The present work was undertaken to identify the genes involved in saponin biosynthesis in *Chlorophtum borivilianum* and analysis of their expression pattern in different tissue. To begin with the isolated saponin from roots and leaves of the plant and analysis the amount by TLC based method. Saponins content analysis provided the preliminary ideas that root has high amount of saponin in compare to leaf tissue. The difference in saponin content may be attributed to differential expression of responsive genes. Thus, differential expression of both tissue was started by Supression subtractive hybridization (SSH) as well as root sequencing of *Chlorophtum borivilianum* root transcriptome. EST generated by SSH librarry in revealed that initial genes involved in saponins biosynthesis were more expressed leaf. Particularly, *CbSQS* and *CbSE* were found to be highly expressed in leaf tissue. While genes related to later of saponin modification were more express in root, which are main storage site the saponins. particularly *GT* and *CYP* were highly expressed in roots. The observed results were sequently confirm by reverse northern blot as well as semiquantitative RT-PCR of the genes related to saponin biosynthetic pathway.

Transcriptome data generated by Illumina Highseq 2000 identified all the genes involved in saponin included; MVA, Non-MVA, and Isoprenoid. Transcription factor regulate these in pathway also were identified . RPKM analysis again confirmed that genes related to early stage of saponins biosynthesis were more abundant in leaf while genes related to later modification were more expresse in root. These results of qRT-PCR confirm the reliability of assembled transcriptome data as well as their expression pattern.

The present study of identify all the transcripts associated with saponins biosynthetic pathway. *CbSQS* and *CbSE* and *CbOSC* were found to be promising target to be important in saponin content in *Chlorophtum borivilianum*. 