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Master Thesis Defense

<u>Entitled</u> MOLECULAR AND PHYSIOLOGICAL ASSESSMENT OF SALINITY STRESS TOLERANCE IN TRANSGENIC ARABIDOPSIS LINES EXPRESSING A SOLANUM TUBEROSUM RIBOSOME-BINDING PROTEIN.

> <u>by</u> Onoud Rashed Saeed Ali Alyammahi <u>Faculty Advisor</u> Dr. Mayank Gururani, Department of Biology College of Science <u>Date & Venue</u> 12:30 PM Sunday, 15 November 2020

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<u>Abstract</u>

Ribosomal proteins are highly conserved components of basal cellular organelles, primarily associated with translation of mRNA leading to protein synthesis. Additionally, some of these proteins are known to play critical role in plants RNA metabolism during stress responses, growth, and development. In this study, transgenic Arabidopsis plants expressing a ribosomal protein S27 (hereafter D26) isolated from Solanum tuberosum was subjected to NaCl-induced salinity stress conditions, to evaluate their putative stress resistance. Transgenic plants were exposed to high salinity stress, induced by 200 mM NaCl and physiological and biochemical assays were performed. The D26 transgenic plants demonstrated improved plant height and root length accompanied with higher chlorophyll and carotenoids accumulation compared to wild-type (WT) control plants under stressed conditions. Electrolyte leakage and stomatal conductance, indicators of stress-related tissue damage and plant water status respectively, were significantly lower in D26 plants compared to WT plants under NaCl-induced salinity stress. Accumulation of proline was recorded higher in D26 plants compared to WT plants. Similarly, lower accumulation of malonaldehyde in D26 plants than the WT plants indicated that D26 suffered relatively lesser oxidative lipid damage than WT under stress. Higher relative expression of three genes encoding major reactive oxygen species (ROS) scavenging enzymes, Ascorbate peroxidase (APX), Catalase (CAT) and Superoxide dismutase (SOD) further indicated improved ROS detoxification capacity in D26 plants. In terms of the damage to photosynthetic components, our Chlorophyll-a fluorescence kinetic analyses revealed that the overexpression of S. tuberosum S27 gene improved the performance indices (Pl_{ABS} and Pl_{total}), and quantum yields and efficiencies of photosystem II (PSII) measured in eleven critical photosynthetic parameters, in D26 plants under salinity stress. Further characterization of D26 plants through RNA-seq analysis is underway.

Keywords: Abiotic stress, Chlorophyll-a fluorescence, Osmotic stress, Quantitative PCR, Reactive oxygen species.