Characterization of Solanum tuberosum Ammonium Transporter Gene Using Bioinformatics Approach

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Abstract : Plants require nitrogen (N) to support desired production levels. There is a need for better understanding of N transport mechanism in order to improve N assimilation by plant root. Nitrogen is available to plants in the form of nitrate or ammonium, which are transported into the cell with the aid of various transport proteins. Ammonium transporters (AMTs) play a role in the uptake of ammonium, the form in which N is preferentially absorbed by plants. Solanum tuberosum AMT1 (StAMT1) was amplified, sequenced and characterized using molecular biology and bioinformatics methods. Nucleotide database sequences were used to design 976 base pairs AMT1-specific primers which include forward primer 5'-GCCATCGCCGCCGCCGG-3' and reverse primer 5'-GGGTCAGATCCATACCCGC-3'. These primers were used to amplify the Solanum tuberosum AMT1 internal regions. Nucleotide sequencing, alignment and phylogenetic analysis assigned StAMT1 to the AMT1 family due to the clade and high similarity it shared with other plant AMT1 genes. The deduced amino acid sequences showed that StAMT1 is 92%, 83% and 76% similar to Solanum lycopersicum LeAMT1.1, Lotus japonicus LjAMT1.1, and Solanum lycopersicum LeAMT1.2 respectively. StAMT1 fragments were shown to correspond to the 5th-10th trans-membrane domains. Residue StAMT1 D15 is predicted to be essential for ammonium transport, while mutations of StAMT1 S76A may further enhance ammonium transport.

Keywords : ammonium transporter, bioinformatics, nitrogen, primers, Solanum tuberosum