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The publication of the mouse and human genomes enables comparative genomics to elucidate gene structure and function within these organisms, classed together within the Metazoa. To find the same functional and evolutionary information for animals in general, it is necessary to expand the comparison beyond the Metazoan lineage. In the July 18 Science, Nicole King and colleagues at the Howard Hughes Medical Institute report *in silico* investigations of the expressed sequence tags (ESTs) of the next most closely related lineage of eukaryotes to the Metazoa - the choanoflagellates. These investigations reveal those genes that existed before animals evolved into the multicellular organisms we see today (*Science* 2003, **301:**361-363).

King *et al.* analyzed more than 5000 ESTs from two choanoflagellate species and determined the phylogenetic distribution of the proteins or domains within eukaryotes, bacteria, archaea, and viruses. They then looked within the eukaryotes for distribution among non-animals including fungi and plants and finally examined the distribution of specific protein domains among these groups. They showed that choanoflagellates and Metazoa share complex signaling proteins and pathways and that their genomes include G-protein - coupled receptors, fibrinogen, somatomedin, and complement control protein domains, and also members of the cadherin, C-type lectin, and tyrosine kinase families. In addition, the extent of tyrosine kinase signaling in choanoflagellates provided evidence of activation of signaling pathways in response to extracellular stimuli.

"The discovery of multiple signaling and adhesion gene family members in choanoflagellates demonstrates that key proteins required for animal development evolved before the origin of animals," write the authors. Sequencing the entire choanoflagellate genome will yield information on "the repertoire of transcription factors and the potential representation of families of proteins that regulate cell differentiation and development in animals," they conclude.

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