CANDIDATE GENE ASSOCIATION MAPPING OF DROUGHT AND SALINITY RESISTANCE IN DURUM WHEAT

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Association or linkage disequilibrium (LD) mapping is a strategy to identify associations between the alleles or haplotypes present in natural populations or collections of germplasm and the trait of interest. Association studies exploit recombination events accumulated over many generations, therefore only markers in LD with the causal allele will show statistical associations with the trait of interest, allowing to improve the mapping resolution. Marker-trait associations can be found either saturating the genome with markers (whole genome scan) or looking at variation in specific genes (candidate gene association mapping). We carried out a candidate gene association study to identify genes that are involved in the genetic control of drought and salinity resistance in durum wheat. Candidate genes were selected among those involved in the control of the trait of interest in Arabidopsis and rice. To verify the presence of polymorphic sites in the candidate gene sequence, genes were preliminarily sequenced on 12 inbred lines, that greatly differ in terms of genetic diversity and stress resistance. This preliminary analysis revealed the presence of polymorphic sites in 26 out of 72 genes sequenced resulting in a SNP frequency of 0.17%. Moreover, no significant decay of LD was observed in the sequenced regions. The polymorphic genes were then sequenced on the rest of the inbred lines that were characterized phenotypically during the project (87 inbred lines in total). In the association studies correction for population structure is essential to avoid spurious associations. The analysis of 20 SSR loci revealed the presence of 5 subpopulations in the germplasm considered and the estimates of population structure were incorporated in the association tests. We performed the association tests between 35 polymorphisms able to distinguish the haplotypic variations in the germplasm and 8 phenotypic traits (among others, yield, a thousand seeds weight and heading date). The LD mapping method allowed to detect statistical significant associations and to identify genes putatively responsible for the phenotypic variability. We present and discuss results of the association tests and of the further characterization of the genes associated with the phenotype, including the determination of their position and of the extent of the associated region.