

## Abstract

Aluminium (Al) toxicity is one of the most critical abiotic stresses which limit crop production in acid soils. The plant epigenome is vulnerable to environmental factors and may become dysregulated under stress conditions. In this study, morphological, physiological and epigenetic changes in DNA cytosine methylation due to Al toxicity and low pH were investigated using standardized Al-sensitive Kenyan tropical maize (KTM) line against a Chinese temperate maize (CTM) line. Growth responses were measured after 4, 24 and 48 hrs exposure to 200  $\mu$  M Al<sup>3+</sup> and at pH 4.5 in MSN nutrient solution. Root tolerance indexes (RTi) showed a high Al<sup>3+</sup> stress response in KTM while CTM showed a more rapid adjustment response to low pH. A methylation-sensitive amplified polymorphism (MSAP) analysis of the CG methylation level range was high at pH 4.5 in KTM but, reached the highest value (5.30%) in CTM at 200  $\mu$  M Al<sup>3+</sup>. The % CNG methylation level in CTM was 6.76 - 7.3% compared to 6.03 - 7.13% in KTM. Isolated and sequenced MSAP variant bands revealed Al<sup>3+</sup> toxicity as a primary stress inducer of epigenetic stress regulatory mechanisms. This study provides an alternative possible explanation for the complexity of Al tolerance mechanism from an epigenetic aspect.