

Press release for: Fortunato SAV, Adamski M, Mendivil O, Leininger S, Liu J, Ferrier DEK and M Adamska. Calcisponges have a ParaHox gene and dynamic expression of dispersed NK homeobox genes. *Nature* **514**, 620–623 (30 October 2014) doi:10.1038/nature13881

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Sponge genomes: genes lost, genes found

Discovery of key developmental regulatory genes in Norwegian sponges shows that the ancestor of all animals possessed was more complex than previously thought.

Hox and ParaHox genes regulate development of animals by providing cells with information on their identity and position within the developing embryo. Cells expressing these genes “know” whether they belong in the brain or in the gut, or whether they are positioned within the neck or the tail. These genes are found in vertebrates, insects, and jellyfish, but until now they have not been found in sponges, which are likely to be the earliest evolved of currently living multicellular animals. Their absence in sponges has been interpreted as demonstrating that Hox and ParaHox genes originated after sponges separated from the lineage leading to complex animals. The broader implication of this absence was that appearance of these gene classes was connected with the origin of morphological complexity in the animal kingdom.

However, two lines of evidence suggested that these genes might have been present in the common ancestor of sponges and other animals, and were lost in sponges: one was based on analysis of their sequences, and the other one on similarity of regions (neighbourhoods) in a sponge genome to the regions containing Hox and ParaHox genes in other animals. This latter scenario has been published by group led by D. Ferrier from the University of St. Andrews in a 2012 *Current Biology* paper, but some scientists remained sceptical. The “ghost loci”, as these genomic regions were called, could be compared to the smoking guns – but the bullets were still missing.

Meanwhile, team led by M. Adamska at the Sars Centre in Bergen, Norway decided to sequence genomes of two sponge species characterized by presence of calcareous skeletons (and thus called calcareous sponges or calcisponges), *Sycon ciliatum* and *Leucosolenia complicata*. These genomes revealed that repertoires of developmental regulatory genes of calcisponges differ dramatically from those previously described in sponges with silica-based skeletons (siliceous sponges). One of the most spectacular findings was presence of a ParaHox gene in the calcisponge genomes discovered by S. Fortunato, then a PhD student in Adamska lab.

The two teams joined forces to confirm the finding of the “missing bullet” and gain insight into possible function of the identified gene and the remaining members of the gene family. Strikingly, expression of the calcisponge ParaHox gene suggests it is likely to be involved in embryonic development and regulate formation of the sponge’s equivalent of a gut – exactly like its vertebrate counterparts! Thus, presence – and likely also a function – of ParaHox genes can be dated back to the last common ancestor of sponges and other animals. “Our work emphasizes the importance of investigating a much wider range of species than are commonly used, so we can really understand what the very first animals that lived over 600 million years ago were like, and the evolutionary history of the complex animals living around us today” says Adamska. The study is reported in the 30th of October issue of *Nature*.



Three specimens of *Sycon ciliatum*, calcareous sponges from the Norwegian fjords. Genome of this species contains a surprising array of genes similar to those governing development of humans, including a ParaHox gene reported by Fortunato et al. in the current issue of *Nature*. Photo credit: M. Adamski