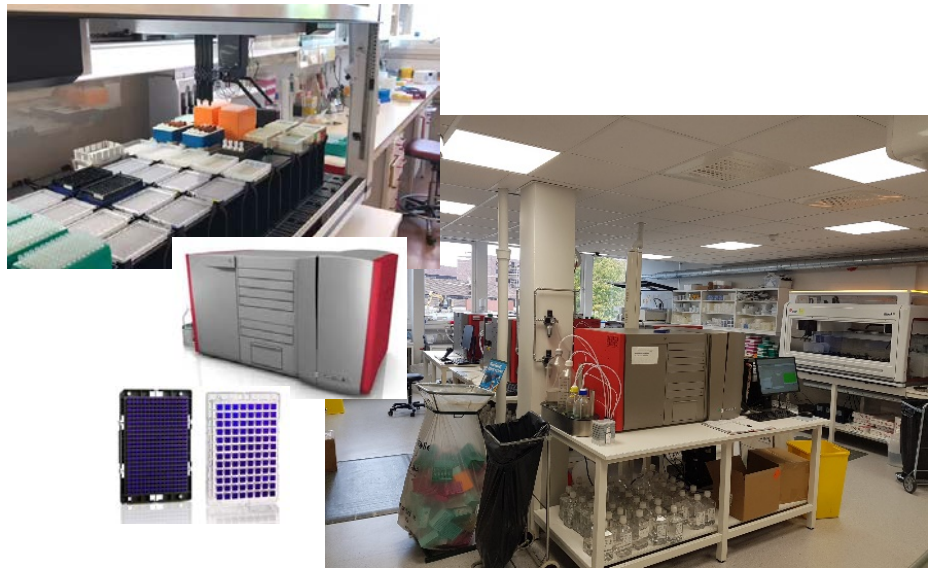
CIGENE lab

- ✓ Established 2003 as a FUGE platform
- ✓ High througput SNP-genotyping facility



Well equipped genomics lab:

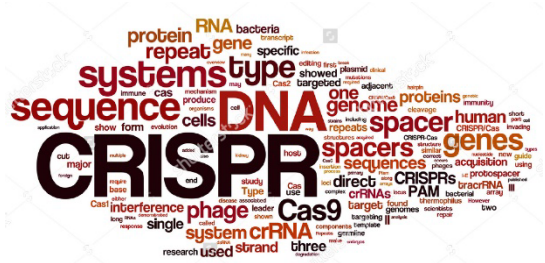
- ✓ Sequencing
- ✓ Functional genomics assays
- ✓ Gene editing (CRISPR)
- ✓ Cell lab

CIGENE
Centre for Integrative Genetics

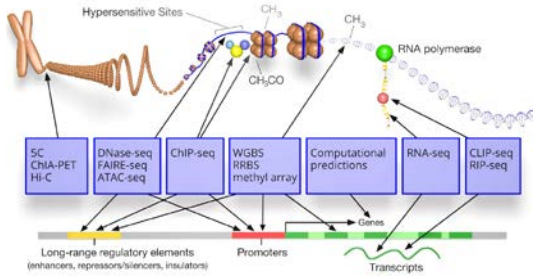
Genome biology, IHA, BIOVIT

Muliggjørende verktøy og teknologier

‘Long-read’ sekvensering



Funksjonell annotering for å forstå genomfunkjon



DIGITAL SALMON

CIGENE lab

- Lønn til labpersonell og andre personer tilknyttet labdrift
- Oppgradering av utstyr:
  - 2017 -> 8,1 mill.
  - 2018 -> 3,8 mill.
  - 2019 -> 1,1 mill.
- Servicekontrakter (3 mill. pr. år)
- Investering i nye teknologier og metoder

- Genomsekvensering
- Funksjonell annotering
- Bioinformatikk
- Geneditering (CRISPR)

ORION
Computer cluster

CIGENE
Centre for Integrative Genetics

Faggruppe genombiologi,
IHA, BIOVIT

2018

- Oppgradering av CIGENE lab
- 2 mill. kr

Budsjett 2019

Oppdragsaktivitet

Genotyping	Prøver	Omsetning	Consumables	Inntekt
Aviagen, AquaGen	450 000	22 500 000	6 300 000	16 200 000
Agena Genotyping	6 500	236 979	148 958	88 021
SUM			**6 448 958**	**16 288 021**

Personale

Ansatte	Stillinger	Lønn	Andel	Lønnsutgifter
CIGENE, labstab	7,85	692 114		-5 433 097
Forskere				
Sum lønn				**-7 469 476**

