

AN IN-DEPTH STUDY OF R2R3-MYB TRANSCRIPTION FACTORS AND TRANSCRIPTOMIC RESOURCES TO ENHANCE DURUM WHEAT STRESS RESPONSE

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This study aims at expanding the research on durum wheat (*Triticum turgidum* subsp. durum) transcription factors (TFs), leveraging genomic and transcriptomic resources to better dissect wheat stress responses. MYB transcription factors, specifically R2R3-MYBs, are critical to the plant resilience to adverse environmental conditions, therefore they are significantly interesting for crop breeding. We carried out a genome-wide identification of R2R3-MYB TFs in durum wheat (PMID ref.: 35795353), leading to the discovery of 233 R2R3-TdMYBs and three Poaceae-specific MYB clusters, one of which was identified here for the first time. We focused on a small subset of genes falling into the abiotic stress response orthogroup and found that most of them responded primarily to salt and drought stress, revealing 41 gene targets for three TdR2R3-MYBs, thereby offering new gene candidates for future functional analyses. Subsequently, to provide a useful resource for omics research in durum wheat, we summarized the available transcriptomic resources for durum wheat (PMID ref.: 36986956), giving exhaustive information on various anatomical levels, phenological phases, environmental conditions, and highlighting the insights gained on abiotic and biotic stress responses. We present these resources, along with crucial databases, tools, and approaches, to assist comparative transcriptomics and omics data integration for the discovery of candidate genes for bio-agronomical traits. The knowledge and resources here generated are central for a comprehensive study and characterization

of a selection of Apulian local varieties in the frame of the project PSR Puglia 2014-2020; Operazione 10.2.1 “Biodiversità dei cereali antichi pugliesi per la sostenibilità e della qualità - SAVEGRAINCER”. On the whole, our research presents an extensive overview of the transcriptomic resources generated in durum wheat and provides valuable insights for future breeding programs for this important crop, aiming at elucidating the molecular responses to unfavorable climate conditions.