

IDENTIFICATION OF COMMON RESISTANCE LOCI OF WHEAT TO THREE RUST SPECIES BY GWAS AND MULTI-LOCATION TRIALS

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Rusts are very common pathogens in tetraploid wheat, above all in Durum wheat (*Triticum turgidum* ssp. *durum*) which is the tetraploid species with higher economic importance, because of its use for human consumption. They are destructive diseases and can cause important production losses and downgrading in quality for durum wheat. Stem, Leaf, and Stripe rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), *P. triticina* (Ptr), and *P. striiformis* f. sp. *tritici* (Pst), respectively, represent an epidemical problem occurring on a continental scale because of the widespread dispersal of urediniospores.

The genetic bases of resistance are generally studied by reaction to single species approach, and have a complex basis with qualitatively acting R genes coupled to a number of QTLs for partial resistance.

A Genome wide association mapping approach (GWAS) was used in this study for identifying loci associated with resistance to the three rusts species by using the wheat 90K iSelect single nucleotide polymorphism (SNP) chip. Phenotyping was carried out by multi-locational trials in different areas of the world, in different growth conditions such as field trials /growth chambers, natural infection / artificial infection, in 2016 and 2017.

Different Marker-Traits-Associations (MTAs) were found diffused on the A and B genomes for specific rust species and also in common between different rusts, both in seedling and adult plant stages. Some resistance loci were confirmed by previous studies as coincident with rust resistance genes already discovered, and some new ones were identified. The results were reviewed by using the durum wheat reference genome sequence of cultivar Svevo.

The common resistance loci identified of resistance to the three rust species can represent pivotal loci for breeding of new durably resistant varieties.