Driftskostnader

Servicekontrakt				-3 000 000
Diverse utviklingskostn. lab.				-1 000 000
Lab fee				-300 000
Kompetanseheving CIGENE labstab				-100 000

Nytt utstyr

Nytt utstyr				
Beckman i5 S8 pipetteringsrobot				-875 000
Binder kjøleinkubator				-70 000
Mikrosentrifuger og vortex ny lab				-35 000
Pipetter til ny lab				-55 000
Stoler til ny lab				-80 000
Sum utstyr				**-1 115 000**

NFR-prosjekter

Lønn fra REWIRED				214 575
FILOPAT	2 000	250 000	28 000	222 000
QE2	3 000	375 000	42 000	333 000
EcoEvoGene	2 000	250 000	28 000	222 000
Primmer	1 500	187 500	21 000	166 500
Nanopore sequencing				60 000
Markørpanel for Arktisk røye				400 000
Andre prosjekt inntekter				500 000
SUM				**2 118 075**
TOTAL				**5 421 620**

Prof., ass.prof., prof. II


Sigbjørn Lien


Dag Inge Våge


Simen Sandve


Guro Sandvik


Jon Olav Vik
25%


Øivind Andersen
20%

Adm.


Lise Fjellsbø

CIGENE
Centre for Integrative Genetics
Genome biology

Researchers


Matthew Kent


Nicola Barson


Torfinn Nome


Yang Jin


Amine Namouchi


Hien To


Sahar Hassani


Marie Gulla


Filip Rotnes


Gareth Gillard


Jørn Henrik Sønstebø

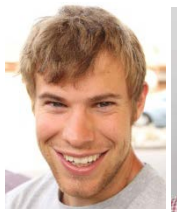

Victor Boyartchuk


Fabian Grammes
33%

Postdocs


Lars Grønvold


Marie-Odile Baudement


Michel Moser


Thomas Harvey


Olga Paulouskaya


Tomasz Podgorniak

PhD-students


Tina G. Kirubakaran


Mathilde Holen


Line Røsæg


Øystein Monsen


Live Rud-Johansen


Darshan Young


Kristina Stenløkk


Noman Reza

Technicians


Kristil Sundaasen


Silje Karoliussen


Mariann Arnyasi


Therese Andersstuen


Tan Thi Nguyen


Øystein Milvang

Kristin Udjus

Nina Falk Peterson

\+

- 3 technicians
- 2 Phd
- 5 postdocs

> 50 people

Prof., ass.prof., prof. II


Sigbjørn Lien


Dag Inge Våge


Simen Sandve


Guro Sandvik


Jon Olav Vik
25%


Øivind Andersen
20%

Adm.


Lise Fjellsbø

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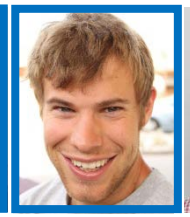
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Therese Andersstuen


Tan Thi Nguyen


Øystein Milvang

Kristin Udjus

Nina Falk Peterson

\+

- 3 technicians
- 2 Phd
- 5 postdocs

> 50 people

Ny master i «Genome Science» (genomvitenskap)

- Rekruttere studenter fra bachelorstudiene i biologi, bioteknologi, plante-, husdyr- og 'havbruk'/akvakultur, samt studenter fra andre læresteder
- Opptak med krav om «grunnpakke» av relevante kurs innen genetikk/genomikk, matematikk/statistikk/informatikk, biokjemi/molekylærbiologi/bioteknologi...
- Bred innretning mot bioinformatikk, funksjonell genomikk, genombasert avl, epigenetikk, genomevolusjon, ernæringsgenomikk, mikrobiota, mikroorganismer, patogener, ...
- BIOVIT: Genombiologi, Avl og kvantitativ genetikk, Genetikk og planteforedling, Plantebiologi og bioteknologi. KBM: Biostatistikk, bioinformatikk, mikrobiota/mikrobiell genomikk. REALTEK: Data Science. VET: Sykdomsgenetikk, patogener, diagnostikk?
- Introduksjonskurs som kombinerer data-generering (lab) med data-analyse
- **Labkurs i funksjonell genomikk/genredigering/sekvensering**
- Nye kurs med appell for studenter også på andre studieretninger

World leading on salmonid genomics

ARTICLE

OPEN

doi:10.1038/nature17164

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 A. Yorke[6], Alexander J. Nederbragt[14], Ave Tooming-Klunderud[14], 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]

