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MAPPING OF QTLS FOR RESISTANCE TO STEM RUST IN TETRAPLOID WHEATS

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The recent emergence of new widely virulent and aggressive strains of Stem Rust (SR, Puccinia graminis) is threatening world as well as Italian durum wheat production, especially under the trend of higher temperature and humidity. A big effort has been undertaken to explore the genetic variability for resistance to this fungal pathogen and discovering novel resistance genes. As large untapped sources of genetic diversity, panels of tetraploid wheat lines provided of several thousands of SNP markers were used for association mapping. This large collection consisted of a group of durum wheat cultivars, produced by the last century breeding, a collection of wild emmer wheats (T. dicoccoides), and lines belonging to other wild and domesticated tetraploid subspecies. In a tight cooperation with the University of Minnesota, this collection was evaluated for reaction to several SR races, including the known Ug99 and the recently emerged TTTTF, in controlled greenhouse and field conditions. Among the genotypes belonging to the collection are parents of two segregating populations (Cirillo x Neodur, Latino x MG5323) that were used for the validation of mapping results. Novel resistance loci were identified, that can be incorporated into new durum varieties through breeding programs. The QTLs found in this study, together with those available in literature, were projected to the recently sequenced durum wheat reference genome (cv Svevo) in order to define more precisely the chromosome regions and candidate genes involved in resistance to rusts. Lines which were resistant to multiple races of rust pathogens were also found among both T. dicoccoides and durum wheat cultivars as a source of resistance genes whose cloning will be undertaken based on the results here ob-

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