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Field Crops Research

Volume 115, Issue 3, 5 February 2010, Pages 270-278

Review

Diversity maintenance and use of *Vicia faba* L. genetic resources

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<https://doi.org/10.1016/j.fcr.2008.10.003>

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Abstract

The faba bean (*Vicia faba* L.) is an ancient crop that is represented in collections by cultivated forms only. Botanic and molecular data suggest that the wild ancestor of this species has not yet been discovered or has become extinct. This fact makes *ex situ* collections more crucial for the present and future breeding activities of this crop, especially when the modernization of agriculture reduces genetic diversity.

At the world level, more than 38,000 accession entries are included in at least 37 listed collections. The partial allogamous status of this crop makes maintenance activity of genotypes more expensive and difficult. In addition to the requirement of fixed genotypes to support new association genetics strategies, there is a need for more research on pollinators and maintenance of genetic diversity within populations.

A large genetic variability has already been identified in *V. faba* in terms of floral biology,

seed size and composition, and also tolerance to several biotic and abiotic stresses. More knowledge is needed on the interactions of *V. faba* with parasitic and pollinator insects, on traits related to environmental adaptation and impacts, on nitrogen fixation in interaction with soil *Rhizobia* and on bioenergy potential, which strengthens the demand for new and large phenotyping actions. Diversity analysis through genotyping is just beginning. The use of amplified fragment length polymorphism (AFLP) or simple sequence repeat (SSR) markers has allowed genetic resources to be distinguished according to their geographic origin and the structuring of collections. Conservation of gene sequences among legume species and the rapid discovery of genes (particularly in the model species *Medicago truncatula* and *Lotus japonicus*), together with robotic developments in molecular biology, offer new possibilities for the analysis of sequence diversity for *V. faba* genes and to evaluate their impact on phenotypic traits. Combined genotyping and phenotyping projects must continue on *V. faba* so that core collections can be defined; these will help in the discovery of genes and alleles of interest for breeders.



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Keywords

Vicia faba; Faba bean; Genetic resources; Diversity; Collections; Genotyping; Phenotyping

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