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Review

Faba bean breeding for disease resistance

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ABSTRACT

Faba bean is a major grain legume widely cultivated in many countries for food and feed purposes. A number of aerial fungi, together with soil-borne pathogens associated with foot and root rot complexes, nematodes, parasitic weeds and viruses may cause severe diseases in faba bean crops. The use of genetic resistance is the most economical and environmentally friendly control method. However, to date no efficient sources of resistance have been described to some diseases, or it is scarce and of complex nature, making necessary the implementation of other control measures. Phenotypic expression of resistance is usually poorly described. As a consequence of this, and of the poorly developed genomic resources available, the genetic basis of resistances is, in most cases, largely unknown. Effectiveness of MAS might soon increase with the adoption of new improvements in marker technology together with the integration of comparative mapping and functional genomics. In this paper we will review and critically discuss current and future strategies on breeding faba bean for disease resistance.

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1. Introduction

Faba bean (*Vicia faba* L.) is one of the oldest legume crops mainly grown as a valuable protein rich food both, for human and animal feed, in this later case providing an alternative to soybean meal in the temperate regions. Like other grain legumes, faba bean contributes to sustainable agriculture by fixing atmospheric nitrogen in symbiosis with the soil bacteria *Rhizobium leguminosarum*. This unique ability reduces the dependence of farmers on extensive use of chemical fertilizers protecting soil and water quality. However, the total area in the world dedicated to faba bean cultivation is declining (Jensen et al., 2010). One of the main

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reasons is the unreliable yields, mainly due to susceptibility of the crop to pests and diseases. A number of aerial fungi, together with soil-borne pathogens associated with foot and root rot complexes, nematodes, parasitic weeds and viruses may cause severe diseases in faba bean crops (Stoddard et al., 2010).

Breeding for disease resistance is regarded the most cost-efficient method of control. However, in contrast to other crops or legumes such as common bean or soybean for which complete monogenic resistance exist and is efficiently used in marker assisted selection (MAS) (Miklas et al., 2006; Garcia et al., 2008), most of the resistance reactions described so far in faba bean are incomplete and poorly understood. Phenotypic expression of resistance is usually poorly described. As a consequence of this, and of the poorly developed genomic resources available, genetic basis of resistances is, in most cases, largely unknown. Only in a few cases preliminary mapping studies have been performed (see Torres et al., 2010) but the relatively large distance between the quatitative trait loci (QTLs) and their associated molecular markers hampers their efficient use for MAS. The scarce genomic resources developed for faba bean and the limited saturation of the genomic regions bearing putative QTLs make difficult to identify markers tightly linked and to determine the accurate position of QTLs (Torres et al., 2010; Rispail et al., 2010).

Effectiveness of MAS might soon increase with the adoption of new improvements in marker technology together with the integration of comparative mapping and functional genomics. The purpose of this paper is to review and critically discuss current and future strategies on breeding faba bean for disease resistance. Little emphasis will be made on description of epidemiology and other control methods as this has been reviewed by Stoddard et al. (2010).

2. Rust

Uromyces viciae-fabae (Pers.) J. Shört. is the causal agent of faba bean rust, and is one of the most serious diseases of faba bean throughout the world. It is a major disease in the Middle East, North Africa, Europe and China, where moderate to substantial yield losses can occur (Rashid and Bernier, 1991; Jellis et al., 1998).

Different control methods have been proposed against rust, ranging from cultural practices to the use of chemical and biological control methods. Cultural practices, such as sowing density, nitrogen availability or crop mixtures can significantly influence faba bean rust infection (Fernández-Aparicio et al., 2006). Chemical control is possible (Marcellos et al., 1995; Emeran and Rubiales, 2001), but other cost-effective and environmentally friendly alternatives to the extensive use of fungicides should be provided. On the other hand, the use of biological control (Gaunt, 1983) or systemic induced resistance (Murray and Walters, 1992; Rojas-Molina et al., 2004) is not yet available at the commercial level (Stoddard et al., 2010).

