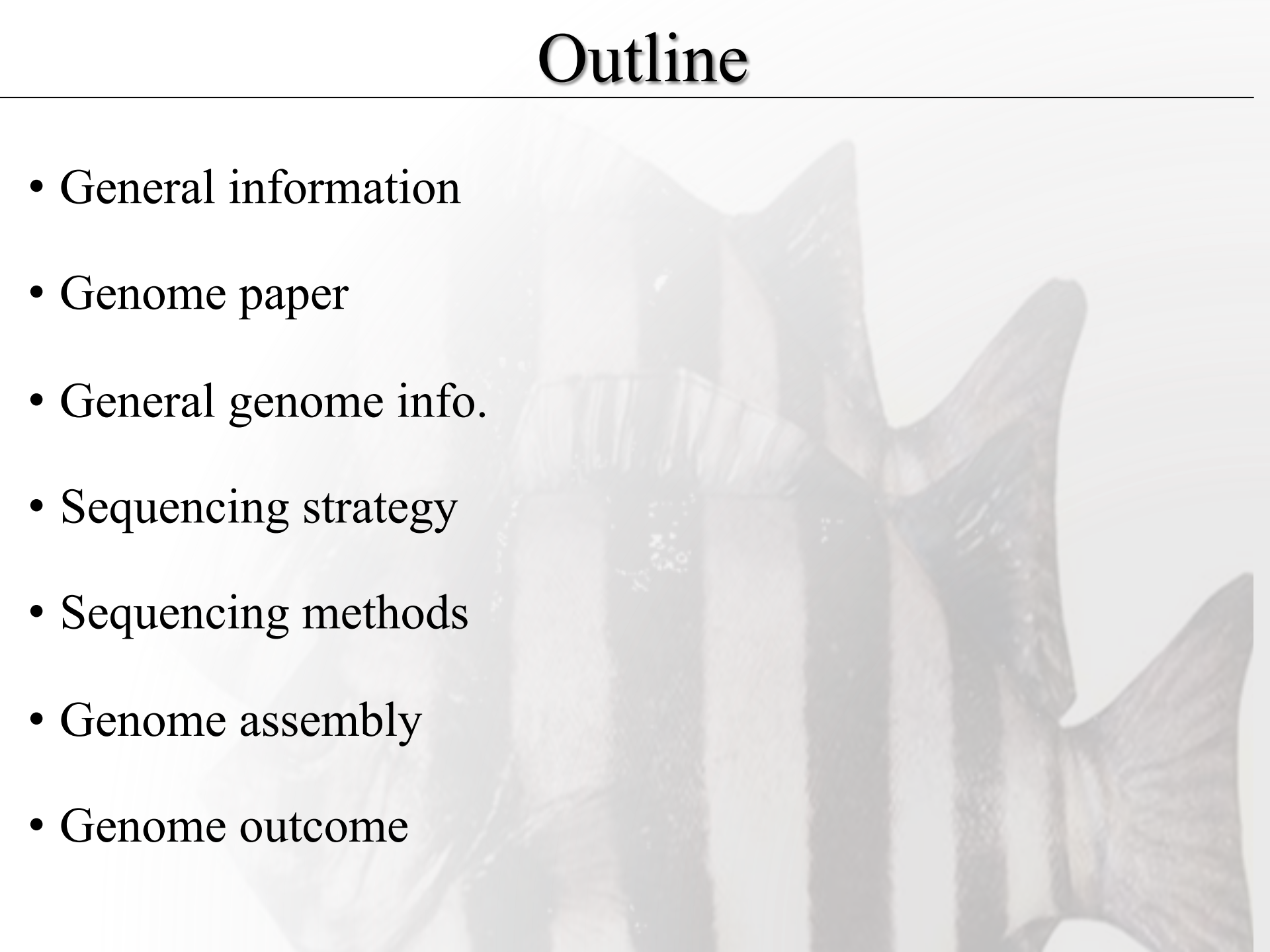


The genome of Barred Knifejaw



- **By: Amina Alenzi**
- Introduction To Genomics 485
- Fall 2021

Outline

- General information
 - Genome paper
 - General genome info.
 - Sequencing strategy
 - Sequencing methods
 - Genome assembly
 - Genome outcome
- 

General Information

- The striped beakfish (*Oplegnathus fasciatus*), also known as the barred knifejaw
- From family Opleganthidae



General Information

- Strong teeth
- Length : 80.0 cm
- maximal recorded weight is 6.5 kg



General Information

- It is native to the northwestern Pacific Ocean



- Hawaii, Korea and Japan

Genome Paper

Journal



(GIGA)ⁿ
SCIENCE

Year published

GigaScience, 8, 2019, 1–8

doi: 10.1093/gigascience/giz013




Advance Access Publication Date: 1 February 2019

Data Note

DATA NOTE

Common name Scientific name

Genome sequence of the barred knifejaw *Oplegnathus fasciatus* (Temminck & Schlegel, 1844): the first chromosome-level draft genome in the family Oplegnathidae

authors Yongshuang Xiao ^{1,2,3,†}, Zhizhong Xiao ^{1,2,3,†}, Daoyuan Ma ^{1,2,3},
Jing Liu^{1,2,3,*} and Jun Li^{1,2,3,*}

¹Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao, 266071, China, ²Laboratory for Marine Biology and Biotechnology, Qingdao National Laboratory for Marine Science and Technology, 7 Nanhai Road, Qingdao, 266071, China and ³Center for Ocean Mega-Science, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao, 266071, China

*Correspondence address. Jing Liu, Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao, 266071, China. Tel: +86-053282898790; E-mail: jliu@qdio.ac.cn; Jun Li, Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao, 266071, China. Tel: +86-053282898718; E-mail: junli@qdio.ac.cn

[†]Contributed equally to this work. † Senior author.

General Genome Information

Genome size 245.0 Gb

Gene number 24,003 genes

Number of chromosome 24 chromosomes

Sequencing method PacBio & Illumina

Sequencing strategy

Contig N50 2.1 Mb

Scaffold N50 33.5 Mb

Sequencing Strategy

- The source of genome is from muscle tissue and blood samples from a single female *O. fasciatus*.

Sequencing Method

- Pacific Bioscience (PacBio) Sequencing:
- Illumina:

Genome Assembly

| The first chromosome-level draft genome of *Oplegnathus fasciatus*

Figure 1: Summary of *Oplegnathus fasciatus* genome assembly and annotation

	Genome assembly	
	Draft scaffolds	Chromosome-length scaffolds based on Hi-C
Length of genome (bp)	778,731,089	768,808,243
Number of contigs	1,692	1,372
Contigs N50 (bp)	2,149,025	2,130,780
Number of scaffolds	/	24
Scaffold N50 (bp)	/	33,548,962
Genome coverage (X)		314.6
Number of contigs (≥ 100 kb)	693	708
Total length of contigs (≥ 100 kb)	735,235,962	732,827,446
Mapping rate of contigs (≥ 100 kb)(%)	/	99.67
	Genome annotation	
Protein-coding gene number		24,003
Mean transcript length (kb)		16.1
Mean exons per gene		10.1
Mean exon length (bp)		217.7
Mean intron length (bp)		1,527.4

Genome Outcome
