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A High Resolution Structural and Proteomic Atlas of the Developing Rice Leaf

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The C3 grass rice (*Oryza sativa*) is a major food crop and full genome sequences of two rice ecotypes greatly facilitates rice research. Leaf photosynthesis is a key factor in determination of biomass production and grain yield. Here we provide an integrated view of development transitions of a young rice leaf with clear sink- and source zones as determined by ¹⁴C-labeling. The leaf structural transitions, including vascular development, and development of the organelles from non-photosynthetic sink zone to photosynthetic source zone, were quantified by microscopy and complemented by photosynthetic pigment analysis. Large scale quantitative proteomics (140 nanoLC-ESI-LTQ-Orbitrap runs; 2 million MSMS spectra) of seven narrow leaf sections, followed by hierarchical cluster analysis and functional annotation, identified >4000 proteins (>6000 protein models) and resolved the major leaf developmental transitions. Rice proteins were annotated for subcellular location and function based on homology to maize and Arabidopsis, taking advantage of our extensive analysis of the maize and Arabidopsis proteome and the Plant Proteome Database (PPDB). This study provides a structural and proteome atlas of the developing rice leaf; we will highlight several transitions along this rice developmental leaf gradient and comment on differences with the leaf gradient of the C4 maize leaf.

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