

# Call attention to The Black rockfish genome



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# The Outline

- General information
- Genome paper
- General genome information
- Sequencing strategy
- Sequencing methods & assembly
- Genome assembly outcome
- Genome outcome
- Interspersed repeats of *S. schlegelii*

# General information

- Black rockfish are important viviparous marine teleost.
  - Japan, Korea, and China.



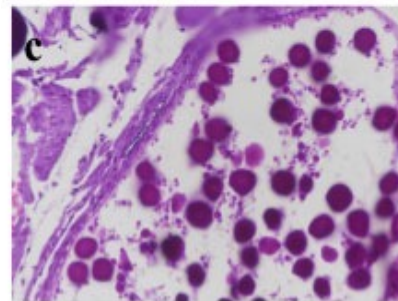
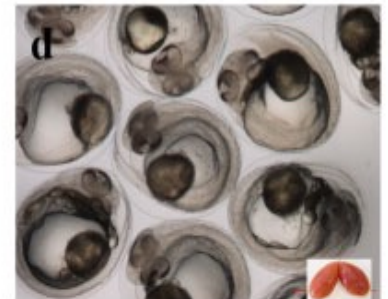
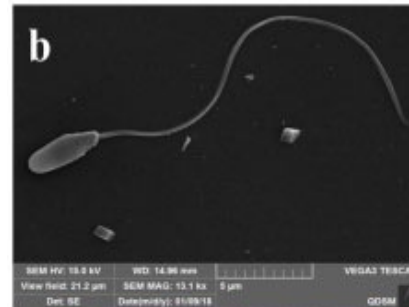
# General information

- Reaches 5 kg and maximum length of 69 cm.
- Females reach larger sizes than males.



# General information

- Breed via internal fertilization
  - Long-term storage of sperm in female ovary
  - Fertilization and embryo hatching occur internally.



# Genome paper

*DNA Research*, 2019, 26(6), 453–464

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Advance Access Publication Date: 23 November 2019

Full Paper

The logo for Oxford University Press, consisting of the word "OXFORD" in a serif font inside a dark grey square.

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Full Paper

## Sequencing of the black rockfish chromosomal genome provides insight into sperm storage in the female ovary

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# General genome information

Number of Chromosomes:	24 chromosomes
Genome Size:	848.31 Mb
# of protein-coding genes:	26,979
Sequencing Strategies:	Whole genome shotgun (WGS)
Sequencing Methods:	PacBio, Illumina, 10x Genomics, and Hi-C
Genome Coverage (X)	101X
Contig N50:	2.92 Mb
Scaffold N50:	35.63 Mb
Assembly Software:	<i>de novo</i>

# Sequencing strategy

- Collect male Black Rockfish (2 years).
- Fresh muscle samples were obtained.
- Genomic DNA was obtained and assessed.
- The *S. schlegelii* fish was shotguned by WGS.



# Sequencing methods

- Multiple genome methods were done and compared:
- PacBio sequencing, then assembled by FALCON assembler.
- 10x Genomics technology, then assembled by fragScaff
- Hi-C technology, library was prepared to enhance a chromosomal level assembly with Lachesis software.
- Illumina sequencing method, short-reads were mapped to the chromosomal-level genome assembly by Pilon software.