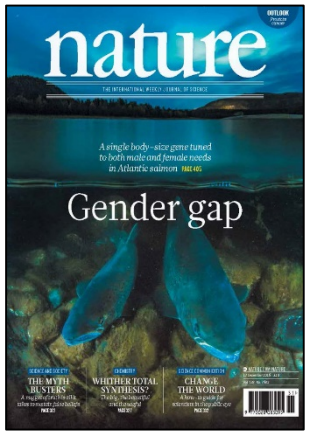
The whole-genome duplication 80 million years ago of the common ancestor of salmonids (salmonid-specific fourth vertebrate whole-genome duplication, Ss4R) provides unique opportunities to learn about the evolutionary fate of a duplicated vertebrate genome in 70 extant lineages. Here we present a high-quality genome assembly for Atlantic salmon (*Salmo salar*), and show that large genomic reorganizations, coinciding with bursts of transposon-mediated repeat expansions, were crucial for the post-Ss4R rediploidization process. Comparisons of duplicate gene expression patterns across a wide range of tissues with orthologous genes from a pre-Ss4R outgroup unexpectedly demonstrate far more instances of neofunctionalization than subfunctionalization. Surprisingly, we find that genes that were retained as duplicates after the teleost-specific whole-genome duplication 320 million years ago were not more likely to be retained after the Ss4R, and that the duplicate retention was not influenced to a great extent by the nature of the predicted protein interactions of the gene products. Finally, we demonstrate that the Atlantic salmon assembly can serve as a reference sequence for the study of other salmonids for a range of purposes.

LETTER

doi:10.1038/nature16062

Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon

Nicola J. Barson[1*], Tutku Aykanat[2*], Kjetil Hindar[3], Matthew Baranski[4], Geir H. Bolstad[3], Peder Fiske[3], Céleste Jacq[4], Arne J. Jensen[3], Susan E. Johnston[5], Sten Karlsson[3], Matthew Kent[1], Thomas Moen[6], Eero Niemelä[7], Torfinn Nome[1], Tor F. Næsje[3], Panu Orell[7], Atso Romakkaniemi[7], Harald Sægrov[8], Kurt Urdal[8], Jaakko Erkinaro[7], Sigbjørn Lien[1] & Craig R. Primmer[2]



New Results

Comment on this paper

Title: Sex-dependent dominance maintains migration supergene in rainbow trout

Devon E. Pearse, Nicola J. Barson, Torfinn Nome, Guangtu Gao, Matthew A. Campbell, Alicia Abadía-Cardoso, Eric C. Anderson, David E. Rundio, Thomas H. Williams, Kerry A. Naish, Thomas Moen, Sixin Liu, Matthew Kent, David R. Minkley, Eric B. Rondeau, Marine S. O. Brieuc, Simen Rød Sandve, Michael R. Miller, Lucydalila Cedillo, Kobi Baruch, Alvaro G. Hernandez, Gil Ben-Zvi, Doron Shem-Tov, Omer Barad, Kirill Kuzishchin, John Carlos Garza, Steven T. Lindley, Ben F. Koop, Gary H. Thorgaard, Yniv Palti, Sigbjørn Lien

doi: https://doi.org/10.1101/504621

This article is a preprint and has not been peer-reviewed [what does this mean?].

Abstract | Full Text | Info/History | Metrics | Preview PDF

Abstract

Traits with different fitness optima in males and females cause sexual conflict when they have a shared genetic basis. Heteromorphic sex chromosomes can resolve this conflict and protect sexually antagonistic polymorphisms but accumulate deleterious mutations. However, many taxa lack differentiated sex chromosomes, and how sexual conflict is resolved in these species is largely unknown. Here we present a chromosome-anchored genome assembly for rainbow trout (*Oncorhynchus mykiss*) and characterize a 56 Mb double-inversion supergene that mediates sex-specific migration through sex-dependent dominance, a mechanism that reduces sexual conflict. The double-inversion contains key photosensory, circadian rhythm, adiposity, and sexual differentiation genes and displays frequency clines associated with latitude and temperature, revealing environmental dependence. Our results constitute the first example of sex-dependent dominance across a large autosomal supergene, a novel mechanism for sexual conflict resolution capable of protecting polygenic sexually antagonistic variation while avoiding the homozygous lethality and deleterious mutation load of heteromorphic sex chromosomes.

Nature Ecology & Evolution, (in press)