

Flexibility of gene arrangement in the genome of *Oikopleura dioica*

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Oikopleura dioica in brief:

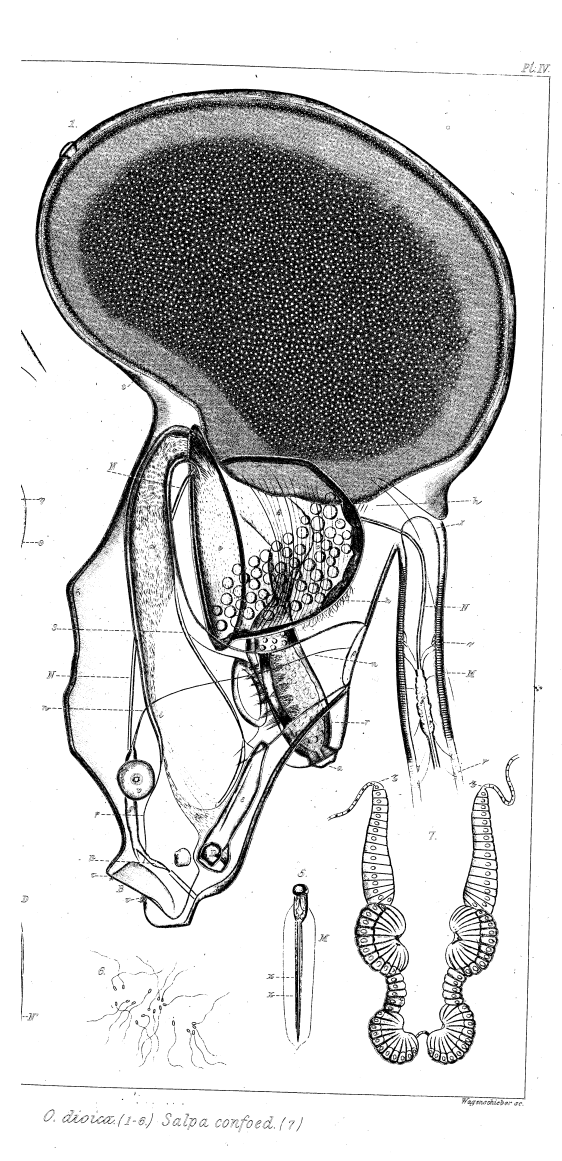
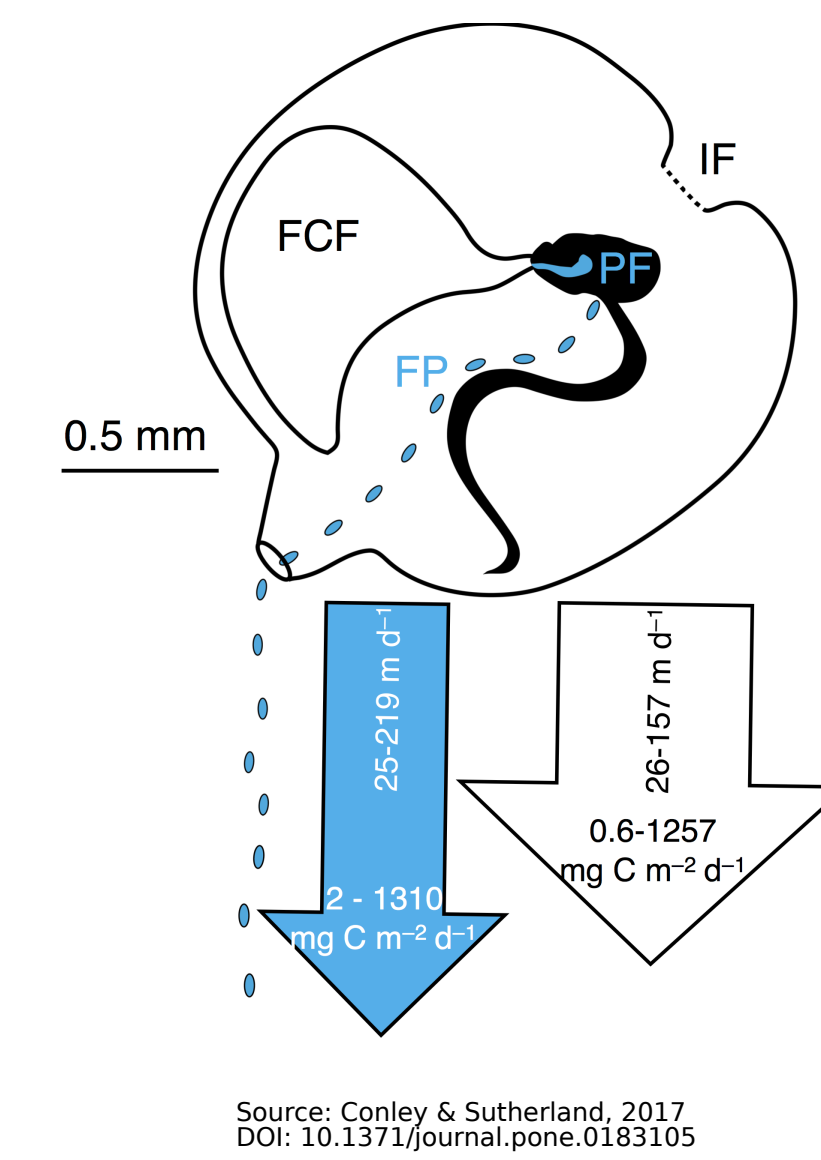
- Japanese name: オタマボヤ
- *Oikopleura dioica* is a globally distributed marine animal. It is evolutionarily closer to human than are model organisms such as yeast, nematodes or fruit flies. As it belongs to the chordate phylum it has features common with vertebrate embryonic development, such as a dorsal nerve cord, or 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 10 % 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 (fecal pellet and "houses") that sediment to the sea floor.
- **Evolution:** as it belongs to the tunicate phylum, it is among the invertebrates that are evolutionary 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 3D microfluidic filter that enables *Oikopleura* to prey on microbes significantly smaller than itself. *Oikopleura* have even reported to capture and ingest bacteriophage viruses. The *Oikopleura* house is synthesised from a specialised epithelium on the epidermis. Cellular arrangement in this epithelium is always the same between individuals.

