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Sequencing and Bioinformatics Analysis of *HSS1* Gene from Medicinal Plant, *Senecio vulgaris* L.

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Abstract

The first pathway-specific enzyme for pyrrolizidine alkaloid (PA) biosynthesis is Homospermidine synthase. HSS catalyzes the NAD1-dependent transfer of an aminobutyl group of spermidine to putrescine. Putrescine, spermidine and spermine are three polyamines which are naturally positively charged compounds found in virtually all living cells. These compounds bind to DNA and have been implicated in a number of crucial processes such as cell division, differentiation and membrane function. Very few studies on expression of *homospermidine synthase* gene in *Senecio vulgaris* have been reported. The objective of current research was to sequencing the *HSS1* gene, and then examine the gene in terms of bioinformatics in order to explain a number of parameters. PCR bands amplified to carry out Sanger sequencing. To sequense genes derived from gene amplification (*HSS1*), primers were designed to cover the entire length of the gene. After receiving the complete sequence, several bioinformatics analyzes were performed to verify the near-homologues of the homologues, examining the number and position of the exons and introns by the FGENESH program, the position of the protein in the cell by the TargetP tool. To determine if the protein will eventually be deployed, check the UNIPROT protein function and other protein-related parameters by the PROTPARAM tool. After sequencing the cloned gene in the vector was determined that the gene contained 1989 base pair (recorded in NCBI by accession number MH042529.1), which contains 65.36% A+T, 64.64% G+C Is. It was also found that the *HSS1* gene has 6 exons with different lengths. The gene identified in this study is well preserved in the genus *Senecio*, as it was 96% in the *Senecio vernalis* plant and 97% similar.

Keywords: Bioinformatics analysis, sequencing, alkaloid, protein function

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