



LEGUME

PERSPECTIVES



Faba bean takes the spotlight

The Journal of the International Legume Society

Issue 24 • December 2023

ISSN

2340-1559 (electronic issue)

Quarterly publicationJanuary, April, July and October
(additional issues possible)**Published by**

International Legume Society (ILS)

Co-published byCSIC, Institute for Sustainable Agriculture, Córdoba, Spain
Instituto de Tecnologia Química e Biológica António Xavier
(Universidade Nova de Lisboa), Oeiras, Portugal**Office and subscriptions**CSIC, Institute for Sustainable Agriculture
International Legume Society
Apdo. 4084, 14080 Córdoba, Spain
Phone: +34957499215 • Fax: +34957499252
diego.rubiales@ias.csic.es**Front cover:**Henry Laugel
Göttingen Universität, Germany**Publishing Director**Diego Rubiales
CSIC, Institute for Sustainable Agriculture
Córdoba, Spain
diego.rubiales@ias.csic.es**Editor-in-Chief**M. Carlota Vaz Patto
Instituto de Tecnologia Química e Biológica António Xavier
(Universidade Nova de Lisboa)
Oeiras, Portugal
cpatto@itqb.unl.pt**Technical Editor**Matilde Calado Sanches
Instituto de Tecnologia Química e Biológica António Xavier
(Universidade Nova de Lisboa)
Oeiras, Portugal
matsanches@itqb.unl.pt**Legume Perspectives Design**

Aleksandar Mikić

Assistant EditorsAlfonso Clemente
Estación Experimental del Zaidin, CSIC, Granada, SpainDiego Rubiales
Instituto de Agricultura Sostenible, CSIC, Cordoba, SpainJose C. Jimenez-Lopez
Estación Experimental del Zaidin, CSIC, Granada, SpainKevin McPhee
Montana State University, Bozeman, USALars Kamphuis
Center for Crop and Disease Management, Curtin University, Perth, AustraliaMaria Carlota Vaz Patto
Instituto de Tecnologia Química e Biológica António Xavier (ITQB
NOVA), Universidade NOVA de Lisboa (UNL), Oeiras, PortugalMarion Prudent
UMR Agroecology, Institut National de Recherche pour l'Agriculture,
l'Alimentation et l'Environnement (INRAE), Dijon, FranceNelson Nazzicari
Consiglio per la ricerca in agricoltura e l'analisi
dell'economia agraria (CREA), Lodi, ItalyPaolo Annicchiarico
Consiglio per la ricerca in agricoltura e l'analisi
dell'economia agraria (CREA), Lodi, ItalyPei Xu
China Jiliang University, Hangzhou, ChinaPeter Smykal
Palacky University, Olomouc, Czech RepublicPietro Iannetta
The James Hutton Institute, Dundee, Scotland, UKStefano Pavan
University of Bari, Bari, ItalyTom Warkentin
University of Saskatchewan, Saskatoon, Canada



This special issue of Legume Perspectives focuses on the faba bean crop. Faba bean is cool-season legume, grown as staple food and feed whose global area of cultivation declined since the 1960s. This negative trend is now being reverted and the crop is regaining the place it deserves in the cropping systems worldwide. In this issue we gathered the contributions of a number of key authors, with the aim to provide a comprehensive overview of current faba bean programs to a broad audience, highlighting constraints and prospects. On behalf of the Legume Society, we wish to thank the authors of the articles in this issue for their concise and well-written contributions.

*Hamid Khazaei
and Diego Rubiales*



CARTE BLANCHE

- 3 Diego Rubiales and Hamid Khazaei

RESEARCH

- 4 Faba bean breeding for global mandate: Status and future progress
7 A faba bean pan-genome for advancing sustainable protein security
10 Breeding faba bean for sub-tropical region of Australia
13 *Vicia faba* plant genetic resources preserved in home gardens in Sweden
15 Management factors affecting faba bean yield
18 Current faba bean research at Göttingen, Germany
21 Progress in faba bean breeding for adaptation to Southern European rain fed farming systems with a focus on stress resistance
23 Status of Faba bean in North and East Africa, limitations, and prospects
26 Faba bean in North America – Status and potential
28 Prospects of genebank genomics in faba bean
30 The limitations and prospects of the faba bean industry in China

ANNOUNCEMENTS

- 31 ILS webpage
32 Event: ICLGG 2024
33 Event: ILS 5
34 ILS Webinars 2024

diego.rubiales@ias.csic.es

Institute for Sustainable Agriculture, CSIC

Córdoba, Spain



After decades of neglect, there is growing interest in the reintroduction of faba beans into farming systems due to their enormous potential to contribute to sustainable agriculture and protein security. We need to produce more natural nitrogen, more sustainable plant-based proteins, and less atmospheric carbon. Cultivating faba beans could assist us in achieving all of those goals. The latest protein shortage happened in the 1970s and created a short-term emphasis on faba bean research after which many programs were frozen or even terminated in quite some countries. However, this time faba bean is here to stay. Societal concerns on environmental issues is driving to a regained attention to reintroduction of more legumes in cropping systems, with a special interest on faba bean. This can only be achieved through an integrative approach leading to the adjustment of cropping practices and the development of more adapted and productive quality cultivars. A number of national and international projects are now covering faba bean research, so agronomy, genetic, and genomic development are now moving rapidly in concert. Germplasm collections are being characterized and breeding programs re-launched. The giant diploid faba bean reference genome has recently been decoded and is being expanded to pan-genomes. These valuable resources now enable us to propel faba bean into the genomics-based breeding era to address resilience, sustainability, and quality traits.



hamid.khazaei@luke.fi

Natural Resources Institute (Luke)

Helsinki, Finland



Faba bean breeding for global mandate: Status and future progress

by Fouad MAALOUF*, Lynn Abou KHATER

Abstract: Faba bean (*Vicia faba* L.) is an important cool season legume grown in diverse environments. ICARDA improvement program developed more than 75 cultivars in collaboration with National research institutes in target countries. Focused products profiles were designed with NARS partners and new tools for crop improvement were adopted such as shortening breeding cycle and developing efficient phenotyping and molecular tools. Kompetitive Allele Specific PCR genotyping system (KASP) markers for most traits with economic importance like drought, heat, herbicide tolerance and phenological and agronomic traits were recently identified. These tools will allow to increase genetic gain and improve faba bean productivity to meet the demand of the population growth and in target counties.

Key words: Faba bean, speed breeding, genetic gains, modernization of breeding program, biotic and abiotic stresses

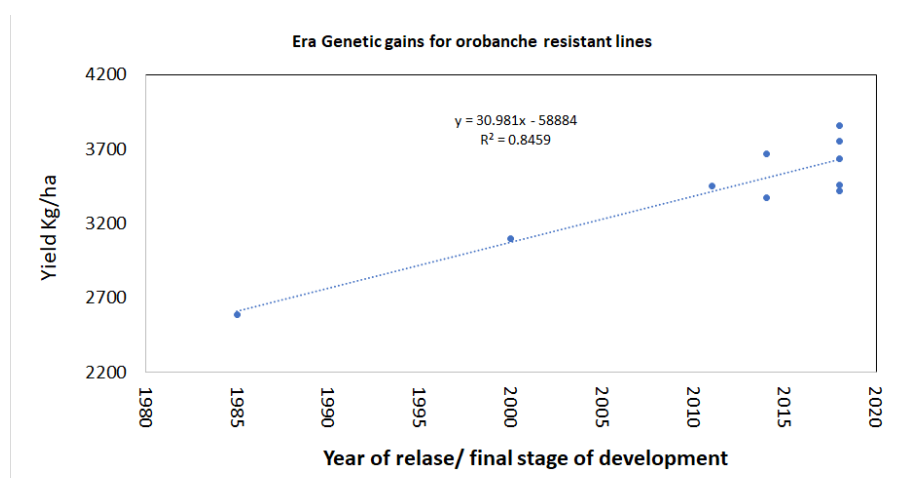


Figure 1. Era genetic gains of resistant lines to orobanche-Terbol 2022

Faba bean is an important cool season food legume grown for its dry and green seeds in 65 countries with total area of 3.05 million ha globally in 2021 [1]. Dry grains occupy approximately 90% of the total world faba bean area. The total production of dry faba bean grains was 5.9 million tons in 2021 which is 25% higher than the first reported value in 1961. The total green production is currently around 2.7 million tons. The dry grains productivity per hectare has increased from 0.9 tons to 2.2 tons over the same period. This increase was due to efforts made in crop improvement and in agronomy research. The top faba bean producer countries are China, Ethiopia, Egypt, Sudan, United Kingdom, Australia, Germany, France, and Morocco.

Faba bean is a highly nutritious crop rich in protein, fibers, vitamins, minerals, and especially essential amino acids [2,3] which make it an

essential crop for human diet and animal feeding. However, the crop is threatened by various biotic and abiotic stresses [4,5]. The major biotic stresses affecting faba bean production in various regions are *Orobanche crenata*, chocolate spot, gall disease and ascochyta blight and faba bean necrotic yellow viruses. Parasitic weeds are a major constraint that can lead to significant reduction of area and productivity [6,7]. *Orobanche crenata* extended in the last decade in Ethiopia and Sudan, while chocolate spot and rust became the most important diseases worldwide. Viruses were one of the major enemies of this crops mainly faba bean leaf roll virus (FBLRV) and faba bean necrotic yellow virus (FBNYV). On the other hand, the major abiotic stresses are heat and drought occurring mainly during reproductive phase [5].

ICARDA has global mandate for faba bean

1 International Center for Agricultural Research in Dry Areas (ICARDA), Terbol, Lebanon

* f.maalouf@cgiar.org

improvement and conserves more than 32% (> 10000 accessions) of the global collection with unique materials collected from 71 countries. Genetic resources are very valuable for any breeding program to develop breeding lines that are resistant to biotic and tolerant to abiotic stresses. More than 2500 faba lines were screened for disease resistance, conducting to the identification of more than 100 lines with resistance to chocolate spot, ascochyta blight and/or rust [8] and sources for heat [9], herbicide [10] and drought tolerance. These useful genetic resources were used in the breeding program to improve the resistance of faba bean crop in North and East Africa and to develop multiparent MAGIC (multiparent advanced generation inter-cross) lines (2400 RILs) constructed by intercrossing eight diverse parents, generation challenge program diverse set (GCP set), diversity panels constructed with 300 diverse lines and Focused Identification of Germplasm Strategy (FIGS sets) for drought [11], heat and cold tolerance. As a result of the efforts made, 75 varieties were released over the last five decades in collaboration with National Agricultural Research System (NARS) in Egypt, Sudan, Ethiopia, China, Tunisia, Syria, Morocco, and Lebanon. These released varieties ensured sustainable increase of the yield as it is reported in Ethiopia [12] and in Egypt (Figure 1).

Currently ICARDA developed breeding product profiles for different target countries to align the program with excellence in breeding platform and worked jointly with NARS breeding programs to define product profile to breed better and targeted cultivars. These product profiles have been prioritized to increase the production in farmers' fields in North and East Africa based on the following agro-ecologies: (a) wheat based irrigation system in Egypt and in Sudan (b) cereal based rainfed targeting in North Africa and West Asia, and (c) cereal based high rainfed system (Table 1).

In addition to the mentioned product profiles, ICARDA collaborates with Chinese partners to develop cultivars with large seeds and pods and with Indian Center for Agricultural Research (ICAR) to develop low vicine-convicine faba bean lines for human consumption.

To accelerate genetic gains, shuttle faba bean breeding with two generations per year using

Table 1. Details of product profiles developed for target countries.

Ecosystem	Countries	Varieties to be replaced	Areas (ha)	Must have economic traits	Other desirable traits
West Asia and North Africa					
Low rainfall Cool	Morocco, Tunisia, Algeria, Syria	Aguadulce, Najah, Hama2	277000	Orobanche, disease resistance, cooking time, herbicide tolerance	Large seed and pods size, Small seed size, Cooking time, Stem borer
East Africa					
High Rainfall	Ethiopia, Eritrea	Walkie, Gelebcho, Tumsa	500000	Earliness, Orobanche, foliar diseases	High biomass, Large seed size
Nile Valley					
Irrigated environments	Egypt, Sudan	Giza843, Eddamer	100000	Orobanche, heat stress, Earliness	Large seeds and pods size, Cooking time

winter and summer seasons, was established at Terbol station since 2012 with different photoperiod and temperature extremes. Speed breeding is also applied to faba bean breeding to advance breeding materials from F1 to F5 using the ICARDA breeding facility at Rabat Morocco. At this platform, four cycles are successfully completed per year (Figure 2). This is essential to reduce breeding cycle and ensure

higher genetic gains in faba beans. ICARDA also developed phenotyping tools at ICARDA Marchouch, Morocco, with a phenomobile system (PhenoBuggy). This technique applied to faba bean allows to record different useful traits such as vegetation index, green fraction, green area index, fraction of intercepted radiation, average leaf inclination angle, canopy and leaf chlorophyll content, steam and ear density, plant



Figure 2. Advancement of F3 faba bean lines under Speed breeding facility at Rabat Morocco during 2023 season.

density and stem diameter (Figure 3).

Moreover, efforts were made towards the applications of molecular breeding. Recently 192 Kompetitive Allele Specific PCR genotyping system (KASPs markers) were designed for drought, heat and herbicide tolerance and other traits such crop phenology, grain yield and its components [4,9]. Validations of the results will allow the implementation of genomic selection in the faba bean international breeding program.



Figure 3. Phenomobile system working in faba bean field.

