Chapter 1: Introduction
INTRODUCTION

Plants are faced with highly variable forms of environmental stresses, including drought, cold, salt and temperature extremes. Although plants gradually evolved a remarkable ability to cope with such highly variable environmental onslaughts, the stresses nevertheless represent a primary cause of crop loss worldwide. While estimated yield loss caused by phytopathogens range typically from 10-20%, average yield loss by abiotic stresses for major crop plants are shown to be by more than 50% (Flowers et al., 2004). Therefore to meet the increasing demands for plant based agricultural commodities it would be imperative to enhance productivity land in current use as to expand agriculture to marginal lands. If crops can be redesigned to better cope with abiotic stress, agricultural production can be increased dramatically.

Salinization is a major problem in lands that receives little rain (due to insufficient water to leach salts) and is a growing problem for irrigation agriculture because long-term irrigation leads to accumulation of salts. In principle, adequate drainage systems and leaching the soil profile with adequate quality water could reduce much of soil salinity. However the prohibitive expenses limit the practical feasibility. Most agriculturally important plants are glycophytes, making soil salinity a significant factor restricting plant growth and hindering crop yield in large areas of the world (Zhu, 2001). In fact, no toxic substance restricts plant growth more than salt on a worldwide scale. It has been estimated that salinity affects at least 20% of world’s arable land and more than 40% of irrigated land to various degrees (Hasegawa et al., 2000).

At the genetic level, salinity tolerance has been considered to be a quantitative trait and generally resistant to improvements by plant breeding. Since quantitative traits maximally influence plant yield, introducing a trait that improves tolerance to saline conditions may actually lower the potential yield under normal conditions. Molecular approaches such as generation of transgenics could therefore help in achieving salt tolerance. With the exception
of complex, multicellular salt excreting glands there is no clear distinguishing phenotypic feature of salt tolerant plants. It is the capacity for ion selectivity, efficient compartmentation, high efficiency of water use and lower water use ability that delineates the tolerant and the sensitive plants (Zhu, 2003). Transcriptome analysis shows that the Arabidopsis genome includes most of the genes that have been associated with tolerance, in other species and yet Arabidopsis is not tolerant to salinity. A comparison with a naturally salt tolerant genetically tractable relative of Arabidopsis, Thellungiella halophytica (salt cress), reveals the constitutive overexpression of a set of certain genes allows for its survival at salt concentrations upto 500 mM (Taji et al., 2004). Thus it is the strength, tissue specificity and as well as the nature of the gene product over expressed that determine the tolerance levels. A delicate balance between the tolerance limits without diminishing the yield potential is critical in achieving tolerance.

With this background Pennisetum glaucum, a monocot belonging to the family Poaceae has been used as a model system for the present study. It is commonly known as the Pearl millet and is a hardy crop that can stand most of the abiotic stresses, like drought, poor soils, floods, salt etc. We hypothesized that identification of mechanisms that control the regulation gene expression patterns in this would provide a more in vivo approach for transferring salinity tolerance capabilities to other plants.

Of the several strategies employed by plants to cope with saline soils, ion compartmentalization is the most successful. This is because it couples growth by cell expansion (mainly due to an increase in the vacuolar size) with ion sequestration and detoxification from the cytosol. Sodium ions provide an energetically favored osmoticum that help balance the cellular osmotic potential with the hypertonic soil solution, thereby alleviating the water deficit associated with saline environments.
The present study was undertaken on the following lines towards the molecular characterization of the Na\(^+\)/H\(^+\) gene from *Pennisetum glaucum* with the following objectives:

- Isolation and cloning of the gene and isoforms from *P. glaucum*.
- Study the regulation of the transcript of the gene and other isoforms in response to various abiotic stresses.
- Isolation of the promoter and studying the binding specificity of transacting factors to the cis-elements by GMSA.
- To identify the possible interacting proteins of *P. glaucum* Na\(^+\)/H\(^+\) antiporter, PgNHX with the aim of identifying its regulation at the post-translational level.
- To functionally validate the PgNHX by raising transgenic plants (*Brassica juncea*) over expressing the gene.