

PROJECT TITLE: Exploration of genomic resources and bio prospecting of genes for adaptability and stress response in Sea Weeds (*Phragmatic Karka*) in the brackish water lagoon Chilika

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PROJECT SUMMARY:

Salinity is one of the major abiotic stresses in plant agriculture and a major limiting factor for plant productivity worldwide. Nearly 20% of the world's cultivated area and about half of the world's irrigated lands are affected by salinity (Kaya et al., 2002). Plants have evolved a number of biochemical and molecular mechanisms that involve complex salt-responsive signaling and metabolic processes at the cellular, organ and whole-plant levels leading to products and processes that improve salt tolerance. A fundamental understanding and knowledge of the effects of salt stress on plants is necessary for understanding the plant response to salinity and to apply the same principle/mechanism for ameliorating the impact of salinity on plants. Plants vary in the degrees of salt tolerance; depending on their salt-tolerating capacity, some are either obligate and characterized by low morphological and taxonomical diversity with relative growth rates increasing up to 50% sea water or facultative and found in less saline habitats along the border between saline and non-saline upland and characterized by broader physiological diversity which enables them to cope with saline and non-saline conditions (Parida and Das, 2005). One such plant which grows and withstands varying salt environments is the reed *Phragmites karka* widely seen in Chilika (10°43'N85°19'E), a brackish water lagoon in the state of Odisha. Phragmites karka forms monoculture dense patches in Chilika lagoon and is considered a highly invasive weed. *Phragmites* is well-adapted to a range of salinity, nutrient, and hydrological conditions, and grows both in northern sector of the lagoon with low salt concentration and southern sector where salt concentration tends to be at 18-20 ppm. However, the molecular and physiological mechanism governing the differential response and adaptability to salt stress is yet to be ascertained in this environmentally significant reed species. Therefore, there is a strong rationale to understand the complex genetic network through exploration of the genomic resources in *Phragmites karka* and elucidate the alterations in the proteins / genes as a part of the adaptation mechanism(s) of reed *Phragmites* karka, surviving in the varied salt environments of Chilika lagoon under omics platform.