

Comparative Analysis of the Genetic Diversity of Faba Bean (*Vicia faba* L.) - Abstract

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Summary

Faba bean (*Vicia faba* L.) is an important grain legume with high protein content (approximately 25- 30%) and high nutritional value. It is broadly cultivated in temperate areas for human consumption and as an animal feed. Although the exact origin of Faba bean is unknown, it is accepted that it was one of the earliest food legumes to be domesticated and has probably been cultivated since the Neolithic period. According to FAOSTAT (2016), the total cultivated area of Faba bean reached approximately 2.15 million ha, yielding more than 4.14 million tons. Faba bean production ranked seventh among all legume crops worldwide. Nevertheless, Faba bean cultivars have anti- nutritional compounds such as tannins, which are primarily located in the seed coat which limit their use for both human and animal consumption. In this respect, the characterization of the genetic diversity in Faba bean is an important parameter for genetic and biodiversity studies, germplasm characterization, as well as for introducing genetic variability in plant breeding. Technical advances in molecular genetics allowed the application of molecular markers for measuring genetic variation at the DNA level. The advantages of using DNA markers is that they are not affected by environmental factors, plant developmental stages and have been successfully used for studying the genetic diversity in various crop species, including Faba bean. The present study aims to assess the genetic diversity among 53 varied Faba bean populations provided by the Hellenic Agricultural Organization “DEMETER” seed bank. To determine the genetic diversity of the studied populations, six SCoT DNA markers were used. A total of 114 loci were obtained with 37.95% being polymorphic and 62.05% monomorphic within or between populations. Among the populations, VF37 exhibited the highest level of polymorphisms (P= 57.02%) and VF78 the lowest (P= 21.05%). According to Shannon’s information index VF37 had higher levels of genetic variation (0.328) compared to other populations. In addition, population VF36 showed two private bands followed by VF37 and VF57 with one private band. Furthermore, the AMOVA (Analysis of Molecular Variance) showed that 56% of the total genetic variation was attributed to differences within populations and the rest (44%) was attributed to differences among populations. SCoT markers are useful tool for the detection of genetic diversity among Faba bean populations and encourage targeted crossing strategies. The present study is a first step towards the development of an efficient breeding program.

Proceedings of HAICTA 2022, September 22–25, 2022, Athens, Greece

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CEUR Workshop Proceedings (CEUR-WS.org)

Keywords

Faba bean, genetic diversity, SCoT molecular markers, seed bank, population genetic