

FINAL OUTCOME

➤ Our result suggest that nsLTPs are coexpressed with genes involved the phenylpropanoid pathway.

➤ This pathway includes the starting compound for biosynthesis of lignin which suggests a role for nsLTPs in lignin formation.

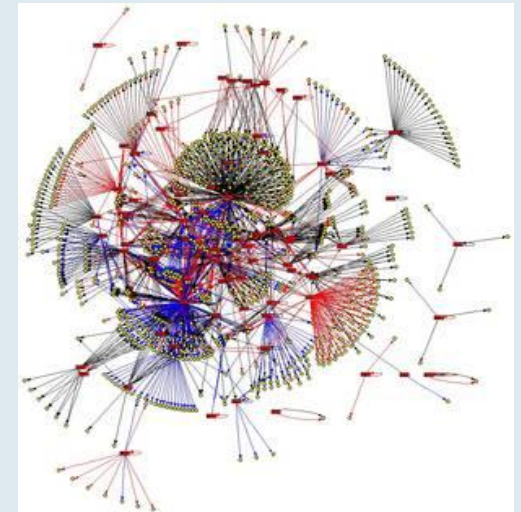
Acknowledgements

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Lastly, I offer my regards and blessings to all of those who supported me in any respect during the completion of the project.



**A bioinformatics approach to
investigate the function of non-specific
lipid transfer proteins in *Arabidopsis
thaliana***



**Master Thesis
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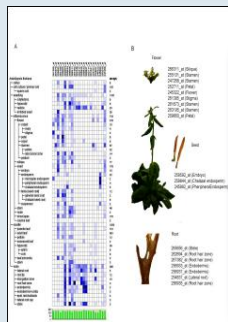
BACKGROUND

Plant non-specific lipid proteins were firstly identified from the spinach leaves and hence named for their property to mediate in vitro transfer of phospholipids between membranes. NsLTPs are widely distributed in the plant kingdom, but an exact biological role is not clearly understood. We have exploited the large amount of Arabidopsis transcriptome data in possible databases to learn more about the function of nsLTPs.

FOCUS OF STUDY

- To analyze the expression profile of the Arabidopsis nsLTPs genes under different response.
- To obtain the Arabidopsis nsLTPs genes co-expression network.
- To employ Gene Ontology (GO) enrichment analysis of the nsLTP expression networks in order to assign a functional context for the nsLTPs..

FINDINGS



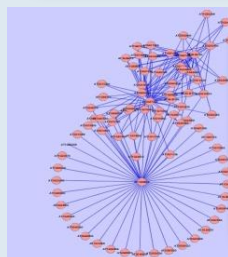
GENEVESTIGATOR

- This tool reveals the expression of nsLTPs genes in the different tissue of *Arabidopsis thaliana*.
- It shows that the expression of some nsLTP genes are root specific, but others are specific for tissue above the ground.



BIO ARRAY RESOURCE (BAR)

- Coexpression analysis of nsLTPs genes from Expression angler (BAR) helps to form several network of nsLTPs genes which shows same co-regulation.
- Different module of nsLTPs genes shows the similar biological process in this network design.



CORNET

- CORNET database provide the correlated coexpression of query genes with neighbour gene.
- This graphical view of module I was obtained via Cytoscape software in the CORNET.

MAIN FINDING

GENE ONTOLOGY (GO)

- Enrichment GO term analysis gives the functional aspect of nsLTPs genes.
- We used BiNGO V 2.3 plugin in cytoscape for all the four modules.
- This plugin able to provide the significant over-represented enrichment GO term for each module.
- Result obtained from BiNGO v 2.3 shows that several genes coexpressed with nsLTPs are involved in the phenylpropanoid pathway.

TOOLS USED

Genevestigator:

<https://www.genevestigator.com/gv/index.jsp>

AtGenExpress Database:

<http://www.weigelworld.org/resources/microarray/AtGenExpress>

Bio Array Resource (BAR):

<http://bar.utoronto.ca/>

CORNET:

<https://bioinformatics.psb.ugent.be/cornet/>