References

- [1] FAOSTAT (2023) Food and Agriculture Organization of the United Nations. Available online: <http://www.fao.org/faostat/en/#data> (accessed on 24 August 2023).
- [2] Crépon K, Marget P, Peyronnet C, *et al.* (2010) Nutritional value of faba bean (*Vicia faba* L.) seeds for feed and food. *Field Crops Res* 115: 329–339.
- [3] Martineau-Côté D, Achouri A, Karboune S, L'Hocine L (2022) Faba Bean: An untapped source of quality plant proteins and bioactives *Nutrients* 14(8): 1541.
- [4] Abou-Khater L, Maalouf F, Jighly A, *et al.* (2022) Genomic regions associated with herbicide tolerance in a worldwide faba bean (*Vicia faba* L.) collection. *Sci Rep* 12: 158.
- [5] Maalouf F, Hu J, O'Sullivan DM, *et al.* (2019) Breeding and genomics status in faba bean (*Vicia faba*). *Plant Breed* 138: 465–473.
- [6] Maalouf F, Seid A, Patil S (2018) Developing improved varieties of faba bean. In *Achieving sustainable cultivation of grain legumes*. Volume 2; Sivasankar S, B.D., Gaur P, Kumar S, B.S. and T.M., Eds.; Burleigh Dodds Science Publishing Limited, 2018.; London, 2018; Vol. 2 ISBN: 9781786761408.
- [7] Maalouf F, Khalil S, Ahmed S, *et al.* (2011) Yield stability of faba bean lines under diverse broomrape prone production environments. *Field Crops Res* 124: 288–294.
- [8] Maalouf F, Ahmed S, Bassam B, *et al.* (2016) New faba bean germplasm with multiple resistances to ascochyta blight, chocolate spot and rust diseases. *Euphytica* 211: 157–167.
- [9] Maalouf F, Abou-Khater L, Babiker Z, *et al.* (2022) Genetic dissection of heat stress tolerance in faba bean using GWAS. *Plants* 11(9):1108.
- [10] Abou Khater L, Maalouf F, Patil SB, *et al.* (2021) Identification of tolerance to metribuzin and imazethapyr herbicides in faba bean (*Vicia faba* L.). International Center for Agricultural Research in the Dry Areas (ICARDA), Terbol, ICARDA, Rabat Morocco. Lebanese University, Faculty of Agriculture.
- [11] Khazaei H, Street K, Bari A, *et al.* (2013) The FIGS (Focused Identification of Germplasm Strategy) approach identifies traits related to drought adaptation in *Vicia faba* genetic resources. *PLoS ONE* 8(5): e63107.
- [12] Tolessa TT, Keneni G, Mohammad H (2015) Genetic progresses from over three decades of faba bean (*Vicia faba* L.) breeding in Ethiopia. *Aust J Crop Sci* 9(1): 41–48.



A faba bean pan-genome for advancing sustainable protein security

by Petri AUVINEN¹, Wei CHANG^{1,2}, Liisa HOLM¹, Martyn JAMES¹, Marko JÄÄSKELÄINEN^{1,2}, Hamid KHAZAEI³, Pia K. LAINE¹, Lars PAULIN¹, Marco SALGADO¹, Frederick L. STODDARD^{2,4}, Jaakko TANSKANEN^{2,3}, Petri TÖRÖNEN¹, Alan H. SCHULMAN^{1,2,3*}

Europe and much of the world urgently needs its own sufficient sources of plant-based food and feed protein. World consumption of meat and dairy products have risen dramatically since 1960, first in the West and recently in newly affluent parts of the developing world, made possible by the parallel growth in plant productivity driven by nitrogen fertilizers. Worldwide, ~1.3% of CO₂ emissions arise from conversion of methane to ammonia, in addition to the energy used in the process [1].

While protein consumption has risen worldwide, many parts of the world nevertheless suffer from a deficit in local plant protein production, relying on imports subject to trade disruption and to the environmental consequences of rainforest and tropical woodland clearance for fields in the countries of export. Europe (EU-27+3), for example, imported 33.5 Mt of soybeans and soy meal in 2021 and produced about

2.7 Mt itself [2]. The import of soy into the EU represented about 10% of the total world soy production and required about 13 Mha of land [2]. Given the strong stratification of Europe into climatic zones [3], neither soy nor any other single protein crop can provide a complete solution for protein production in Europe. In sum, continual growth in feed protein harvests, made possible by fossil-fuel-based fertilizers, in order to produce sufficient protein for growing populations and consumption is not sustainable; alternatives need to be found [4,5]. Legume-based protein sources are one key, and many species are available for the different agroclimatic zones.

Having an average protein content of 29%, faba bean (*Vicia faba* L.) is a widely adapted protein crop that could substantially improve protein sovereignty and security, for both food and feed. It is well suited to regions worldwide where it is a traditional, staple food. Its range of climatic adaptation is complementary to soy, which is adapted to warm regions and does poorly where faba bean does well. Moreover, it is highly efficient at capturing nitrogen from the air, fixes ~60 kg of N, taking up 20 kg from soil, leaving 40 kg behind, and incorporating 40 kg into the grain per ton of grain, at the top end for common legume crops [6]. Faba bean fixes N efficiently even if the soil already contains N, unlike soy [6,7]. Increasing the use of nitrogen-fixing faba bean could thus enormously contribute to closing the N cycle and reducing fossil fuel use in temperate and cool regions worldwide.

Faba bean, like other crops, faces challenges from the biotic and abiotic stresses made worse by climate change. Breeders need new genetic tools to develop sustainable and reliable crops

more efficiently, with the properties that processors need and consumers want, both for feed and for both traditional and novel food uses [8]. Assembled genome sequences for plants greatly aid the development of these tools, because they define the identity and physical position of the genes in a crop, enable association of a specific gene and sequence with a trait of interest, allow the development of molecular markers linked to the particular gene, and unlock the search or generation of new variants for novel traits. Assemblies of varying degrees of contiguity have been made for the genomes of at least 12 other legumes, including pea, common bean, and lentil, as well as the model species *Medicago truncatula* and *Lotus japonicus*. Although these support interpretation of the faba bean genome, the imperfect correspondence to the gene content and organization as well as to the traits of these other genomes mean that they cannot substitute for a faba bean genome itself.

The large size of the faba bean genome (13 Gbp diploid) had until recently hindered a high-quality assembly, but new advances enabled production of a highly contiguous reference genome [9]. The reference genome conferred a clear overview of *V. faba* genes and their regulatory regions as well as the massive repetitive component of the genome, which comprises mostly retrotransposons and satellite repeats. We were able to show that the faba bean genome expanded to its current massive size through a higher rate of amplification than loss of retrotransposons and satellite repeats. In contrast to large cereal genomes [10], gene density and recombination frequency shows no sharp telomere to centromere gradient across chromo-

¹Institute of Biotechnology, HiLIFE, University of Helsinki, Finland

²Väikki Plant Science Centre (ViPS), University of Helsinki, Finland

³Natural Resources Institute Finland (LUKE), Helsinki, Finland

⁴Department of Agricultural Sciences, University of Helsinki, Finland

* alan.schulman@helsinki.fi

somes; the gene space is quite compact considering the genome size. We were able to put the reference genome to practical use through a targeted genotyping assay and a high-resolution genome-wide association (GWA) analysis to dissect the genetic basis of seed size and of hilum colour.

Current progress towards a pan-genome

The basis of control of key traits including disease resistance, abiotic stress response, flowering time, the synthesis and properties of storage starch and protein, anti-nutrient accumulation, and nitrogen fixation and nutrient use efficiency, as well as genome structure and evolution, all require a genomic data. Contiguous and complete sequence data is needed not only to identify structural variations in the crop's proteins and the DNA sequences that codes for them, but also in the promoters and other regions that control their expression. A reference genome, no matter how complete, represents only a single facet of the total diversity space of a species. Hence, we embarked upon assembling a pan-genome for faba bean. The concept of pan-genomes originates in the bacterial world but was brought to the plants through analysis of the vast genetic differences between inbred lines of maize [11]. The gene complement shared across a species is called the “core” genome, the unique genes the “accessory” genome, and the total complement of genes found in the species the “pan”-genome. The genomic dynamism found in maize is not unique to this crop; indeed, pan-genomics has proven its relevance across the plant kingdom [12-15].

In the PanFaba project funded by the Jane and Aatos Erkko Foundation of Finland, we are now producing a pan-genome spanning the diversity space of *Vicia faba* to deliver the insight and tools needed for rapid improvement of faba bean. We have assembled the genomes of five accessions spanning the diversity space of *V. faba*; these will be complemented by at least 16 others by colleagues at other institutions in a coordinated international effort. The assemblies are complemented by transcriptomics and gene annotation. The PanFaba project will enable the high-resolution linkage of genotype to phenotype that is needed to improve faba bean as a protein crop and adapt it to likely future cli-

matic conditions in various regions worldwide. Methodologically, the genomes have been sequenced by the PacBio HiFi long-read technology, assembled with Hifiasm, and scaffolded with a hybrid approach using Bionano optical mapping, Nanopore long-reads, and OmniC (HiC) proximity sequencing. Gene models are being aided by PacBio long-read RNA sequencing from several tissues of the accessions in the pan-genome, grown in parallel (Figure 1).

Prospects

The genome sequence will yield all the faba genes and their copy number variation, regulatory sequences, and positions, allowing discovery of the basis for the stress and disease tolerance, agronomic traits, and quality in this crop. The pan-genome will identify global gene variation, including presence-absence variation, copy number variation, global single-nucleotide variation and small structural variation (insertions

and deletions) within genes. It will also enable discovery, difficult otherwise, of inversions, that interfere with recombination, as well as other structural variations such as translocations (Figure 2). The pan-genome will facilitate development of large numbers of molecular markers with defined physical positions and order, linked to genes. This will in turn enable the genotypic characterization of germplasm diversity sets for conservation and input to breeding, as well as the construction of high-density genetic maps for trait localization.

Knowledge of the identity and map location of agriculturally important genes, together with high-density markers derived from genome sequencing, form the foundation for parental selection and for genomic breeding methods, including marker-assisted selection, marker-assisted backcross selection, “breeding by design” (ideotype-based), and genomic selection (GS). The application of GS requires genotypic and phenotypic datasets for training populations in order to predict the breeding value of lines. Importantly, selection based on sequence allows simultaneous and synergistic marker discovery, validation, and genotyping. The application of GWA is already providing an understanding of the molecular basis of complex traits such as flowering time, maturity and yield. High density genetic markers derived from the physically ordered genes of the genome sequence are essential for GWA.

We look forward to the development of additional tools from the genotypes in the pan-genome, which will facilitate understanding both of gene function and the basis of useful traits in faba bean. These include mutant collections and TILLING populations, as well as biparental RIL populations, multi-parental MAGIC populations, and NAM populations for the assignment of gene function. The de novo assemblies which form the framework of the pan-genome, combined with the genomics tools mentioned above, will facilitate the analysis of genetic diversity, which is needed for germplasm management, conservation, and exploitation. It will enable detection of signatures of natural and human selection in the genome and development of understanding of the crop's environmental adaptation. Given the falling price and rising efficiency of short-read sequencing as well



Figure 1. Faba bean accessions for the pan-genome grown in parallel, spring 2023, in the greenhouse on the Viikki campus of the University of Helsinki. The accessions include Mélodie/2, ILB 938/2 (IG 12132), NV153 (IG 12658), RV322 (IG 132238), and Hiverna/2-5. Samples were collected of roots, young leaves, flowers, expanding pods, and filling seed for long-read RNA sequencing.

as of long-read technologies such as PacBio and Nanopore, we fully expect the number of accessions in the faba bean pan-genome to expand to by an order of magnitude over the next several years, increasing its utility for understanding and improving this crop.

Genome and gene sequence data is essential for the design and deployment of genome editing technology, in order to direct edits to the relevant members of gene families and to minimize off-target effects. In parallel to the development of the pan-genome, we and several other labs are working to develop gene editing methods for *V. faba*. We expect that the pan-genome, together with populations for genetics, genetically characterized diversity sets, and gene editing tools will facilitate collaborative research on agronomically important genes and traits in faba bean, increase interest in this crop within

the scientific community, and thereby accelerate its improvement in breeding programs worldwide, leading to increased productivity and reliability of the crop and its role in providing plant-based protein. 🌱

Acknowledgements

PanFaba is funded by the Jane and Aatos Erkkö Foundation.

References

- [1] Pach JD (2007) Ammonia production: energy efficiency, CO₂ balances and environmental impact. In: Meeting of The International Fertiliser Society. 2007. London, UK: International Fertiliser Society.
- [2] European Soy Monitor 2021 (2023) Insights on European uptake of certified, responsible, deforestation, and conversion-free soy in 2021. Prepared by Schuttelaar & Partners. 2023, Schuttelaar

& Partners: the Hague, the Netherlands. Available at: <https://www.idhsustainabletrade.com/publication/european-soy-monitor-2021/#:~:text=The%20report%20also%20shows%20that,compared%20to%2043.8%25%20in%202020>. Accessed on 17 December 2023.

- [3] Metzger MJ, Bunce RGH, Jongman RHG, *et al.* (2005) A climatic stratification of the environment of Europe. *Glob Ecol Biogeogr* 14: 549–563.
- [4] Foley JA, Ramankutty N, Brauman KA, *et al.* (2011) Solutions for a cultivated planet. *Nature* 478: 337–342.
- [5] Cole MB, Augustin MA, Robertson MJ, *et al.* (2018) The science of food security. *NPJ Sci Food* 2: 14.
- [6] Baddeley JA, Jones S, Topp CFE, *et al.* (2013) Biological nitrogen fixation (BNF) by legume crops in Europe. *Legume Futures Report 1.5*. Available from www.legumefutures.de.
- [7] Hardarson G, Danso SKA, Zapata F, *et al.* (1991) Measurements of nitrogen fixation in fababean at different N fertilizer rates using the ¹⁵N isotope dilution and 'A-value' methods. *Plant Soil* 131: 161–168.
- [8] Khazaei H, O'Sullivan DM, Stoddard FL, *et al.* (2021) Recent advances in faba bean genetic and genomic tools for crop improvement. *Legume Sci* 3: e75.
- [9] Jayakodi M, Golicz AA, Kreplak J, *et al.* (2023) The giant diploid faba genome unlocks variation in a global protein crop. *Nature* 615: 652–659.
- [10] Mascher M, Gundlach H, Himmelbach A, *et al.* (2017) A chromosome conformation capture ordered sequence of the barley genome. *Nature* 544: 427–433.
- [11] Morgante M, De Paoli E, Radovic S (2007) Transposable elements and the plant pan-genomes. *Curr Opin Plant Biol* 10: 149–155.
- [12] Naithani S, Deng CH, Sahu SK, *et al.* (2023) Exploring pan-genomes: An overview of resources and tools for unraveling structure, function, and evolution of crop genes and genomes. *Biomolecules* 13(9): 1403.
- [13] Jayakodi M, Schreiber M, Stein N, *et al.* (2021) Building pan-genome infrastructures for crop plants and their use in association genetics. *DNA Res* 28(1): dsaa030.
- [14] Della Coletta R, Qiu Y, Ou S, *et al.* (2021) How the pan-genome is changing crop genomics and improvement. *Genome Biol* 22: 3.
- [15] Bayer PE, Golicz AA, Scheben A, *et al.* (2020) Plant pan-genomes are the new reference. *Nat Plants* 6: 914–920.

