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## Transcriptome sequencing analysis of *Oryza meyeriana* reveals the differences in disease resistance with *Oryza sativa*

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*Oryza meyeriana* (*O. meyeriana*), a GG genome type ( $2n=24$ ), accumulated plentiful excellent characteristics with respect to tolerance to shade, blast and bacterial blight. However, limited genomic or transcriptomic data of *O. meyeriana* are currently available. In this study, we present the first comprehensive characterization of the *O. meyeriana* transcriptome using RNA-seq. We obtained 185,323 contigs with an average length of 1,692 bp and an N50 of 2,391 bp. Through differential expression analysis, we found there were most tissue-specifically expressed genes in roots, and next to stems and leaves. By similarity search against protein databases, 146,450 had at least a significant alignment to existed gene models. Comparison with the *Oryza sativa* (*O. sativa*) genome revealed similar rate of alignment across different plant species, however 13% of the *O. meyeriana* contigs had not been detected as expressed in *O. sativa*. Furthermore, the enrichment of the plant-pathogen interaction pathway in *O. meyeriana* showed difference with *O. sativa*, including the similarity of these aligned candidate genes and the absence of candidate genes involved in the plant-pathogen interaction pathway. In addition, we identified 52 contigs as disease resistance protein which was not existed in *O. sativa*. Taken together, there are significant differences between *O. meyeriana* and *O. sativa* in disease resistance. This information provides a foundation for future investigations into the discovery of a huge amount of novel genes which will facilitate gene mining and provides a basis for comparative studies within the genus *Oryza*.

### Biography

Bin He is studying at Sichuan University of Life Science Institute as a PhD student. His research concerns the transcriptome and genome of wild rice, including *Oryza meyeriana*, *Oryza officinalis* and *Oryza rufipogon*. He is committed to mining new resistant resource; apply new elite resistant genes to improve the resistance of rice. He has published several papers in some journals, such as BMC genomics.

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