

Bioactive Secondary Metabolites Associated Genes from High Value Rare Medicinal Plants are Panacea for Metabolic Engineering

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Editorial

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Editorial

Medicinal plants have drawn considerable attention as a matter of fact that human all over the world requires medicine. Consumption of herbal medicine has been increasing. Harvesting the medicinal plants from wild for this purpose is great loss of biodiversity. Himalayan region of India is considered as one of the hot spots of biodiversity. The gene mining and their functional characterization of rate limiting steps of concerning pathways are essential to provide several clues for targeting gene function for upscale production of medicinally significant components *in vitro* as well as *in vivo*. Various studies have been performed so far on isolation and characterization of rate limiting genes in several medicinal plants. Gene over expression analysis is also being successfully carried out to correlate the role of other associated key genes transcript level and secondary metabolite in many plant species. Over expression studies in which HMG-Co a reductase gene (hmgr) from *Catharanthus roseus* and amorpha-4, 11-diene synthase (ads) gene from *Artemisia annua* were over-expressed in *A. annua* plants to find their effect on artemisinin content. The expression of hmgr and ads at the transcriptional level were also confirmed in each transgenic line employing RT-PCR assays. The HPLC analysis showed that the artemisinin content was significantly increased in these transgenics upto 7.65-fold higher compared to non-transgenic wild plant. Expression analysis of isoprenoid pathway in the presence of two inhibitors mevinolin and fosmidomycin in suspension cultures of *Arnebia euchroma* suggested a positive correlation between shikonin content and expression of 3-hydroxy-3-methylglutaryl-CoA reductase (Ae hmgr) and (Ae pgt)

suggesting critical role played by these genes in shikonins biosynthesis. Picroside-I & II, Derived from *Picrorhiza kurroa*, an iridoid glycoside, is used as an active ingredient of various commercial herbal formulations available for the treatment of liver ailments. Expression studies of Picroside biosynthesis in which four genes of MEP pathway; DXPS, ISPD, ISPE, MECPS and one gene of MVA pathway PMK from *Picrorhiza kurroa* showed elevated levels of transcripts (57-166 folds) in shoots and (5-15 folds) in stolons with Picroside-I. Further HDS and DXPR genes of MEP pathway showed higher expression ~9-12 folds in roots having Picroside-II. The expression of ISPH and ISPE was also high ~5 folds in roots accumulating Picroside-II. GDPS was the only gene with high transcript level in roots (9 folds) and shoots (20 folds). Differential biosynthesis and accumulation of picrosides would assist in regulating quantity of active ingredients for herbal medicine. The DXPR expression is also known to be positively correlated with the isoprenoid biosynthesis in peppermint and diterpenoid tanshinone accumulation in hairy roots of *Salvia miltiorrhiza*. *Withania somnifera*, also known as Indian ginseng/ ashwagandha is known to contain valuable bioactive compounds, called withanolides. Nine fast growing hairy root lines of *Withania somnifera* were analyzed for their growth and withanolide content. Hairy root line W9 was selected due to its high specific growth rate (0.196 ± 0.005 d⁻¹) and high withanolide content. The response to different concentrations of elicitor's methyl jasmonate and *Piriformospora indica* cell homogenate were assessed in the W9 hairy root line. qPCR is presently the effective way to understand

expression patterns of different genes from MVA, MEP and PPP for terpene pathway. Though gene expression and withanolide content were found to be elevated in almost all elicitor treatment and different time durations. The results suggest that the elicitation potential of methyl jasmonate was higher than that of *P. indica* cell homogenate for increasing withanolide levels in hairy roots of *W. somnifera*.

Efforts have been made throughout the globe to understand plant secondary metabolism and its regulation. Due to fact that the genes/enzymes of secondary metabolites biosynthesis are under strict control of various elicitors in a particular environment and need to understand before pathway engineering to safeguard biodiversity in one hand and their efficient utility for human demand on other hand.