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## **Transcriptome Profiling of Glucosinolate Biosynthesis in Radish (*Raphanus sativus* L.) roots**

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### **[Introduction]**

Radish (*Raphanus sativus* L.) is a major root vegetable in *Brassicaceae* family worldwide. Glucosinolates (GLs) content and composition are important breeding target in radish cultivars that are beneficial to human health on inflammation, carcinogenesis and cardiovascular protection. However, molecular mechanisms of their metabolism in radish have been a few reports. In this study, we performed a RNA sequencing (RNA-seq) technology for comprehensive analysis of transcriptome in radish root.

### **[Materials and Methods]**

A total of 63 radish (*Raphanus sativus* L.) accessions were collected from Rural Development Administration, Leibniz Institute of Plant Genetics and Crop Plant Research, and National Agriculture and Food Research Organization for identification of total GLs were used in this study. Two radish transcriptome (var. *hortensis* x cv. Aokubi doubled haploid (DH) line and cv. WK10039 inbred line) were used as reference genome sequence for a RNA-seq. The quantitative RT-PCR (qRT-PCR) was carried out for conducting expression of candidate genes.

### **[Results and Discussion]**

The trimmed read between 25,046,852 ~ 59,463,280 from RNA-seq technology were mapped on the 2 reference genome sequences. We selected 90 and 79 candidate genes and analyzed by heatmap and qRT-PCR, respectively. The majority of the genes related to GLs biosynthesis were investigated in the candidate genes. This transcriptome data will provide the information of comprehensive gene expression in radish root and will facilitate the biotechnological approaches for molecular breeding of radish.

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