007.
- Badjona, A., Bradshaw, R., Millman, C., Howarth, M. and Dubey, B. 2023. Faba Bean Processing: Thermal and Non-Thermal Processing on Chemical, Antinutritional Factors, and Pharmacological Properties. *Molecules*, 28(14), 5431; <https://doi.org/10.3390/molecules28145431>
- Brar, P.S., Bhardwaj, G. and Mohit Bhardwaj, M. 2023. Broad Bean. In: (Eds. Ranga, A.D. and Singh, J.) *Underutilized vegetable crops-importance and cultivation*

- Byrne, P. 2023. Fava Bean (*Vicia faba*). In: Chen K, Byrne P (Eds.) Understudied Indigenous Crops. Fort Collins, Colorado: Colorado State University. Date accessed. Available from <https://colostate.pressbooks.pub/understudiedindigenouiscrops/chapter/fava-bean/>
- Chaudhary, V., Kajla, P., Shobhit (2022). Chemistry, Nutrient Composition and Quality of Fava Beans. In: Punia Bangar, S., Bala Dhull, S. (eds) Fava Bean: Chemistry, Properties and Functionality. Springer, Cham. https://doi.org/10.1007/978-3-031-14587-2_4
- Cubero, J.I. 1984. Taxonomy, Distribution and Evolution of the Fava Bean and its Mild Relatives. In: Witcombe, J.R., Erskine, W. (eds) Genetic Resources and Their Exploitation — Chickpeas, Fava beans and Lentils. Advances in Agricultural Biotechnology, vol 6. Springer, Dordrecht. https://doi.org/10.1007/978-94-009-6131-9_12
- De Angelis, D., Pasqualone, A., et al., 2020. Data on the proximate composition, bioactive compounds, physicochemical and functional properties of a collection of faba beans (*Vicia faba* L.) and lentils (*Lens culinaris* Medik.). Data in Brief 34 (2020) 106660
- Dhull, S.B., Mohd. Kashif Kidwai, Muhammad Siddiq, Jiwan S. Sidhu. 2021. Fava (Broad) Bean Production, Processing, and Nutritional Profile. In: Book Editor(s): Muhammad Siddiq, Mark A. Uebersax. First published: 17 December 2021. <https://doi.org/10.1002/9781119776802.ch14>
- Duc, G. 1997. Fava bean (*Vicia faba* L.). In: Field Crops Research, 53(1–3): 99–109
- El-Dawy, E.G.A.E.M., Gherbawy, Y.A. and Hussein, M.A. 2021. Morphological, molecular characterization, plant pathogenicity and biocontrol of *Cladosporium* complex groups associated with faba beans. Sci Rep., 11, 14183.
- Hou, W., Zhang, X., Liu, Y., Liu, Y. and Feng Bl. 2023. RNA-Seq and genetic diversity analysis of faba bean (*Vicia faba* L.) varieties in China. PeerJ., 11:e14259. <https://doi.org/10.7717/peerj.14259>
- Jayakodi, M., Golicz, A.A., Kreplak, J., et al., 2023. The giant diploid faba genome unlocks variation in a global protein crop. Nature, 615: 652–659
- Kambrekar, D.N., Raikar, M.R. and Gudadur, K. 2019. Abundance of insect pollinators associated with broad bean *Vicia faba* L. var. major (Fabales: Fabaceae) in North Karnataka. Journal of Pharmacognosy and Phytochemistry, 8(2): 1449–1452
- Khazaee, H., Donal M. O'Sullivan, Frederick L. Stoddard et al. 2021. Recent advances in faba bean genetic and genomic tools for crop improvement. Legum Sci., 3(3): e75.
- Kosev, V. and Georgieva, N. 2023. Evaluation of the genetic diversity in broad bean (*Vicia faba* L.) accessions. Bulg. J. Agric. Sci., 29(4), 682–689
- Kosterin, O.E. 2014. The lost ancestor of the broad bean (*Vicia faba* L.) and the origin of plant cultivation in the Near East. Vavilov Journal of Genetics and Breeding, 18(4/1): 831–840.
