

First ostracod draft genomes provide insights into ostracod biology and evolution

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Introduction

- Ostracods have the most extensive fossil record of all extant Arthropoda => ideal model organisms for evolutionary research
- But: known genomic resources of the Ostracoda are still extremely limited
- Here, we assembled & annotated the first genomes of ostracod species (Figure 1) with asexual & sexual reproduction
- We used short read Illumina technology for DNA (genome) and RNA (transcriptome) sequencing

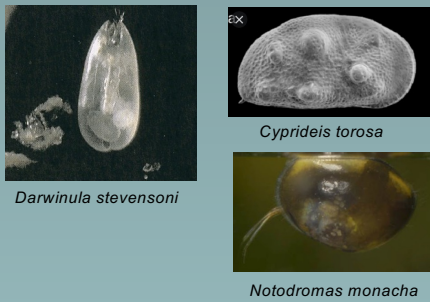


Figure 1: The three ostracod species for which the first genomes were published.

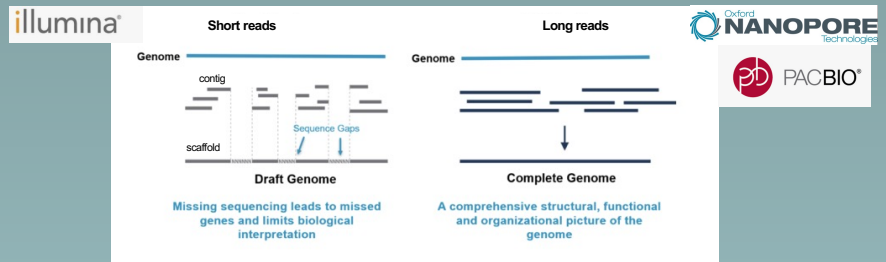


Figure 2: Two kinds of high throughput sequencing for genomic assemblies, producing short & long reads and consequently, short or long contigs & scaffolds.

Features of first ostracod genomes

Ostracod species	Reproduction	N50	Nr of scaffolds	Genome size Assembly/Flow Cytometry	BUSCO complete genes	Predicted genes	Heterozygosity
<i>Darwinula stevensoni</i>	Putative ancient asexual	56,000bp	62,118	362/420 Mb	93.7%	15,453	0.92-0.99%
<i>Notodromas monacha</i>	Sexual	42,000bp	62,251	385/425 Mb	92.7%	13,771	1.32-1.43%
<i>Cyprideis torosa</i>	Sexual	16,000bp	132,611	320Mb/not known	86.6%	17.776	Not estimated – assembly too fragmented

Table 1: Quality, completeness and heterozygosity of ostracod genomes (Tran Van et al. 2021).

N50 = sequence length of the shortest contig at 50% of the total genome length. bp = basepairs. Mb = megabases – 1 million bp. BUSCO = Benchmarking Universal Single-Copy Orthologs = nr of ortholog single copy genes

Conclusions

- Quality (N50 & nr of scaffolds) similar to other crustacean genomes with Illumina (Table 1)
- Genome of *C. torosa* most fragmented (N50, nr of scaffolds) & least complete (BUSCO score)(Table 1)
- Similar nr of predicted genes as in other crustacean genomes (Tran Van et al. 2021)
- Heterozygosity of D.s. < in polyploids (1.8-33%) or hybrids (1.5-8.7%), > diploid asexuals (0.03-0.83%) => *D. stevensoni* is most likely a diploid asexual and not of hybrid origin
- Diverse, abundant (19-26%) and still active transposable elements (TEs) in the genome of *D. stevensoni* (Figure 3) <=> different to TEs of other asexuals (e.g. *Daphnia*) & putative ancient asexuals (rotifers, mites)

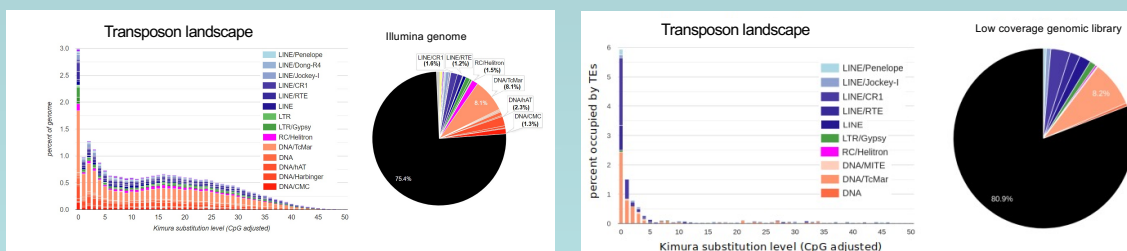


Figure 3: Occupancy of transposable elements (TEs) (pie chart), TE diversity (different colours) and activity (substitution plot) in the genome of *D. stevensoni*. From Schön et al. (2021).

A Kimura substitution level of 0 indicates recent transposon activity.

References
 Schön I., Rodriguez F., Dunn M., Martens K., Shribak M. & Arkhipova I.R. 2021. A survey of transposon landscapes in the putative ancient asexual ostracod *Darwinula stevensoni*. *Genes* 12, 403.
 Tran Van P., Anselmetti Y., Bast J., Dumas Z., Galtier N., Jaron K., Martens K., Parker D., Robinson-Rechavi M., Schwander T., Simon P. & Schön I. 2021. First annotated genomes of draft genomes of three non-marine ostracods (Ostracoda, Crustacea) with different reproductive modes. *Genes, Genomes, Genetics* 11, jkab043.