

**Protein-protein Interaction (PPI) Network Module Analysis for Detecting Sub-modules and Hub Proteins Associated in Root Development of *Oryza sativa*.**

**W. G. A. S. Sandareka<sup>1\*</sup>, S. P. C. Fernando<sup>1</sup>, T. L. S. Tirimanne<sup>1</sup>**

<sup>1</sup>Department of Plant Sciences, University of Colombo, Colombo, Sri Lanka

\*2015s15477@stu.cmb.ac.lk

*Oryza sativa* (rice) is one of the main global staple foods, and improved varieties are required to enhance its yield to supply for the increasing population. It is essential to study the root system for plant improvement because it contributes immensely to plant growth and stress tolerance. When producing improved varieties, revealing the molecular mechanisms behind phenotypes, such as root development, is indispensable and requires the identification of associated genes and their interactions. Phenotypes are governed by multiple proteins forming complex interactions; hence, it is important to analyze these interactions rather than focusing on individual proteins. This is achieved via protein-protein interaction (PPI) network module analysis in bioinformatics. This also allows identifying the sub-modules within a particular module for a phenotype, which correspond to different biological pathways governing the final phenotype. Also, there are proteins with higher importance than others, i.e., hub proteins, which have a higher number of interactions compared to non-hub proteins. These hubs can be identified using network analysis. The efficiency of PPI network analysis has been proven in human disease research, but to our knowledge, this method has never been used on root development in rice. Therefore, to better understand the protein interactions involved with root development, PPI network analysis was used to analyze sub-modules and identify hub proteins. Rice PPI network from the STRING database was retrieved and genes with experimental evidence for their contribution to root development were extracted from the literature. These were used to predict 75 new gene candidates. Then, the PPI network module for the root development was extracted and visualized, and sub-modules and hubs were identified. Enrichment analysis was performed to detect the biological pathways related to sub-modules and those pathways and hubs were analyzed using the literature. Altogether, 6 sub-modules, 20 intramodular hubs, and 2 intermodular hubs (DRO1 and FH1) were identified and analyzed. They were mainly associated with root hair development, auxin regulation, cytokinin regulation, and cell wall organization, which are related to the root development, confirming the applicability of our approach.

**Keywords:** PPI, Rice, Root