

DEVELOPMENT OF A LINKAGE MAP TO DISSECT THE GENETIC BASES OF LEAF RUST RESISTANCE IN DURUM WHEAT

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Leaf rust, caused by the fungus *Puccinia triticina* (formerly *P. recondita* f. sp. *tritici*) is one of the most important diseases for wheat, causing significant yield losses annually in many wheat-growing regions of the world. The utilization of resistance genes is the most viable and economical strategy to minimize the yield losses. Many studies on genetic resistance were carried out on hexaploid wheat (*Triticum aestivum*) in which more than 60 resistance genes and QTLs have been described but little is known regarding leaf rust resistance in durum wheat (*Triticum turgidum*).

We are currently developing a genetic linkage map on a RIL population derived from a cross between two durum wheat varieties, Creso and Pedroso, for the dissection of the genetic bases of leaf rust resistance. Creso is a durum wheat cultivar whose resistance has been postulated to be durable and Pedroso is a susceptible cultivar. 123 F9 Recombinant Inbred Lines are now available from this cross and more than 400 biochemical and molecular markers (SSR) with known map position have been tested on the parental lines, resulting in 125 polymorphic markers.

Diversity Array Technology (DArT) can detect and type DNA variation in several hundred genomic loci in parallel and it can be effectively applied to genetic mapping in wheat. The DArT has been utilized to develop the map, resulting in about four hundred markers positioned on durum wheat genome.

The phenotypic characterization of the RIL population for hypersensitive response and durable resistance to leaf rust at different growth stages will allow to identify genetic determinants of qualitative and quantitative aspects of resistance to leaf rust in durum wheat.