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## Abstract

Climate change and harsh agricultural practices are increasing the amount of salt and heavy metals in soil, drastically decreasing the amount of arable land while simultaneously lowering crop yields. However, some plants grown in poor soil have adapted diverse mechanisms to cope with harsh environments. It has been hypothesized that the biochemical mechanisms responsible for salt tolerance overlaps with heavy metal tolerance, yet the similarities in these mechanisms are still unknown. Lessons from naturally salt and heavy metal tolerant plants can be applied to crops to increase resilience or be used in phytoremediation efforts. Here, we use the salt and heavy metal tolerant plant *Cakile maritima* as a model system for phytoremediation by using a large-scale multi-omics approach, combining ionomics, metabolomics, transcriptomics, and genomics, to understand the metabolic responses following NaCl and cadmium stress. We have developed an automated pipeline for tracking salinity, as well as using elemental analysis to monitor intracellular concentrations. We will perform RNA-seq to understand patterns of differential gene expression, gather a list of candidate genes, and use comparative genomics to understand the potential influence of ancient polyploidy on stress tolerance. Combining this with metabolomics will enable a fully integrated understanding of salt stress response and allow us to know if *Cakile maritima* is predisposed for salt stress or has a rapid stress response. Coupling this with transcriptomics will allow us to identify important pathways and neofunctionalized genes that may be specific for *C. maritima* stress response and be applied to crop species to enhance resilience.



**NAPPN Annual Conference Abstract: Halophytes and Heavy Metals: A multi-omics approach to understanding phytoremediation**

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