COMPARATIVE GLYCOMICS REVEALS CHANGES IN N-GLYCOME PATTERNS IN MULTICELLULARITY AND EARLY ANIMAL EVOLUTION

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Extensive self and non-self cell recognition and division of labor between groups of cells are key requirements of animal multicellularity. In mammals, N-glycosylation is tissue-specific and cancer cells are known to have altered glycosylation patterns. However, little N-glycosylation data from early branching animals or their closest unicellular relatives is available, leaving the evolutionary patterns in the dark.

To overcome this gap, we conducted a systematic, comparative N-glycomics study that includes representatives of early branching animal groups (ctenophores, sponges, placozoans and cnidarians), as well as their closest protist relatives (filastereans, choanoflagellates, ichthyosporeans and corallochytreans) and additional eukaryotic outgroups.

Here, we report a huge variety of N-glycan structures, including novel compositions. The data suggest that N-glycan complexity is positively correlated with organismal complexity and linked to lifestyle. Ichthyosporeans, which have a complex life cycle and often are animal parasites, synthesize a wide variety of N-glycan structures, similar to animals. In contrast, facultatively multicellular protists (*C. owczarzaki*, *S. rosetta*) synthesize simpler oligomannose N-glycans, despite possessing the genes encoding for glycan branching. Our results indicate that the N-glycan biosynthetic pathway became more important for obligate multicellularity, both as a mechanism of protein quality control and a way to synthesize recognition tags. This study provides a foundation for future work on non-canonical species by establishing several reference stage-specific glycomes. Further, single species-focused studies are needed to unravel the significance of the observed structures for each organism.

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