**Ginger and turmeric expressed sequence tags identify signature genes for rhizome identity and development and the biosynthesis of curcuminoids, gingerols and terpenoids**

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Abstract
Background

Ginger (Zingiber officinale) and turmeric (Curcuma longa) accumulate important pharmacologically active metabolites at high levels in their rhizomes. Despite their importance, relatively little is known regarding gene expression in the rhizomes of ginger and turmeric.

Results

In order to identify rhizome-enriched genes and genes encoding specialized metabolism enzymes and pathway regulators, we evaluated an assembled collection of expressed sequence tags (ESTs) from eight different ginger and turmeric tissues. Comparisons to publicly available sorghum rhizome ESTs revealed a total of 777 gene transcripts expressed in ginger/turmeric and sorghum rhizomes but apparently absent from other tissues. The list of rhizome-specific transcripts was enriched for genes associated with regulation of tissue growth, development, and transcription. In particular, transcripts for ethylene response factors and AUX/IAA proteins appeared to accumulate in patterns mirroring results from previous studies regarding rhizome growth responses to exogenous applications of auxin and ethylene. Thus, these genes may play important roles in defining rhizome growth and development. Additional associations were made for ginger and turmeric rhizome-enriched MADS box transcription factors, their putative rhizome-enriched homologs in sorghum, and rhizomatous QTLs in rice. Additionally, analysis of both primary and specialized metabolism genes indicates that ginger and turmeric rhizomes are primarily devoted to the utilization of leaf supplied sucrose for the production and/or storage of specialized metabolites associated with the phenylpropanoid pathway and putative type III polyketide synthase gene products. This finding reinforces earlier hypotheses predicting roles of this enzyme class in the production of curcuminoids and gingerols.

Conclusion

A significant set of genes were found to be exclusively or preferentially expressed in the rhizome of ginger and turmeric. Specific transcription factors and other regulatory genes were found that were common to the two species and that are excellent candidates for involvement in rhizome growth, differentiation and development. Large classes of enzymes involved in specialized metabolism were also found to have apparent tissue-specific expression, suggesting that gene expression itself may play an important role in regulating metabolite production in these plants.

Keywords:
Ginger; Turmeric; EST; Microarray; Metabolite; Rhizome development