

# Largest study of sponges sheds new light on animal evolution

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Sponges are an important animal for marine and freshwater ecology and represent a rich animal diversity found throughout the world, from tropical climates to the arctic poles. For evolutionary biologists, they also present an interesting animal for comparative study because they are simple filter feeders, and lack nervous, digestive or circulatory systems, suggesting that they diverged early from other animals.

To provide a wider framework for understanding the molecular complexity behind the evolution of [sponges](#), authors Riesgo, Windsor, Farrar, Giribet, and Leys (from the University of Barcelona, University of Alberta and Harvard University), performed the largest sequencing study to date on the genes of representatives from eight sponge genera covering all four currently recognized sponge classes. They performed comparative analysis of animal genes important for signaling, neuronal and ionic conduction, epithelia, immunity and reproduction.

One of the remarkable results of this work, published in the journal *Molecular Biology and Evolution*, is the understanding that most higher animal genes, or the greater complement of genes involved in more complex gene pathways, are also present in all sponge groups. They found a number of genes that previously had been associated with complex structures of higher [animals](#) and were thought to be absent in sponges. This provides an important new resource to the question of which molecules might have been present in early animal groups, and more importantly, provides the framework for posing new hypotheses on determining gene function in sponges and the evolution of animal

complexity.

Provided by Oxford University Press

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