Phylogenetic Approach to Mine Novel β-1,4-Galactosyltransferases for Glycoengineering

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 β -1,4-Galctosyltransferase (β 4-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 β 4-GalT as a query sequence, we have identified 114 putative β 4-GalT sequences in 34 organisms belong to four kingdoms except plant. Phylogenetic tree analysis indicated that β4-GalTs would be split into two distinct groups; Eukaryotic β4-GalT and Bacterial β4-GalT. Multiple amino acid sequence alignments of eukryotic 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). Eukaryotic \(\beta 4-GalTs \) were further divided into 8 subfamilies, including \(\beta 4-GalT \) I, II, III, IV, V, VI, VII, and Strongylocentrotus group; An ortholog to the ancestor present before the split of β 4-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, reinforming the notion that bacterial \beta4-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 allows us to identify novel bacterial enzyme useful to engineer glycosylation pathways for the production of humanized glycoproteins.

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Recent Publication

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