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De novo transcriptome assembly and identification of cold and freeze responsive genes in sea buck-thorn

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Sea buckthorn (*Hippophae rhamnoides L.*) is well known for its immense medicinal, nutritional and ecological value, and also for its ability to grow in extreme environments. We used next generation Illumina sequencing to gain a comprehensive view of the sea buck-thorn transcriptome. A total of 86,253,874 high quality short reads were assembled using different assembly tools and parameters. The use of short read assembler ABySS with an additive k-mer approach followed by TGICL suite was found most promising for *de novo* transcriptome assembly. Finally, 88,297 transcripts (>100 bp) were generated representing 53 Mb transcriptome. The average transcript length and N50 length remained 610 bp and 1,193 bp, respectively and 91% of the short reads uniquely mapped back to the sea buck-thorn transcriptome. Further, 41,340 (46.8%) transcripts showed significant similarity with the sequences present in nr protein databases of NCBI (E-value <1E-06). Assembled transcripts were also screened for the presence of transcription factors and simple sequence repeats. Next, DeepSAGE, a tag based approach was also followed to identify differentially expressed genes under cold and freeze stress. In all, 11,922 differentially expressed genes (DEGs) were identified including 6,539 up regulated and 5,383 down regulated genes. Gene ontology and KEGG pathway analysis was performed to assign gene ontology term to DEGs and ascertain their biological functions. Expression of selected 22 DEGs was validated using qRT-PCR.A combination of *de novo* transcriptome assembly and DeepSAGE analysis proved to be a powerful method for transcriptome analysis and identifying abiotic stress responsive genes in seabuckthorn.

Biography

Saurabh Chaudhary is presently pursuing his PhD under the guidance of Prof P C Sharma, Dean, University School of Biotechnology, GGSIPU, New Delhi, India. His research area includes transcriptome analysis of sea buckthorn, a medicinally and ecologically important plant. He has studied digital gene expression profiling under cold and freeze stress using DeepSAGE in sea buckthorn. The major achievements of his work are: comprehensive study of sea buckthorn transcriptome, assembly of 88,297 putative uni-genes of sea buckthorn and identification of 11,922 differentially expressed genes under cold and freeze stress in seabuckthorn. He has three research publications in peer reviewed international journals.

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