

Co-expression Pattern and Functional Interaction of Drought-responsive Transcription Factors and Genes in Wheat, Rice, and Maize

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Abstract—We present co-expression networks in wheat, rice, and maize to unravel the interactions of drought-responsive genes underlying the complex molecular mechanisms governing drought tolerance in the three species. The largest co-expression network was created for wheat (3321 nodes, 819 066 edges) followed by rice (2471 nodes, 600 155 edges) and maize (1779 nodes, 212 353 edges). A comparison of the co-expression networks of these three species showed that, under drought stress, rice had more signalling genes and comparatively fewer carbon-metabolizing genes than wheat and maize did. Osmoregulation could be a secondary mechanism for drought tolerance in rice because it had the lowest number of osmoregulating genes in its co-expression network among the three species. Of the 17 important drought-specific transcription factor (TF) families in the network, MYB was the most numerous in all, followed, by bHLH, ERF, C2H2, NAC, and bZIP with little variation in connectivity across the three species. The interaction of these genes offered fresh insights in studying the function of drought-responsive genes across species and in identifying the target pathways for improving drought tolerance.