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Comparative proteomic study on response to chilling stress in different silicon-accumulator rice (*Oryza sativa* L.)

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In rice (*Oryza sativa*) plant, silicon accumulation is directly involved in broad spectrum stress alleviation. Presently, two rice lines; LSD and HSD responses were studied under chilling stress (12° C/10° C; D/N). Physiological responses were detected through RWC% and REL% measurement. Molecular responses were detected through comparative two-dimensional electrophoresis and qPCR. Enhanced Si uptake protected leaf cells from excessive water loss as RWC% in HSD leaves remained within 80%-95% while in LSD leaf tissues it reduced up to 50%; and also kept REL% below toxic. Among 93 leaf reproducible, differential proteins; 57 proteins up regulated and 36 down regulated respectively based on ≥1.5 (up regulation) and ≤0.5 (down regulation) parameter. On the basis of MapMan functional gene ontology (GO), these proteins were found to be involved in 13 important groups; photosynthesis (23%), stress defense response (5%), redox defense response (10%), signaling proteins (2%), carbohydrate metabolism (4%), amino acid metabolism (5%), secondary metabolism (4%), nucleotide metabolism (6%), RNA regulation (4%), TCA (4%), protein metabolism (16%), Development (2%) and unknown functional annotation (4%). qPCR depicted coincidence with proteomics findings. G-proteins signaling including guanine nucleotide-binding and GTP-binding nuclear protein Ran2 up-regulated to transmit chilling signal inside cell which transduced redox homeostasis through superoxide dismutase, OsAPx and thioredoxin expression to scavenge ROS along with stromal 70 kDa heat shock-related protein and heat shock protein 82, stress specific proteins up regulation as PCRC. This PCRC induced photosynthetic, carbohydrate, mitochondrial and also proteins related to amino acid metabolism such as transaminase/transferase, nucleotide metabolism such as glutathione S-transferase and RNA regulation such as mRNA binding protein as SCRC to chilling stress adaptation. Conclusively, *LSi1* overexpression enhanced Si induced cell's physiological and molecular defense through insoluble silica gel deposition as well as the bio-actively soluble silica form with the enzymes to trigger chilling defense pathway.

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