Genomkartlegging – er det noe nyttig for havbruksnæringen?

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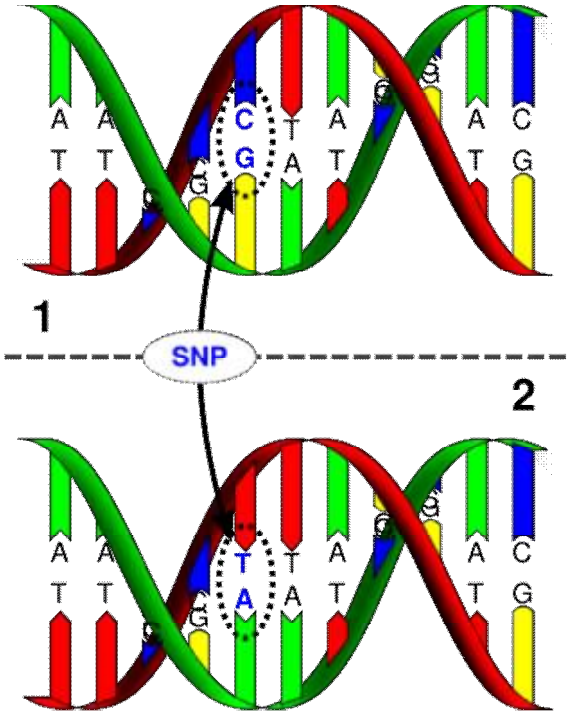
CIGENE
Centre for Integrative Genetics

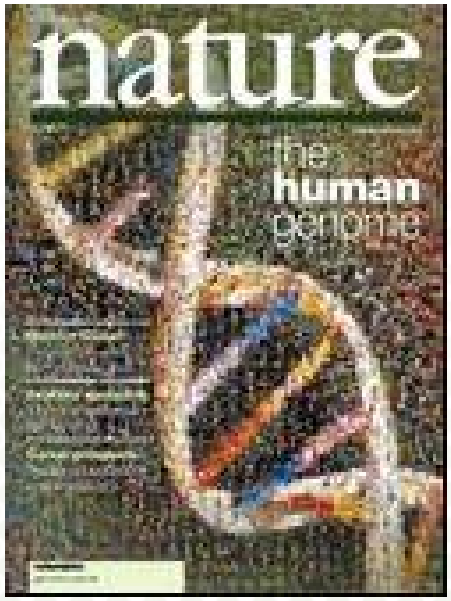
- Etablert i 2003 og finansiert av FUGE som nasjonal plattform for storskala genotyping og analyse av SNP informasjon
- Mest forskning relatert til produksjonsbiologi
- Spesielt fokus på arter innen landbruk og akvakultur

FUGE
Funksjonell genomforskning

Single Nucleotide Polymorphisms (SNPs)



- Representerer den mest vanlige variasjonen i genomet (finnes hver 300bp)
- Tillater automatisert genotyping
- Finnes i kodende og ikke kodende regioner
- Kan være funksjonelle og dermed direkte anvarlige for variasjon i fenotyper