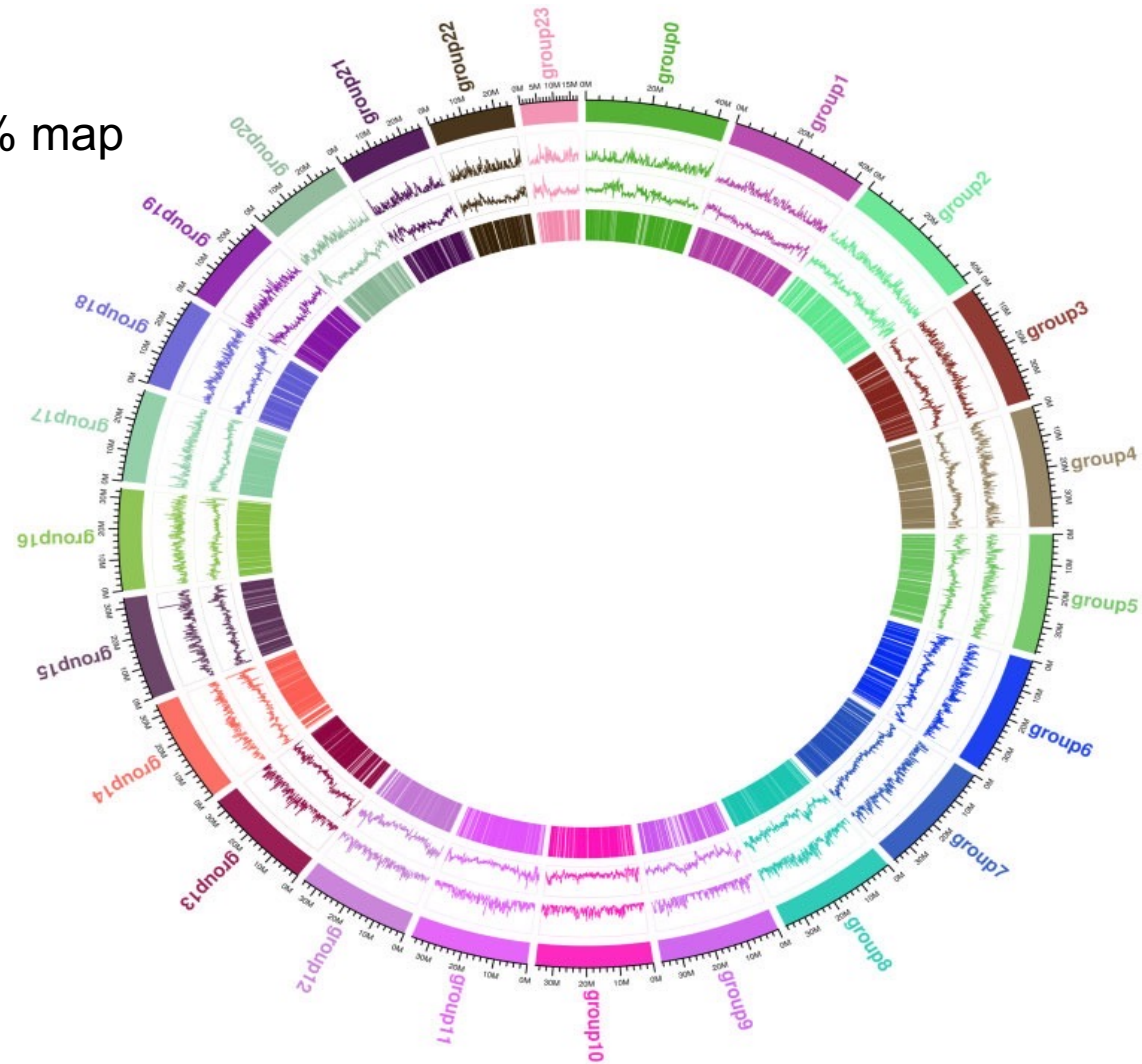
# Genome assembly



- They were *de novo* assembled.
- 2.96 Mb N50 contigs.
- 35.63 Mb N50 scaffold.
- 26,979 protein-coding genes were functionally annotated.
- 0.00038% SNP.

# Genome outcome

- A total of 97.93% of the short sequence reads covered 99.61% map of the genome assembly map.



# Structural and Functional annotation

- Were conducted using *de novo*, homolog-base, and RNA-seq methods.
- Compared the structural characters with the genome of closely related species.

# Interspersed repeats of *S. schlegelii*

- The DNA transposable elements were 18.06% more than in humans (3.2%), but less than in zebrafish (39%).
- The retrotransposable elements (17.93%) were more than in zebrafish (11%), and less than in humans (44%).



# Questions

- Where there any researches regard the viviparous type?
- Why we generate multiple genome assemblies in this paper?

