Rice is a global staple crop that requires ample amount of water for growth and development. Drought is one of the severe abiotic stresses that affects the productivity of rice. Therefore, there is need to select drought tolerant rice varieties that can efficiently grow in drought-prone areas. The traits responsible for enhancing or adapting drought resistance in rice plants can be selected and studied to improve their growth under stress conditions. Remarkable progress has been made in the direction of trait selection criteria.

Comparative analysis of various traits has been conducted on drought tolerant and drought sensitive rice varieties. In our study, we have studied morphological, physiological, anatomical, biochemical and molecular variation of different rice varieties. Various root related biochemical and morphological traits such as root length, diameter, area, volume, Relative Water Content (RWC), xylem number, xylem area, proline content, Malondialdehyde (MDA) content, protein and gene expression have been investigated for a comparative study of the plant response to drought stress in different rice varieties. In addition, we implemented novel automated frameworks based on computer vision algorithms for high-throughput quantification of xylem and stomata. This task has been accomplished using Scanning Electron Microscopy images.

The results of transcriptome analysis revealed variation in expression of Med37, RSOsPR10, OsPIP2;5 and OsNIP2;1 genes among various rice varieties. The differential proteome analysis using 2-D followed by MALDI-based identification shows role of chitinases in drought tolerance. The learning generated both, through computational/digital image
analysis as well as biochemical studies can contribute significantly towards the field of rice phenomics.

**Highlights**

The salient findings of this work are as follows:

1. Reduction in xylem area as well as xylem number in drought tolerant varieties under drought stress.
2. Lower stomatal density in drought tolerant varieties.
3. Significant correlation of aquaporin genes with the root length.
4. Significant higher root length, area, diameter and volume of root in drought tolerant varieties.
5. Upregulation of *OsPIP2;5* and downregulation of *OsNIP1;2* was observed in roots of drought tolerant variety.
6. Proline content in the roots found to be significantly higher in tolerant variety.
7. Negative correlation between proline content and RWC.
8. MDA content in tolerant variety under drought is significantly lower.
9. Five proteins (including chitinase) identified that are induced during drought stress.