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Cloning and In-silico Analysis of Senescence Associate Protein in Maize (*Zea mays* L.)

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ABSTRACT: Maize (*Zea mays* L.) is one of the most important cereal crop cultivated across the world and a relevant source of food, feed, and industrial products. The current global annual production and crop yield are reduced due to environmental constraints such as drought, high salinity and low temperature which drastically affect plant growth and development. Among such environmental stresses, drought is one of the most devastating abiotic stresses which lead to significant yield loss in maize. Hence, it is imperative to genetically improved maize for drought stress tolerance. It is now well established that drought tolerance is regulated by several genes, including transcription factors that enable plants to withstand unfavourable conditions. Senescence associated genes (SAGs) are related to many biological processes, including abiotic stress response in plants. However, only little information regarding SAGs is available in maize. Here, we isolated 822 bp of Senescence associated gene by PCR-based approach using cDNA generated from leaf tissue of HKI 1015 inbred line of maize. The cloned sequence consists of highly conserved domain of tetraspanin membrane protein which plays role in abiotic stress in rice. Unlike animals, these membrane proteins have not been intensely investigated in plants. Therefore, *in-silico* approaches were used to predict the structure and function of this protein. Structural identification of the target protein shows sequence identity with PDB ID: 5tcx.1.A. Comparative modelling and crystal structure stereochemistry was identifed by PyMOL and PDBSUM. The Subcellular localization prediction shows presence of major (71.6%) part of the targeted protein in plasma membrane. Presence of Helix-loop-Helix type secondary structure was predicted. Phylogenetic analysis of non-redundant sequence was done to study the evolutionary relationship among group of organism.Prediction of protein–protein interaction suggest that this protein has Wrky 115,Wrky92,Wrky48,Wrky83 as a major interacting partners.

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