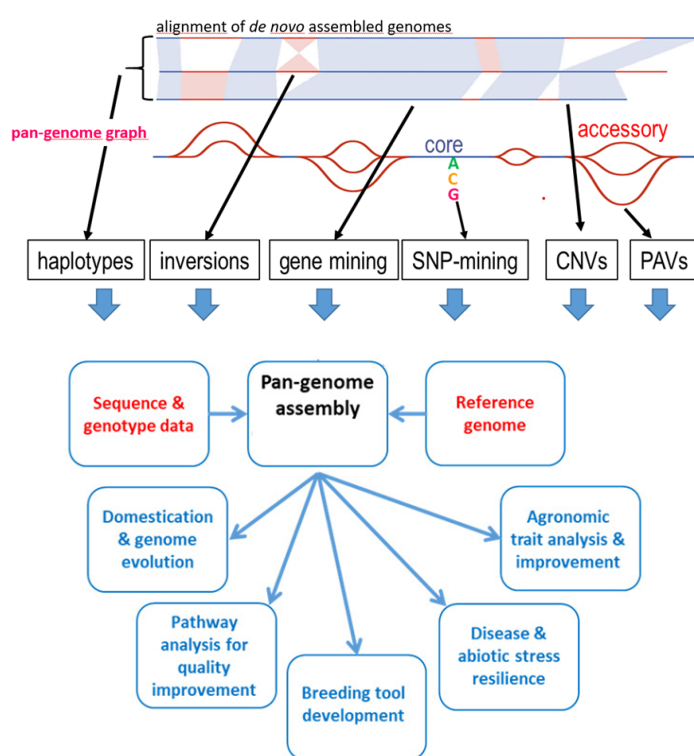


Figure 2. Scheme for pan-genome analysis and exploitation. Aligned pan-genome assemblies (top) are used to construct graphical models (upper middle) to represent all inter-genome variation at various scales. Divergent regions are represented by alternative pathways that may be shared by one or more accession. These then serve for identification of different kinds of variation, including single-nucleotide polymorphisms (SNPs), copy number variations (CNVs), and presence-absence variations (PAVs), which can then be exploited (bottom). Figure based on Bayer *et al.* [15].

Breeding faba bean for sub-tropical region of Australia

by Kedar Nath ADHIKARI*

Abstract: Faba bean (*Vicia faba* L.) is an important rotational crop in Australia providing \$50-\$100/ha indirect benefit to growers through break in disease cycle, change of weed spectrum and the nitrogen fixation. It is primarily grown as an export commodity to the Middle eastern countries, mainly Egypt, Saudi Arabia and United Arab Emirates. Its production in sub-tropical region is constrained by rust (*Uromyces viciae-fabae* (Pers.) Schroet.), chocolate spot (*Botrytis fabae* Sard.) and certain viral diseases, but sufficient resistance has been developed in new varieties to combat these constraints. Likewise, successful breeding has been carried out for better seed quality, tolerance to certain herbicides, heat and drought stresses.

Key words: breeding, disease resistance, faba bean, herbicide tolerance, protein quality

Challenges for faba bean production in sub-tropical Australia

Foliar diseases

Faba bean rust (*Uromyces viciae-fabae* (Pers.) Schroet.) can cause moderate to high yield losses in North Africa, Ethiopia and Australia. Up to 70% yield losses have been reported in Australia [1]. The disease is found throughout the faba bean growing areas in the world except North America. Several sources of resistance have been reported [1,2], but the level of resistance is only partial. Newer Australian varieties, such as PBA Warda, PBA Nasma and PBA Nanu have moderate level of resistance to the disease and require only limited fungicidal sprays. In the breeding program, new genotypes with rust resistance, viz. Ac1866#15013, Ac1231#14905, Ac1653#14919, Doza#12034 and Ac1655, have been identified. Doza#12034 and Ac1655 have been already characterised for rust resistance; they possess single dominant genes which are independent to each other [1]. The resistance gene in Doza#12034 is named as Uvf-2 and located in Chromosome III and the gene in Ac1655 as Uvf-3 and located in chromosome V for which KASP markers VF_0703 and Ac×F165 for Uvf-2 and Uvf-3, respectively are available [3]. The resistant genes in Ac1231#14905, Ac1866#15013 and Ac1653#14919 are yet to be characterised. Our preliminary results indicated that Ac1866#15013 may have adult plant resistance gene.

Chocolate spot (*Botrytis fabae* Sard.) can be the most damaging disease of faba bean when conditions are conducive for the disease develop-

ment as observed in 2016 in Australia. A high level of resistance to the disease has not been found and the resistance is believed to be controlled by multiple genes. Recently, Gela *et al.* [4] reported identification of five quantitative trait loci contributing to the resistance on chromosome 1 and 6. Some sources of resistance to the disease are available in Australia and recently a variety, PBA Amberley, has been released in Australia with a significant improvement to the disease.

Although ascochyta blight (*Ascochyta fabae* Speg) is a devastating disease causing up to 90% yield losses, it is not a problem in sub-tropical region of Australia. Stemphylium blight (*Stemphylium* spp) occurs occasionally, but no significant losses have been reported from this disease.

Soil-borne diseases

Aphanomyces root rot is one of the concern root diseases in Australia, but it has not yet become a major issue. However, it has been reported frequently where the crop rotation is short. Genetic variation for resistance to the host has been reported [5], but no genetic studies have been done yet. Due to a wide crop rotation, the disease might have been controlled. This has been demonstrated by widespread occurrence of the pathogen in insect-proof enclosures in our breeding program when faba bean is alternated by cereal crops for just one season.

Viruses

Faba bean is infected by many viral pathogens, but most important viruses in Australia are: bean leaf roll virus (BLRV), bean yellow mosaic virus (BYMV) and pea seed borne mosaic vi-

The University of Sydney, School of Life and Environmental Sciences, International Crop and Digital Agricultural Research Centre, Narrabri NSW 2390 Australia

* kedar.adhikari@sydney.edu.au

rus (PsbMV) causing sporadic losses [6]. Some of the viruses are transmitted through infected seeds and others through vectors like aphids. Seed transmission of virus in Australia is almost absent except for PsbMV. Because of the uncertainty of virus epidemics and the lack of effective control options, growers can perceive viruses as a higher risk than fungal diseases. In 2020, BYMV losses up to 70% were reported in northern New South Wales and no reliable resistance has been found, but there is a high level of resistance in our breeding program for BLRV and all new varieties are resistance to it.

Insects-pests

Cowpea aphid (*Aphis craccivora* Koch), black bean aphid (*A. fabae* Scopoli) and green peach aphid (*Myzus persicae* (Sulzer)) damage faba bean by sucking as well as transmitting viruses. Recently, a new species of aphid, *Megoura crassicauda*, has been found active among faba bean and vetch crops in northern NSW. These aphids survive on other pasture legumes, such as lucerne and sub-clover making it persistent all year around. The most damaging insect pests in Australia are *Heliothis armigera* and *H. punctigera*. *H. punctigera* is native to Australia and is the major insect pest of faba bean. Green mirids (*Creontiades dilutus*, *C. pacificus*), which is mainly a mung bean pest feeding on immature green pods, is becoming a faba bean pest in sub-tropical Australia. No resistance to these pests has been identified and the chemical method of control has been widely adopted.

Abiotic stress tolerance

Frost tolerance

Faba bean is vulnerable to frost, particularly in the flowering, early pod formation and pod-filling stages. Variation exists in the breeding germplasm for frost tolerance at the vegetative stage ranging from almost no damage to 60% stem collapse. The newer varieties of faba bean are more tolerant than the older varieties, such as Fiord and Fiesta. A gradual improvement was observed on the tolerance level from PBA Nanu to Fiord in the order of PBA Nanu>PBA Warda>Doza>Cairo>Fiord. The level of toler-



Figure 1. Frost damaged faba bean pods (left) and immature and dead seeds (right) from such pods.



Figure 2. Effect of residual phenoxy herbicides at seedling stage (left) and spray drift at adult stage (right) in faba bean.

ance found in the germplasm is strong enough to withstand the severe frost in the northern region. However, little variation was found at flowering and pod development stage which are the most damaging phases. Frost tolerance at the vegetative stage has been continuously improved by including newly identified germplasm in the breeding program.

The severely damaged pods turn black and abort (Figure1). The less damaged pods have fewer seeds which are not fully developed and

stained resulting not only substantial yield loss, but also reduced seed quality. Plants become more susceptible to frost at the reproductive stage than at the vegetative stage. Young pods were the most sensitive to cold temperatures and the flowers were much hardier [7]. Although no comparative studies are conducted on frost damage in Australia, our experience indicates 20-30% yield loss would be common in older varieties, such as Fiord. In severe cases the losses can be as high as 60% (Figure1). Frost dam-

age will be higher in the moisture limited conditions. Therefore, drought can aggravate the effect of frost.

Heat and drought tolerance

Faba bean is mostly grown as a rainfed crop and suffers from lack of moisture and increased heat stress towards the later part of growing season. Only limited research has been conducted on these aspects. It has been shown that carbon isotope discrimination at leaf level can be used to measure water use efficiency and this technique can be used as a selection criterion for improving drought tolerance in faba bean [8]. We also found a wide variation in faba bean root length that might be associated with drought tolerance.

Early flowering trait has been used as an escape mechanism to avoid heat stress. Yield losses as high as 62% were observed due to heat stress and yield reduction started when the mean temperature increased from 22°C. Podding and grain filling were the most sensitive developmental stages to heat stress. Early research indicated the existence of genetic variability and tolerant genotypes. Genotypes 11NF014b-14, 13NF433b 2, PBA Nasma, and 13NF439c-1 were identified as more tolerant to heat stress than others. Some of these lines are included in the crossing program to increase the heat tolerance.

Herbicide tolerance

Faba bean has better ability to compete weeds compared to chickpea and lentil because of its early vigor and larger canopy. Effective control can be achieved by pre-emergence herbicides as post-emergence herbicides are available only for grassy weed species. Weed control, however, is now becoming more difficult due to widespread evolution of herbicide-resistant weed biotypes. Therefore, continuous spraying with the same group of herbicides for a long time should be avoided by adopting crop rotations using differ-


ent herbicides. Faba bean is sensitive to phenoxy herbicides containing endogenous plant hormones, such as MCPA, 2,4-dichlorophenoxyacetic acid (2,4-D) and 2,4,5-trichlorophenoxyacetic acid (2,4,5-T). Residual effect and chemical drift from such herbicidal sprays can travel long distances causing severe damage (Figure 2). Integrated weed management involving crop rotations, rotation of herbicide groups, and combination of both chemical and non-chemical methods are recommended for weed control.

Extensive research is carried out to develop faba bean varieties with resistance to certain group of herbicides. PBA Bendoc has been released with tolerance to imidazolinone (Imi) (Group B) herbicide and several lines have been identified with tolerance to metribuzin (Group C). Recently a molecular marker linked to Imi tolerance has been identified and this marker has been used regularly for selection. Once such varieties are available it will make easier to control in-crop weeds in faba bean.

Breeding for better seed quality

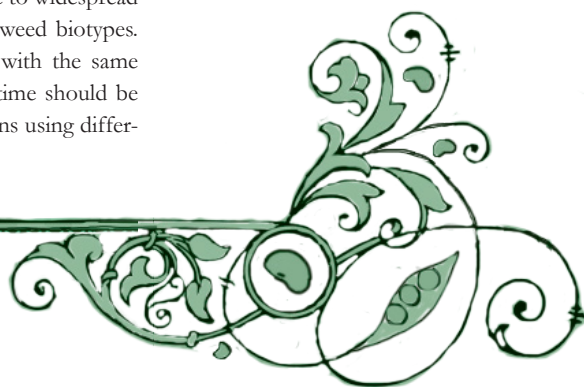
Faba bean protein content is relatively higher (24 to 35%) on dry basis than other cool season legumes. However, its grain contains two β -glucosides (up to 2% in dry weight basis): vicine and convicine (vc) which can cause favism to people lacking glucose-6-phosphate dehydrogenase (G6PD) enzyme in their body system. This can cause acute haemolysis, causing death in the absence of a proper medical care.

A single recessive gene, designated as vc-, controls the vc content. Although light hilum in the

seed cotyledon is linked to low vc content [9], this linkage is loose and it cannot be reliably used as a selection criteria. Recently, molecular markers are available for detecting its presence/absence [10]. We are employing molecular markers for selecting low vc lines in the breeding program and such lines will be commercially available for cultivation in the near future. 

References

- [1] Adhikari KN, Zhang P, Sadeque A, *et al.* (2016) Single independent genes confer resistance to faba bean rust (*Uromyces viciae-fabae*) in the current Australian cultivar Doza and a central European line Ac1655. *Crop Pasture Sci* 67: 649–654.
- [2] Sillero JC, Villegas-Fernández AM, Thomas J, *et al.* (2010) Faba bean breeding for disease resistance. *Field Crops Res* 115: 297–307.
- [3] Ijaz U, Sudheesh S, Kaur S, *et al.* (2021) Mapping of two new rust resistance genes Uvf-2 and Uvf-3 in faba bean. *Agronomy* 11: 1370.
- [4] Gela TS, Bruce M, Chang W, *et al.* (2022) Genomic regions associated with chocolate spot (*Botrytis fabae* Sard.) resistance in faba bean (*Vicia faba* L.). *Mol Breed* 42: 35.
- [5] van Leur JAG, Southwell RJ, Mackie JM (2008) *Aphanomyces* root rot on faba bean in northern NSW. *Aust Plant Disease Notes* 3: 8–9.
- [6] Rose I, van Leur J (2006) Breeding faba beans (*Vicia faba*) for adaptation to short season environments in Australia. In: *Proceedings of the breeding for success: Diversity in action. 13th Australasian Plant Breeding Conference*. Christchurch, New Zealand 18–21 April 2006. pp. 34–38.
- [7] Alharbi NH, Alghamdi SS, Migdadi HM, *et al.* (2021) Evaluation of frost damage and pod set in faba bean (*Vicia faba* L.) under field conditions. *Plants* 10: 1925.
- [8] Mukhtadir MA, Merchant A, Sadeque A, *et al.* (2022) Carbon isotope and soluble metabolites reflect physiological status among contrasting faba bean genotypes in response to water deficit. *Front Plant Sci* 13: 955406.
- [9] Duc G, Bao S, Baum M *et al.* (2010) Diversity maintenance and use of *Vicia faba* L. genetic resources. *Field Crops Res* 115: 270–278.
- [10] Khazaei H, Purves RW, Song M, *et al.* (2017) Development and validation of a robust, breeder-friendly molecular marker for the vc- locus in faba bean. *Mol Breed* 37: 140.



