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Identification of key genes involved in purple shoot tea

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Statement of the Problem: Purple shoot tea attributing to the high anthocyanin accumulation is of great interest for its wide health benefits. However, the underlying mechanisms involved in purple buds and leaves formation in tea plants still remain elusive. To better understand this issue, comparative transcriptome profiling were performed on three purple tea individuals and three green tea individuals from a F1 population ('Longjing43'x'Baihao zao') to reduce background disturbance. Nearly 300 million RNA-Seq reads were obtained and they were finally assembled into more than 110,000 unigenes. The average length of assembled sequences reached 759 bp and the N50 sequence length was 1081 bp, indicating the RNA-Seq analysis was of good quality. A total of 2193 unigenes showed significant differences in expression levels between green and purple tea samples, with 1143 up- and 1050 down-regulated in the purple tea. Further real time PCR analysis was consistent with the RNA-Seq results. Our study identified 28 differentially expressed transcriptional factors and *A CsMYB* gene was found to be highly similar to AtPAP1 in Arabidopsis. Further analysis of differentially expressed genes involved in anthocyanin biosynthesis and transportation showed that the late biosynthetic genes and genes involved in anthocyanin transportation were largely affected but the early biosynthetic genes were less or none affected. Overall, the identification of a large number of differentially expressed genes offers a global view of the potential mechanisms associated with purple buds and leaves formation, which will facilitate molecular breeding in tea plants.

Biography

Kang Wei has his research interest in the accumulation of flavonoids (including catechins, anthocyanins, etc.) in different tea cultivars and relative mechanisms. Currently, he is working on LC MS to detect chemicals in tea leaves of different cultivars. He has experience in RNA-SEQ and iTRAQ technologies to get the transcriptome and proteome data.

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