DIVERSITY AND EVOLUTION OF THE VERTEBRATE SIALYLTRANSFERASE REPERTOIRE

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Sialic acids (SA) are commonly found on cell surface glycoproteins and glycolipids. Biosynthesis of sialylated molecules is an essential pathway that controls cellular functions like embryonic development or host-pathogen interactions. It involves biosynthetic enzymes known as sialyltransferases (STs), that catalyze the stereo- and regio-specific transfer of SA from activated sugar donors (CMP-SA) to a variety of acceptor substrates [1].
We used bioinformatics to identify and predict the function of animal sialyltransferase genes of the CAZy GT#29. Four ST families (ST3GAL, ST6GAL, ST6GALNAC and ST8SIA) are identified in Metazoa [2]. Phylogenomic and protein sequence analyses shed light into the origin ST and sialic acid pathway in Eukaryota and we showed that the major actors of the sialic acid pathway were already present in the Last Common Ancestor of Eukaryotes (LECA) [3].
We focused on the ST8SIA family comprised of mono-, oligo- and poly-α2,8-sialyltransferases and we showed that while the mammalian ST8SIA family is comprised of six subfamilies, nine vertebrate ST8SIA subfamilies originated from genome duplication events that occurred at the base of vertebrates. Comparative genomics analyses highlighted the diversity and heterogeneous distribution of the *st8sia* genes among teleost fish and sequence-based analyses unveiled potential changes of function after gene or genome duplications [4]. We developed a glyco-tool box with engineered recombinant enzymes and chemo-enzymatically synthetized donor substrates (both natural and functionalized) and we set cell-free enzymatic assays that enabled us to characterize novel fish ST8SIA activities [5]. Computational approaches and molecular dynamic simulations were used to investigate the structural and biochemical determinants of the donor substrate specificity in vertebrate ST8Sia IV [6]. Collectively, our data underscore molecular and functional evolution of vertebrates ST8SIA that account for the wide diversity of vertebrate sialoglycoconjugates.

References:

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