Vicia faba plant genetic resources preserved in home gardens in Sweden

by Matti W. LEINO^{1, 2*}

Abstract: Plant genetic resources of cultivated plants have rarely been preserved in commercial agriculture and horticulture in Sweden. Instead, many local cultivars have been found in home gardens. Over the last decades many, and variable, accessions of faba bean (*Vicia faba*) have been gathered and are now preserved at the Nordic gene bank – NordGen.

Keywords: ethnobotany, gene bank, *in situ* conservation, landrace, local cultivars.

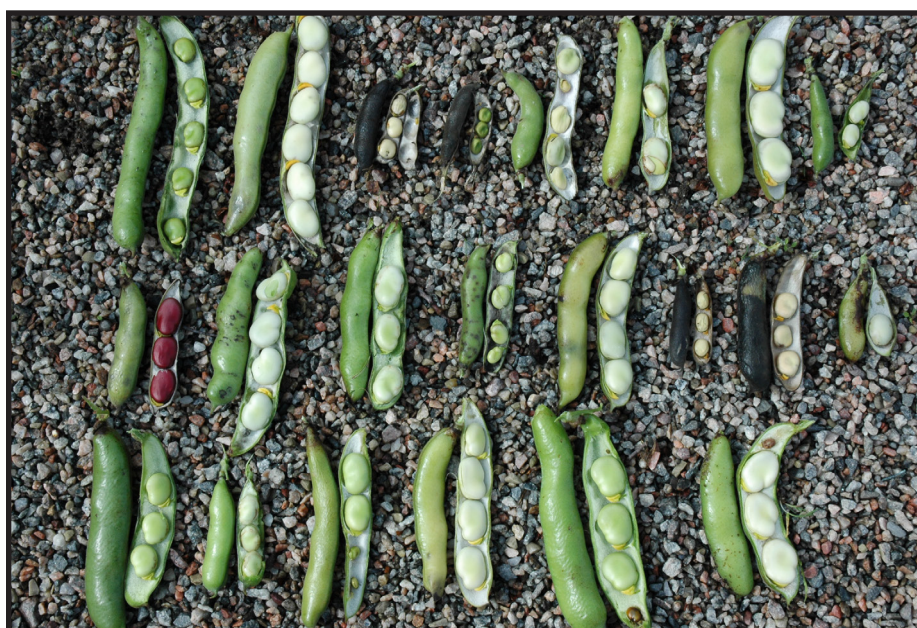


Figure 1. Pods from 22 of the 35 Swedish local cultivars. The material display large variation in earliness, seed and pod size.

Already in the early 20th century, farmers and gardeners in Sweden began to abandon their traditional varieties of cereals and legumes and replace them with modern varieties produced by plant breeding [1]. Thus, when the Nordic gene bank was inaugurated in the 1970s, efforts to gather local varieties and landraces from farms and market gardens were met with limited success. As suggested by Galluzzi *et al.* [2] an alternative source of plant genetic resources are small-scale home gardens where traditional crops have been preserved for other reasons than maximized harvests.

Since the 1990s, the Nordic Gene bank, the National program for diversity of cultivated plants and different NGOs, have launched several calls and inventories directed to home gardens [3]. These have been particularly successful in finding local material of grain legumes, mainly peas (*Pisum sativum*), but also beans (*Phaseolus vulgaris*) and faba beans (*Vicia faba*).

In total, 35 accessions of faba beans were found in Sweden and are today preserved at the Nordic gene bank – NordGen. Geographically, most accessions originated in the southern part of Sweden, but not in the regions with the high-

¹ AFL, Stockholm University, Stockholm, Sweden


² Grain legume working group, NordGen, Alnarp, Sweden

* matti.leino@arklab.su.se

est average temperatures or longest growing seasons. In these regions, common beans were instead more abundant. Broad beans dominated among the finds, but some accessions were smaller seeded faba beans and some were intermediate in shape. Most accessions are clear garden types, but some had originally been cultivated in field scale and were more recently transferred to and preserved in gardens.

Many accessions had been preserved as family heirlooms, associated with family or culinary traditions, typically various kinds of bean porridge. In many cases, their history could be traced back one hundred years or more. A special case are several accessions from the western archipelago. Here, the local varieties of faba beans were used

as a supporting crop for tall-stemmed field peas. In some other locations, faba beans had been intercropped with potatoes.

Test cultivation of the accessions reveal large morphological variation (Figure 1). The traits of the material and its potential use in breeding remains to be fully evaluated, but some accessions have already proved valuable. For example, the local cultivar 'Gubbestad', proved to have the highest protein content in a characterisation of North European modern and landrace cultivars [4]. Other putatively interesting traits could be related to climate adaptation, such as earliness and day light response. The material is freely available for research and breeding at NordGen (www.nordgen.org). 

References

- [1] Leino MW (2021) Primitive landraces: Swedish farmers' perception on seed traits before the era of crop improvement. In: BG Karlsson, A Rabo (eds.), *Seedways: The Circulation, Control and Care of Plants in a Warming World*. (KVHAA: Stockholm).
- [2] Galluzzi G, Eyzaguirre P, Negri V (2010) Home gardens: neglected hotspots of agro-biodiversity and cultural diversity. *Biodivers Conserv* 19: 3635–3654.
- [3] Nygård L, Leino MW (2013) Klint Karins kålrot och Mor Kristins böna: om Fröuppropets kulturarv. SLU, Programmet för odlad mångfald.
- [4] Bodner G, Kronberga A, Lepse L, *et al.* (2018) Trait identification of faba bean ideotypes for Northern European environments. *Eur J Agron* 96: 1–12.



AdobeStock™ image

Management factors affecting faba bean yield

by Kiflemariam Y. BELACHEW^{1,2}, Annika SÖDERHOLM-EMAS^{2,3}, Cairistiona F.E. TOPP⁴,
Christine A. WATSON^{5,6}, Frederick L. STODDARD^{2,6*}

Abstract: Faba bean yields are often lower than they could be if appropriate interventions were taken. We surveyed literature on quantitative impacts of management choices related to region of adaptation, soil and water management, nitrogen nutrition and pollination. At least six adaptation classes can be resolved, differing in autumn vs spring sowing and maturity time. The crop is very responsive to alleviation of drought, soil compaction, soil acidity and waterlogging. The crops dependence on bee-mediated pollination is well known, but there are no guidelines on the adequacy of pollination in a commercial crop. Recognition of stress symptoms and the application of appropriate inputs can enable farmers to greatly increase crop yields.

Key words: *Vicia faba*, pollination, irrigation, adaptation, phenology, drought

Faba bean (*Vicia faba* L.) was one of the original crops domesticated in the Fertile Crescent about 10,000 years ago. It is grown on all inhabited continents, with about 4 million tonnes produced each year. Of the starch-containing legumes, it has the highest protein content, the global average being 29% of dry matter and its global average yield is 2.0 t/ha, equal to that of pea [1], so its potential protein yield per hectare is high. In favourable conditions, its yields exceed 5 t/ha, and there is a competition in the UK for the first 10 t/ha crop. Yield is, however, constrained by many biotic and abiotic stresses, some of which can be ameliorated by on-farm practices. In the recent ERANET SusCrop project 'LegumeGap', we reviewed the potential for crop management factors to affect yield of faba bean, with the main focus on Europe. Data points were extracted from 256 articles and some of the key quantitative outcomes are given here.

Classes of adaptation

Appropriate phenology is necessary for optimum yield. The germplasm of this crop falls into a handful of discrete adaptation classes, based on the combination of adaptation analyses and agro-climatic maps. The crop needs to flower when there is no risk of frost and mature when conditions are suitable for harvest, neither too wet nor too hot.

Mediterranean-adapted cultivars are sown in the autumn under shortening days and harvested in the spring under lengthening days, before

conditions become too hot and dry. Time of flowering, soon after the winter solstice, is a critical trait [2]. In the oceanic climate of northwestern Europe, winter-hardy cultivars have a growing season of up to 11 months, with a vernalization requirement that prevents flowering until spring [3]. Spring-sown material showed separate adaptation into continental and oceanic adaptation classes [4], and more recent experience shows that sub-Boreal material, with its shorter growing season, forms a third class. Germplasm in South America and Australia is largely derived from Mediterranean material, while that in central North America is primarily of European continental origins with some admixture from China. Ethiopian highland germplasm is distinctive, being adapted to moderate day-length and high rainfall. In China, faba bean is grown in as wide a range of climates as in Europe.

Seed size is a critical factor for both markets and adaptation. In the sub-boreal climates of northern Europe and central Canada, small seeds (< 350 mg) are preferred because of the necessity for rapid seed-filling and post-harvest drying. Even smaller seeds (150–200 mg) are typical of Nepalese and Bangladeshi cultivars that have a very short growing season between other crops. Large seeds (> 1 g) are preferred for food use in the Mediterranean basin and western Asia, in spite of their long seed-filling period and low multiplication rate. Some of these accessions have massive root systems that explore the soil volume for water and nutrients, which may be an adaptive advantage in these low-rainfall regions [5].

1 Department of Geosciences and Geography, University of Helsinki, Finland

2 Department of Agricultural Sciences, University of Helsinki, Finland

3 Länsi-Uudenmaan vesi ja ympäristö, Lohja, Finland

4 Department of Agriculture, Horticulture and Engineering Sciences, Scotland's Rural College, Edinburgh, UK

5 Rural Land Use Department, Scotland's Rural College, Aberdeen, UK

6 Department of Crop Production Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden

* frederick.stoddard@helsinki.fi



Figure 1. Faba bean plots in Finland suffering from (a) drought and (b) waterlogging; plots in Ethiopia (c) at pH 4.2 and (d) limed to pH 6.0; flowers in Finland being pollinated by (e) a honeybee and (f) a bumblebee.

Soil and water management

Faba bean is recognized as a drought-sensitive crop and in most climates it performs best on a moisture-retentive clay-rich loam with a pH near neutral. The lower rainfall limit for its growth in rainfed agriculture is about 400 mm [6]. It survives waterlogging (Figure 1) and soil compaction better than some other crops, but yield losses are still large; in nine comparisons, yield losses due to soil compaction were 10 to 50%, averaging 28%.

Irrigation brought yield benefits in about 75% of cases, but there was a risk of providing too much water (Figure 2). The average yield benefit was 33% when the amount of irrigation water was calculated from the measured moisture deficits, and 53% at drier sites where the amounts of required water were simply estimated. The largest effects, up to 3-fold, were seen when water was supplied during and after flowering in Mediterranean climates of western Asia and southern Australia. Nevertheless, in northern Europe, the yields of rainfed field experiments track the amount of growing season rainfall closely [7] and national average yield figures clearly show the effects of drought years.

Irrigation should be more widely used on this crop.

It is well known that soil acidity restricts faba bean growth both directly due to pH and indirectly due to solubilization of Al^{3+} ions. We have found no reports of experiments titrating responses to rootzone pH across a range of values, so one is in progress at SRUC. A soil pH value below 5.5 requires correction. In field experiments in Ethiopia, plots at an uncorrected soil pH of 4.2 died during the flowering stage, but those limed to a pH of 6.0 produced a harvestable yield of 3 tonnes/hectare (Figure 1 c and d).

Zero tillage almost always showed a yield advantage over conventional, where the soil is turned to a depth of 20–25 cm (Figure 2). The average benefit was 25%, with the greatest values from experiments in Spanish vertisols where the benefits included moisture retention, maintenance of soil organic matter, aggregate stability, and agrochemical control of the parasitic weed, broomrape [8]. Other modified tillage systems, whether shallow or deep, had little effect on crop yield compared with conventional tillage (Figure 2).

Is there enough biological nitrogen fixation?

The bacterium responsible for biological nitrogen fixation in symbiosis with faba bean, *Rhizobium leguminosarum* biovar *viciae*, is widespread in arable soils, so it may be asked whether it is worth inoculating the seeds with an effective race before sowing. Our dataset suggests that it is (Figure 2). In no case was there a significant detriment from inoculation and even when it was only one year since a related crop had been grown, there was, on average, a 19% yield benefit from inoculation. The mean benefit was 33% when the interval since the previous related legume was two years and 60% when there was no history of legumes in the field. More than half of the data points came from papers where there was no mention of previous history of legumes in the field, and the mean benefit from inoculation was 41%. Inoculation costs the farmer time, so the economic threshold for benefit is several percent above the statistically significant threshold.

On average across 140 studies, 71% of nitrogen was derived from atmosphere [9]. How much N fertilizer does a faba bean crop need? Our review found little evidence of yield benefits across a range from 50 kg/ha to 600 kg/ha of applied N. Starter N at 20–40 kg/ha is widely recommended by advisory agronomists, but there is little scientific evidence for or against it.

