

2nd International Conference on **Agricultural & Horticultural Sciences**

Radisson Blu Plaza Hotel, Hyderabad, India February 03-05, 2014

Computational mining of transcriptomes for transcription factors controlling various biological processes in *Podophyllum* spp.

Pawan Kumar, Tarun Pal, Varun Jaiswal, Hemant Sood and Rajinder S Chauhan
Jaypee University of Information Technology, India

Sinopodophyllum hexandrum Royle (syn. *P. emodi* Wall) is a critical endangered medicinal plant native to alpine and sub-alpine regions of Himalayan countries like India, Nepal, Pakistan, China and Bhutan (2500-4200m) commonly known as “bankakri or Giriparpat” in North- Western Himalayan region. This medicinal plant is well known for anticancer compounds podophyllotoxin and its derivatives. Till date, *Podophyllum* species have been the source of podophyllotoxin, the preliminary compound for the production of the semi-synthetic anti-cancer drugs etoposide (VP-16-213), teniposide (VM-26), etopophos, Pod-Ben- 25, Condofil, Verrusol, Warticon etc. which are used in the treatment of leukaemia, lung, testicular cancer and rheumatoid arthritis.

The biology of various physiological and biochemical processes contributing to total plant biomass and yield of podophyllotoxin is not fully understood, thereby, limiting genetic intervention approaches. In addition to biosynthetic pathways, the transcription factors (TFs) and transcription regulators (TRs) play important role in regulating the production of podophyllotoxin. *Podophyllum hexandrum* and *Podophyllum peltatum* are the two important species of *Podophyllum* having 4.3% and 0.25% podophyllotoxin respectively. Different tissues (leaf, stem, root, rhizome) of both the species synthesizes different amounts of podophyllotoxin and its derivatives. Podophyllotoxin was found in the leaf tissue of *P. peltatum* but not in *P. hexandrum*. Current study is aimed at identification of TFs/TRs through the computational mining of transcriptomes from different tissues of *P. hexandrum* and *P. peltatum*. Transcriptome data of *P. hexandrum* (2, 27, 885 contigs) and *P. peltatum* (1, 47, 960 contigs) were collected from the Medicinal Plant Transcriptomics Database. TFs/TRs were identified according to presence of InterPro domains using PlantTFcat. All contigs were annotated to proteins (according to possible open reading frames) and searched through InterProScan. PlantTFcat classified these contigs into 108 known TF and TR families. We identified total 3652 and 4412 TF/TR-encoding transcripts (contigs) which belonged to 97 and 95 TF/TR families in *P. hexandrum* and *P. peltatum* respectively. Differentially expressed TFs/TRs in leaf, stem, root and rhizome tissues of *P. hexandrum* and *P. peltatum* were identified according to contribution of tissue specific small reads in TFs/TRs encoding contigs. 3477, 3617 and 3517 TFs/TRs encoding transcripts were found in the leaf, stem and rhizome tissues of *P. hexandrum* respectively. Similarly 3383, 3307 and 3824 TFs/TRs encoding transcripts were found in leaf, stem and root tissue *P. peltatum* respectively. These transcripts are expected to be involved in various tissue specific biological processes like photosynthesis, disease resistance, secondary metabolite synthesis etc. 175, 81 and 35 TF/TR encoding contigs were absent in leaf, stem and rhizome tissues of *P. hexandrum*. Similarly 1029, 1105 and 588 TF/TR encoding contigs were absent in leaf, stem and root tissues of *P. peltatum*. The differentially expressed TFs/TRs may provide valuable information related to tissue specific biochemical processes occurring in leaf, stem, root and rhizome e.g. podophyllotoxin synthesis is known to be rhizome/root specific and TFs/TRs uniquely present in rhizome can be further explored for their role in podophyllotoxin biosynthesis.

This study will provide a platform for better understanding the biology of physiological and biochemical processes in *Podophyllum* species (*P. hexandrum* and *P. peltatum*).

Biography

Pawan Kumar has worked as a Research Fellow in the CSIR-Institute of Himalayan Bioresource Technology from April 2011 to January 2013. Currently, he is pursuing PhD in the Dept. of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Himachal Pradesh, India. His current research interests emphasizes on the Metabolomics, Metabolic Engineering, Plant Tissue Culture, Computational Biology, Plant Molecular Biology.

pwn.verma2008@gmail.com, rajinder.chauhan@juit.ac.in