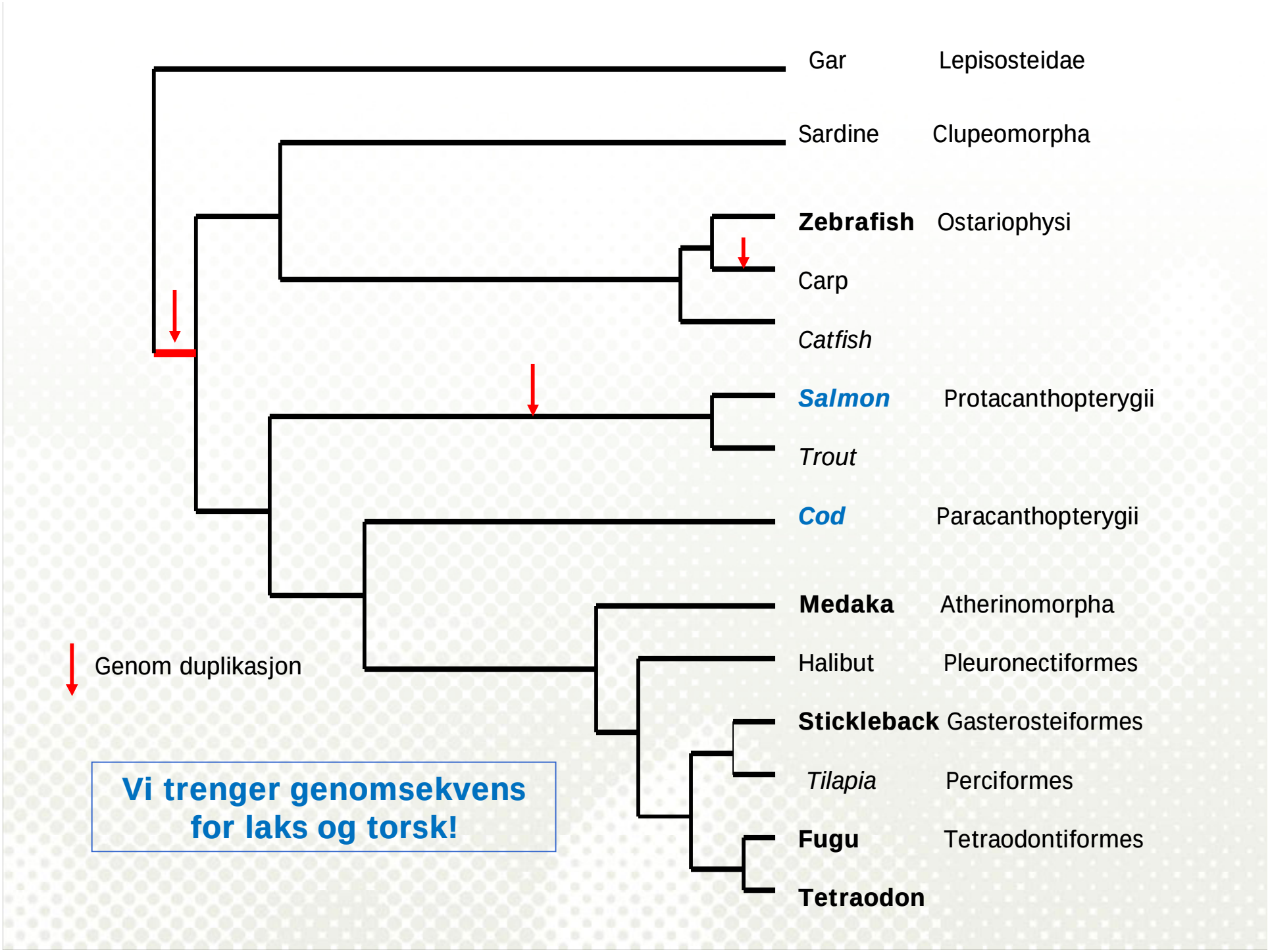


Human genom-sekvens

- publisert i 2001
- tok >10 år å produsere

Genom sekvensering

GENOME	STATUS
Storfe	Science, 2009
Hest	Science, 2009
Gris	Ferdig
Sau	Snart ferdig
Torsk	Snart ferdig
Laks	I gang
...	
...	


Gar
Lepisosteidae
Sardine
Clupeomorpha
Zebrafish
Ostariophysi
Carp
Catfish
Salmon
Protacanthopterygii
Trout
Cod
Paracanthopterygii
Medaka
Atherinomorpha
Halibut
Pleuronectiformes
Stickleback
Gasterosteiformes
Tilapia
Perciformes
Fugu
Tetraodontiformes
Tetraodon
Genom duplikasjon
Vi trenger genomsekvens for laks og torsk!