Pollination: beans need bees

Much work has been done on the mixed breeding system of faba bean, to define the proportion of flowers that can pollinate themselves in the absence of bee activity (autofertility) and how that varies between cultivars and environments. Other work has evaluated the relative importance of honeybees and various wild bee species as effective pollinators (Figure 1 e and f), and measured the impact of bee activity on the growth and vigour of the subsequent crop. Honeybees and short-tongued bumblebees collect only pollen from the front of the flowers during pollinating visits and collect nectar from holes bitten at the base of the flower (note black

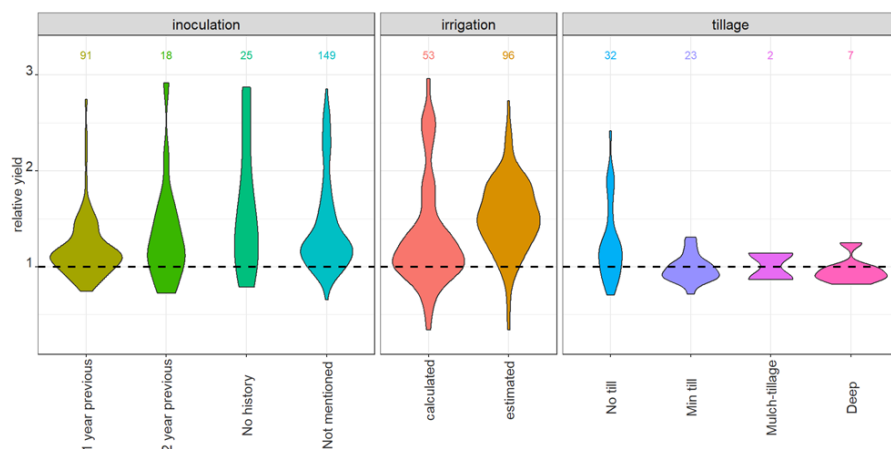


Figure 2. Relative yield in experiments testing the effects of inoculation with *Rhizobium leguminosarum* bv viciae compared with no inoculation, irrigation with amounts either calculated or estimated from water deficit compared with rainfed, or subjected to different tilling treatments compared with conventional tillage. Numbers above the plots show the number of observations per treatment.

mark in Figure 1 e). Long-tongued bees collect both pollen and nectar in pollinating visits. The average yield reduction without insect-mediated pollination was 33%, and it was 80% certain that pollination would result in a higher yield [10]. In terms of crop management, however, the most important question for a farmer is: How much of that 33% of yield is my crop in danger of losing, given its current bee population? Is my crop getting enough pollination, or should I bring in hives of honeybees? The question is hard to answer because of heterogeneity between and within fields, cultivars and seasons. Surveys of British crops found that as little as 25% of early flowers on autumn-sown (winter) beans were pollinated in some fields at the same time as nearly 75% were in others [11]. Even so, that minimum equated to two flowers per raceme, which is a typical load for a healthy plant. By quantifying criteria such as the number of effective visits per minute and the number of flowers per square metre, it would be possible to develop a rule of thumb on the number of honeybees per square metre needed for full pollination of a crop.

Conclusion

National average yields of faba bean fall well short of what the most productive crops achieve. Many of these shortfalls can be fixed by timely decisions and interventions, such as relieving soil compaction or liming to raise soil pH. Inoculation with *Rhizobium* and contracts with local beekeepers are low-cost insurance mechanisms for these unpredictable biotic interactions. Water management, especially during flowering and early pod-filling, appears to be the greatest determinant of yield, and the intervention requiring the greatest investment in infrastructure. A survey conducted under the LegumeGap project has shown that there are substantial gaps in farmer knowledge about these important issues (papers in preparation).



Acknowledgements

The work was financed by the SusCrop- ERA-NET' project LegumeGap (Grant 031B0807B) with funding from the Ministry of Agriculture and Forestry of Finland (MMM) and the Department for Environment, Food and Rural Affairs of the UK (DEFRA), with further support from the Scottish Government's Strategic Research Programme.

References

- [1] FAOstat (2023) Faostat.fao.org. Visited 10.08.2023
- [2] Mwanamwenge J, Loss S, Siddique K, *et al.* (1998) Growth, seed yield and water use of faba bean (*Vicia faba* L.) in a short-season Mediterranean-type environment. *Aust J Exp Agric* 38: 171–180.
- [3] Flores F, Nadal S, Solis I, *et al.* (2012) Faba bean adaptation to autumn sowing under European climates. *Agron Sustain Dev* 32: 727–734.
- [4] Flores F, Hybl M, Knudsen JC, *et al.* (2013) Adaptation of spring faba bean types across European climates. *Field Crops Res* 145: 1–9.
- [5] Belachew KY, Nagel KA, Fiorani F, *et al.* (2018) Diversity in growth responses to moisture deficit in young faba bean (*Vicia faba* L.) plants. *PeerJ* 6: e4401.
- [6] López-Bellido R, López-Bellido L, López-Bellido F, *et al.* (2003) Faba bean (*Vicia faba* L.) response to tillage and soil residual nitrogen in a continuous rotation with wheat (*Triticum aestivum* L.) under rainfed Mediterranean conditions. *Agron J* 95: 1253–1261.
- [7] Skovbjerg CK, Knudsen JN, Füchtbauer W, *et al.* (2020) Evaluation of yield, yield stability and yield-protein relationship in 17 commercial faba bean cultivars. *Leg Sci* 3: 39.
- [8] López-Bellido R, Benítez-Vega J, López-Bellido L (2009) No-tillage improves broomrape control with glyphosate in faba-bean. *Agron J* 101: 1394–1399.
- [9] Palmero F, Fernandez JA, Garcia FO, *et al.* (2022) A quantitative review into the contributions of biological nitrogen fixation to agricultural systems by grain legumes. *Eur J Agron* 136: 126514.
- [10] Bishop J, Nakagawa S (2021) Quantifying crop pollinator dependence and its heterogeneity using multi-level meta-analysis. *J Appl Ecol* 58: 1030–1042.
- [11] Stoddard FL (1986) Pollination and fertilization in commercial crops of field beans (*Vicia faba* L.). *J Agric Sci* 106:89–97.

Current faba bean research at Göttingen, Germany

by Lisa BRÜNJES, Wolfgang Ecke, Alex WINDHORST, Henri Laugel, Wolfgang LINK*

Abstract: Faba bean breeding research at Göttingen has been held for over five decades. Current projects include studies on freezing tolerance, pollinators and reproductive behavior, seed-weight variance, as well as identifying highly inbred individuals existing a priori in faba bean populations. The focus of the projects is on plant breeding methodology, to improve future breeding schemes.

Key words: breeding methodology, inbred lines, QTL, synthetics, seed weight, winter hardiness

The grain legume faba bean is cultivated as both a spring- and autumn-sown crop in Europe. While in the Mediterranean Basin, faba beans are typically sown in autumn to exploit the rain-fed winter months, they are mainly cultivated as spring crop north of the Alps. The genuine winter faba bean is only cultivated in North-West (NW) Europe. Mild winter conditions favor large-scale winter faba bean production in the UK and France, where winter beans accounted for approximately 40% (75,000 ha) and 75% (51,308 ha) of the respective total faba bean cultivation area in 2022 [1]. Despite the yield advantage over the spring-type, the cultivation of winter faba bean remains limited in other countries of NW Europe due to the insufficient winter hardiness of current cultivars. Consequently, breeding for improved winter hardiness is of great importance to facilitate local plant protein production in NW European countries, like Germany. One substantial aspect of winter hardiness is tolerance against frost

in winter and against frost in early spring (late-frost), which occurs in early spring when plants have lost their cold acclimation, i.e., are dehardened.

In our ongoing project, we have adapted the sophisticated climate chamber frost stress protocol, initially developed in 2003 and subsequently refined [2,3,4], to include late-frost treatments on dehardened plants [5]. We tested a broad panel of inbred lines, most derived from the “Göttingen Winter Bean Population” plus further diverse types. The lines were exposed to frost in a climate chamber and phenotyped. Utilizing recent developments in faba bean genomics, such as the 60K Vfaba_v2 Axiom SNP array [6] and the V. faba reference genome, we identified via genome-wide associations studies (GWAS) multiple validated quantitative trait loci (QTL) associated with tolerance against frost and late-frost, e.g., for freezing damage (Figure 1) and survival after frost. Currently, we are developing genomic prediction models for winter-frost and late-frost tolerance as well as field-based traits such as yield.

Faba bean is a partially allogamous species. European faba bean cultivars are usually synthetic populations which utilize part of the het-



Figure 1. Differentiation for frost damage among four different winter faba bean inbred lines on juvenile potted plants after frost stress in a climate chamber experiment. Shown are two plants per inbred line and pot corner. Frost damage is visible as loss of leaf turgidity and loss of color in leaf and stem (blackening of tissue).

Georg-August University Göttingen, Division of Plant Breeding Methodology, Germany

* wlink@gwdg.de

erosis. As yield and yield stability are improved in heterozygous and heterogeneous crop stands, increasing the share of heterosis in synthetic cultivars is a promising breeding strategy. High rates of cross-fertilization increase the share of heterosis realized in synthetic cultivars. Hence, the degree of cross-fertilization is a crucial parameter in breeders' yield predictions and used to predict inbreeding and share of heterosis. Available yield predictions assume that all genotypes contribute equally to the cross-fertilized seeds. We found genotypes to significantly and markedly differ in success rates as pollen donors [7]. Yet, allowing such differences in paternal outcrossing success in a population increases its inbreeding, thus decreases yield. Hence, differences in paternal success should be avoided.

To circumvent expensive paternity assessments, reproductive traits that are easier to assess were estimated for the same sixteen genotypes. Pollen production and pollen viability were highly correlated with paternal success in inbred lines (Brünjes and Link, under preparation). Hence, these traits could be used as proxy

for paternal outcrossing success when selecting inbred lines as components of a synthetic.

As higher degrees of cross-fertilization improve seed yield in the next generation, we studied the pollination efficiency of individual bee species to pollinate faba bean. The most efficient pollinator species that enhanced cross-fertilization and seed set was *Bombus hortorum*, a less frequent and more specialized pollinator species with long head and long tongue (Figure 2). It effectuated 45% cross-fertilization, while the other species including honeybee realized less than 20% cross-fertilization each [8]. Thus, synthetic populations should be propagated in environments with large and vital *B. hortorum* populations, to maximize the genotype-specific degree of cross-fertilization and realize higher heterozygosity in subsequent generations, to better manage and exploit heterosis in faba bean.

To compose a synthetic, inbred lines are used. To develop them is tedious, as no doubled haploid technique is available, and faba beans need manual 'tripping' and bee-proof cages for selfing. Yet due to its mixed mating, faba bean pop-

ulations a priori contain individuals with very different inbreeding status, including highly inbred individuals (expectedly > 5%). We use KASP SNP markers and the 60K Vfaba_v2 Axiom SNP array [6] to investigate and exploit this situation within the 'Göttingen Winter Bean Population'. Moreover, Genomic selection will be applied to 'chipped seed'; a non-destructive method to extract DNA from faba bean seed cotyledons. In the end, the use of inbred lines in both line and population breeding will be facilitated to optimize breeding schemes [9].

The huge differences in faba bean's seed size made us analyse this domestication trait. First, from a cross of two lines differing strongly in seed weight, 'HediLin' (Thousand seed weight (TSW) 350 g) × 'PietraLin' (TSW 3000 g), we developed two near isogenic lines (NILs), one small-seeded and one large-seeded. These NILs are much more similar in growth and development than the initial parents, but still show an about two-fold difference in seed weight. Crossing these two NILs, we obtained N=180 recombinant inbred lines that were used to map

Table 1. QTL for seed weight in faba bean mapped in our RIL population.

Mapped QTL					Effects		Confidence intervals		
No.	QTL	LG	Position [cM]	LOD	Add. [mg]	Variance explained [%]	^b Low [cM]	^b Up [cM]	^b Size [cM]
1	sw1c.1AB	c.1AB	1.40	16.2	-36.2	6.6	0.56	2.24	1.68
2	sw1c.1CDsgl	c.1CDsgl	38.93	36.8	-72.6	20.3	38.08	39.49	1.41
3	sw2c.1CDsgl	c.1CDsgl	57.49	13.9	-37.2	5.5	56.64	63.00	6.36
4	sw1c.1EF	c.1EF	34.33	8.5	-25.2	3.1	28.06	38.82	10.75
5	sw1c.1GHI	c.1GHI	5.91	12.2	-30.8	4.7	4.00	7.32	3.32
6	sw2c.1GHI	c.1GHI	40.25	7.6	+14.0 ^a	2.8	36.00	44.18	8.18
7	sw1c.2J	c.2J	1.00	12.0	-30.6	4.6	0.00	3.40	3.40
8	sw1c.4N	c.4N	13.52	19.7	-40.3	8.5	12.39	14.91	2.52
9	sw2c.5RSTU	c.5RSTU	4.00	6.6	-25.9	2.4	1.40	6.73	5.33
10	sw1c.5RSTU	c.5RSTU	17.98	12.2	-32.9	4.7	15.18	18.83	3.64
Full model		-	-	79.5	-	87.4	-	-	-

LG: linkage group, c.1 to c.5 indicate the chromosomes to which the linkage groups belong, A to U refer to the segments polymorphic between the NIL parents of the mapping population that make up the linkage groups.

LOD: logarithm of the odds showing the statistical probability (10^{LOD}) of the QTL being real.

^a the positive sign indicates that the allele of the small-seed parent increases seed size; ^b Low = Lower confidence interval, Up = Upper confidence interval, and Size of LOD 2.0 support intervals for the QTL positions



Figure 2. Long-tongued *Bombus hortorum*, the most efficient pollinator among five local bee species at Göttingen.

ten QTLs for seed weight. For nine of them, the allele of the large-seeded parent 'PietraLin' increased seed weight, yet, for one QTL (Table 1), the 'increase' allele came from small-seeded 'HediLin'. With a model including all 10 QTL, we could explain 87.4% of the phenotypic variance for seed weight in this cross. Hence, our QTL mapping captured the majority of the seed-weight loci.

In the past decades, only the Georg-August University Göttingen (www.uni-goettingen.de/de/48273.html) was home to a German academic group working on faba bean breeding. Recently, new groups in Germany joined faba bean research (University Giessen, JKI Quedlinburg, IPK Gatersleben) meaning good prospects for progress in research and in farmers' fields. 🌱

Acknowledgements

Donal O'Sullivan, University of Reading, UK for the Axiom SNP array. Funding: ProFaba/SusCrop, DFG (LI 486/9-1), DBU-20014/302, BLE/BMEL_2820EPS003, Eigen-Brauer-Foundation.

