

## ABSTRACT

A major component of the diatom cell wall is silica, derived from silicon. Due to limiting environmental concentration of silicon, and a substantial requirement during cell wall synthesis, diatoms must transport silicon in to the cell against a steep concentration gradient. This is accomplished through the silicic acid transporters (SITs). The SITs were first identified in the marine pinnate diatom *Cylindrotheca fusiformis*. In the present work an analyses has been made to determine the homology amongst the twenty nine full length and partial amino acid sequences of SITs downloaded from two websites. The study revealed considerable extent of homology in the N-termini of the sequences while no such homology was observed in the C-termini. A short seven amino acid long conserved sequence was found in all the SIT sequences. The overall negative charge present on the proteins validated the membrane protein nature of the SITs which are hydrophobic. Leucine and tryptophan have been found to be the most abundant and least frequently occurring amino acid residues respectively, in the SITs analysed.

Analysis of the transmembrane regions in the sequences revealed that these regions are mostly located in the N terminal sides of the proteins. With respect to the orientations of the two termini towards the cytosolic and extracytosolic region, it was found that the C-termini are always towards the cytosolic region but there is no such fixed orientation in the N-termini.

Analysis of the signal peptide sequences in the SITs with SignalP3.0 software revealed that there is no fixed cleavage site in the signal peptide sequences.

Comparison with transport membrane proteins (sodium ion/potassium ion/calcium ion sodium ion/ proton, sodium-coupled phosphate transporter protein, acetylcholine receptor (cattle), acetylcholine receptor (*Homo sapiens*)) showed that the SITs do not share any homology with the sequences of these proteins. There are also differences in terms of the abundance of amino acid residues in these proteins.