Oikopleura dioica: a plankton predator that:

lives in a house made with cellulose

has a muscular tail, for flowing food to its mouth

never sleeps and releases its gametes in only 5 days

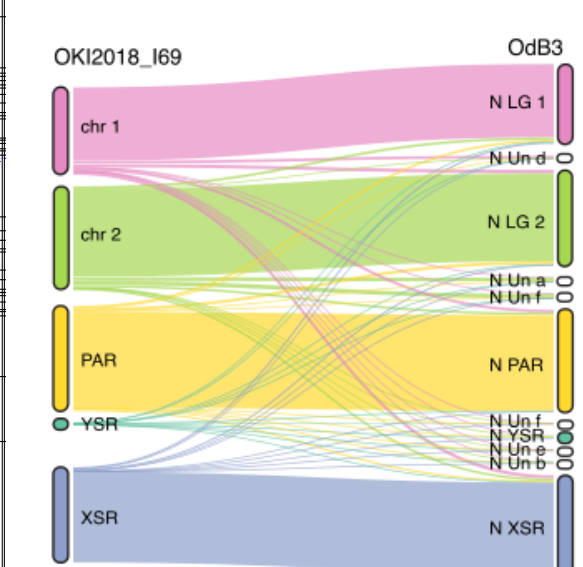
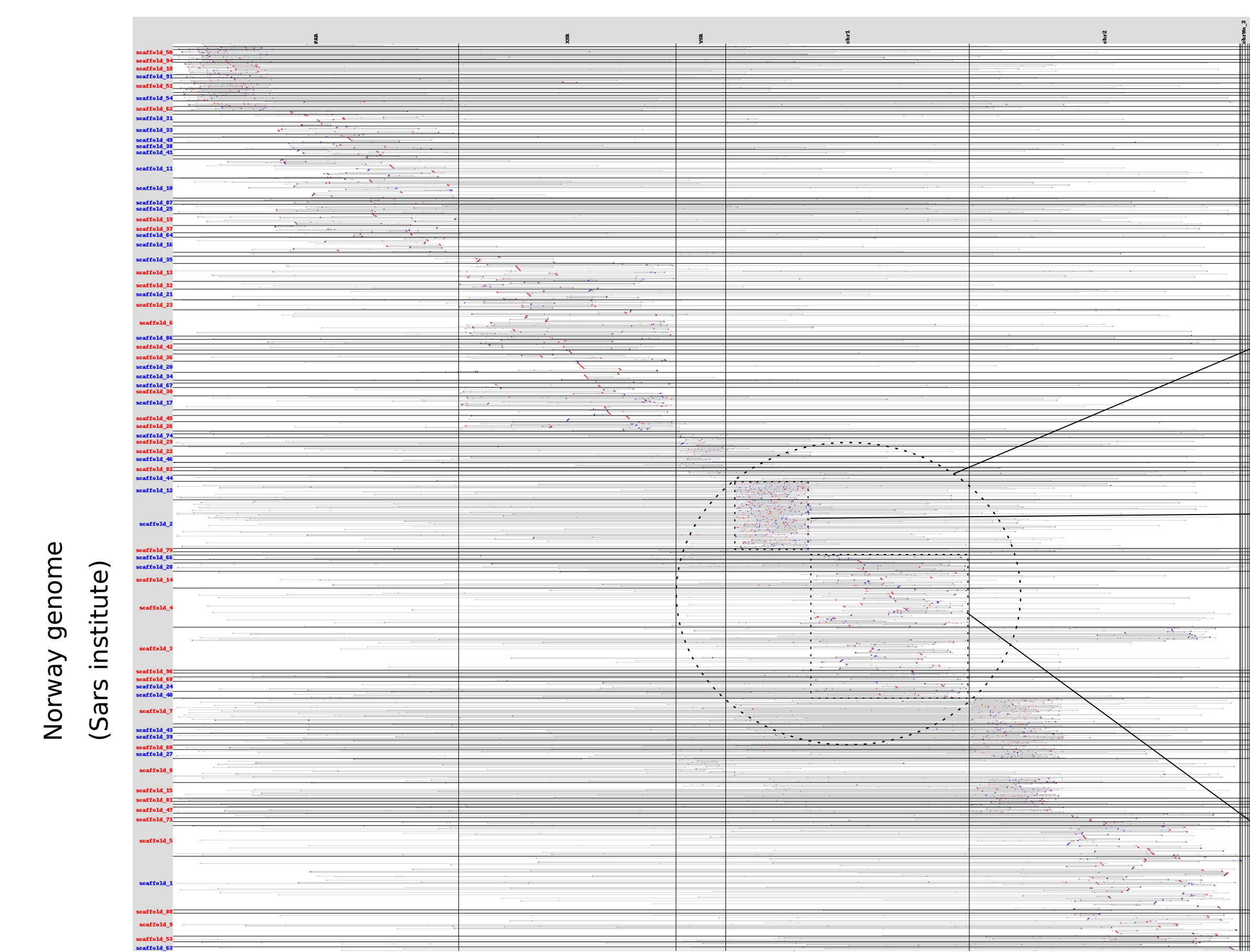
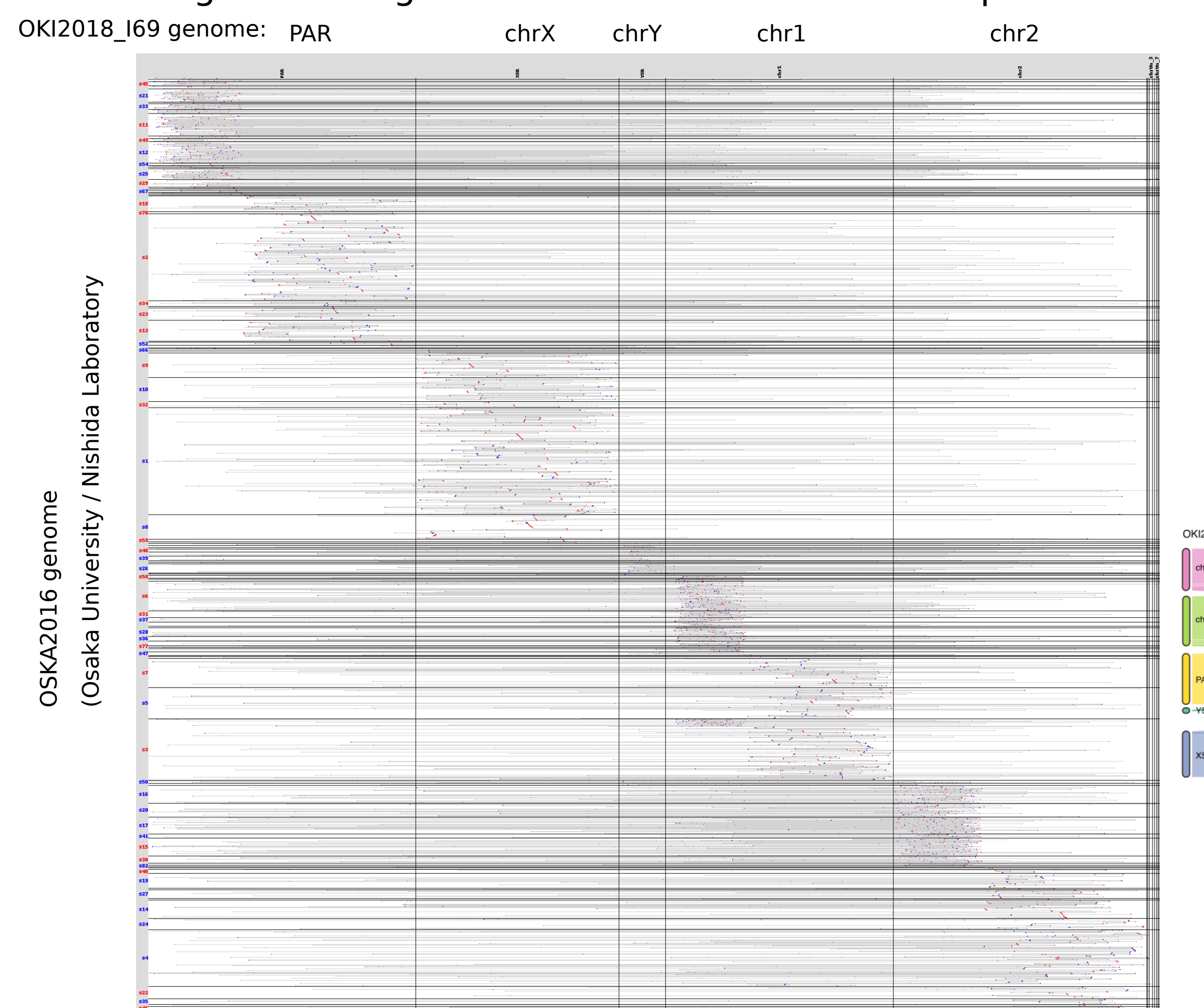