References

- [1] Sass O (2022) Ackerbohnen und Erbsen – ist die Züchtung aus den Startlöchern? UFOP Pflanzenprotein Symposium "Local Heroes". Nov 22, 2022, Berlin. https://www.ufop.de/index.php/download_file/view/12001/2049/. (Accessed Jan 31, 2023)
- [2] Arbaoui M, Balko C, Link W (2008) Study of faba bean (*Vicia faba* L.) winter-hardiness and development of screening methods. *Field Crops Res* 106: 60–67.
- [3] Roth F, Link W (2010) Selektion auf Frosttoleranz von Winterackerbohnen (*Vicia faba* L.): Methodenoptimierung und Ergebnisse. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 60. Jahrestagung 2009, Raumberg-Gumpenstein, Austria, pp. 31–37.
- [4] Ali MBM, Welna GC, Sallam A, *et al.* (2016)

Association analyses to genetically improve drought and freezing tolerance of faba bean (*Vicia faba* L.). *Crop Sci* 56: 1036–1048.

- [5] Windhorst A, Skovbjerg CK, Andersen SU, *et al.* (2023) Improving overwintering in times of climate change - A GWAS for late-frost tolerance of winter faba bean. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 73. Jahrestagung 2022, 21-23 November, Raumberg-Gumpenstein, Austria, pp. 29-36.

- [6] O'Sullivan DM, Angra D, Harvie T, *et al.* (2019) A genetic toolbox for *Vicia faba* improvement. In: International conference on legume genetics and genomics, May 13–17, 2019. Dijon, France.

- [7] Brünjes L, Link W (2021) Paternal outcrossing success differs among faba bean genotypes and impacts breeding of synthetic cultivars. *Theor Appl Genet* 134: 2411–2427.

- [8] Marzinzig B, Brünjes L, S Biagioni S, *et al.* (2018) Bee pollinators of faba bean (*Vicia faba* L.) differ in their foraging behaviour and pollination efficiency. *Agric Ecosyst Environ* 264: 24–33.

- [9] Adhikari KN, Khazaei H, Ghaoui L, *et al.* (2021) Conventional and molecular breeding tools for accelerating genetic gain in faba bean. *Front Plant Sci* 12: 744259.



Progress in faba bean breeding for adaptation to Southern European rain fed farming systems with a focus on stress resistance

by Diego RUBIALES*, Ángel M. VILLEGAS-FERNÁNDEZ

Abstract: Faba bean is a temperate grain legume whose cultivation declined largely in Europe after the onset of modern agriculture. In Southern Europe there is an interest in reintegrating faba bean into rain fed farming systems what requires locally adapted cultivars that can satisfy the needs of both the producers and of the consumers. Germplasm with varying levels of resistance to some of the major diseases have been identified but are not always readily incorporated into elite cultivars. A few DNA markers have already been developed for key diseases such as ascochyta blight, rust and for the parasitic weed broomrape although have insufficiently used so far in marker assisted selection. Some progress has been achieved to identify genotypes with tolerance to drought, which will probably be a major issue in the near future. Faba bean resistance breeding will undoubtedly speed up with the adoption of rapidly developing genomic resources, complemented with proper phenotyping and speed breeding techniques.

Key words: genomics, phenomics, resistance, diseases, parasitic weeds

State of the art on faba bean breeding for stress resistance:

Faba bean (*Vicia faba* L.) is an annual grain legume crop with high protein that plays a major role in sustainable agriculture. Its cultivation in Southern Europe has suffered a decline since the middle of 20th century, with acreage decreasing from more than 830,000 ha in the beginning of the 1960s to just 109,000 ha in 2021. There is a growing interest in revalorizing the crop globally, but particularly in Mediterranean rainfed farming systems, where there is a tradition of use faba bean types for human food in addition to the most known types for animal feed. There is also great potential of faba bean crop in organic farming.

One of its major challenges is the existence of an array of biotic and abiotic stresses that affect the plants and compromise yields. Deployment of genetic resistance against major pests and disease is core in any integrated control strategy. However, the insufficient understanding of the genetic basis in many instances [1] and the slow development of genomic resources has retarded the successful application of molecular assisted selection (MAS) in faba bean breeding programs comparing to other legume crops. In recent decades, however, genomic resources are speedily expanding, which will facilitate MAS and gene discovery in faba bean.

In Southern Europe, the most widespread fungal diseases, and the better characterized ones, are rust, ascochyta blight and chocolate spot. There exist also other diseases that may reach importance at the local level, such as downy mildew, alternaria blight or cercospora leaf spot, but no doubt the major biotic constraints are root parasitic weeds.



Figure 1. Rust susceptible accession, with well-formed pustules (left), compared with an accession displaying incomplete, late action hypersensitive response.

Rust is incited by *Uromyces viciae-fabae*, which presents host specialization, so that faba bean isolates do not infect well lentil or vetches, and the other way around. Races have been suggested within the faba bean infecting isolates, but their distribution has not been systematically monitored anywhere. Partial resistance not based in hypersensitive response is rather common, but its inheritance has been insufficiently studied, with no QTLs reported so far. Monogenic resistance causing “late acting” hypersensitivity (Figure 1) is also known [2]. A number of accessions presenting several degrees of resistance to rust have been described in the region, mainly in Spain, where the disease was extensively studied at Córdoba in past decades: V-300, V-313, V-1271, V-1272, V-1273, V-1335 2N34, 2N52, LPF 120, BPL 710, 132-3, 158-1, and 095-3 [1, 3]. Registered cvs. Joya and Omeya present hypersensitive resistance, while registered cv. Borjana shows intermedium levels of non-hypersensitive resistance.

Institute for Sustainable Agriculture, CSIC, Córdoba, Spain

* diego.rubiales@ias.csic.es



Figure 2. Leaves and stems (left) and pods (right) of faba bean showing symptoms of ascochyta blight.

Ascochyta blight (Figure 2) is a foliar disease incited by *Didymella fabae* (anamorph *Ascochyta fabae*). Spores are carried and distributed by infected seeds and crop debris. Infection can also be started by wind dispersed ascospores. Then, rain and wind disperse the conidiospores. There is no consensus in the definition of races. Some levels of incomplete resistance are available. In Southern Europe the screening for resistance has been carried out mainly at Córdoba where promising accessions have been identified (i.e., L-831818, V-6, V-26, V-255, V-958, V-1020, V-1085, and V-1117) [1, 4]. Earlier reports pointed towards major gene inheritance, but recent studies suggest complex inheritance with some QTLs identified [5]. To the far of our knowledge no cultivars with resistance to ascochyta blight have been registered in this area.



Figure 3. Faba bean plant showing chocolate spot symptoms.

Chocolate spot (Figure 3) is incited mainly by *Botrytis fabae*. *B. fabae* specialization on faba bean has been ascribed to its production of the phy-


totoxins botrytone and regiolone. Variation in virulence has been suggested among *B. fabae* isolates but no races have been described so far. Accessions with a high degree of resistance have been selected at Córdoba BPL 1763, 135-1, and IBL 4726 among others) [1, 3] and some resistant cultivars have been developed, including cvs. Arrechana, derived from accession 135-1, and cv. Borjana, derived from BPL 710, are moderately resistant.

Root parasitic weeds like broomrapes are the largest problem the Mediterranean Basin and Middle East. *Orobancha crenata* which is the most widespread, and the only one problematic at present in southern Europe although attention should be paid also to *O. foetida* that is problematic in Tunisia and to *O. aegyptiaca* that can be a problem in eastern Mediterranean countries. Resistance breeding has been extensive in several Mediterranean programs (Figure 4). Interestingly, reported resistances use to be effective in multiple environments, even against both *O. foetida* and *O. crenata* or even against *P. aegyptiaca*. Most breeding programs relied on the Egyptian G402 as donor of resistance. In



Figure 4. Genotypes of faba bean resistant (left) and susceptible (right) to broomrape in experimental fields in Córdoba.

addition to this at Córdoba we are incorporating additional sources of resistance like the ones conferring reduced induction of broomrape seed germination or hampered establishment by reinforcement of cell walls by callose deposition, complemented by lignification of endodermal cells [6]. Interestingly, occasional observations suggest that the inheritance of this non-germination trait in faba bean may be simple, which would facilitate resistance breeding and its pyramiding with other resistance mechanisms. Cvs. Baraca, Joya, Omeya and Habanita, developed at Córdoba are resistant to broomrape.

Abiotic stresses: Southern European climate is characterised by mild winters and warm springs, with erratic rain concentrated in winter, causing periodic episodes of intermittent and terminal drought by the end of the season. With climate change, higher temperatures occur earlier and droughts become more common, making tolerance to heat waves and to drought a priority in faba bean breeding. Preliminary screenings identified drought tolerance in BPL 710, Baraca, 135-1, V-1020, and V-255. 

References

- [1] Rubiales D, Khazaei H (2022) Advances in disease and pest resistance in faba bean. *Theor Appl Genet* 135: 3735–3756.
- [2] Avila CM, Sillero JC, Rubiales D, *et al.* (2003) Identification of RAPD markers linked to *Uryf-1* gene conferring hypersensitive resistance against rust (*Uromyces viciae-fabae*) in *Vicia faba* L. *Theor Appl Genet* 107: 353–358.
- [3] Villegas-Fernández AM, Sillero JC, Emeran AA, *et al.* (2011) Multiple-disease resistance in *Vicia faba*: Multi-environment field testing for identification of combined resistance to rust and chocolate spot. *Field Crops Res* 124: 59–65.
- [4] Rubiales D, Avila CM, Sillero JC, *et al.* (2012) Identification and multi-environment validation of resistance to *Ascochyta fabae* in faba bean (*Vicia faba*). *Field Crops Res* 126: 165–170.
- [5] Atienza SG, Palomino C, Gutiérrez N, *et al.* (2016) QTLs for ascochyta blight resistance in faba bean (*Vicia faba* L.): validation in field and controlled conditions. *Crop Pasture Sci* 67: 216–224.
- [6] Rubiales D (2018) Can we breed for durable resistance to broomrapes? *Phytopathol Mediterranea* 57(1): 170–185.

Status of faba bean in North and East Africa, limitations, and prospects

by Lynn ABOU KHATER, Fouad MAALOUF*

Abstract: Being a multi-purpose crop, faba bean (*Vicia faba* L.) is highly valued in North and East Africa, however its production is still below the demand and its productivity remains low in many countries. This is primarily due to a combination of factors including the dominance of low yielding cultivars, the weak seed system in many countries, the susceptibility to abiotic and biotic stresses, the lack of improved cultivars and the lack of extension. These limitations should be addressed by scientists and agricultural policy makers for a more successful and promising faba bean production.

Key words: East Africa, faba bean, limitations, North Africa, prospects

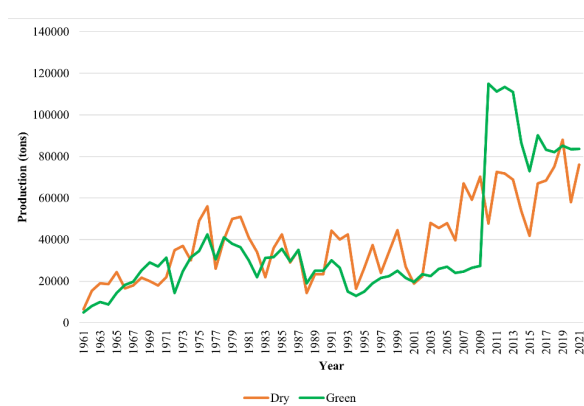


Figure 1. Evolution of faba bean dry and green productions over the years.

Faba bean (*Vicia faba* L.) ranks first among the cool season food legumes grown in North and East Africa, with production averaging 1.6 and 0.7 million tons harvested from 0.76 and 0.07 million ha for dry and green faba bean respectively [1]. The decreasing trend of faba bean acreage in North Africa contradicts with the one of East Africa; however, the production has increased in both regions which can be attributed to agronomic achievements and breeding efforts, but this production does not seem to meet the high consumption of faba bean.

Not until this year that the green faba bean data were included in FAOSTAT which resulted in a more accurate estimation of the total production and acreage. Besides being primarily consumed as dry seeds in North and East Africa, faba bean green pods and grains have become very popular in many north African countries like Egypt for example (Table 1) where their production has surpassed the one of dry seeds in the recent years as illustrated in Figure 1. This can be attributed to changes in consumer preferences in the Nile Delta, to the opportunity

of using the produce as a cash crop and to the high yield of green faba bean compared to the one of dry faba bean grains.

Table 1. Production (tons) of dry and green faba bean in the main producer countries of North and East Africa.

	Country	Production (tons)	
		Dry	Green
North Africa	Algeria	39629	277353
	Egypt	105051.6	190937
	Morocco	131208.3	72338
	Tunisia	76000	83605.1
East Africa	Sudan	176691.7	NA
	Ethiopia	1089489	11510.5

Egypt leads the dry faba bean exports on both regional and global levels, whilst Ethiopia leads the faba bean production and is the second major producer on the global level [1]. But the productivity of faba bean in Ethiopia is still far below its yield potential which prevented the ex-

International Centre for Agricultural Research in Dry Areas (ICARDA)

* f.maalouf@cgiar.org

port of the crop as almost all the production is sold in the domestic markets.

Faba bean is a versatile crop; it is of great value for both human and animal nutrition. It is considered a staple food in the diet of millions of people in North and East Africa and considered an affordable source of protein [2] in many low-income countries like Ethiopia, Sudan, and Egypt. Although the use of faba bean as animal feed has been limited due to its antinutritional components [3], faba bean straw is considered a cash crop in Egypt and Sudan [4]. In addition, faba bean offers many services for the agroecosystem [5]. However, recent statistics suggest that North and East African countries are still adopting the cereal monoculture cropping system. The limited inclusion of faba bean in their cropping system might be due to many factors like: a) the seasonal prices instability and low productivity of the local cultivars as the dry small seeds continues to dominate the total faba bean acreage (91% in 2021) [1], b) lack of extension and the absence of a well-functioning supply chain that connects farmers to the market as the majority of farmers in the region are still growing local landraces that do not meet the preferred quality traits of the domestic and international markets, c) the poor cultural practices, d) the weak seed system in many countries resulting in shortage of improved seeds and e) the absence of modern faba bean cultivars that presents many farmers desired traits like mechanical harvesting and tolerance to different biotic and abiotic stresses [6].

