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Entitled

TRANSCRIPTOMIC ANALYSIS OF THE GLYCOPHYTIC CROP *IPOMOEA AQUATICA* UNDER SALINITY CONDITIONS COMPARED TO ITS WILD HALOPHYTE RELATIVE *IPOMOEA PES-CAPRAE*

by

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11:00 am

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Online-zoom

The link :

<https://uae-u.ac-ae.zoom.us/j/94588086493?pwd=b1BWNTAzdHB5MTJ2aEhCeXdBaDdvQT09>

Abstract

This study focuses of the glycophytic crop *Ipomoea aquatica* (commonly known as water spinach) and its wild halophytic relative *Ipomoea pes-caprea*. *I. aquatica* is a crop with economic value, however it is unable to tolerate high levels of salinity. On the other hand, it's relative *I. pes-caprea* is able to grow and thrive in the harsh environment of the UAE. The main objective of this study is to analyze the genetic differences underlying the variation in the two plants' response to salinity and determine the genetic components that can be used to enhance *I. aquatica*'s tolerance to salinity. The plants were subjected to salinity stress and their physiological responses were closely monitored. The transcriptomes of the two plants were also analyzed to find mRNAs, miRNAs, and pathways that were enriched under salinity stress. The analysis determined several crucial genetic differences between *I. aquatica* and *I. pes-caprea* during salinity stress. Some of these differences include the upregulation of High-affinity Potassium channel (HKT) in *I. pes-caprea* as well as the upregulation of a NAC3-like transcription factor. These differences can be used to genetically modify *I. aquatica* in order to enhance its salt tolerance levels.

Keywords: *Ipomoea aquatica*, *Ipomoea pes-caprea*, Bioinformatics analysis, Transcriptome analysis.