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### 2<sup>nd</sup> International Conference on

# **Transcriptomics**

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### The transcriptomic studies on rice (Oryza sativa) developing embryo and endosperm

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Respectively. We used RNA-seq to reveal the molecular mechanisms involved in rice endosperm development. Three cDNA libraries were taken from rice endosperm at 3, 6 and 10 days after pollination (DAP), which resulted in the detection of 21,596, 20,910 and 19,459 expressed genes, respectively, and 10,371 genes were differentially expressed in the early and middle stages. Plant hormone, galactose metabolism and carbon fixation related genes showed a significant increase in expression at the middle stages. Plant hormone, galactose metabolism and carbon fixation related genes showed a significant increase in expression at the middle stages. Plant hormone, galactose metabolism and carbon fixation related genes showed a significant increase in expression at the middle stages, whereas genes for defense against disease or response to stress as well as genes for starch/sucrose metabolism were strongly expressed during the later stages of endosperm development. The RNA-Seq result confirmed the expression characteristics of rice endosperm development.

#### Biography

Jianbo Wang has completed his PhD from Wuhan University, China. He is interested in the research on plant reproductive development, and has published more than 40 papers in reputed journals.

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