

Abstract

Aluminum toxicity is one of most distributed plant abiotic stress in the world, causing root inhibition and therefore crop losses. Plants continuously adapt its defense to abiotic stresses through different mechanisms including DNA methylation. The methylome variation is influenced by external cues from environment or by hormonal signals. Salicylic acid is one of the most important hormones in plants, directing growth and defense. Its application is seen having the capacity to elicit plant defense mechanisms. In this study, the effects of aluminum toxicity and salicylic acid on DNA methylation were carried out in pearl millet using MSAP epigenotyping and ELISA test. The methylation analysis revealed aluminum treatment increased the global and CCGG methylation level whereas application of salicylic acid had reverse effects. Moreover, most of the methylation or demethylation due respectively to aluminum and salicylic acid, occurred at the external cytosine. This finding reveals that salicylic acid could overcome the negative effects of aluminum toxicity through DNA demethylation pathways.