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Poster Abstract - D.13

NUCLEOTIDE DIVERSITY AND LEVELS OF LINKAGE DISEQUILIBRIUM IN CANDIDATE GENES FOR DROUGHT AND SALINITY RESISTANCE IN DURUM WHEAT

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The genetic factors that underlie complex quantitative traits can be identified by using linkage disequilibrium (LD) mapping. Such an analysis allows to exploit natural populations to map the genetic determinants of a trait of interest. In this way it relies on many more informative meioses (i.e., all those occurred in the history of the genotypes) than those contained in a traditional mapping population. Association analysis has the potential to identify a single polymorphism within a gene that is responsible for the phenotypic variation. In this study we used the candidate gene approach to localize the genes that contribute to the drought and salinity resistance in durum wheat (*Triticum turgidum* ssp. *durum*). An initial set of 100 candidate genes was determined by choosing genes with known function in Arabidopsis and rice. This set comprises stress-inducible transcription factors belonging to many different classes, including the bZIP, MYB, ERF/AP2, WRKY and zinc finger families. Primers have been designed on the basis of the wheat ESTs homologous to these genes. In the case of co-amplification of more than one locus, the primers have been redesigned from the single sequences obtained by cloning the PCR product. 30 genes have been analysed so far with this procedure. For a number of genes more than one locus per gene was amplified and sequenced. In total 46 loci have been sequenced in a subset of the 12 lines that are representative in terms of genetic diversity and stress resistance of the whole set of 88 lines that will be characterized phenotypically during the project. Overall, we found a low SNP frequency (equal to 0.20%, i.e. one SNP every 510bp) and, as a consequence, a very low nucleotide diversity in most loci (on average equal to 0.00066). It has been observed that in the sequenced regions LD does not decay significantly within physical distances of 1kb. This approach will potentially allow to establish statistically significant associations between nucleotide diversity at the candidate loci and the phenotypic variation for the traits of interest and, thus, to identify the genes responsible for such variation to use in durum wheat breeding programs.