



Analysis of alterations to the transcriptome of Loquat (*Eriobotrya japonica* Lindl.) under low temperature stress via *de novo* sequencing

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ABSTRACT. Loquat (*Eriobotrya japonica* Lindl.), which originates from the cooler hill regions of southwestern China, is a typical subtropical evergreen tree. Loquat is one of the most important economic crops in China, but the available genomic information is very limited. Here, we present the first deep transcriptomic analysis of loquat. *De novo* assembly generated 116,723 contigs and 64,814 unigenes using Illumina sequencing technology. A total of 45,739 unigenes were annotated by Nr, GO, and COG datasets. In addition, we analyzed the gene expression profiles of loquat fruit under low temperature stress and 4017 differential expressed genes were identified. We found that the unigenes involved in the brassinosteroid biosynthesis and phosphatidylinositol signaling systems were upregulated, indicating that they have an important role in the resistance of plants to low temperature. Our results provide an invaluable resource for identification of specific genes and proteins involved in loquat development and response to low temperatures.

Key words: Loquat; Illumina sequencing; Low temperature stress; Transcriptome