Source: Conley & Sutherland, 2017
DOI: 10.1371/journal.pone.0163105

Credit: C. Cañestro via Nature (doi:10.1038/447153a)

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Pairwise genome alignments visualised with the dot plot method



Okinawa Chr1 aligned to various scaffolds of Norway genome assembly

Okinawa Chr1's short arm sequences align preferentially to two Norway scaffolds, in a typical pattern that forms a square. We conclude that these scaffolds are Norway genome Chr1's short arm.

Same as above for the long arm. Note that the length of the homologous regions (blue and red diagonals) tends to be longer.

Massive rearrangements between *O. dioica* genomes

There are 3 genome assemblies available for *Oikopleura dioica*:

- OdB3 (Denoeud and coll., 2010), a Sanger sequencing of the laboratory strain of the Thompson laboratory in **Norway**.

- OSKAZ2016 (Wang and coll., 2020), a PacBio sequencing of the laboratory strain of the Nishida laboratory in **Osaka**, Japan.

- OKI2018_I69 (Bliznina and coll., 2020 under peer review), a Nanopore sequencing of a single individual of a laboratory strain of the Luscombe laboratory in **Okinawa**, Japan.

Our **OKI2018 I69 assembly has chromosome-scale resolution** thanks to Hi-C scaffolding. More details are available in our bioRxiv preprint: "*Telomere-to-telomere assembly of the genome of an individual Oikopleura dioica from Okinawa using Nanopore-based sequencing*", Bliznina and coll., 2020, <https://doi.org/10.1101/2020.09.11.292656>.

← Pairwise comparisons of these genomes show that homologous DNA segments are found on homologous chromosomes. This Sankey plot on the left illustrates it for the comparison between the Okinawan (OKI2018_I69) and the Norway (OdB3) genome.

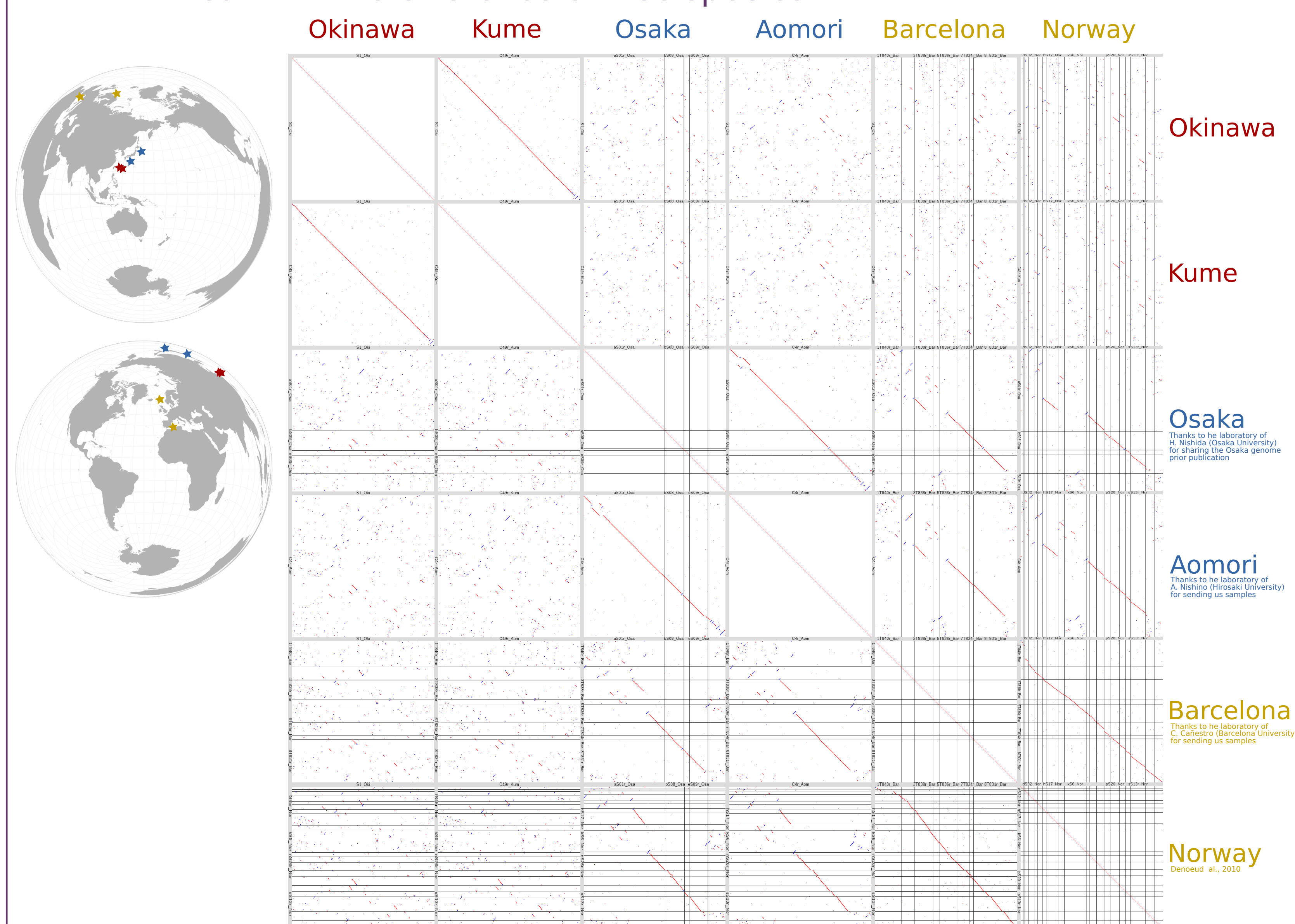
The dot plots on the left display the homologous DNA segments in spatial context. They show that a) the unit of conservation is chromosome arms, b) intra-arm rearrangements are massive, and c) the scale of rearrangement is finer in short arms.

