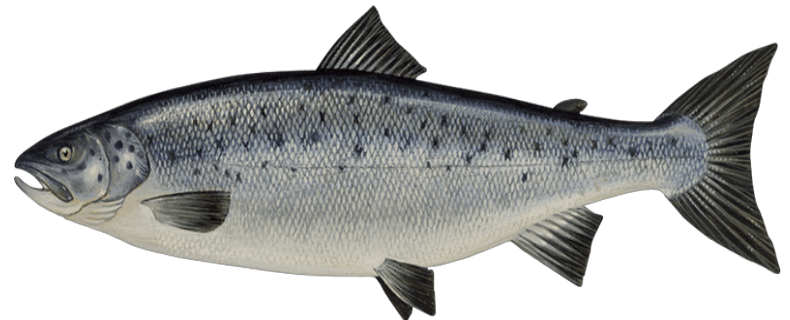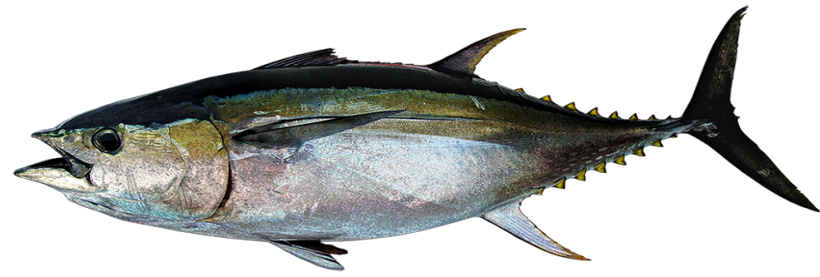# A journey of Edibles fish
(Sardine -Salmon- Tuna- Trout)

Presented by: Haya Adel, Shouq Alazmi, Noor Alotaibi, Haneen Badran

Introduction to Genomics 485
Fall 2019

Outline

- Facts about the species.

- Sequencing strategy

- Sequencing method

- Assembly

- Annotation

- Interesting genomic fact

- Questions

ARTICLE

The Atlantic salmon genome provides insights into rediploidization

Sigbjørn Lien[1], Ben F. Koop[2], Simen R. Sandve[1], Jason R. Miller[3], Matthew P. Kent[1], Torfinn Nome[1], Torgeir R. Hvidsten[4,5], Jong S. Leong[2], David R. Minkley[2], Aleksey Zimin[6], Fabian Grammes[1], Harald Grove[1], Arne Gjuvsland[1], Brian Walenz[3], Russell A. Hermansen[7,8,9], Kris von Schalburg[2], Eric B. Rondeau[3], Alex Di Genova[10,11], Jeevan K. A. Samy[1], Jon Olav Vik[1], Magnus D. Vigeland[12], Lis Caler[3], Unni Grimholt[13], Sissel Jentoft[14], Dag Inge Våge[1], Pieter de Jong[15], Thomas Moen[16], Matthew Baranski[17], Yniv Palti[18], Douglas R. Smith[19,20], James R. Yorke[6], Alexander J. Nederbragt[14], Ave Tooming-Klunderu[?], Kjetill S. Jakobsen[14], Xuanting Jiang[21], Dingding Fan[21], Yan Hu[21], David A. Liberles[8,9], Rodrigo Vidal[22], Patricia Iturra[23], Steven J. M. Jones[24,25], Inge Jonassen[26], Alejandro Maass[10,11], Stig W. Omholt[27] & William S. Davidson[25]
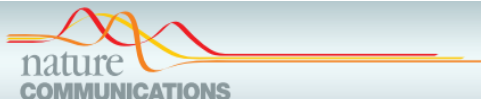
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nature COMMUNICATIONS

