MYCORRHIZA-MEDIATED DISEASE RESISTANCE - A MINI-REVIEW

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Abstract

Arbuscular mycorrhizal fungi (AMF) play an essential role as one of the primary mutualistic plant-microbe symbioses. Plants benefit from root endophytes that extend their zone of activity beyond the rhizosphere (Feddermann *et al.*, 2010; Hohmann *et al.*, 2011, 2012). The main known benefits of mycorrhiza involve nutrient mobilisation (mainly phosphorus), improved tolerance against abiotic (mainly drought) and biotic stresses (mainly soil-borne pathogens) (Azcón-Aguilar & Barea, 1996; Parniske, 2008). An increasing number of studies highlight a significant role of AMF in the mediation of disease resistances. Besides an improved phosphorus use efficiency, individual reports have shown enhanced levels of defence-related compounds (such as glucanases, chitinases and phenolics) in mycorrhizal plants, and there is first evidence of certain phytohormone pathways (in particular jasmonate signalling) to be involved in mycorrhiza-mediated disease resistance (Jung *et al.*, 2012).

Despite their ecological and nutritional importance, legume crops receive less and less attention in breeding programmes and crop rotations. Increasing problems with fungal diseases seem to be a main cause for the decline in yield (Wilbois, 2011; Finckh *et al.*, 2013). However, legumes are known to show particularly strong interactions with important symbionts such as AMF and *Rhizobium* spp. and, therefore, provide a valuable model system to identify genotypes that interact efficiently with symbiotic microbes.

Linkage mapping was used to identify quantitative trait loci (QTL) and genes in pea that are linked to resistance against various pathogens (Prioul-Gervais *et al.*, 2007; Pereira *et al.*, 2009; Fondevilla *et al.*, 2011; Hamon *et al.*, 2011; Li *et al.*, 2012). The ability of plants to respond to AMF can vary widely between plant species and among genotypes (Parke & Kaeppler, 2000; Sawers *et al.*, 2010). Genotypic differences in the response to AMF have been observed in various crops (Powell *et al.*, 1982; Hetrick *et al.*, 1993; Kaeppler *et al.*, 2000; Tawaraya *et al.*, 2001). Such differences in mycorrhizal responsiveness indicate a genetic basis for plant-AMF interactions. Galván et al. (2011) were the first to report on QTL governing responses of onion species to AMF based on shoot biomass. However, little is known about the genetic basis for mycorrhiza-mediated disease resistance and more research is needed to exploit genotypic differences, e.g., via marker-assisted selection.

For legume crops, the use of association mapping has been restricted in the past due to insufficient genome-wide marker coverage. Most recently, 384 pea accessions of the United States Department of Agriculture – Agricultural Research Service (USDA-ARS) pea core collection were genotyped for 20.000+ single nucleotide polymorphism (SNP) marker using genotyping-by-sequencing. These SNP markers are currently being mapped *in silico* using *M. truncatula* to establish a physical genetic map. Further, a linkage map of a portion of these SNP markers will also soon be created using a pea recombinant inbred population. This high density genotyped association mapping panel can now be used for genome-wide association studies as demonstrated for barley (Pasam *et al.*, 2012; Shu *et al.*, 2012).

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