



Category: Bioinformatics

An insight into structural and functional characteristics of 3-hydroxy 3-methyl glutarylCoA reductase from *Ocimum* species

Shilpi Bansal¹ and Neelam Singh Sangwan¹

¹CSIR-Central Institute of Medicinal & Aromatic Plants, Lucknow (U.P.), INDIA

Presenting author: shilpi.success@gmail.com

Abstract

Secondary metabolites, the biological compounds secreted by plants as an aid to support their growth and development under stress conditions or as a part of their defense mechanism, now hold equal importance for mankind who employs it immensely for medication, flavorings, aroma, etc. Wide applicability of these compounds instigates one to understand the biosynthesis, structure and regulation of these bioactive molecules. Terpenoids form the largest group of secondary metabolites which comprise of a wide range of structurally and functionally distinct metabolites synthesized either via mevalonate pathway or non-mevalonate pathway. Targeting a key regulatory enzyme of this pathway, modulation of which would alter the carbon flux would be beneficial to enhance our knowledge about the above issue. For this the transcriptome (from SRA) of different *Ocimum* species was mined out for important pathway genes using various bioinformatics approaches. Amongst them 3-hydroxy 3-methyl glutaryl CoA reductase (HMGR) was selected which is the rate limiting enzyme in mevalonate pathway which controls the conversion of HMG-CoA to mevalonic acid. Isolation, cloning, protein expression, purification, etc. would be discussed in detail in the meeting. Full length protein was also characterized through bioinformatics tools to study its structure, properties, conserved domains, etc. Increase in secondary metabolite production by alteration of HMGR pool along with transcript modulation studies *in planta* revealed that HMGR gene governs the biosynthesis of secondary metabolites. Transcriptome mapping of different HMGR homologs which on comparison within member of same genus revealed its divergent nature which could account to its multifunctional role in different plants. Besides, providing a deep insight about the enzyme function combination of such molecular, transgenic and bioinformatics tools would help to develop strategies to engineer the HMGR mediated flux and also valuable metabolites in plants.

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