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Poster Abstract – A.10

FINDING A MOLECULAR MARKERS LINKED TO THE DEHYDRATION RESPONSIVE TRANSCRIPTION FACTOR 1 GENE (*TdDRF1)*

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Triticum durum, Dehydration Responsive Transcription Factor 1 (TdDRF1), Simple Sequence Repeat (SSR), Random Amplified Polymorphic DNA (RAPD)

The *Triticum durum TdDRF1* gene encodes for dehydration responsive transcription factors. The expression profile of this gene is being evaluated in both greenhouse and field environments, under well-watered and dehydrated conditions. Moreover, we are getting more and more information about the function of these factors. All the data obtained spotlight that the targeting of this gene could help the selection of cultivars for improving the plant tolerance to drought.

For this reason, one effective goal is to find some *TdDRF1* gene-associated molecular markers. Actually, molecular markers are becoming a powerful tool for crop improvement, permitting to characterize and evaluate the allelic diversity of germplasms.

Our analyses was lead on sequences coming from several Italian durum wheat varieties of economical interest for pasta production, some CIMMYT released cultivars with good adaptation to rainfed environments and some durum wheat wild ancestors, *Triticum urartu* and *Aegilops speltoides*.

In particular, here we focused on a Simple Sequence Repeat (SSR), which is localized in the 5' terminal codifying region of the gene and presents a repeating unit of 3 bp in length encoding for an Alanine. Among the analyzed sequences some of them showed a stretch of seven Ala, while others a stretch of six.

In parallel, we used an approach derived from the Random Amplified Polymorphic DNA (RAPDs) technique to screen the *TdDRF1* gene in several genotypes. We selected some specific primers and put at point a multiplex reaction in order to obtain a genotype-dependent band profile. We are performing this PCR assay using both genomic DNA and cDNA, proceeding from stressed plants.

Both the worklines would allow us to compare and cluster the analyzed genotypes based on the similarities concerning the SSR region and the fingerprints of the PCR results.

Hopefully, in the future, we would be able to associate the particular marker allele to the phenotypic response of the wheat genotypes to dehydration conditions.

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