

Insights into the genesis of the pan-metazoan toolkit from the sponge genome

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Our understanding of the evolutionary transition to metazoan multicellularity is currently being transformed by the analysis of recently sequenced choanoflagellate, poriferan (sponge), cnidarian and placozoan genomes. Amongst these, Porifera is considered the earliest branching animal phylum living today and thus ideally suited for unravelling the origin of metazoan multicellularity. Comparison of the structure, composition and function of the genome of the demosponge *Amphimedon queenslandica* with choanoflagellate and eumetazoan genomes has allowed us to begin to reconstruct the ancestral animal genome and its role in building cells, tissues, organs and skeletons. It is clear that the ancestor from which all extant metazoans stemmed was far more sophisticated than widely appreciated, possessing almost all the genomic innovations required to undergo complex development and differentiation, regenerate body parts via stem cells, and discern self from nonself (allorecognition). Therefore, we can infer that the morphogenetic tools used by all modern animals evolved well before the Cambrian explosion.