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Transcriptomic Analysis of Fragrant Rice Reveals the Involvement of Post-transcriptional Regulation in Response to Zn Foliar Application

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Abstract : Alternative splicing (AS) is an important post-transcriptional regulatory mechanism to generate transcripts variability and proteome diversity in plants. Fragrant rice (Oryza sativa L.) has a high economic and nutritional value, and the application of micronutrients regulate 2-acetyl-1-pyrroline (2-AP) production, which is responsible for aroma in fragrant rice. However, no systematic investigation of AS events in response to micronutrients (Zn) has been performed in fragrant rice. Furthermore, the post-transcriptional regulation of genes involved in 2-AP biosynthesis is also not known. In this study, a comprehensive analysis of AS events under two gradients of Zn treatment in two different fragrant rice cultivars (Meixiangzhan-2 and Xiangyaxiangzhan) was performed. A total of 386 and 598 significant AS events were found in Meixiangzhan-2 treated with low and high doses of Zn, respectively. In Xiangyaxiangzhan, a total of 449 and 598 significant AS events were found in low and high doses of Zn, respectively. Go analysis indicated that these genes were highly enriched in physiological processes, metabolism, and cellular process in both cultivars. However, genotype and dose-dependent AS events were also detected in both cultivars. By comparing differential AS (DAS) events with differentially expressed genes (DEGs), we found a weak overlap among DAS and DEGs in both fragrant rice cultivars, indicating that only a few genes are post-transcriptionally regulated in response to Zn treatment. We further report that Zn differentially regulates the expression of 2-AP biosynthesis-related genes in both cultivars, and Zn treatment altered the editing frequency of SNPs in the genes involved in 2-AP biosynthesis. Finally, we showed that epigenetic modifications associated with active gene transcription are generally enriched over 2-AP biosynthesis-related genes. Taken together, our results provide evidence of the post-transcriptional gene regulation in fragrant rice in response to Zn treatment and highlight that the 2-AP biosynthesis pathway may also be post-transcriptionally regulated through epigenetic modifications. These findings will serve as a cornerstone for further investigation to understand the molecular mechanisms of 2-AP biosynthesis in fragrant rice.

Keywords : fragrant rice, 2-acetyl-1-pyrroline, gene expression, zinc, alternative splicing, SNPs
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