

## **Tandem Duplication of a Flavonol Synthase Gene *FtFLS1* and Its Association with Rutin content in Tartary Buckwheat**

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### **[Introduction]**

Tartary buckwheat (*Fagopyrum tataricum*) is a valuable crop due to its characteristic functional component, rutin for medicine and health. Flavonol synthase (FLS) genes involved in rutin biosynthesis had been already isolated from tartary buckwheat, but *FtFLS1* has not been characterized so far in whole genome of *F. tataricum*. In this study, we isolated and characterized the *FtFLS1* involved in regulation of the rutin biosynthetic pathway from *F. tataricum*.

### **[Materials and Mehtods]**

To elucidate rutin-biosynthetic pathway, we conducted transcriptome analysis in flowers, stems, roots and leaves of tartary buckwheat along with the analysis of a high-quality draft genome of *F. tataricum*.

### **[Results and Discussions]**

Comparative analyses of *FLS1* loci demonstrate that these genes of *F. tataricum* expanded through sequential tandem duplications differently of genes from common buckwheat (*F. esculentum*). The tandem duplicated *FLS1* showed flower-specific expression in *F. tataricum*. Correspondingly, rutin content increased in flowers of *F. tataricum*, compared to other parts. These results suggest that the tandem duplicated *FtFLS1* in tartary buckwheat result in the increased rutin content, compared to common buckwheat. In further work, by a dedicated qPCR array platform, the transcript levels of rutin biosynthetic genes, including paralogs, will be determined in flowers, leaves, stems and roots to elucidate the pathway regulatory mechanisms.

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