

International Conference on **Transcriptomics**

July 27-29, 2015 Orlando, USA

Transcriptome and small RNA gene expression changes in synthetic allohexaploids of Brassica

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Polyploidy played important roles in promoting plant genome evolution through genomic merging and doubling. We compared transcriptome and small RNA expression differences between a synthetic Brassica allohexaploid and its parents using RNA-seq approach. Total of 29260, 29060 and 29697 genes were expressed in B. rapa, B.carinata and the allohexaploid respectively. The majority of the 3184 DEGs between the allohexaploid and B. rapa were involved in photosynthesis, biosynthesis of secondary metabolites and circadian rhythm. For the 2233 DEGs between the hexaploid and B. carinata, many played roles in photosynthesis, plant hormone signal transduction, biosynthesis of secondary metabolites and limonene and pinene degradation. There were more differences between the allohexaploid and its paternal parent than that between it and its maternalparent in gene expression. Many methyltransferase genes and transcription factor genes showed differential expression between the hexaploid ard its parents. On the other hand, we detected 613, 784 and 742 miRNAs expressed in B. rapa, B. carinata and the allohexaploid respectively and 618 miRNA genes were differentially expressed between Brassica hexaploid and its parents while 425 miRNA genes showed non-additive expression in the allohexaploid. Moreover, many non-additively expressed miRNAs were repressed in the allohexaploid and there was a bias towards repression of B. rapami RNA genes which is consistent with progenitor biased gene repression in these allopolyploids. Our study represented the comprehensive analysis of functional gene and small RNA gene expressions in allopolyploid which would lead to better understanding of plasticity of allopolyploid genomes.

Biography

Jianbo Wang has completed his PhD from Wuhan University. He is interested in the research on plant molecular evolution and has published more than 30 papers in reputed journals.

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