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***OxF3H* Gene Increases Insect Resistancy in Rice through Transcriptomic Changes and Regulation of Multiple Biosynthesis Pathways**

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[Abstract]

In this study, we analyze RNA-seq data from *OxF3H* and WT at several points (0 h, 3 h, 12 h, and 24 h) after WBPH infection. A number of the genes were further validated by RT-qPCR. Results revealed that highest number of DEGs (4,735) between the two genotypes detected after 24 h of infection. Interestingly, many of the DEGs between the WT and *OxF3H* under control conditions were also found to be differentially expressed in *OxF3H* in response to WBPH infestation. These results indicate that significant differences in gene expression between the “*OxF3H*” and “WT” exist as the infection time increases. Many of these DEGs were related to oxidoreductase activity, response to stress, salicylic acid biosynthesis, metabolic process, defense response to pathogen, cellular response to toxic substance, and regulation of hormones level. Moreover, genes involved in salicylic acid (SA) and Ethylene (Et) biosynthesis were upregulated in *OxF3H* plants while jasmonic acid (JA), Brassinosteroid (Br), and abscisic acid (ABA) signaling pathways were found downregulated in *OxF3H* plant during WBPH infestation. Interestingly, many DEGs related to pathogenesis such as *OsPRI*, *OsPRIb*, *NPRI*, *OsNPR3* and *OsNPR5* were found significantly upregulated in *OxF3H* plants. Additionally, genes related to MAPKs pathway, and about 30 *WRKY* genes involved in different pathways were found upregulated in *OxF3H* plants after WBPH infestation. This suggests that overexpression of the *OxF3H* gene leads to multiple transcriptomic changes and impact plant hormones, pathogenic related and secondary metabolites related genes and enhancing the plant resistance to WBPH infestation.

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