The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates

Camille Berthelot[1,2,3,4,5], Frédéric Brunet[6,*], Domitille Chalopin[6,*], Amélie Juanchich[7,*], Maria Bernard[4,8], Benjamin Noël[4], Pascal Bento[4], Corinne Da Silva[4], Karine Labadie[4], Adriana Alberti[4], Jean-Marc Aury[4], Alexandra Louis[1,2,3], Patrice Dehais[9], Philippe Bardou[9], Jérôme Montfort[7], Christophe Klopp[9], Cédric Cabau[9], Christine Gaspin[10,11], Gary H. Thorgaard[12], Mekki Boussaha[8], Edwige Quillet[8], René Guyomard[8], Delphine Galiana[6], Julien Bobe[7], Jean-Nicolas Volff[6], Carine Genêt[8], Patrick Wincker[4,13,14], Olivier Jaillon[4,13,14], Hugues Roest Crollius[1,2,3] & Yann Guiguen[7]

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genes MDPI

"Out of the Can": A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, *Sardina pilchardus*

André M. Machado [1,†], Ole K. Tørresen [2,†], Naoki Kabeya [3,†], Alvarina Couto [1,4], Bent Petersen [5,6], Mónica Felício [7], Paula F. Campos [1,4], Elza Fonseca [1,8], Narcisa Bandarra [7], Mónica Lopes-Marques [1], Renato Ferraz [1,9], Raquel Ruivo [1], Miguel M. Fonseca [1], Sissel Jentoft [2,10], Óscar Monroig [11,*], Rute R. da Fonseca [4,12,*] and L. Filipe C. Castro [1,8,*]

# Evolutionary changes of multiple visual pigment genes in the complete genome of Pacific bluefin tuna

Yoji Nakamura[a,1], Kazuki Mori[b], Kenji Saitoh[a], Kenshiro Oshima[c], Miyuki Mekuchi[a], Takuma Sugaya[a], Yuya Shigenobu[a], Nobuhiko Ojima[a], Shigeru Muta[b], Atushi Fujiwara[a], Motoshige Yasuike[a], Ichiro Oohara[a], Hideki Hirakawa[d], Vishwajit Sur Chowdhury[e], Takanori Kobayashi[a], Kazuhiro Nakajima[f], Motohiko Sano[a,2], Tokio Wada[f], Kosuke Tashiro[b], Kazuo Ikeo[g,h], Masahira Hattori[c], Satoru Kuhara[b], Takashi Gojobori[g,h,1], and Kiyoshi Inouye[f]

[a]Research Center for Aquatic Genomics, National Research Institute of Fisheries Science, Fisheries Research Agency, Kanazawa, Yokohama 236-8648, Japan; [b]Department of Bioscience and Biotechnology, Faculty of Agriculture, Kyushu University, Higashi-ku, Fukuoka 812-8581, Japan; [c]Department of Computational Biology, Graduate School of Frontier Sciences, University of Tokyo, Kashiwa 277-8561, Japan; [d]Department of Plant Genome Research, Kazusa DNA Research Institute, Kisarazu 292-0818, Japan; [e]Division for Arts and Science, Faculty of Arts and Science, Kyushu University, Nishi-ku Fukuoka 819-0395, Japan; [f]Fisheries Research Agency, Nishi, Yokohama 220-6115, Japan; [g]Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics, Mishima 411-8540, Japan; and [h]Department of Genetics, School of Life Science, The Graduate University of Advanced Studies (SOKENDAI), Shonan Village, Hayama, Kanagawa 240-0193, Japan

