

Transcriptome analysis of a rice cultivar reveals the differentially expressed genes in response to wild and mutant strains of *Xanthomonas oryzae* pv. *oryzae*

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Supplementary files:

Supplementary Table 1. Description of RNA-Seq paired end data produced by Illumina sequencing.

Supplementary Table 2. Detailed list of 1,235 DEGs at different time points in CBB23 genotype after infection of PXO99^A and P99M2 strains. The significant DEGs were retrieved by Log₂FC ≥ 1 (up-regulated genes) or ≤ -1 (down-regulated genes) as a threshold level. The gene ID, FPKM based expression pattern, and chromosomal position are mentioned in the table.

Supplementary Table 3. Description of differentially expressed TFs in CBB23 after infection of PXO99^A and P99M2 strains at different time points.

Supplementary Table 4. Significantly enriched peroxidase responsive genes in CBB23 after PXO99^A and P99M2 infection.

Supplementary Table 5. Summary of GO enrichment in CBB23 after PXO99^A and P99M2 infection.

Supplementary Table 6. Significant GO terms (FDR ≤ 0.05) of DEGs after infection of PXO99^A and P99M2 strains in CBB23 at different time periods.

Supplementary Table 7. Significant KEGG pathway (p -value ≤ 0.05) in CBB23 after PXO99^A and P99M2 infection at different time points.

Supplementary Table 8. MapMan analysis of DEGs involved in host-pathogen interaction pathway in CBB23 genotype. The gene ID, bin code, gene description, and average Log₂FC values are presented in the below-mentioned table.

Supplementary Table 9. Co-expression network analysis of nominated differentially expressed TFs with other rice genes.

Supplementary Table 10. List of qRT-PCR primers used for RNA-Seq data validation.