Mining and Phylogenetic Analysis of β-1,4-Galactosyltransferase

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Abstract

β-1,4-Galctosyltransferase (β4-GalT) is a key enzyme involved in the biosynthesis of glycoproteins found mainly in mammalian species (1). From a systematic search of databank, using human β4-GalT as a query sequence, we have identified 114 putative β4-GalT sequences in 34 organisms belong to four kingdoms except plant. Multiple amino acid sequence alignments of β4-GalTs showed these transferases have a typical Golgi type II transmembrane domain at their N-terminal region and share four conserved motifs involved in transferring galactose from UDP-galactose to *N*-acetylglucosamine (2). Phylogenetic tree analysis indicated that β4-GalTs would be split into two distinct groups; Eukaryotic β4-GalT and Bacterial β4-GalT. Eukaryotic β4-GalTs were further divided into 8 subfamilies, including β4-GalT I, II, III, IV, V, VI, VII, and *Strongylocentrotus* group; An ortholog to the ancestor present before the split of β4-GalT I, II, III, and IV was detected in arthropods. An ortholog to the ancestor before the split of β4-GalT V and VII was found in sea urchin. All bacterial β4-GalTs, however, were grouped into a single family. Interestingly, most bacterial enzymes were detected from parasitic microorganisms in the human body, suggesting that bacterial β4-GalTs could plays an important role in establishing the host-parasite relationship. Database mining and subsequent phylogenetic analysis of enzymes involved in the N-glycan synthesis will allow us to engineer glycosylation pathways for the production of humanized glycoproteins.

References

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