Common name: The pacific Bluefin tuna
scientific name: *thunnus orientals*
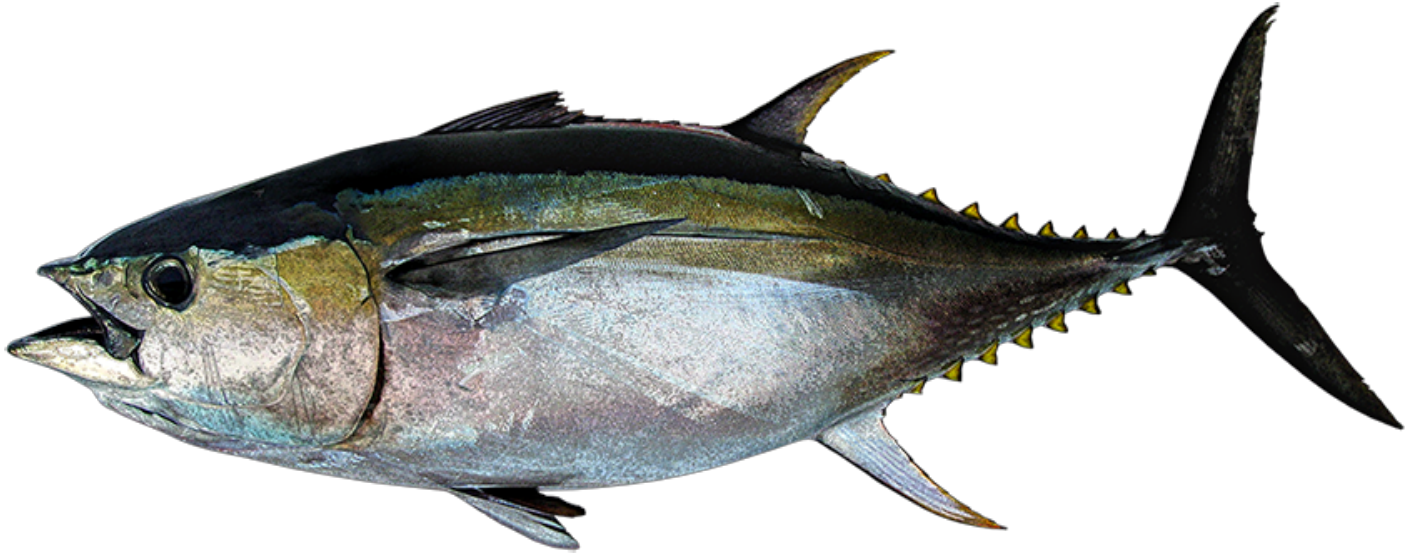
Fact:

❖ Tuna are large fish and they are nomadic, which means that they do not spend their entire life on a single place. They often change their location.

❖ They are "ultimate fish" because they are top predators in ocean ecosystem.

❖ Colour of the body provides excellent camouflage in the water.
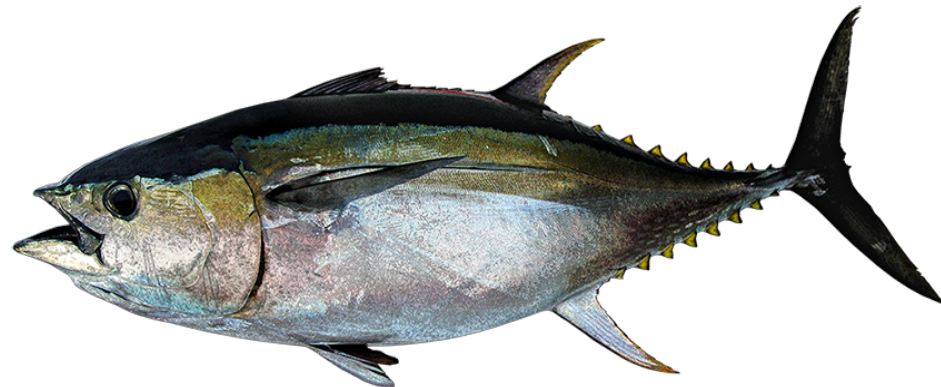
❖**Sequence strategy:** WGS
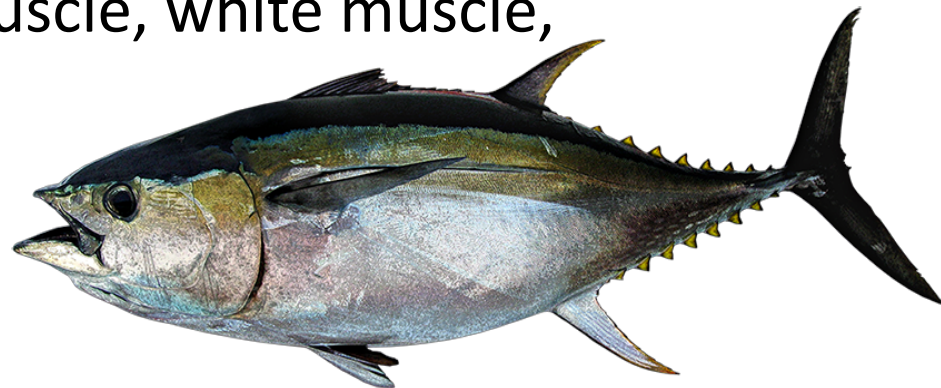
❖**Sequencing method**: Illumina

