SEARCHING NATURAL VARIATION FOR WATER STRESS RESPONSE IN MAIZE

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Drought is the most pervasive and severe abiotic stress that affects crop potential and is therefore the greatest challenge to agriculture. Maize is of utmost importance to meet the food, feed, and industrial material demands of a growing world population, especially because it is a highly consumed crop and harbors a wide range of genetic diversity for stress tolerance. Whole-genome sequences of several maize lines are already available, enabling the search for natural genetic diversity associated with important agronomic traits. Thus, the objective of this study was to explore natural genetic variability in maize to find potential candidate genes related to drought tolerance using datasets from the public literature. Firstly, we review all GWAS papers about drought stress in maize. From this review, 20 papers were selected and the genes identified by

them were further investigated. We chose the trait anthesis silking interval (ASI) to update the genomic information because most part of the genes identified in the literature is related to it. The literature review indicated 48 candidate genes associated with ASI, and the list increases to 279 after the re-scan in the new version of maize genomes, including 133 uncharacterized ones. We performed two different analyses to identify the best set of potential candidate genes, namely, differentially expression gene analysis (DEG) and expression of protein, by protein protein interaction network (PPI). DEG analysis was performed based on the expression data, under the control and water stress condition, for eight traits available in the qTeller database. The PPI analysis was performed using the String website to construct the protein network, and the Cytoscape software was used to find clusters of genes and the most important ones in the network. The expression data for eight traits pointed out 73 differentially expressed genes. 39.73% of these DEG were upregulated and 60.27% of them were downregulated under drought compared to the control condition. Gathering the results for all the eight traits, we had 33 different genes. Only six were differentially expressed for at least four traits. The expression protein data provide other 42 relevant genes according to the results of the five analyses done, that is, three clusters of genes, number of connections for each gene in the network and the score for each one. Gathering the five results, we had 24 different genes. Only four of them were present in at least three results and were taken as promising candidates. No gene was common between the two approaches, namely, DEG and expression of proteins. So, we had ten final genes to investigate their potential to control drought tolerance in maize. Two of these genes are uncharacterized and will be used as candidate targets for genome editing in our laboratory.