Workshop on Sequencing Salmonid Genomes
UMB, Aas, October 2005

Goals of the Atlantic Salmon Genome Sequencing Project (ASGSP)

Produce a genome sequence that:

1. Identifies and physically maps all of the genes in the Atlantic salmon genome.
2. Can act as a reference / guide sequence for the genomes of other salmonids (e.g., rainbow trout).

Genome BritishColumbia
Leading > Investing > Connecting

Logo InnovaChile

The Research Council of Norway

FHF

marineharvest
excellence in seafood

cermaq

SalmoBreed

AquaGen

Laksen som blir sekvensert

Dobbel haploid laks produsert ved mitotisk androgenese

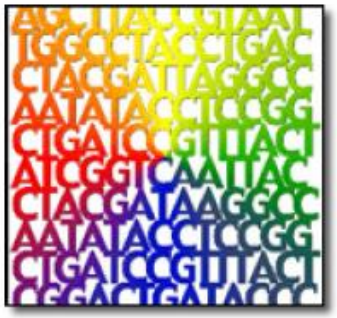
Beyond Sanger: Toward the $1,000 Genome

NIH NEWS RELEASE

National Institutes of Health — National Human Genome Research Institute

NHGRI Seeks Next Generation of Sequencing Technologies

New Grants Support Development of Faster, Cheaper DNA Sequencing



BETHESDA, Md., Thurs., Oct. 14, 2004 - The National Human Genome Research Institute (NHGRI), part of the National Institutes of Health (NIH), today announced it has awarded more than $38 million in grants to spur the development of innovative technologies designed to dramatically reduce the cost of DNA sequencing, a move aimed at broadening the applications of genomic information in medical research and health care.

NHGRI's near-term goal is to lower the cost of sequencing a mammalian-sized genome to $100,000, which would enable researchers to sequence the genomes of hundreds or even thousands of people as part of studies to identify genes that contribute to cancer, diabetes and other common diseases. Ultimately, NHGRI's vision is to cut the cost of whole-genome sequencing to $1,000 or less, which would enable the sequencing of individual genomes as part of medical care. The ability to sequence each person's genome cost-effectively could give rise to more individualized strategies for diagnosing, treating and preventing disease. Such information could enable doctors to tailor therapies to each person's unique genetic profile.

Next-Gen sekvensering

454 LIFE SCIENCES

Solexa

SOLiD™ System

Plattform	Distributor	Model	Leselengde	Total sequence
454	Roche	Titanium	500nt	1Gb
SOLiD	ABI	SOLiD	50nt	20-60Gb
Solexa	Illumina	GAIIx	2x106bp	10-50Gb
Solexa	Illumina	HiSeq2000	2x106bp	200Gb