❖**Specimen sequenced:** DNA from reared male(diploid genome)

❖ **Specimen for cDNA analysis :** from reared female

❖ (Total RNAs were isolated from fin, gill, heart, intestine, kidney, liver, red muscle, white muscle, pyloric caeca, and stomach)

Assembly sequencing: diploid genome

❖ **Genome size**: ~800Mb

❖ **Number of contigs:**192,169

❖ **N50 contigs** :7,588bp

❖ **Number of scaffolds**:16,802

❖ **Scaffold N50**: 136,950bp

❖ **Genome coverage:** 11.9x**,** 43X

❖ **Assembly strategy:** roche 454 FLX titanium ,
 illumine GaIIx platforms

Assembly: cDNA sequencing

❖**Number of contigs**:180,512

❖**N50 contigs**:836bp

Interesting genomic fact:

❖The pacific Bluefin tuna genome possessed 10 visual pigment genes

Common name: sardine
Scientific name: *sardine pilchardus*

Fact about species: sardine

❖ Sardines are small ,silvery, elongated fishes with a single short dorsal fin.

❖ Sardine is also known as the European pilchard because is one of the most commercially important species.

❖ Sardine live in Atlantic Ocean.

1. **Source for sequencing** :
- ❖ DNA from muscle
- ❖ RNA from liver

2. Seq. strategy:
- ❖ Whole genome shutgan

3. **Sequencing methods**:
- ❖ Illumina

Assembly:

❖ Sequencing reads is 412,914,751bp

❖ Genome size:850Mb

❖ Number of contigs: 90,290

❖ Contig size: 640Mb

❖ N50 size: 10,878bp

❖ GC%: 44.45%

❖ Number of scaffolds: 45,321

❖ Scaffold N50: 25,577bp

❖ Genome coverage: 59x

5. annotation:
- ❖ By use two pass iterative MAKER pipeline
- ❖ Genes contained: 29,701
- ❖ Coding genes: 23,336

Interesting fact:
- ❖ Sardine is one of the oily fish species represent unique sources of the healthy omega-3-long chain polyunsaturated fatty acids.

Common Name: Rainbow Trout
Scientific Name: *Oncorhynchus Mykiss*

Facts about Rainbow Trout

❖ Rainbow Trout (*Oncorhynchus mykiss*) is a member of the salmonid family that is of a major ecological interest worldwide.

❖ It is one of the most studied fish species and is extensively used for research in many fields such as carcinogenesis, toxicology, immunology, ecology, physiology and nutrition.

❖ Rainbow trout get their name from the beautiful colors that shine on their skin. Coloration of the rainbow trout varies widely in relation to sex, habitat, and maturity.

❖ Rainbow trout are predators, and will eat almost anything that they can catch, including insects, small fish, and crustaceans. They will also eat fish eggs, including the eggs of other rainbow trout, and will scavenge on leftover carcasses as well.

❖ The rainbow trout has been introduced to every continent except Antarctica.

