PROTEOMIC ANALYSIS OF GERMINATED RICE (*Oryza sativa* L.) UNDER SALT STRESS

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ABSTRACT

Salt stress caused a dramatic decline of rice production. Proteome study of salt tolerance mechanism supplied a span-new viewpoint and valuable clue to rice tolerant improvement projects. Aim of this study was to identify the salt tolerant capacity and stress response proteins of seven Thai rice (*Oryza sativa* L.) cultivars at germination stage. To achieve these goals, seven Thai rice varieties: Pathumthani, Phitsanulok2, RD29, RD31, RD41, RD47, and Riceberry were germinated under 200mM NaCl for 4 days. Based on germination rate, Pathumthani, Phitsanulok2 and RD31 cultivars were categorized as tolerant, while RD29, RD41 and Riceberry were moderately tolerant and RD47 as susceptible. GeLC-MS/MS analysis of total proteins prepared from 7 rice seeds grown under salt stress identified 1339 proteins, 51 of which were expressed only in salt tolerant cultivars including Pathumthani, Phitsanulok02 and RD31. These proteins were distributed on cell membrane, cytoplasm, peroxisome, plastid, mitochondrion and nucleus. They played role in development, protein modification, signal transduction, stress response, transport and transcription. Proteome mechanism during the process of seed germination under salt stress was proposed.