U.S. Department of Health and Human Services

NIH News

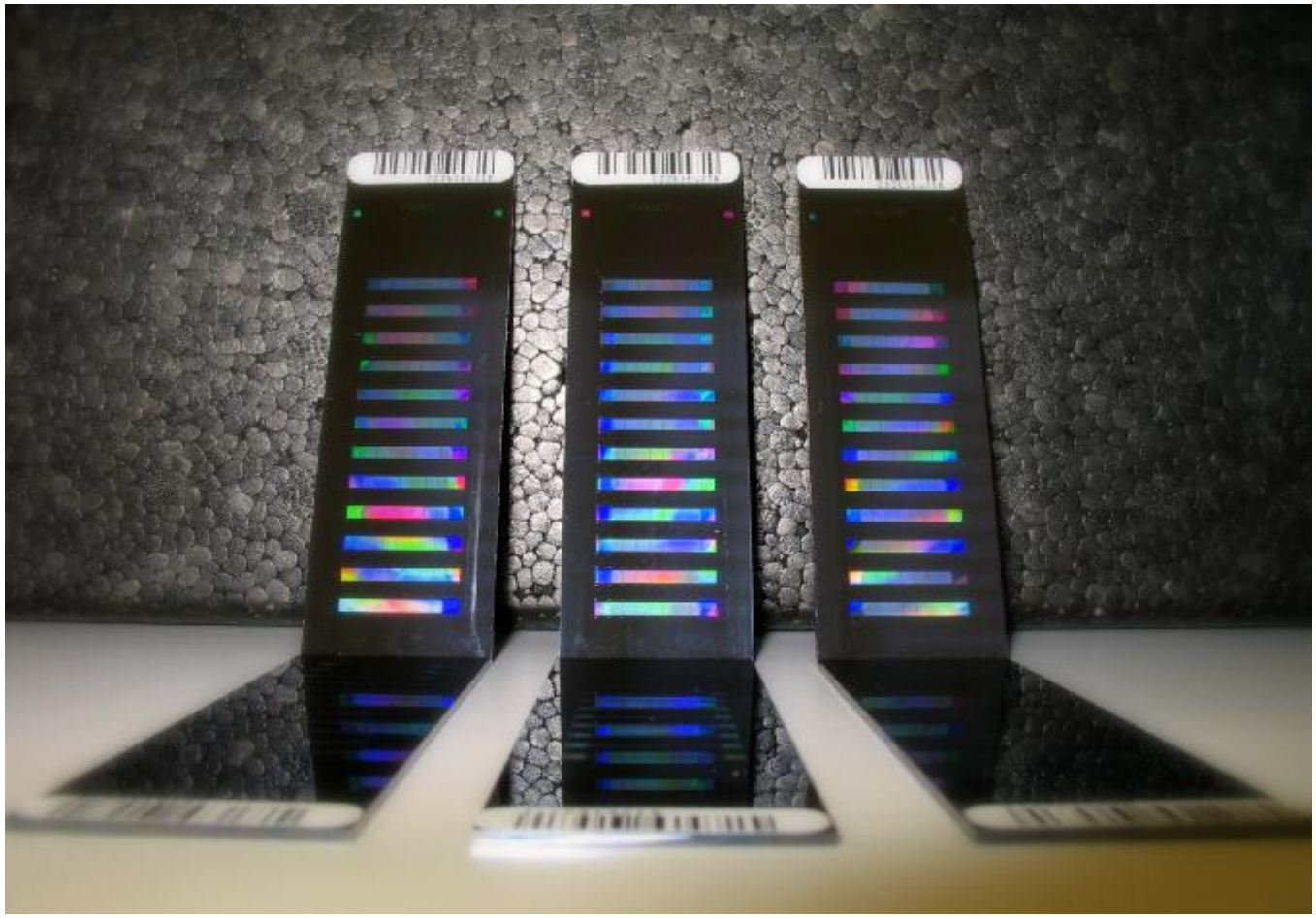
National Institutes of Health

International Consortium Announces the 1000 Genomes Project

Major Sequencing Effort Will Produce Most Detailed Map of Human Genetic Variation to Support Disease Studies

Bethesda, Md., Tues., Jan.22, 2008 — An international research consortium today announced the 1000 Genomes Project, an ambitious effort that will involve sequencing the genomes of at least a thousand people from around the world to create the most detailed and medically useful picture to date of human genetic variation. The project will receive major support from the Wellcome Trust Sanger Institute in Hinxton, England, the Beijing Genomics Institute, Shenzhen (BGI Shenzhen) in China and the National Human Genome Research Institute (NHGRI), part of the National Institutes of Health (NIH).

