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KWANKAO KARNPAKDEE: METABOLITE PROFILES OF 'KDML 105' AND SALT-TOLERANT 'UBN 02123-50R-B-2' RICE *Oryza sativa* L. IN RESPONSE TO SALINITY STRESS. ADVISOR: ASST. PROF. SUPAART SIRIKANTARAMAS, Ph.D., CO-ADVISOR: ASST. PROF. NUCHANAT WUTIPRADITKUL, Ph.D., pp.

In this research, I studied metabolic responses in the two cultivars of Thai rice, moderately salt sensitive rice 'KDML 105' and salt-tolerant rice 'UBN02123-50R-B-2' (UBN). I found different physiological appearance in both cultivars when treated with 80 mM NaCl at 12 and 24 h. The metabolite profiles of six replicates of leaves and roots were then investigated using GC-TOF/MS and LC-MS/MS. The results showed that metabolites in glycolysis, energy metabolisms, and amino acid metabolisms were up-accumulated faster in UBN when compared to KDML 105 at 12h under salinity stress. At 24h, those metabolite levels in UBN were declined in contrast to those in KDML 105 that showed higher up-accumulation. To investigate stress-related gene expressions, several candidate genes, e.g. L-galactono-1,4-lactone dehydrogenase, glutamate decarboxylase, pyrroline-5-carboxylate reductase, and riboflavin synthase, were selected. I found that the genes encoding glutamate decarboxylase and pyrroline-5-carboxylate reductase, which involved in the osmoprotectant biosynthesis, were significantly higher expressed during salinity treatment at 24h in UBN than KDML 105. In contrast, the gene encoding riboflavin synthase was significantly lower expressed in KDML 105 than UBN. Secondary metabolite analyses showed the up-accumulation of ferulic acid in roots of the UBN. These results suggest that UBN can response to salinity stress much better than KDML105 through the higher up accumulation of primary metabolites and osmoprotectants, implying the higher salinity tolerance ability in the salt-tolerant rice 'UBN02123-50R-B-2'.

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