Faba bean production in North and East Africa is threatened by a number of abiotic and biotic stresses causing growth and performance impairment and season to season yield fluctuations [reviewed recently in [7] and [8]]. The most common and of economic importance stresses are presented in Table 2. Abiotic stresses affect the plant-water relationship causing damages. With the projected climate change that is anticipated to increase the harmful effects of these stresses and the high management cost of some abiotic stresses that the poor farmers cannot afford, the development of tolerant faba bean lines is becoming very crucial to ensure yield stability and to encourage farmers to further plant faba bean. This is the case in Sudan where an increase in the faba bean acreage has been observed after the

release of heat tolerant faba bean varieties. In this framework, the efforts of the regional faba bean breeding programs led to the development of sources for tolerance and to the release of tolerant varieties.

Moreover, biotic stresses like foliar diseases, pests, viruses, and weeds (Table 2) hinder faba bean production in the Northern and East African regions and can cause complete yield loss. Although huge progress was made in improving the detection and management methods of these pests, the projected climate change is complicating the timely management and therefore the development of resistant lines is highly recommended.

In this end, national research systems in collaboration with ICARDA developed and released faba bean cultivars that are resistant/tolerant to key traits with high yield potential (Table 2), but the majority of these lines provides partial resistance only. Hence, additional efforts are needed to develop varieties with complete and combined resistance.

Although great achievements were made in up-scaling faba bean traits, additional national and scientific efforts are still required to boost both production and productivity. The key stakeholders in the region should work together to highlight the impressive nutritional values of faba bean, to promote its dual consumption (green and dry) and the improved varieties, and to ensure that the seeds of the improved faba bean varieties are available for farmers by strengthening the seed delivery system. The extension programs should raise awareness about sustainable agriculture in general and about the economic and ecological benefits that will result from including faba beans in their cropping system in particular. In addition, the faba bean breeding programs need to conduct additional research to address all the constraints described above and develop climate smart, nutritious, and pest-resistant varieties. 🌱

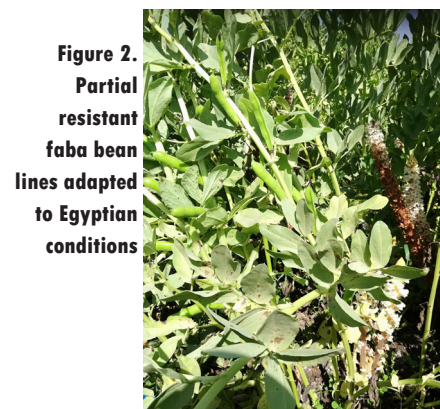


Figure 2.
Partial
resistant
faba bean
lines adapted
to Egyptian
conditions

References

- [1] FAOSTAT (2023) Food and Agriculture Organization of the United Nations. www.faostat.fao.org Accessed 25 June 2023.
- [2] Rahate KA, Madhumita M, Prabhakar PK (2021) Nutritional composition, anti-nutritional factors, pretreatments-cum-processing impact and food formulation potential of faba bean (*Vicia faba* L.): a comprehensive review. *LWT* 138: 110796.
- [3] Multari S, Stewart D, Russell WR (2015) Potential of faba bean as future protein supply to partially replace meat intake in the human diet. *Compr Rev Food Sci Food Saf* 14(5): 511–522.
- [4] Muehlbauer FJ, Abebe T (1997) *Vicia faba* L. New crop factsheet. Center for New Crops and Plant Products. Purdue University, USA.
- [5] Jensen ES, Peoples MB, Hauggaard-Nielsen H (2010) Faba bean in cropping systems. *Field Crops Res* 115(3): 203–216.
- [6] Abobatta WF, El-Hashash EF, Hegab RH (2021) Challenges and opportunities for the global cultivation and adaptation of legumes. *J Appl Biotechnol Bioeng* 8(5): 160–172.
- [7] Adhikari KN, Khater LA, Maalouf F (2022) Application of genetic, genomic strategies to address the biotic stresses in faba bean. In: Kole C (eds) *Genomic designing for biotic stress resistant pulse crops*, Springer International Publishing, pp. 353–380.
- [8] Maalouf F, AbouKhater L, Babiker Z, et al. (2022) Genetic and genomic research for abiotic stresses in faba bean. In: Kole C (Eds) *Genomic designing for abiotic stress resistant pulse crops*, Springer, Cham, pp. 249–270.
- [9] Maalouf F, Ahmed S, Shaaban K, et al. (2016) New faba bean germplasm with multiple resistances to ascochyta blight, chocolate spot and rust diseases. *Euphytica* 211: 157–167.

Table 2. Major abiotic and biotic stresses affecting North and East Africa, and the availability of resistance in the region.

	Stress	North Africa	East Africa	Released varieties	Sources for resistance
Abiotic	Heat	✓	✓	Basabeer, Ed-Damer, Hudeiba-93	VF420, FB2648, IG11908, IG11982, IG12110, IG13945, IG99664, Vf351, FB2509, IG14026, IG12659, IG13958, FB1165, Vf301, VF626
	Drought	✓	✓	NA	FLIP06-010FB, Sakha 1, Sakha 4, Nubariya 1, Nubariya 3
	Waterlogging	✓	✓	Selale, Wayu, Walki, Hachalu, Didia, Ashebeka, Dagm	NA
	Soil acidity		✓	NA	Dosha, NC 58, Kassa
	Soil salinity	✓		NA	G429, G843, M1
Biotic	Ascochyta blight	✓		NA	IG72433, IG102181, IG10583, IG105860, IG105863, IG106583
	Chocolate spot	✓	✓	Gora, Moti, Gebelcho, Obsie, Didea, Walki, Dosha	BPL710 and accessions listed in Maalouf <i>et al.</i> [9]
	Rust	✓	✓	Dosha	BPL710, ILB938
	Gall disease		✓	Dosha, Tumsa, Walki and Hachalu, Degaga, Nc 58	NA
	Stem borer	✓	✓	NA	IG72498, IG 11561
	Sitona weevil	✓		NA	
	Black bean aphid	✓	✓	NA	NA
	Seed weevil	✓	✓	NA	NA
	Faba bean necrotic yellow virus	✓		NA	IG159170, IG159165, IG159163, IG159162
	Bean yellow mosaic virus		✓	Selection from BPL 758, BPL 1311, BPL 1314, Giza 3	NA
	Bean leaf roll virus		✓	NA	BPL756, BPL 757, BPL758, BPL769, BPL5278, BPL5279
	Broomrapes	✓	✓	Misr 3, Giza 429, Giza 674, Giza 843, Hashbenge, Baraca	ILB4358

Faba bean in North America – Status and potential

by Albert VANDENBERG¹, Hamid KHAZAEI²

Abstract: Over the past 15 years, plant breeders have developed adapted low vicine-convicine, white-flowered, small-seeded, round faba beans which are suitable for production in western Canada. A considerable expansion of faba bean production is anticipated over the next several years. It will help to satisfy the demands of the new and rapidly expanding plant-based protein extraction industry in North America.

Key words: *Vicia faba*, protein industry, breeding, new markets, vegetable-type faba bean

Since the early 1970s, the faba bean industry in North America has grown sporadically but has not expanded to the extent of pea and lentil. At that time, in Canada, a perceived global shortage of plant protein resulted in the investment and establishment of two full time faba bean breeding programs at the universities of Manitoba and Saskatchewan. Both program efforts diminished over time, largely because of the slow pace of export market development for faba bean and complete lack of a domestic market. Both faba bean programs were down-sized and then

faba bean varieties for potential production in the northern third of the Canadian prairies [1]. The production was largely targeted toward feeding livestock with small quantities of traditional directed toward traditional human markets in North America and the Middle East.

As concerns increased more recently about both prices of nitrogen fertilizer and environmental contributions to atmospheric carbon dioxide, faba bean once again came into focus as a potential way to reduce use of nitrogen fertilizer in crop rotations, and to help extend rotations



Figure 1. The direction of breeding for small-seeded round faba beans.

evolved to become more focussed on breeding of canola and flax, crops which had better market demand. The efforts related to faba bean crop development slowly diminished, while emphasis was increased on development of other grain legumes, especially pea and lentil. Both of these are now mature crops in the northern Great Plains of the USA and the Canadian prairie regions. Since the 1970s, faba bean genetic improvement was maintained at a low level in Saskatchewan, and European breeding programs sporadically introduced white-flowered

of the pea crop that was increasingly affected by *Aphanomyces euteiches* Drechs., the causal organism of aphanomyces root rot (ARR). Simultaneously, concerted efforts were expanded for in the development of the plant-based protein industry for use in food products, especially over the past 10 years through investments made by Protein Industries Canada. The main obstacles to increased production of faba bean was the large seed size and its content of vicine-convicine (v-c). Interest in investment faba bean breeding for the northern great plains of

¹ Department of Plant Sciences, University of Saskatchewan, Saskatoon, Canada
bert.vandenberg@usask.ca

² Natural Resources Institute Finland (Luke), Helsinki, Finland
hamid.khazaei@luke.fi

Canada was re-initiated over the past 15 years at the University of Saskatchewan. The specific focus was on reducing seed size, improving seed shape to round (Figure 1), and altering/improving the seed biochemistry by genetic reduction of v-c and tannins in the seed. More recently, leading farmers in the pulse crop industry became proponents of expansion of faba bean production, and seed fractionation companies became interested in the higher protein content and processing qualities of faba bean relative to pea.

The discovery of the genetic marker for the low vicine-convicine gene *vc1* [2, 3] was an essential and most important step in renewed interest and expansion of faba bean. Breeding programs were able to rapidly develop isolated breeding nurseries for low v-c and white flower simultaneously. Using faba bean germplasm from central and south Asia, it was possible to introgress smaller seed size and improved (round) seed shape. This allowed significant potential for reduction in the cost of seeding and improvements in the handling systems at the farm level. At the leading edge of breeding programs, the shape of faba bean seeds now is close to being round, similar to that of green and yellow pea (Figure 2).


Interest in expansion of faba bean in crop rotations will continue to increase based on demand for plant-based protein, demand for longer crop rotations and the incentive to reduce the use (and cost) of nitrogen fertilizer. Early results of nitrogen management research indicate that growing a faba bean crop for grain in the northern great plains can leave fixed residual soil nitrogen of 100 kg/ha, and that subsequent nitrogen-requiring crop yields are increased substantially due to the slow release of the organic nitrogen throughout the growing season. Interest in increased use of faba bean is expanding rapidly as agronomists conduct more research on the benefits in crop rotations and intercropping. Significant economic and biological rationale exists for reduction of nitrogen fertilizer use in prairie cropping systems.

The main short-term potential for faba bean is its expanding use as a grain crop for plant-based protein extraction in North America. Economic potential exists for millions of hectares of production - this would result in expansion of ni-



Figure 2. From left to right: yellow pea, yellow cotyledon faba bean, green pea, and green cotyledon faba bean seeds.

trogen fixation benefits in the existing cereal-oil-seed-legume crop rotations of the cooler climatic regions where pea and lentil are now used. It should be possible to extend crop rotations to some extent to include faba bean to help mitigate problems with ARR that has become a limitation for pea and lentil production. There is also increasing potential for using small-seeded faba bean in southern cropping regions as a winter green manure in some grain and vegetable production systems. This could include use as a vegetable crop similar to fresh garden pea, or even as a stem vegetable for stir frying. Use of faba bean in the seed vegetable form would benefit from introduction and expansion of the green cotyledon trait to enhance stable vegetable colour, similar to green pea. It may also be possible to develop faba bean in a form similar to that of the snow or snap pea if sufficient variation can be discovered or developed for these

traits. Future research efforts will include deeper research into the potential for increased protein and improvement in protein quality. In all scenarios, the superior nitrogen fixation and crop rotation benefits of faba bean could enhance crop rotations and production systems across North America. 

References

- [1] Khazaei H, Hawkins G, Vandenberg A (2021) Historical review of faba bean improvement in western Canada. *Leg Sci* 3[4]:e92.
- [2] Khazaei H, Purves RW, Song M, *et al.* (2017) Development and validation of a robust, breeder-friendly molecular marker for the *vc*- locus in faba bean. *Mol Breed* 37:140.
- [3] Khazaei H, Purves RW, Hughes J, *et al.* (2019) Eliminating vicine and convicine, the main anti-nutritional factors restricting faba bean usage. *Trends Food Sci Technol* 91:549–556.



Prospects of genebank genomics in faba bean

by Hailin ZHANG, Axel HIMMELBACH, Ulrike LOHWASSER, Andreas BÖRNER, Nils STEIN, Murukarthick JAYAKODI*

Abstract: Genebanks hold comprehensive collections of cultivars, landraces and crop wild relatives, but their detailed characterization has so far been applied to major crops. The IPK Genebank houses more than 2,000 faba bean accessions which can have promising alleles for faba bean improvement. However, the lack of cost-effective genotyping technology limits the characterization of such germplasm. Here, we optimize the cost-effective sequence-based approach to genotype entire faba bean accessions at IPK Genebank. Our efforts will lead to the efficient utilization of genetic diversity for faba bean breeding and research.