Atlantisk laks 7K SNP-chip

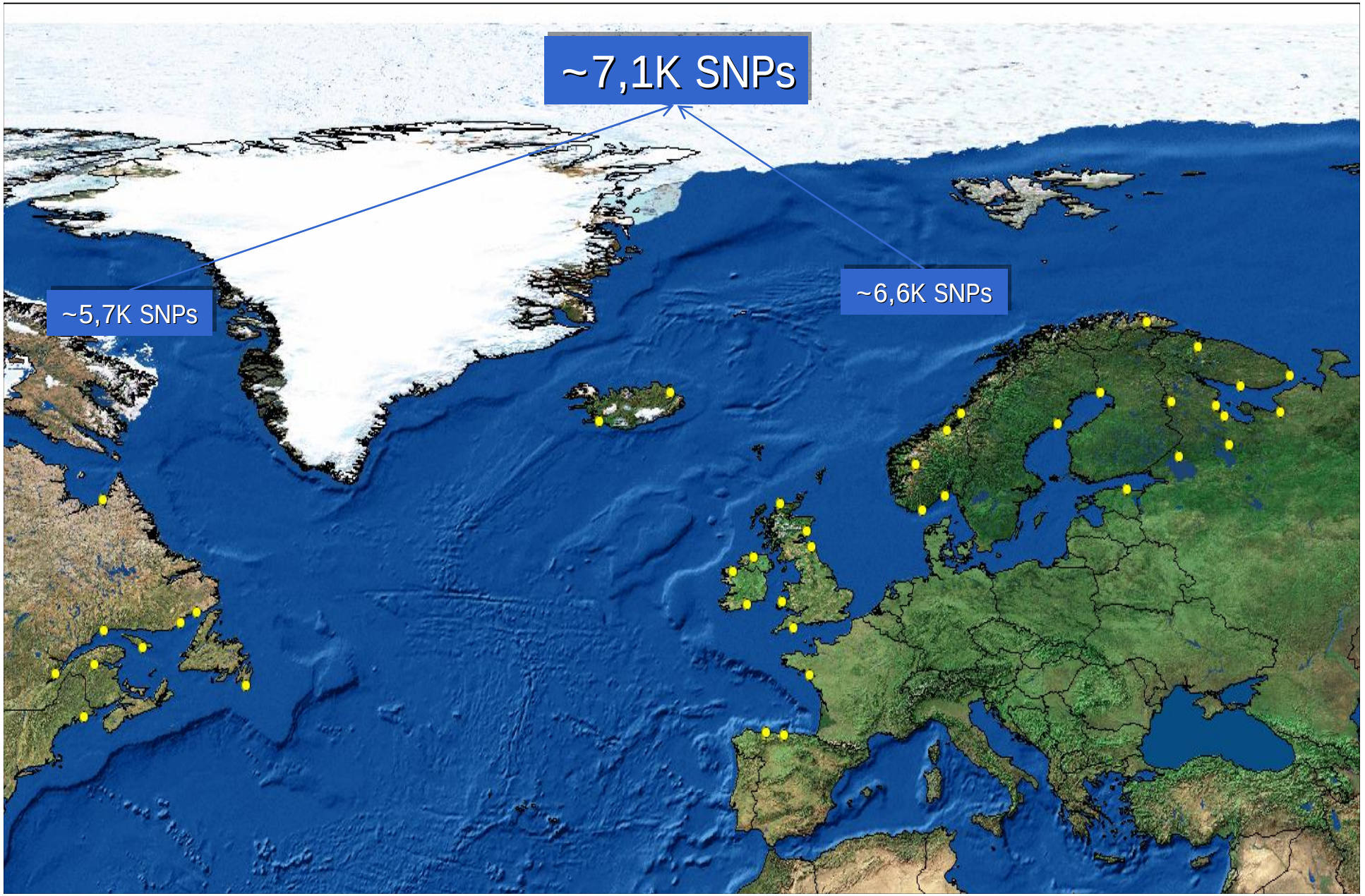


Centre for Integrative Genetics

Anvendelser av SNP-chip (1)

- Studere genetisk variasjon i laks
- Sammenlikne SNP variasjon i villaks og oppdrettslaks
- Konstruere høyoppløselig SNP-kart
- Studere effekter av genomduplikasjon i Atlantisk laks

