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Leininger S, Adamski M, Bergum B, Guder C, Liu J, Laplante M, Bråte J, Hoffmann F, Fortunato S, Jordal S, Rapp HT and Adamska M. 2014. *Developmental gene expression provides clues to relationships between sponge and eumetazoan body plans*. **Nature Communications**. DOI: 10.1038/ncomms4905

Scientists from the Sars International Centre for Marine Molecular Biology and their colleagues from the Universities of Bergen and Oslo discover that when it comes to usage of developmental regulatory genes, the nerve-less, muscle-less and gut-less sponges are not so different than other, more sophisticated animals.

Majority of animals, including vertebrates (such as humans) and the familiar invertebrates like butterflies and snails, are collectively called “bilaterians” because of their bilateral symmetry established by two body axes: head to tail (anterior to posterior) and belly-to-back (ventral to dorsal). During embryonic development, the bodies of bilaterians arise from three distinct layers: the outer-most ectoderm (producing skin and nervous system), the inner-most endoderm (producing the gut) and the mesoderm, which is sandwiched between the two other layers, and produces muscles.

Cnidarians (corals and jellyfish), which are the nearest relatives of bilaterians, are much simpler: they have only one axis of symmetry: bottom-to-top (basal to apical) which likely corresponds to the anterior-posterior axis of bilaterians. They are also built of only two layers, the ectoderm and the endoderm (which bears similarity to both endoderm and mesoderm of bilaterians).

Sponges are possibly the most ancient of the living animal phyla, and are one of the simplest: they have no nerves, no muscles, and no gut. Instead, sponges obtain their food by filtering particles out of water, which is propelled through the canal system by action of cells equipped with flagella and collars. These cells, called collar cells or choanocytes, form the innermost epithelial layer of sponges, the choanoderm. Water enters the sponge body through multiple tiny pores (hence the Latin name of sponges, Porifera = pore bearing) and exits through much larger openings, called oscula. Many species of sponges have highly plastic, “amorphous”, bodies with multiple oscula, and on the first sight do not even resemble animals. However, some species, for example *Sycon ciliatum*, an extremely common sight in the fjords around Bergen, have only a single osculum, a clear apical-basal body axis and are radially symmetrical.

These features prompted a group of scientists led by Maja Adamska from the Sars Centre in Bergen and including researchers from the Sars Centre, the University of Bergen and the University of Oslo, to use *Sycon ciliatum* as a model to investigate similarities between sponges and “true animals”, especially cnidarians. “One of the major challenges of

evolutionary biology is to understand how the different body plans of animals from diverse phyla are related to each other. In the recent years scientists have learned a lot about similarity of cnidarian and bilaterian body plans by comparing expression of conserved genes regulating their development. The genome of another sponge, *Amphimedon*, was sequenced a few years ago, revealing that many of these genes are also present in sponges, but because *Amphimedon* looks so different than “true animals” we never dared to compare the adult body plans then” says Adamska, who was also a co-author on the *Amphimedon* genome paper. “But *Sycon*, despite being built of basically the same cell types, looks so different – it is exquisitely simple and elegant, so we decided to identify its developmental regulatory genes and study their expression during development and in adult bodies”.

Using the Next Generation Sequencing technology and producing billions of sequences at the Norwegian Sequencing Centre in Oslo, the team was able to make two startling findings reported in their Nature Communications paper published on 20 May 2014: One, that the number of genes for signalling molecules involved in axial patterning in *Sycon* is quite similar to the numbers known from complex bilaterians. Two, expression patterns of a large number of developmental regulatory genes are very similar to those known from cnidarians and bilaterians. In particular, genes associated with the apical end of cnidarians are strongly expressed around the osculum (also at the apical end) of *Sycon*, and genes connected with development of endoderm of cnidarians and bilaterians are expressed in the choanoderm of *Sycon*. “This is definitely not the end of the story; we now have the challenging task of finding out if function of the identified genes is as conserved as their expression. We also want to know why does a simple sponge need so many developmental genes, and how did it get them. We are already looking into genomes of several other sponges, and each of them has a story to tell” concludes Adamska.



Sponge *Sycon ciliatum*: individual specimen (left) and large numbers of individuals growing on kelp from the fjord near Bergen. Images: left, Leininger et al. Nature Comm. DOI: 10.1038/ncomms4905, right, M. Adamski.