❖ The average lifespan for a rainbow trout is 4 to 6 years in the wild.

❖**Source of DNA:** Genomic DNA was extracted from fin clips from a single homozygous doubled haploid YY male from the Swanson River (Alaska)

❖**Sequencing Strategy:** Public Sanger BAC-end sequences (BES).

❖**Sequencing Methods:** Sanger, Illumina, Roche 454

Assembly:

❖ Genome size: 2.4 Gb

❖ N50 contig: 7.7 Kb

❖ Number of contigs: 445, 600

❖ N50 scaffold: 383.6 Kb

❖ Number of scaffolds: 79,941

❖ Genome coverage: 70 fold

❖ Method: Public Sanger BAC-end sequences (BES) and Roche 454 reads were assembled with Newbler.

Annotation:

❖ Number of genes: 55,735

❖ Number of coding genes: 46,585

❖ Low complexity sequences using DUST
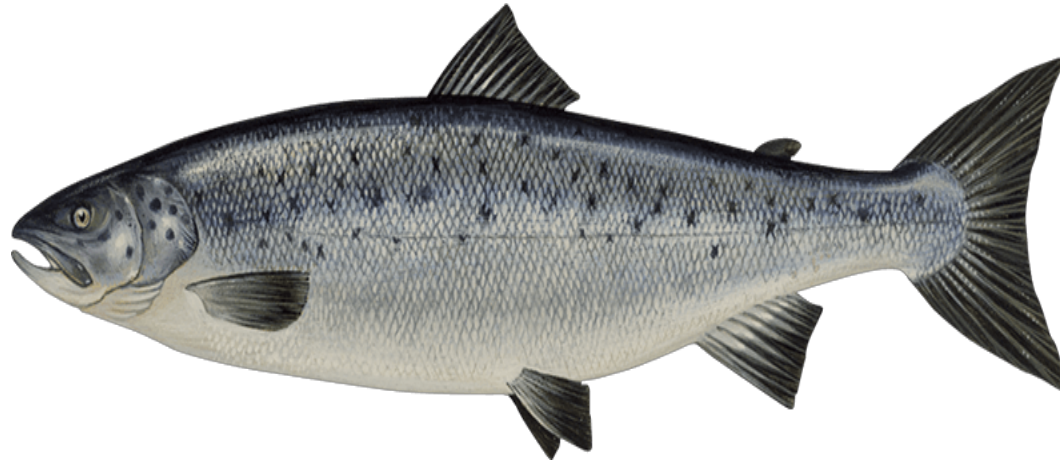
❖ Tandem repeats using Tandem Repeat Finder

Interesting Genomic Facts

❖The Rainbow Trout genome sequence provides for the very first time in any vertebrate a unique opportunity to build a possible scenario in the early steps of gene fractionation occurring after a WGD event.

Common Name: Atlantic Salmon
**Scientific Name:** *Salmo Salar*

- **Facts about the species**:

❖ Atlantic Salmon found near River in France, North American, European and Baltic water.

❖ It belongs to salmonid lineage which comprises to 11 genera, with at least 70 species.

❖ It has a 29 chromosome.

❖ They are carnivorous, which means they eat other animals such as sand eels.