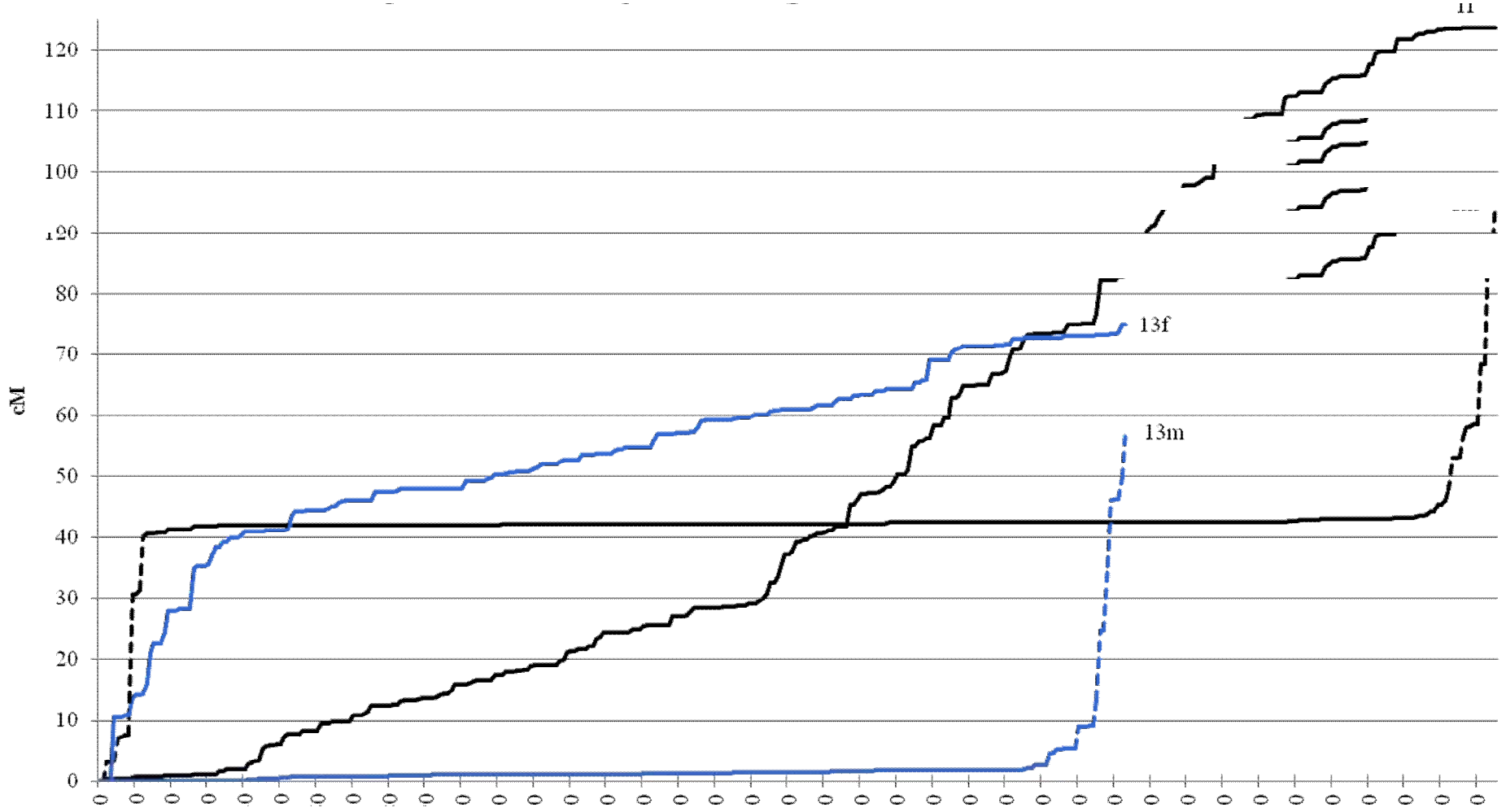
SNP-variasjon i ville laksepopulasjoner



Høyoppløselig SNP-kart i Atlantisk laks

- 3034 laks
- 263 familier
- 5443 SNPs integrert i kart

Kromosom	SNPer	Hunn	Hann	Ratio
ssa01	385	123.7	94.8	1.30
ssa02	194	106.4	24.2	4.40
ssa03	284	102.9	54.4	1.89
ssa04	210	103.9	89.9	1.16
ssa05	217	102	34	3.00
ssa06	243	104.7	52.2	2.01
ssa07	129	101.2	63	1.61
ssa08	56	52.2	3.2	16.31
ssa09	310	87.7	46.8	1.87
ssa10	295	69.6	50.2	1.39
ssa11	229	73.4	48.9	1.50
ssa12	239	88.2	43	2.05
ssa13	283	74.9	57.4	1.30
ssa14	205	64.7	47.5	1.36
ssa15	213	71.4	53.9	1.32
ssa16	189	58.6	7.9	7.42
ssa17	130	68.6	28.8	2.38
ssa18	163	64.4	13.5	4.77
ssa19	155	59.8	55.9	1.07
