Poster Abstract - C.04

USING A DURUM WHEAT GERMPLASM COLLECTION SUITABLE FOR GENE DISCOVERY VIA ASSOCIATION MAPPING: CHROMOSOME REGIONS FOR RESISTANCE TO SOIL-BORNE CEREAL MOSAIC VIRUS

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A collection of 134 durum wheat accessions chosen to sample the genetic variation present in the major cultivated gene pools has been assembled for genetic association study and allele mining purposes. The collection has been characterized molecularly with SSR markers to evaluate the pattern of long-range linkage disequilibrium (LD) and the presence of population structure (Maccaferri *et al.*, 2005). The phenotypic variation present in the collection is also being studied: various morphological descriptors and agronomically valuable traits have been recorded in comparative field trials carried out during the last three growing seasons. Up to now the collection have been characterized with 100 SSR markers, chosen on the basis of their map position and molecular information content.

A subset of 113 accessions were evaluated in two consecutive seasons (2003 and 2004) for resistance/tolerance to soil-borne cereal mosaic virus (SBCMV), a disease that affects bread and durum wheat in several regions of the world and especially in the north and centre of wheat growing areas in Italy. SSR data were subjected to the marker/phenotype association analysis after accounting for the population structure. A number of chromosome regions (e.g. on chromosome arms 4AL, 4BS, 5BL) showed a significant association with symptom severity and/or virus concentration in both years. These chromosome regions represent good candidates for harbouring valuable resistance genes/QTLs in durum wheat and are now being subjected to a more refined genetic analysis to validate their genetic effects on SBCMV. The results herein presented indicate the feasibility of utilizing association mapping for identifying chromosome regions that influence agronomic traits in durum wheat.