- Kovbjerg, C.K., Angra, D., Robertson-Shersby-Harvie, T. et al. 2023. Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. Theor Appl Genet., 136, 114. <https://doi.org/10.1007/s00122-023-04360-8>
- Li, X. and Yang, Y. 2014. A novel perspective on seed yield of broad bean (*Vicia faba* L.): differences resulting from pod characteristics. Scientific Reports, 4: 6859
- Maalouf, F., Jinguo Hu, . . . et al., 2018. Review Article: Breeding and genomics status in faba bean (*Vicia faba*). Plant Breeding. DOI: 10.1111/pbr.12644
- NCSE. 2024. *Vicia faba*. <https://plants.ces.ncsu.edu/plants/vicia-faba/>
- Nurmansyah, Alghamdi, S.S. and Migdadi, H.M. 2020. Morphological diversity of faba bean (*Vicia faba* L.) M₂ mutant populations induced by gamma radiation and diethyl sulphate. Journal of King Saud University - Science, 32(2): 1647–1658
- O'Sullivan, D.M. and Angra, D. 2016. Advances in Fava Bean Genetics and Genomics. Front. Genet., 7:150. doi: 10.3389/fgene.2016.00150
- Petruzzello, M. 2024. Broad bean, (*Vicia faba*). The Editors of Encyclopaedia Britannica. <https://www.britannica.com/plant/broad-bean>
- PV. 2024. Broad bean, dry. <https://plantvillage.psu.edu/topics/broad-bean-dry/infos>
- Redden, R., Paull, J., Zong, X., Sass, O., Yang, T., Ling, L. 2014. Fava Bean. In: Singh, M., Bisht, I., Dutta, M. (eds) Broadening the Genetic Base of Grain Legumes. Springer, New Delhi. https://doi.org/10.1007/978-81-322-2023-7_4
- Singh, A.K., Bharati, R. C., Manibhushan, N.C. and Pedpati, A. 2013. An assessment of faba bean (*Vicia faba* L.) current status and future prospect. African Journal of Agricultural Research, 8(50): 6634–6641
- Stoddard, F.L. and Bond, D.A. 1987. The pollination requirements of the faba bean. Bee World, 68(3) 144–152
- Sultan, S.M., Raina, S.K., Ahmad, S. and Bha, S.S. 2023. Characterization and Evaluation of Fava Bean (*Vicia faba* L.) Germplasm Collected from Kashmir, India. Indian Journal of Plant Genetic Resource, 36(3) 346–355
- Sylvia. 2017. Broad beans – *Vicia faba*. <https://www.healthbenefitstimes.com/broad-beans/>
- Wettberg, E.J.B.V, and Guerra-Garcia, A. 2023. Huge broad-bean genome could improve yields of an underused crop. Nature, 615: 587–588
- Wikipedia. 2024. *Vicia faba*. https://en.wikipedia.org/wiki/Vicia_faba
- WMDEC. 2024. Health Benefits of Fava Beans
- Zhang, H., Yujiao Liu, Xuxiao Zong et al., 2023. Genetic Diversity of Global Fava Bean Germplasm Resources Based on the 130K TNGS Genotyping Platform. Agronomy, 13(3): 811; <https://doi.org/10.3390/agronomy13030811>
- Zhu, Y., Feng, Q., Zhuqun Jin, Z. and Wu, F. 2021. Differences in Grain Microstructure and Proteomics of a Broad Bean (*Vicia faba* L.) Landrace Cixidabaican in China Compared with Lingxiyicun Introduced from Japan. Plants, 10(7): 1385; <https://doi.org/10.3390/plants10071385>
- Zong, X., Yang, T. and Liu, R. 2019. Fava Bean (*Vicia faba* L.) Breeding. In: Al-Khayri, J., Jain, S., Johnson, D. (eds) Advances in Plant Breeding Strategies: Legumes. Springer, Cham. https://doi.org/10.1007/978-3-030-23400-3_7