Application of a bioinformatics based approach to predict normal and random N-glycosylation of β-secretase-1

Fateme Pakniya[1], Hassan Mohabatkar[1]

[1]Department of Biotechnology, Faculty of Advanced Sciences and Technologies, University of Isfahan, Isfahan

ABSTRACT

β-secretse-1 enzyme is considered as a key factor in Alzheimer's disease. The proteolytic cut of the extracellular amyloid-β precursor protein (APP) is performed by β-secretase-1, which is followed by failed inside the membrane by γ-secretase and amyloid-β peptide is created with 42 roots that form oligomer itself and then form larger amyloid plaques found in brains of Alzheimer's patients. In this study, we investigated regions of this enzyme which are affected by a type of post translational modification (PTM) which is N-glycosylated. At first, using Swiss-Prot, the protein identification code was taken. Then the amino acid sequence of β-secretase was taken using the NCBI site based on FASTA format. In ExPASY site, using the Net NGlyc 1.0 server, the glycosylated areas of this enzyme was predicted. In the following, 100 random sequences were created using the RandSeq tool and N-glycosylated sites of these 100 random sequences were predicted. The natural β-secretase-1 has three N-glycosylation sites. Perdition of N-glycosylation sites for 100 random sequences showed that four percent had three sites, 92 percent were predicted to have less than three sites and four percent were predicted to have more than three sites. Based on the fact that in 92% of random sequences were predicted to have fewer glycosylation sites than natural sequences, it can be interpreted that there is natural pressure or force that controls PTM. In other words, PTMs such as glycosylation are not happening randomly.

Key words: β-secretase-1; N-glycosylation; Alzheimer's disease;