Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
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IPK researchers unlock high potential of faba bean as global protein crop

Press Release

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Gatersleben, 08.03.2023 **Increasing the proportion of locally produced plant protein in currently meat-rich diets could substantially reduce greenhouse gas emission and loss of biodiversity. However, plant protein production is hampered by the lack of a cool-season legume equivalent to soybean in agronomic value. Faba bean (*Vicia faba L.*) has a high yield potential and is well-suited for cultivation in temperate regions, but genomic resources are scarce. An international research team including scientists from the IPK Leibniz Institute reports a high-quality chromosome-scale assembly of the faba bean genome. Today, the results have been published in the journal “Nature”.**

Faba bean is one of the earliest domesticated crop plants. It was part of the Neolithic package of crops that the early farmers took with them as they left the Fertile Crescent. In the 21st century, nutritional quality remains a central breeding goal: new faba bean varieties should be low in the alkaloid glycosides vicine and convicine as well as in tannins. Furthermore, essential amino acids should be balanced better to accommodate human dietary needs, while seed phytate and protease inhibitors should be reduced to improve nutrient bioavailability, all while taking care not to alter seed size or compromise pest resistance and whilst simultaneously improving yield stability.

Using a high-quality chromosome-scale assembly of the faba bean genome the research team shows that it has grown to a massive 13 Gb in size through an imbalance between the rates of amplification and elimination of retrotransposons. They achieved the technical feat of assembling the first ever single large chromosome of 3.3 Gb (chr1), which is even bigger than the human genome. Genes and recombination events are evenly dispersed across chromosomes and the gene space is remarkably compact considering the genome size, though with significant copy number variation driven by tandem duplication. “Demonstrating practical application of the genome sequence, we develop a targeted genotyping assay and use high-resolution genome-wide association analysis to dissect the genetic basis of seed size and hilum colour”, says Dr. Murukarthick Jayakodi, head of IPK’s independent research group “Grain Legume Genomics” and first author of the study.

Faba bean breeders can now face the complex challenges enabled by genomic resources and insights. The reference genome will facilitate the rapid introgression of new traits into elite material and permits powerful and broadly applicable mapping approaches. “Our rich genome-wide annotation now sheds light on these effects, adding an important component to the genomics-based breeding“, says Dr. Murukarthick Jayakodi. Together with target gene identification, this opens up the possibility of gene cloning. “The resources presented constitute a genomics-based breeding platform for faba bean, enabling breeders and geneticists to accelerate improvement of sustainable protein production across Mediterranean, subtropical, and northern temperate agro-ecological zones", emphasises the IPK researcher.

Note:

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Original publication:

Jayakodi *et. al.*: (2023) The giant diploid faba genome unlocks variation in a global protein crop. Nature. DOI: [10.1038/s41586-023-05791-5](https://doi.org/10.1038/s41586-023-05791-5)

Photo (for free use):

https://ipk-cloud.ipk-gatersleben.de/s/MCy9St88qDX36dZ

This picture displays the seed size and color diversity in faba bean. Photo: James Hadley/ Donal O' Sulivan, Univ. Reading