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Identification and Functional Analyses of NO-responsive Transcription Factors Suggest Their Role in Plant Growth and Defense—A Way Forward to Crop Improvement

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[Introduction]

Nitric oxide (NO) has emerged as a key signaling molecule both in plants and animals in the last couple of decades under various stress conditions. These insults typically induce changes in cellular redox state, partly by promoting the production of reactive nitrogen species (RNS). Contrary to other signaling cascades, NO transfers its bioactivity through post-translational modification, the chief of which is *S*-nitrosylation. Transcription factors (TFs) are regulatory proteins that act as on/off relay of gene expression and are crucial particularly in the altered redox state of the cell.

[Materials and Methods]

In the current study using high-throughput RNA seq data from two separate studies, we identified transcription factors that showed differential expression in response to *S*-nitroso L-Cysteine (CySNO) both in Arabidopsis and rice. NO-induced TFs from both species were analyzed for their phylogenetic relationship and to identify common and unique TFs using Venn diagram in both species. Promoter sequences of the common NO-induced TFs were analyzed 1.5 kb upstream of the transcription initiation site for possible cis-regulatory elements. Gene ontology (GO) analyses were performed to associate TFs with respective GO terms.

[Results and Discussion]

About 673 TFs in Arabidopsis and 131 in rice representing major TF families showed differential expression in response to CySNO, one of the NO donor. GO enrichment analysis suggested that more than 95% of NO-induced TFs were successfully mapped to Arabidopsis and rice genomes, respectively and were classified into pathways that regulate various key cellular processes including hormone signaling, protein degradation, growth and development, biotic and abiotic stresses, etc. A comparison of both transcriptomes showed several TFs that showed differential expression in response to NO in both species. For example, certain members of WRKY TFs such as WRKY 4, WRKY61, and WRKY65 were up-regulated in both Arabidopsis and rice suggesting that NO function is conserved across the plant kingdom.

Functional characterization into the role of certain NO-responsive TFs in the model plant Arabidopsis through the functional genomics approach suggested their putative role in plant growth, development, and defense. For example, functional genomics study using knock out (KO) lines of NO-responsive *AtMYB48* showed negative regulation of *R*-gene mediated defense, whereas *AtRAP2.6* showed positive regulation of both basal and *R*-gene-mediated defense response. Concluding this study will help to identify candidate genes involved in the key biological process for improving crop productivity and resistance to phytopathogens.

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