❖ Size: Adults are usually 70 to 76 cm in length. They weigh 4-5 kg. But the heaviest recorded Atlantic Salmon was around 45 kg.
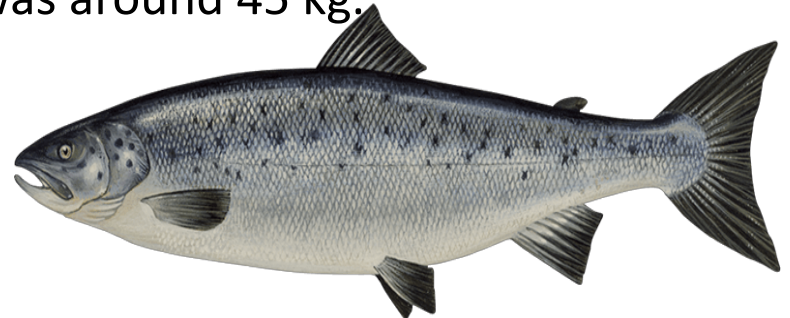
Life cycle of Atlantic Salmon
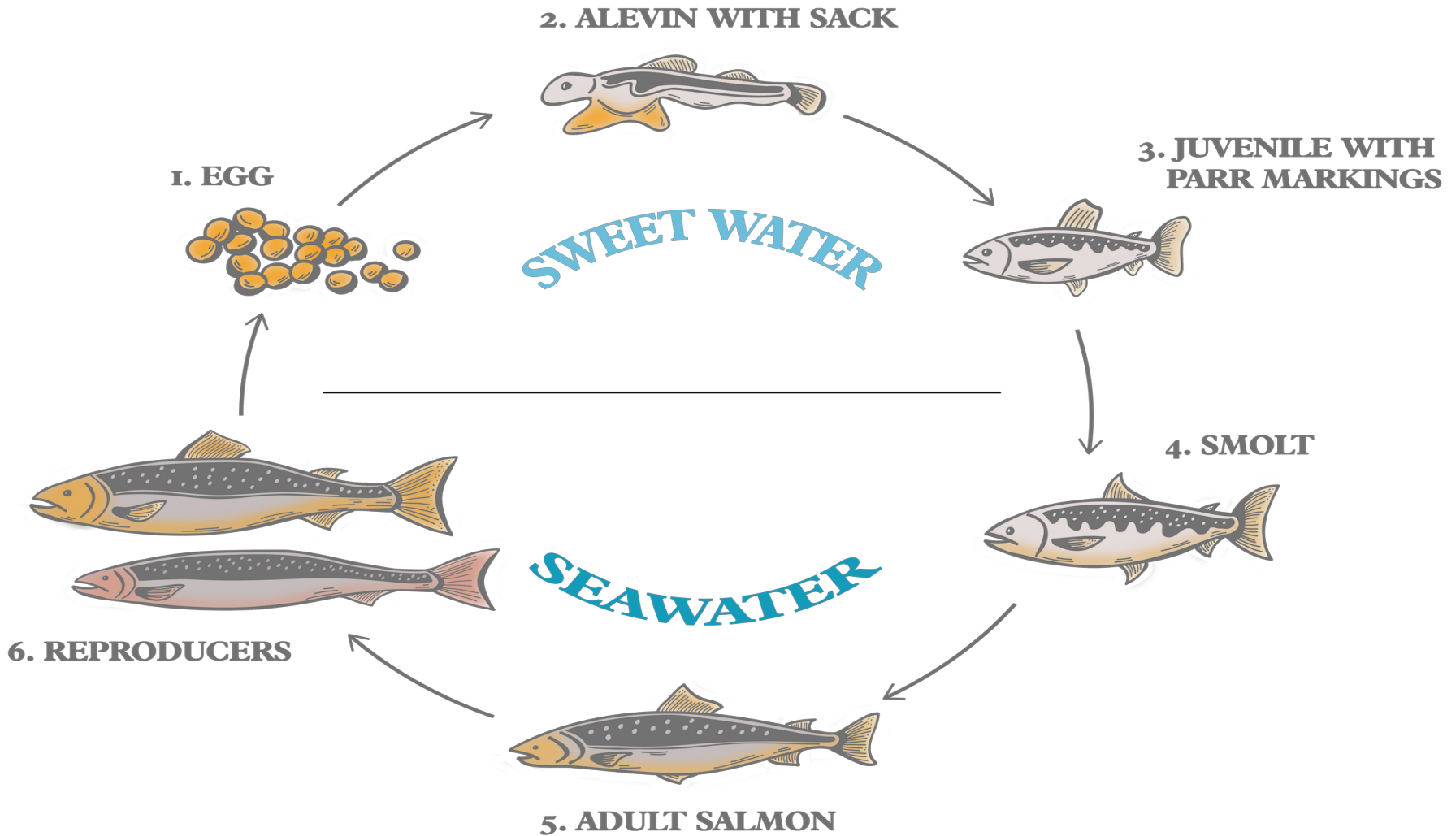
Sequence Strategy

❖ **Specimen:**
DNA from single double-haploid female from AquaGen strain.

