

BIODIVERSITY GENOMICS 2020



POSTER ABSTRACTS

Posters will be available in Spatial.Chat throughout the duration of the conference. Poster presenters are encouraged to be present to chat about their poster during one or more of the following sessions:

Monday 5th- 19:00-20:00 BST

Tuesday 6th- 15:00-16:00 BST

Tuesday 6th- 19:00-20:00 BST

Wednesday 7th- 15:00-16:00 BST

Thursday 8th- 15:00-16:00 BST

Thursday 8th- 19:00-20:00 BST

Friday 9th- 15:00-16:00 BST

The following document contains all the abstracts for posters that will be presented during the conference arranged by subject. These subjects will relate to rooms within Spatial.Chat.

Nanopore-based long reads assembly of sponge *Halisarca dujardini* draft genome
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The evolution of complexity of multicellular organisms manifested in appearance of new systems and organs is driven by large changes in animal genomes. Due the basal phylogenetic position of Porifera, the studies of their genome organization are crucial for such fundamental questions as the origin of morphogenetic processes regulation. Our model, *Halisarca dujardini*, has long drawn interest of morphologists because of its capacity for regeneration, as well as unique programs of morphogenesis, development, and metamorphosis. Transcriptomic data demonstrate involvement of cell-to-cell signaling pathways in axis establishment of sponge body. To improve our understanding of genomic regulation of morphogenetic and regenerative processes a draft genome was assembled. We have sequenced genomic DNA from definitive sponge using three MinION 9.4.1 flow cells and 1D-ligation library preparation (Oxford Nanopore). Approximately 13 Gb of long reads with N50=15 kb were obtained. Additionally we have generated 13 Gb reads using Illumina. Several assembly strategies were compared to obtain best genome assembly which was evaluated using contig N50 and BUSCO scores. As a result, a draft assembly with a total length of 286 Mb, N50=146 kb and metazoan BUSCO score of 76.6% (single:71.8%, duplicated:4.8%, fragmented:6.0%, missing:17.4%, n:978) was produced. We determined genome size to be 286 Mb which is unexpectedly large in comparison with the first sequenced demosponge genome, *Amphimedon* (166 Mb). We are currently working on additional sequencing in order to improve the genome contiguity and quality. We intend to use the genome of *H. dujardini* together with ChIP-seq and ATAC-seq data as resource to study regeneration and developmental morphogenesis in future. The study was supported by the Russian Science Foundation (grant 17-14-01089).