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Title: Differential Network Analysis Reveals Evolutionary Complexity in Secondary Metabolism of

Rauvolfia serpentina over Catharanthus roseus

Authors: Ahuja, P.S. (/jspui/browse?type=author&value=Ahuja%2C+P.S.)

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Abstract:

Comparative co-expression analysis of multiple species using high-throughput data is an integrative approach to determine the uniformity as well as diversification in biological processes. Rauvolfia serpentina and Catharanthus roseus, both members of Apocyanacae family, are reported to have remedial properties against multiple diseases. Despite of sharing upstream of terpenoid indole alkaloid pathway, there is significant diversity in tissue-specific synthesis and accumulation of specialized metabolites in these plants. This led us to implement comparative coexpression network analysis to investigate the modules and genes responsible for differential tissue-specific expression as well as species-specific synthesis of metabolites. Toward these goals differential network analysis was implemented to identify candidate genes responsible for diversification of metabolites profile. Three genes were identified with significant difference in connectivity leading to differential regulatory behavior between these plants. These genes may be responsible for diversification of secondary metabolism, and thereby for species-specific metabolite synthesis. The network robustness of R. serpentina, determined based on topological properties, was also complemented by comparison of gene-metabolite networks of both plants, and may have evolved to have complex metabolic mechanisms as compared to C. roseus under the influence of various stimuli. This study reveals evolution of complexity in secondary metabolism of R. serpentina, and key genes that contribute toward diversification of specific

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