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GENETIC MARKERS ASSOCIATED TO ARBUSCULAR MYCORRHIZAL COLONIZATION IN DURUM WHEAT

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The arbuscular mycorrhizal (AM) symbiosis between soil fungi and plant roots is ecologically and agriculturally important, given its functional role in plant nutrition. The genetic basis of susceptibility to mycorrhizal colonization in wheat sub-species (Triticum spp.) has been investigated. The mycorrhizal status of wild, domesticated and cultivated tetraploid wheat accessions, differing for selection history, origin and/ or year of release, inoculated with the AM species Funneliformis mosseae, was evaluated. In order to detect genetic markers in linkage with chromosome regions involved in AM root colonization, a genome wide association analysis was carried out on 108 durum wheat varieties and two AM fungal species (F. mosseae and Rhizoglomus irregulare). Our findings showed that a century of breeding on durum wheat and the introgression of Reduced height (Rht) genes associated with increased wheat grain yields did not select against AM symbiosis in durum wheat. Moreover, mycorrhizal colonization ranged from 2 to 45% depending on environmental conditions, symbiont identity and wheat accession. Seven putative Quantitative Trait Loci (QTLs) linked with durum wheat mycorrhizal susceptibility in both experiments, located on chromosomes 1A, 2B, 5A, 6A, 7A and 7B, were detected. The individual QTL effects (r²) ranged from 7 to 16%, suggesting a genetic basis for this trait. Marker functional analysis has been carried out to find candidate genes. In conclusion, the genetic mapping of QTLs associated with mycorrhizal colonization will allow a more effective breeding for the development of new genetic material and a start point for further research.

ABSTRACT