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Profiling Metabolites Expressed Corn Root Under Waterlogging

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[Abstract]

Waterlogging tolerance of corn is one of the important factor for cultivate in paddy soil condition to increase cultivation area and self-sufficiency of corn in Korea. In order to develop elite waterlogging tolerance corn, the new corn lines bred by crossing wild corn, Teosinte, and cultivated corn inbred lines. Five accessions among the 2 species, *Zea mays sub spp. mexicana* and *Zea mays spp. parviglumis*, of 81 Teosinte were selected through the waterlogging treatment. The waterlogging treatments were implemented for 7 days at the seedling(V3) stage. The inbred lines were developed by crossing 5 teosinte accessions and cultivated corn lines and they were estimated waterlogging tolerance. It was screened and analyzed the metabolites extracted from roots of 19KT-32(KS141 x teosinte) that was treated waterlogging. We selected 8 of 180 metabolites like as γ -aminobutyric acid(GABA), putrescine, citrulline, Gly, and Ala that expression was remarkably changed over 2.5-times, 7 metabolites increased and 1 metabolite decreased in waterlogging, respectively. Glutamate decarboxylase(GAD) catalyzing GABA accumulation gene have 10 haplotypes, and exon1 was highly conserved, but identified to 135 SNPs after the first intron. Among the 135 SNPs, the number of transversion mutations (52) surpassed the number of transition mutations (38). Most of metabolites were related to abiotic stress in plant that it regulated to pH, osmotic pressure K^+/Ca^{++} and ATPase activity. We are analyzing the association using these results for increase breeding efficiency.

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