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Procedia Environmental Sciences 29 (2015) 72

Procedia

Environmental Sciences

Agriculture and Climate Change - Adapting Crops to Increased Uncertainty (AGRI 2015)

Metabolite Profiling Reveals Sensitivity-Dependent Metabolic Shifts in Rice (*Oryza Sativa* L.) Cultivars under High Night Temperature Stress

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Abstract

Global climate change has an increasing influence on the productivity of crop plants. In the past century this was accompanied by an asymmetric warming with a greater increase of night compared to day temperatures, resulting in a broad decline in the diurnal temperature range. However, little is known about crop physiology and metabolic changes occurring during the early response of rice to high night temperature (HNT) conditions.

We have analyzed the effects of HNT on 12 rice cultivars from both the japonica and indica subspecies and found a clear distinction between tolerant and sensitive cultivars, based on leaf chlorosis estimates.

Physiological differences between tolerance classes in response to HNT were observed. Moreover, GC-MS profiling indicated distinct metabolite patterns under HNT and control conditions. In sensitive cultivars the contents of several metabolites of central metabolism was increased under HNT. The TCA cycle, amino acid and polyamine biosynthesis were the main pathways influenced by HNT. Targeted analysis revealed increased contents of putrescine, spermine and spermidine under HNT restricted to sensitive cultivars, accompanied by enhanced expression of genes encoding enzymes catalyzing the first committed steps of polyamine biosynthesis. Furthermore, tolerant cultivars showed a different metabolic pattern already under control conditions. Correlation analyses have uncovered candidate metabolites that may be suitable as metabolic markers to support breeding for HNT tolerance in rice.

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Peer-review under responsibility of the organizing committee of the Agriculture and Climate Change - Adapting Crops to Increased Uncertainty (AGRI 2015)

Keywords: High night temperatures; *Oryza sativa*; metabolite profiling

References

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