

In silico characterization of alginate lyase produced by different species

Aanandhalakshmi R and B. Vanavil*

Department of Biotechnology, Kalasalingam Academy of Research and Education,
Krishnankoil-626126, Tamilnadu, India

*Corresponding author

ABSTRACT

Alginates are synthesized in abundance as a major structural material in cell-wall and intracellular matrix of brown algae and bacterial species like *Azotobacter* and *Pseudomonas*. Alginate can be depolymerized into alginate oligosaccharides by alginate lyase. Alginate lyase (AL) can be classified into G block, and M block-specific lyases based on the substrate specificity but some enzymes cleave both polyM and polyG. AL can be endolytic and exolytic. Oligosaccharides derived from alginate have many biological activities including immune regulation, anti-coagulation, anti-oxidant, anti-cancer, growth-promoting activities. In the present study, *in silico* characterization of the different reported alginate lyases was carried out. A total of 50 protein sequences of alginate lyase produced by different microorganisms were retrieved from UniProt database and have been subjected to assessment of physiochemical properties, multiple sequence alignment, motif analysis and phylogenetic tree construction. Multiple sequence alignment was carried out using Clustal Omega. The physicochemical parameters analyses were evaluated using the ProtParam tool. The phylogenetic tree was constructed by the Neighbor-Joining method using MEGA-X. Motif analysis of alginate lyase sequences was done by MEME server. Further, the structures of 45 retrieved alginate lyase sequences were modelled using SWISS-MODEL. Multiple sequence alignment showed that there are no conserved regions and sequences are highly variable among different alginate lyases. The total number of amino acid residues ranged from 320 to 1059 with varying molecular weights. The pI value ranged from 4.42 to 9.59. The variability was also observed among these alginate lyases in terms of other physiochemical parameters.

Keywords: Alginate lyase, Multiple Sequence Alignment, Phylogenetic analysis, Motif, Homology Modeling

