Oikopleura dioica in brief:
- Japanese name: おいくぼる
- Oikopleura dioica is a globally distributed marine animal. It is evolutionarily closer to humans than most organisms such as yeast, nematodes or fruit flies. As it belongs to the chordate phylum, it has features common with vertebrate embryonic development, such as a dorsal nerve cord, and the formation of a muscular tail supported by a notochord.
- Ecological importance: O. dioica is a small filter feeder that can account for up to 13% of the total carbon mass in an area. It eats unicellular plankton and was reported to be able to ingest bacterial viruses and microplastics as well. Being an extremely efficient predator, it has an important role in the carbon chain, by producing organic matter (faecal pellets and "houses") that sediment to the sea floor.
- Evolution: As it belongs to the Tunicate phylum, it is among the invertebrates that are evolutionarily closest to humans. Tunicates, like vertebrates, are chordates: they have a muscular tail. They also have a brain, a heart, a gut, etc.
- Compact genome: only 70 Mb. Nevertheless, it contains 18,020 predicted genes, which makes it an interesting model to study how to compactly encode functions homologous to some found in vertebrates.
- O. dioica lives in a "house" made of cellulose and novel proteins. The house is a 30 micrometric filter that enables Oikopleura to prey on microbes significantly smaller than itself. Oikopleura have even been reported to capture and ingest bacteriophage viruses. The Oikopleura house is synthesised from a specialised epithelium on the epidermis. The cellular arrangement in this epithelium is always the same between individuals.

Oikopleura dioica is known as a globally distributed species.

Massive rearrangements between O. dioica genomes:
Chromosomal assemblies of different isolates revealed massive scrambling of gene order, questioning current taxonomy.

Pairwise comparison of whole genomes show conservation of synteny - in the sense of "staying on the same chromosome".

Pairwise alignments of homologous chromosomes (Chr 2) and species phylogenetic cladogram.

Pairwise genome alignment visualised with the dot plot method.

Alignment of 10-Mbp windows in pairs of increasingly distant species.

There are 3 genome assemblies available for Oikopleura dioica:
- OD3 (Denneud and coll., 2010), a Sanger sequencing of the laboratory strain of the Thompson laboratory in Norway.
- OSK2016 (Wang and coll., 2020), a PacBio sequencing of the laboratory strain of the Nishida laboratory in Osaka, Japan.
- OIK2018_169 (Bizzima and coll., 2021), a Nanopore sequencing of a single individual from a laboratory strain of the Luscombe laboratory in Okinawa, Japan.

Our OIK2018_169 assembly has chromosome-scale resolution thanks to Hi-C scaffolding. More details are available in our bioRxiv preprint: "Pacbio-to-nanopore assembly of the genome of an individual Oikopleura dioica from Okinawa using nanopore-based sequencing", Bizzima and coll., 2020, https://doi.org/10.1371/journal.pbio.2142266.

In simple terms: our study shows that the genes move a lot, but within their chromosome arm.

These large-scale rearrangements are likely to cause reproductive isolation and question the assumption that Oikopleura dioica is a single species.

Conclusions and perspectives:
Each change of chromosomal location of a DNA sequence from one genome to the other is related to a break of the DNA molecule. We are now studying the sequence context of these breaks to understand what makes the Oikopleura genome so fluid and how we can utilise this to simplify the design of artificial genomes.

By the way... O. dioica uses the "ascidian" mitochondrial genetic code but some other larvaceans use a different code that was not described before.