❖ Method strategy:
Whole-Shut gun sequence (WGS).

❖ Genome size = 2.97 Gb
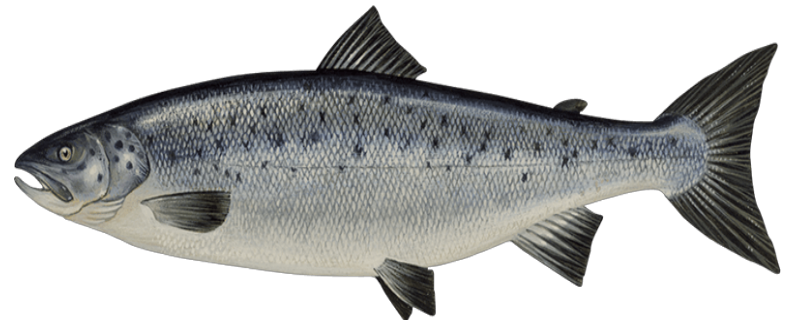❖ # of coding gene = 55,620

❖ Sequence method: Sanger (4x) and Illumine (202x)
NGS technique.

❖ Annotation was done with Blast2GO
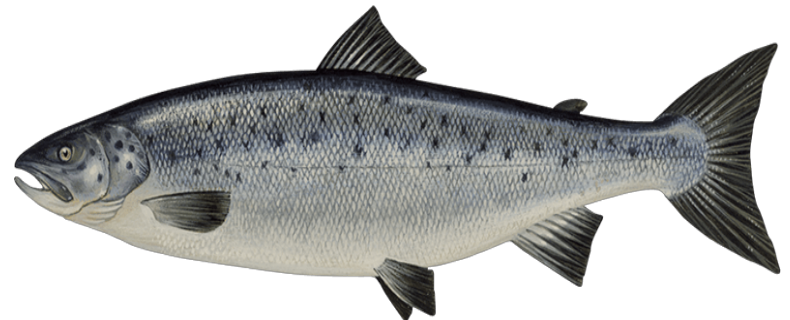Contig N50 = 57.6 kb
Scaffold N50 = 2.97 Mb
# of scaffold = 9,447

Interesting genomic fact

Migration.

❖ when salmon start migration back to spawn, they don't eat. But they live by their body fat.

❖ The maximum age are 14 years old.

❖ They live in both freshwater and sea water.

Comparison of Genome Assembly

Name of organisms	# of chromosomes	Genome size	# of contig	# of scaffold	N50 contig	N50 scaffold	Sequence method
Bluefin tuna	-	~ 800 Mb	192,169 180,512	16,802	7,588 bp 836bp	136,950 bp	Illumine
sardine	-	850 Mb	90,290	45,321	10,878 bp	25,577 bp	Illumine
Rainbow Trout	30	2.4 Gb	445,600	79,941	7.7 Kb	383.6 Kb	Sanger Illumina Roche
Atlantic Salmon	29	2.97 Gb	-	9,447	57.6 kb	2.97 Mb	Sanger, Illumine, NGS

Questions:

1 – How many chromosomes in Atlantic Salmon?

      29 chromosomes.

2 – how many visual pigment genes that the pacific bluefin tuna possessed?

      10 genes.

3- Which sequencing methods Do Not use primers?

      Nanopore, Maxam and Gilbert.

4. What do you think is healthier tuna or sardine?

Sardine

1. More vitamin E
2. More calcium

Thank you