U. viciae-fabae sensu lato is a species complex. Recently, host-specialized isolates that cannot infect *V. faba* have been reported (Emeran et al., 2005), suggesting that *U. viciae-fabae* may be subdivided into at least 3 groups of populations with differential pathogenicity to faba bean, vetch or lentil, respectively. This subdivision has been supported by recent RAPD analysis (Emeran et al., 2008). However, more research is needed to clarify this ultimate classification of the *U. viciae-fabae* complex and to definitively support the separation of *U. viciae-fabae* into *formae specialis*.

Concerning pathogenic diversity, several races of *U. viciae-fabae* have been identified. Conner and Bernier (1982), using a set of differential faba bean lines, described different races on the basis of the colony size. More recently, Emeran et al. (2001) proposed a new differential set that allowed the identification of 16 races, using the infection type, based on the presence or absence of necrosis, as the discriminatory criteria. The same set of differentials has been used more recently to group 27 Spanish and Portuguese isolates into 15 physiological races (Rojas-Molina et al., 2006). The highest virulence was identified in Egyptian populations. The evidence of physiologic specialization in *U. viciae-fabae* described above suggests that the use of single resistance genes in cultivars would likely not result in long time rust control, so to search for strategies to prolong the durability is a major need.

Several sources of resistance against *U. viciae-fabae* have been reported in faba bean in the last decades (Table 1). Incomplete resistance is common (Rashid and Bernier, 1984, 1991; Khalil et al., 1985; Polignano et al., 1990; Sillero et al., 2000; Herath et al., 2001), and hypersensitive resistance has only recently been identified (Sillero et al., 2000). However, the necrotic reaction occurs late, resulting in a reduction of the infection type rather than complete resistance. Both types of incomplete resistance are associated with an increased latent period, a reduction in colony size and a decreased infection frequency. They only differ in the

Table 1
Faba bean germplasm resistant to *Uromyces viciae-fabae*.

Accession name	Material	Reference
Kuzminskie, Latviiskie, Primus, Pikulovichskie	Cultivars	Tÿmchenco (1964)
Altaiskii, Burstinskii, Girov-Doina, Hîngu, Turtulesti	Cultivars	Perseca and Bobes (1968)
2N34, 2N52, 2N293	Breeding lines	Bernier and Conner (1982)
Ackerperle, Diana, Eufordia, Herz Freya	Cultivars	Rashid and Bernier (1984)
2N192, 2N255, 2N311, 2N319, 2N382, 2N435, 2N441, ILB 96, ILB 226, ILB 315, ILB 318, ILB 335, ILB 403, ILB 411, ILB 420, ILB 431, ILB 479, ILB 490, ILB 866, ILB 919, ILB 938	Breeding lines	Rashid and Bernier (1984)
Bergers, Czersdorfer, Columba, Niki, Pluto	Cultivars	Furgal-Wegrzycka et al. (1985)
Reina Blanca	Cultivar	Khalil et al. (1985)
ILB 249/803/80, ILB 249/804/40, ILB 938	Breeding lines	Khalil et al. (1985)
Maris Bead	Cultivar	Rashid and Bernier (1986a)
ILB 159-1, ILB 159-4	Breeding lines	Rashid and Bernier (1986a)
2N6, 2N29, 2N43, 2N122, 2N291, 2N319, ILB (332X133)A, ILB (322X133)B, ILB 697, ILB 866, ILB 938	Breeding lines	Rashid and Bernier (1986b)
BPL 710, BPL 1179	Breeding lines	ICARDA (1987)
MG109253, MG109258	Breeding lines	Polignano et al. (1990)
Aladin, Outlook, 80Fum-1	Cultivars	Rashid and Bernier (1991)
2N5, 2N240, 2N430	Breeding lines	Rashid and Bernier (1991)
BPL 7, BPL 8, BPL 260, BPL 261, BPL 263, BPL 309, BPL 406, BPL 417, BPL 427, BPL 490, BPL 484, BPL 524,BPL 533, BPL 539, BPL, 552, BPL 554, BPL 567, BPL 571, BPL 573, BPL 576, BPL 588, BPL 604, BPL 610, BPL 627, BPL 649, BPL 663, BPL 665, BPL 667, BPL 680, BPL 640, BPL 643, BPL 702	Breeding lines	Bond et al. (1994)
Qi Dou No. 2	Cultivars	Bond et al. (1994)
V-300, V-313, V-1271, V-1272, V-1273, V-1335	Breeding lines	Sillero et al. (2000)