

**International Conference** 

## **FROM SEED TO PASTA III** A Sustainable Durum Wheat Chain for Food Security and Healthy Lives



Bologna - Italy, 19-21 September 2018

## POLYMORPHISMS IN THE *TDDRF1* GENE SEQUENCE DISTINGUISH THE A AND B GENOME COPIES

Patrizia Galeffi, Cristina Cantale

ENEA, Casaccia Research Centre, Via Anguillarese 301, 00123 Rome, Italy Corresponding author: patrizia.galeffi@enea.it

Drought tolerance is one of the main components of yield and its stability in durum wheat, and its improvement is a major challenge to breeders. Genes codifying for transcription factors are particularly interesting, since they are components of the signal transduction pathways that coordinate the expression of several downstream genes. In particular, the dehydration responsive element binding factors (DREB proteins) are trans-acting elements endowed with a highly conserved AP2/EREBP domain, through which they bind specifically to DRE (dehydration responsive element), inducing the expression of functional downstream genes. A DREB2-related gene, namely TdDRF1 (Triticum durum dehydration responsive factor 1), was isolated in durum wheat and its expression was related to the response to water deficit. This gene, producing three transcripts by alternative splicing, was isolates, cloned and sequenced from different varieties and the polymorphisms were analysed. By a comparison with Triticum urartu and Aegilops speltoides homologous sequences, it emerged that both A and B genome copies of the TdDRF1 gene had been identified. The alignments highlighted several features, distinctive for A or B genomes, which could be used for selectively isolate the specific gene copy. Furthermore, polymorphisms were used to investigate preferences in transcription between the two genomes. Indeed, a larger number of transcripts homologous to the A rather than the B genomes were identified in transcripts databases. B genome specific polymorphism resulted in relationship with grain yield in drought condition in a RIL population and the validation as a functional marker is in progress. Finally, the effect of some polymorphisms in the inferred putative proteins was investigated and interesting results are reported.

## ABSTRACT