**Abstract**

Leucas aspera commonly known as ‘Thumbai’ is used traditionally as an antipyretic and insecticide. It is distributed throughout India from the Himalayas down to Ceylon and possess various pharmacological activities like antifungal, antioxidant, antimicrobial, antinociceptive and cytotoxic activity. As this plant distributed throughout India, analysis of genes induced during abiotic stress may give better insights on abiotic stress tolerance. Quantitative real time RT-PCR is a better technique to analyse the differential expression of genes. A major step in gene quantification analysis is data normalisation in real-time RT-PCR . Normalizing through reference genes, or housekeeping genes, can make more accurate and reliable results from reverse transcription real-time quantitative polymerase chain reaction (qPCR). The classical housekeeping genes involved in basic cellular processes such as 18 S rRNA, ubiquitin, actin, b-tubulin, and glyceraldehyde-3-phosphate dehydrogenase have been recurrently used as internal controls for gene expression analysis in plant as they are supposed to have a uniform expression in all samples and experimental conditions tested. To analyse the differential expression of genes involved in abiotic stress, Actin gene homologue was identified from Leucas aspera to use as house keeping genein this experiment. Complete coding region (CDS) of actin gene from different plants were downloaded from NCBI database. Conserved region of the Actin gene was deduced and degenerate primers were designed using bioinformatics tools ClustalW and PriFi. Using the degenerate primers, partial gene homologue of actin from Leucas aspera genomic DNA was amplified and the amplicon was sequenced. The sequence data was annotated for exons and introns were submitted in NCBI database. This gene will be used as housekeeping gene for normalization in differential expression studies in this plant.