

Physiological studies and proteomic analysis for differentially expressed proteins and their possible role in the root of N-efficient rice (*Oryza sativa* L.)

ABSTRACT

The root proteome of nitrogen-efficient and nitrogen-inefficient rice cultivars was compared in this study in order to investigate the differential expression of proteins under deficient (1 mM), low (10 mM) and high (25 mM) levels of nitrogen (N). Nitrogen use efficiency (NUE) was assessed by biochemical assays such as N-uptake kinetics and activities of N-assimilation enzymes. Two-dimensional gel electrophoresis and MALDI-TOF-MS analysis resulted in the identification of 504 protein spots (210 and 294 spots in cvs. Rai Sudha and Munga Phool, respectively). A positive correlation was observed between physiological parameters and the concentration of a number of root proteins. Sixty-three spots showed a significant cultivar N-treatment effect on the level of expression. Functional aspects of eleven spots with major alterations in expression over control were critically analyzed. The data suggest that glutamine synthetase, cysteine proteinase inhibitor-I, porphobilinogen deaminase (fragment) and ferritin were involved in conferring N efficiency to the N-efficient rice cultivars/genotypes. Interestingly, these proteins are involved directly or indirectly in N assimilation. Such studies should help us in identifying and understanding the structural or functional protein(s) involved in the response to the level of nitrogen fertilization.

Keyword: 2DE; MALDI-TOF-MS; N-uptake kinetics; N-use efficiency; Rice genotypes; Root proteome