

A NEW WILD EMMER WHEAT PANEL ALLOWS TO MAP NEW LOCI ASSOCIATED WITH RESISTANCE TO STEM RUST AT SEEDLING STAGE

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Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), is a major wheat disease worldwide, and can cause yield losses of up to 70% or more. A collection of 283 wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides* (Körn. Ex Asch. & Graebn.)) accessions, representative of the entire Fertile Crescent region where wild emmer naturally occurs, was assembled and genotyped, characterized for population structure, genetic diversity, and rate of LD decay. Then the collection was employed for mapping Pgt resistance genes, as a proof of concept of effective Genome Wide Association Studies (GWAS) in wild emmer. The collection was evaluated in controlled conditions for reaction to six common Pgt pathotypes that

currently threaten wheat worldwide (TPMKC, TTTTF, JRCQC, TRTTF, TTKSK/Ug99, and TKTTF). Most resistant accessions originated from the Southern Levant wild emmer lineage, with some showing a resistance reaction toward three to six tested races. Association analysis was conducted considering a 12K polymorphic SNPs dataset, kinship relatedness between accessions and population structure. Eleven significant Marker-Trait Associations (MTA) were identified across the genome, which explained from 17% up to 49% of phenotypic variance and an average of 1.5 additive effect (based on the 1-9 scoring scale). The identified loci were either effective against single or multiple races. Markers significantly linked to resistance were anchored on the wild emmer and durum wheat reference genomes. Some co-localised with known *Pgt* resistance genes, while others represent novel resistance loci useful for durum and bread wheat pre-breeding. Candidate genes with an annotated function related to plant response to pathogens were identified at the regions linked to the resistance and defined according to the estimated small linkage disequilibrium (about 126Kb), as typical of wild species.