

Title : Study on the Mechanisms of Salt Tolerance and Plant Growth Promotion in Selected Actinobacteria

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ABSTRACT

Salt stress is a major environmental factor that significantly affects agricultural productivity. Two plant growth-promoting actinobacteria, *Dermacoccus abyssi* MT1.1^T and *Streptomyces thermocarboxydus* S3 have previously been reported to produce indole-3-acetic acid (IAA) and siderophores and solubilize tri-calcium phosphate. Both strains have been reported to be effective in mitigating salt and drought stress in plants. However, the precise mechanisms by which these actinobacteria mitigate stress remain unclear. Therefore, this study aims to elucidate the salt stress tolerance mechanisms of two actinobacterial strains using physiological evaluation and genome mining approach. Our finding indicated that *D. abyssi* MT1.1^T and *S. thermocarboxydus* S3 could tolerate NaCl concentrations of up to 6% (w/v) and 10% (w/v), respectively. The mechanisms involved in their salt stress adaptation is the accumulation of osmolytes. The mechanism involved in salt stress adaptation in these strains is the accumulation of osmolytes. Under salt stress conditions (4% NaCl), *D. abyssi* MT1.1^T exhibited higher accumulation of total soluble sugars (TSS) and proline in cells compared to non-stress conditions, whereas *S. thermocarboxydus* S3 showed an increase in TSS accumulation only. Additionally, both strains accumulated higher levels of hydrogen peroxide and catalase compared to non-stress condition, while glutathione peroxidase levels were reduced. Notably, *D. abyssi* MT1.1^T demonstrated an increase in antioxidant levels under salt stress, whereas *S. thermocarboxydus* S3 exhibited a decrease. Genomic analysis using the RAST server revealed genes associated with plant growth promotion and response to osmotic and oxidative stresses. These findings provide valuable insight into the salt tolerance mechanisms of actinobacteria, supporting their potential application in enhancing crop resilience in high-salinity environments.

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