In simpler terms: the genes move a lot, but within their chromosome arm.

These large-scale rearrangements are likely to cause reproductive isolation and therefore 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.

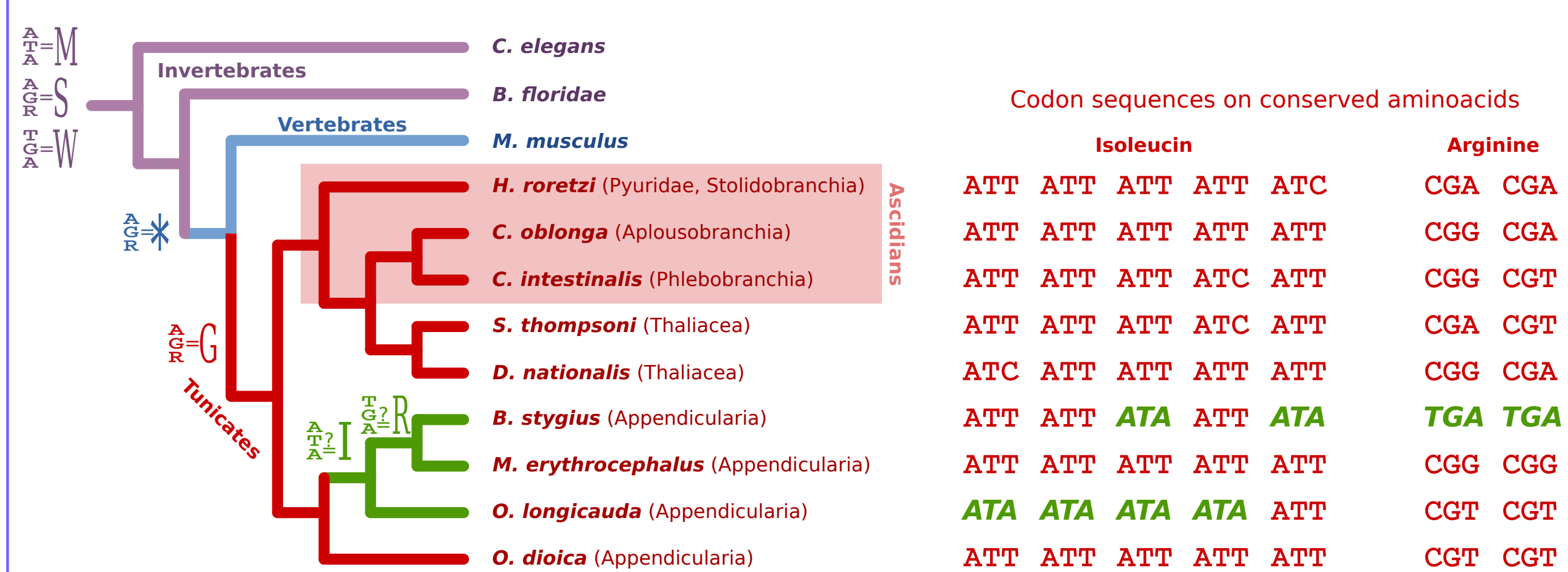
Chromosome X sequences from 6 genomes assembled from populations sampled across different oceans and seas confirm the existence of tree species



Zoom in to see details !

By the way...

A novel genetic code found in mitochondria of appendicularians related to *Oikopleura dioica*



Pichon J, Plessey C, Luscombe N. Widespread use of the "ascidian" mitochondrial genetic code in tunicates F1000Res. 2019 Dec 10;8:2072. doi: 10.12688/f1000research.21551.2