Keywords: plant genetic resources, genebank genomics, genotyping, restriction enzymes, genotyping-by-sequencing

Faba bean (*Vicia faba* L.) is an important protein crop in temperate agriculture due to its better adaptations. Sequence based characterization for faba bean *ex situ* collections offer opportuni-

ties for sustainable crop improvement and protein production. However, in the past, genetic research in faba bean was limited by the giant and complex genome (~13Gb). With interna-

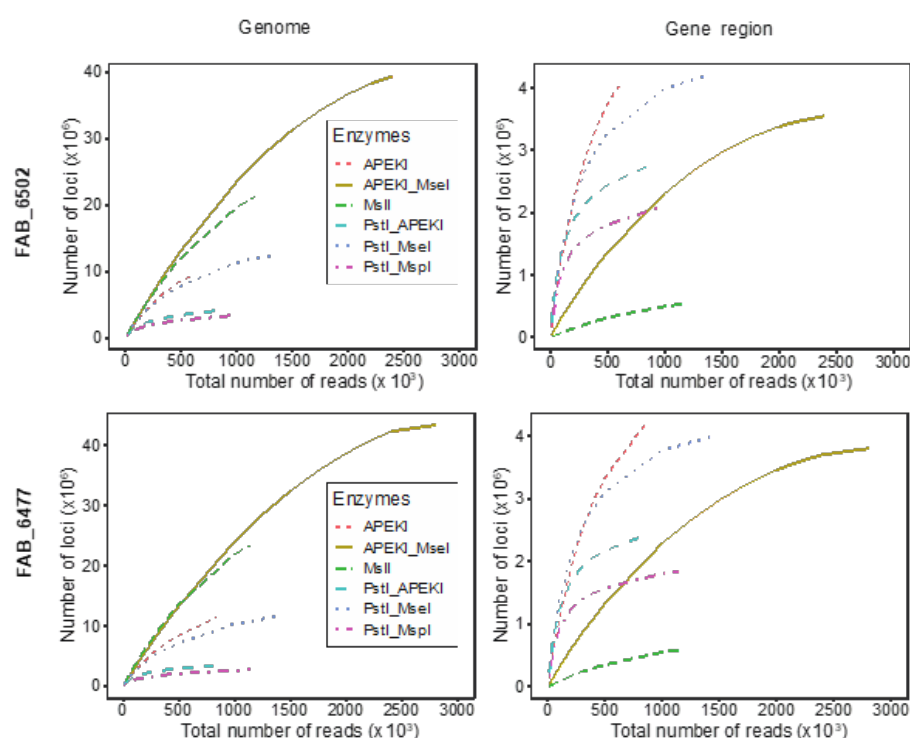


Figure 1. Read depth covering genomic loci distribution in the GBS libraries produced by the various restriction enzyme (RE) combinations used to digest faba bean genomic DNA from two accessions (FAB 6502 and FAB 6477). We have chosen a combination of methylation-sensitive ApeKI and AT-target MseI RE for diversity analysis after testing with various single (ApeKI and MseI) and double (ApeKI/MseI, PstI/ApeKI, PstI/MseI, and PstI/MspI) digestion for GBS optimization in faba bean. The number of loci in genome region showed a saturating curve shape for four enzyme sets (ApeKI, PstI/ApeKI, PstI/MseI, and PstI/MspI).

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Seeland, Germany

* jayakodi@ipk-gatersleben.de

tional collaborative effort, we generated the first high-quality annotated reference genome for faba bean [1]. Recently, we further maximized the quality of the reference genome and gene annotation using optical map and full-length transcripts. Currently, array-based genotyping methods are available for faba bean, which is expensive in genotyping thousands of accessions. Thus, a cost-effective genotyping method is needed for large germplasm characterization, perform genetic studies and identify superior alleles for breeding.

We put effort to optimize a cost-effective genotyping-by-sequencing (GBS) [2]. The genome fraction captured by GBS depends on the restriction enzyme (RE) used. Here, we evaluated GBS with various REs and found the appropriate combination for faba bean given the best library quality, the high number of genomic loci distributed across chromosomes and high enrichment for gene space (Figure 1). With the new optimized protocol, we sequence over two thousand faba bean accessions from diverse sources including genebanks, diversity panels and elite lines to understand the faba bean population structure and global genetic diversity. This study will enable selection of coresets to study important traits, deliver trait-specific novel genetic source and implement genomic selection and pan-genomics. 🌱

References

- [1] Jayakodi M, Golicz AA, Kreplak J, *et al.* (2023) The giant diploid faba genome unlocks variation in a global protein crop. *Nature* 615: 652–659.
- [2] Elshire RJ, Glaubitz JC, Sun Q, *et al.* (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS ONE* 6: e19379.



Shutterstock™ image

The limitations and prospects of the faba bean industry in China

by He YUHUA*

China has the largest cultivation area of faba beans in the world, with over 800,000 hectares harvested annually, being South China the larger producer, with 90% of the total Chinese production [1]. The sowing time is in Autumn in South China and Spring in North China.

Faba bean is an important crop in China, used either as dry seeds, vegetables (fresh seeds or fresh pods). Dry seeds are used as human's food or animal's feeds normally. The dry seeds represent over 60% in total growth area, and 30% are consumed as vegetables in total growth area in south. In the North-West China, faba bean is planted for food production (dry seeds), and only 5% is used for vegetables (fresh seeds or pods) only [2].

Faba bean is a traditional crop which can also be used for green manure and forage, with straws being superb feed for livestock consumption because of their high protein. Faba bean is often grown after rice, tobacco, corn, wheat, potatoes, and rapeseed crops. Faba bean is the most important crop in rotation and short-term intercropping in the Chinese agricultural system.

1- The limitations of Chinese faba bean industry

a) The faba bean seeds industry is weak, with new varieties seldom used. Faba bean is relatively important in southern China, but minor in the northern agricultural production system. Any case, faba bean is not regarded as a major crop in China and has not been supported by key agricultural policies. Still, faba bean has made a great progress in breeding.

b) The labor and modern production techniques are insufficient. The faba bean does grow in unsatisfactory farmlands, and farmers require to input more costs, like labor and techniques. In addition, compared with rice, wheat, corn, and other crops, the faba bean is facing critical climatic factors, such as cold damage in South China, and drought stress in whole faba bean production. Unfortunately, modern machinery is seldom available to grow faba beans in China. This, together with a constant reduction in number of farmers is constraining faba bean industry in China.

2- The prospects of Chinese faba bean industry

a) There is potential to increase faba bean as a food crop as its adaptability is wide, the cold and drought tolerance are outstanding relative to other cool season crops. Faba bean can be used as important measure and supplement for planting in some waste fields in winter, in south China, which increase the total grain output and farmers' income.

b) Faba bean is a traditional food crop in China, used since 2500 years ago. Faba bean is pretty suitable for growing in winter in South China because of the fantastic cold tolerance. The faba bean industry does promote the sustainable and optimum development of the agricultural system and still supplies an abundant consumption option for the population nowadays.

c) Growing faba beans provides a variety of options to deal with the risks of international trade in pulses for China. Faba bean industry is an essential measure to ease the dependence on importing amount in peas and soybean. 🌱



Institute of Food Crops, Yunnan Academy of Agricultural Sciences, China

* trbio@163.com

References

- [1] Yu H, Yang F, Hu C, *et al.* (2023) Production status and research advancement on root rot disease of faba bean (*Vicia faba* L.) in China. *Front Plant Sci* 14: 1165658.
- [2] Zhao N, Miao Y, Wang K, *et al.* (2021) Advances in faba bean production in China. *Legume Perspectives* 21: 24–26.

We invite all ILS members to register their contacts and major expertise, and to integrate the website hub of projects with info on past or current projects that they have coordinated, in:

LEGUMESOCIETY.ORG
The official ILS website



**Conferences, Legume
 Perspective issues ...**

**ILS Members projects
 and profiles...**



... and much more!

Don't miss our news!
Follow us on twitter @LegmSociety

Website contact: nelson.nazzicari@crea.gov.it



Do not miss the 11th International Conference on Legume Genetics and Genomics!

 30 Sep - 3 Oct

 Brisbane/Meenjin, Australia

 <https://www.iclgg2024.org/>



 **ICLGG 2024**
Brisbane / Meenjin, Australia

Chair:
Prof Michael Udvardi



Join...

up to 400 leading national and international researchers,
educators and agri-food representatives

Deadlines:

1 May - Abstract
submission closes
31 Jul - Early bird
registration closes

Share...

the latest breakthroughs in legume
genetics and genomics

Shape...

global strategies to improve legumes for
food security without environmental harm

After the amazing ILS4 Granada...

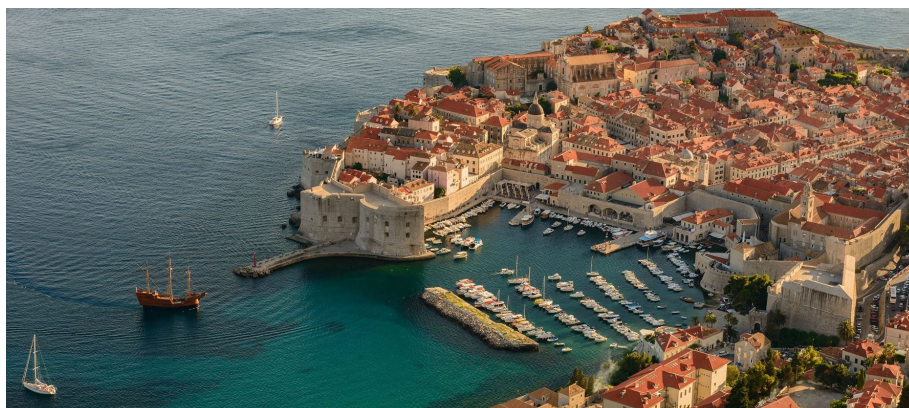


(including another ILS Football Cup event with blue team emerging victorious)



**JOIN US AT THE
ILS5 Conference
8-12 June 2026, Dubrovnik, Croatia**

Save the date



And do not forget to attend ILS webinars!

The webinars donot require an ILS membership and are available to everyone on the ILS website!

2024 calendar:



Jan 9, 4pm CET (UTC+1)

Marion Prudent (INRAE, France)

"Pea resilience to drought"



Feb 6, 4pm CET (UTC+1)

Kristian Holst Laursen (University of Copenhagen, Denmark)

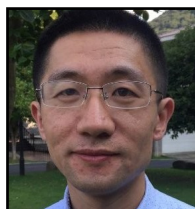
"The impact of plant nutrients on the performance and quality of legumes for plant-based foods"



Mar 5, 4pm CET (UTC+1)

Yongfeng Ai (University of Saskatchewan, Saskatoon, Canada)

"Pulse processing and starch utilization"



Abr 2, 12pm CET (UTC+1)

Pei Xu (China Jiliang University, Zhejiang, China)

"Functional phenotyping offers deeper insights into physiology of legume crops"



Mai 7, 4pm CET (UTC+1)

Paolo Annicchiarico (CREA, Italy)

"Breeding forage and grain legumes for intercropping"



Jun 4, 4pm CET (UTC+1)

Jose Carlos Jimenez (CSIC, Spain)

"Nutraceutical properties of lupin (Lupinus angustifolius) seed proteins"

Legume Perspectives is an international peer-reviewed journal aiming to interest and inform a worldwide multi-disciplinary readership on the most diverse aspects of various research topics and use of all kinds of legume plants and crops.

The scope of Legume Perspectives comprises a vast number of disciplines, including biodiversity, plant evolution, crop history, genetics, genomics, breeding, human nutrition, animal feeding, non-food uses, health, agroecology, beneficial legume-microorganism interactions, agronomy, abiotic and biotic stresses, agroecology, sociology, scientometrics and networking.

The issues of Legume Perspectives are usually thematic and devoted to specific legume species or crop, research topic or some other issue. They are defined by the Editorial Board, led by the Editor-in-Chief with the help from Assistant Editors, who select and invite one or more Managing Editors for each issue. Having accepted the invitation, the Managing Editor agrees with the Editorial Board the details, such as the deadline for collecting the articles and a list of the tentative contributors, from whom he, according to his own and free choice, solicit the articles fitting into the defined theme of an issue. A possibility that every member of the global legume research community, with a preference of the International Legume Society members or established authorities in their field of interest, may apply to the Editorial Board to be a Managing Editor and suggest a theme for his issue is permanently open and can be done simply by contacting the Editor-in-Chief by e-mail, with a clearly presented idea, structure and authors of the potential issue.

Since one of the main missions of Legume Perspectives is to provide as wide global readership with the insight into the most recent and comprehensive achievements in legume science and use, the articles published in Legume Perspectives are usually concise, clear and up-to-date reviews on the topic solicited by the Managing Editor from each author. Managing Editor is solely responsible for collecting the articles from the authors, anonymous peer-review, communicating with the Technical Editor and providing the authors with the proofs of their manuscript prior to the publication.

Apart from review articles, Legume Perspectives is keen on publishing original research articles, especially if they present some preliminary results of an outstanding significance for legume research and before they are published in their full volume, as well as brief reports on already held and announcements about the forthcoming national and international events relating to legumes, descriptions of the projects on legumes, book reviews,

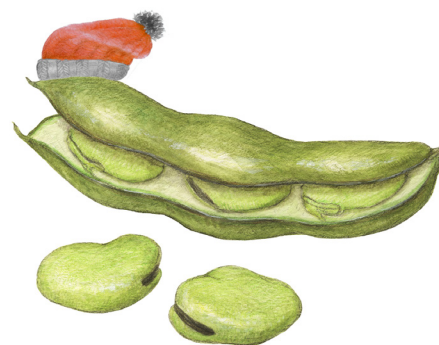
short articles on legumes in popular culture or everyday life, fiction stories on legumes and obituaries. The authors of such contributions are advised to contact the Editor-in-Chief first, in order to present the draft of their idea first and receive a recommendation if it is appropriate.

Regardless of the article category, Legume Perspectives prefers a clear, simple and comprehensive writing style that would make its articles interesting and useful for both academic and amateur audience. Your article is expected to assist in the exchange of information among the experts in various fields of legume research.

Legume Perspectives welcomes either longer (900-1,100 words + up to 3 tables, figures or photos + up to 10 references) or shorter (400-500 words + 1 table, figure, photograph or drawing + up to 4 references) manuscripts. The Editor-in-Chief, depending on the opinion of the Managing Editor, may allow any variation in length or structure, from case to case.

The manuscripts for Legume Perspectives should be prepared in Microsoft Office Word, using Times New Roman font, 12 points size and single spacing. Please provide each manuscript with a 100-word abstract and 4-6 key words listed alphabetically. The references should follow the style of the published papers in this issue, be given in full and listed alphabetically. The tables may be incorporated in the manuscript, while figures, photographs or drawings should be submitted separately as jpg files with a resolution of at least 600 dpi. The authors whose native language is not English are strongly advised to have their manuscripts checked by a native English speaker prior to submission and be persistent in following only one of all the variants of English they themselves prefer.

Publishing articles in Legume Perspectives is free.



AdobeStock™ image

LEGUME PERSPECTIVES *Sponsorship list*



INTERNATIONAL LEGUME SOCIETY
CÓRDOBA, SPAIN
<http://www.ias.csic.es/grainlegumesmagazine/>



SPANISH NATIONAL RESEARCH COUNCIL
www.csic.es



INSTITUTO DE TECNOLOGIA QUÍMICA E BIOLÓGICA ANTÓNIO XAVIER
(UNIVERSIDADE NOVA DE LISBOA)
OEIRAS, PORTUGAL
www.itqb.unl.pt

Want to help the legume research network in Europe and worldwide?

Support Legume Society and its journal today!

legumesociety@gmail.com