

Functional screening for salinity tolerant genes from *Acanthus ebracteatus* Vahl using *Escherichia coli* as a host

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Abstract Salinity reduces plant growth and crop production globally. The discovery of genes in salinity tolerant plants will provide the basis for effective genetic engineering strategies, leading to greater stress tolerance in economically important crops. In this study, we have identified and isolated 107 salinity tolerant candidate genes from a mangrove plant, *Acanthus ebracteatus* Vahl by using bacterial functional assay. Sequence analysis of these putative salinity tolerant cDNA candidates revealed that 65% of them have not been reported to be stress related and may have great potential for the elucidation of unique

salinity tolerant mechanisms in mangrove. Among the genes identified were also genes that had previously been linked to stress response including salinity tolerance, verifying the reliability of this method in isolating salinity tolerant genes by using *E. coli* as a host.

Keywords *Acanthus ebracteatus* · Functional screening · Mangrove · Salinity tolerance

Introduction

Mangroves are taxonomically diverse associations of woody plant communities belonging to several unrelated angiosperm families that dominate tropical and subtropical tidelands (Tomlinson 1986). These plants have developed morphological and physiological adaptations to environments that are of elevated salinity, high temperatures, strong winds, extreme tides, and muddy anaerobic soils (Kathiresan and Bingham 2001). Salinity tolerance in mangroves depends on a range of adaptations, including ion compartmentation, osmoregulation, selective transport and uptake of ions, maintenance of a balance between the supply of ions to the shoot, and capacity to accommodate the salt influx (Ball 1988a).

The effects of salinity on the physiology of mangrove plants have been studied in relation to photosynthetic and stomata responses (Ball and Critchley 1982; Ball and Farquhar 1984), atmospheric concentrations of CO₂ (Ball and Munns 1992), growth and carbon partitioning (Ball 1988b), and lipid composition (Oku et al. 2003). In the recent years, the isolation of salinity tolerant genes from a few mangrove species through the generation and analyses of expressed sequence tags (ESTs) from *Avicennia marina* (Mehta et al. 2004) and *Acanthus ebracteatus*

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