

Sequence analysis and characterization of vacuolar-type H⁺-ATPase proteolipid transcript from *Acanthus ebracteatus* Vahl

ABSTRACT

The vacuolar-type H⁺-ATPase (V-ATPase) is a multimeric enzyme with diverse functions in plants such as nutrient transport, flowering, stress tolerance, guard cell movement and development. A partial sequence of V-ATPase proteolipid was identified among the expressed sequence tags (ESTs) generated from *Acanthus ebracteatus*, and selected for full-length sequencing. The 876-nucleotide cDNA consists of an open reading frame of 165 amino acids. The deduced amino acid sequence displays high similarity (81%) with its homologs from *Arabidopsis thaliana*, *Avecinnia marina* and *Gossypium hirsutum* with the four transmembrane domains characteristics of the 16 kDa proteolipid subunit c of V-ATPase well conserved in this protein. Southern analysis revealed the existence of several members of proteolipid subunit c of V-ATPase in *A. ebracteatus*. The mRNA of this gene was detected in leaf, floral, stem and root tissues, however, the expression level was lower in stem and root tissues.

Keyword: *Acanthus ebracteatus*; Mangrove; Sequence; Transcript; Vacuolar-type H⁺-ATPase proteolipid