ASSOCIATION MAPPING USING CANDIDATE GENES FOR DROUGHT AND SALINITY RESISTANCE IN DURUM WHEAT

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Linkage disequilibrium mapping is a method to determine whether candidate genes are associated with variation in a trait of interest using natural populations and to localize polymorphisms that contribute to this variation. In this project we used the candidate gene approach to identify genes that contribute to the drought and salinity resistance in durum wheat (*Triticum turgidum* ssp. *durum*). A set of candidate genes that includes stress-inducible transcription factors belonging to many different classes, were preliminarily sequenced on 12 inbred lines, that greatly differ in terms of genetic diversity and stress resistance. Hence, each polymorphic site found in the preliminary analysis has been genotyped in 95 samples (87 inbred lines and 8 individuals from different Ethiopian populations) that were characterized phenotypically during the project. In LD mapping studies the population structure has to be taken into account because it may lead to nonfunctional, spurious associations. In order to infer the population structure with random and unlinked genetic markers, we selected, on the basis of a simple sequence repeat (SSR) map of *T. turgidum* previously constructed in our lab, the two most distal SSR markers of each major linkage group. Therefore, all the samples have been genotyped with 28 SSR markers. Here we present and discuss results on nucleotide diversity in a large set of genic regions, on the extent of LD in durum wheat genome and on the genetic variability and the phylogenetic relationships among the lines used in the present study. Association tests, that incorporate estimates of population structure, will enable to detect statistically significant associations between sequence variants in the candidate genes and the phenotypic variation and may lead to the identification of the alleles responsible for this variation in the trait of interest.