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CLUSTERING 288 LINES FROM THE FINAL PANEL OF THE DURUM WHEAT REFERENCE COLLECTION (DWRC) BY TDDRF1 GENE VARIABILITY

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Introduction: Drought tolerance is one of the main components of yield and its stability, and its improvement is a major challenge to breeders. Transcription factors are considered among the best candidate genes for developing functional markers, since they are components of the signal transduction pathways that coordinate the expression of several downstream genes. In the present study, we report preliminary results concerning the ability of various SNPs of *TdDRF1* gene to cluster 288 lines of durum wheat selected from the Durum Wheat Reference Collection (DWRC). The *TdDRF1* gene was isolated, cloned and sequenced in a large number of durum varieties in greenhouse experiments. The sequences were aligned and analyzed in order to highlight SNPs. Among all, 26 polymorphisms were used to design specific KASP markers and some of them were able to cluster the 288 different lines. These results are preliminary, but promising, in view of association studies with interesting agronomical traits.

Keywords: Tolerance, Stability, Transcription factors, Greenhouse, Agronomical traits.

Methodology & Theoretical Orientation: Durum Wheat Reference Collection (DWRC) resulted from an initiative by Durum Wheat Genomics and Breeding Expert Working Group, in the frame of the activities of the wheat initiative, aimed to optimize the utilization of the durum wheat genetic resources. The DWRC panel consists of a stratified collection of 960 accessions extensively genotyped and organized in four main subpanels (elite, landraces, durum relatives and INRA evolution population). In this study, 288 lines were selected, including the whole elite subpanel and some landraces. The KASP (Kompetitive Allele Specific PCR) genotyping technology (patented by LGC Ltd) represents a new high-throughput and low cost genotyping platform, lacking limitations of low throughput, labor intensiveness and high costs characterizing common SNP genotyping, as allele-specific PCR (AS-PCR), cleaved amplified polymorphic sequences (CAPS) and Temperature-Switch PCR (TSPCR). 26 markers designed on *TdDRF1* gene polymorphisms were used to genotyping 288 lines that represented a large spectrum of varieties already analyzed in field trials around the world.

Conclusion & Significance: In our study, the variability inside a functional gene was used as a tool for genotyping. Association studies with agronomic data will be carried out in order to exploit these alleles as new molecular markers. We thank DWGB-EWG for giving us the possibility of using the DWRC.

Biography

Patrizia Galeffi is a Senior Scientist at ENEA, Italian National Agency for New Technologies, Energy and Sustainable Economic Development. Her main scientific activities are focused on Biotechnology, Plant Genetics and Molecular Biology area: molecular study of genes in durum wheat responding to abiotic stresses; functional genomics, transcriptomics and gene expression profiling in plants; plant biodiversity, in particular cereal diversity; plant transformation and transgenic plants; bioinformatics and statistics applied to agronomical and molecular data; triticale as biomass for bioenergy and bioethanol; antibody molecular biology; antibody engineering; antibodies for plant pathogen resistance; plants as a bio-factory to produce antibodies for pharmacological use; molecular design of stable engineered antibodies; nanomaterials. She is an author of around 40 publications in peer-reviewed journals, Active Reviewer of several international scientific journals and member of the Panel Editors of *Journal of Food, Agriculture and Environment.* She is an author of five patents, certified agent for technology transfer and member of ENEA Patent Commission.

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