

# Faba bean: from gene to plate and back again

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## ABSTRACT

Faba bean is doubly an orphan crop: it is both relatively neglected, and lacks a known wild progenitor. Our international collaboration is sequencing the gene space of its large diploid genome, 13 Gbp, and will eventually cover the whole genome. Stress responses and phenology limit the growing of the crop by farmers, and anti-nutritional factors limit use of the crop for food and feed, so these are among the current targets for improvement where genomic information would be valuable for accelerating breeding.

Faba bean is a traditional food in the Mediterranean basin, western Asia and China, and can return to the dining table elsewhere. It has higher yields than pea in 10 EU countries and higher protein yields in 16, because of its higher protein content (world average 29% in faba bean, 23% in pea). The high solubility of its protein makes faba bean a suitable alternative to soybean for people allergic to soy products, and for cool climates where soybean does not thrive.

We have identified sources of large root systems that explore root-zone water effectively, along with sources of stomatal control that limit water loss in different circumstances, and new sources of earliness of flowering and maturity. Vicine and convicine are the main anti-nutritional factors limiting food and feed use, and we have developed markers closer and closer to, and finally within, the currently known gene that causes a 90-95% reduction in their concentration. Further exploration of their biosynthetic pathway should allow their eventual elimination. Novel food processing methods allow elimination of vicine, convicine and their aglycones in a food matrix, and showed the importance of lowering lipoxygenase activity in order to maintain palatability of food products. Our programme encourages dialogue between genomics and application, accessing the gene information that is most needed for impact.