



Aluminum triggers broad changes in microRNA expression in rice roots

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ABSTRACT. MicroRNAs are small 21-nucleotide RNA molecules with regulatory roles in development and in response to stress. Expression of some plant miRNAs has been specifically associated with responses to abiotic stresses caused by cold, light, iron, and copper ions. In acid soils, aluminum solubility increases, thereby causing severe damage to plants. Although physiological aspects of aluminum toxicity in plants have been well characterized, the molecular mediators are not fully elucidated. There have been no reports about miRNA responses to aluminum stress. Modulation of miRNA expression may constitute a key element to explain the mechanisms implicated in aluminum toxicity and tolerance. We examined the expression of at least one miRNA member from each miRNA family in rice roots of *Oryza sativa* spp *indica* cv. Embrapa Taim and *Oryza sativa* spp *japonica* cv. Nipponbare under high concentrations of aluminum. Forty-six miRNA families were effectively detected by quantitative PCR. Among these, 13 were down-regulated and six were up-regulated in roots of the Nipponbare

cultivar after 8 h of aluminum treatment. In roots of the Embrapa Taim cultivar, five miRNAs were down-regulated and three were up-regulated. Analyses of their putative targets suggest that these rice miRNAs are involved in the regulation of various metabolic pathways in response to high concentrations of aluminum.

Key words: Aluminum; MicroRNAs; Abiotic stress; Gene expression