

RNA-sequencing of methyl-jasmonate treated turmeric (*Curcuma longa*) reveals novel protease inhibitor transcripts

ABSTRACT

Turmeric (*Curcuma longa*) has long been known in Southeast Asia as a medicinal plant and been used as folk remedies to treat minor illnesses like diarrhea or skin diseases. Recent studies on turmeric have shown numerous pharmacological properties such as anti-oxidant, anti-inflammatory, anti-pathogenic including anti-viral protease activities. All these beneficial properties make turmeric a suitable candidate for the discovery of novel protease inhibitors (PIs). PIs are commonly found in all organisms to regulate biological processes. In plant, PIs are reported to play important roles in plant defense mechanism. A number of these PIs have been genetically engineered into crop plants to enhance protection against microorganism and pest insects. However over time, the pathogens and pest insects are slowly adapting to the current strategies and overcome the additional defense barrier. Hence, this study was conducted to identify novel PIs genes from methyl jasmonate (MeJA)-treated turmeric plants through the whole transcriptome sequencing approach. From the raw data reads obtained from the RNA-sequencing of MeJA-treated leaf tissues, a single reference transcriptome was assembled de novo using Trinity software. A total of 105,529 contiguous sequences were obtained. Sequence annotation and homology search were performed onto several protein databases such as Uniprot, Pfam, GO and KEGG which resulted in around 50% of the transcripts showed similarity hits to known proteins. The individual expression profile of the transcripts from the control and MeJA-treated turmeric samples were generated and compared in order to identify differential expressed genes. A total of 4274 transcripts had been identified to be differentially expressed where there were 1599 upregulated transcripts and 2715 downregulated transcripts. A total of 21 transcripts showed sequence similarity hits to PIs families and three of the transcripts were identified to be upregulated from the MeJA treatment. These identified PIs transcript can serve as candidate genes for further functional studies and applications.

Keyword: Turmeric (*Curcuma longa*); Protease inhibitor; RNA sequencin