ssa20	176	58	35.5	1.63
ssa21	106	51.5	58.7	0.88
ssa22	159	55.2	54.7	1.01
ssa23	125	47.1	52.2	0.90
ssa24	114	51.1	39.5	1.29
ssa25	117	52.6	53.7	0.98
ssa26	141	77.7	48.5	1.60
ssa27	161	49.5	54.9	0.90
ssa28	95	50.8	40.7	1.25
ssa29	91	52.1	55.8	0.93
TOTALT	5443	1942.6	1282.1	1.52


cM
120
110
100
90
80
70
60
50
40
30
20
10
0
13f
13m

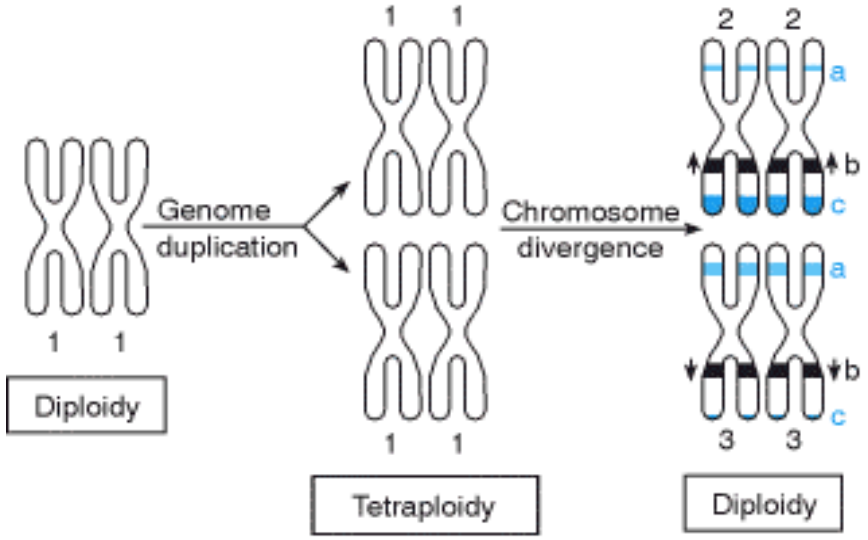
Salmonider som modell for å studere effekter av genomduplikasjon

Genomduplikasjon førte til en fordobling av antall kromosomer og gener:

Ancestral karyotype: 2n = 48

Genome duplication: (4n) 2n = 96, NF = 96

Atlantic salmon	2n = 56-60	NF = 74
Brown trout	2n = 80	NF = 100-102
Rainbow trout	2n = 58-64	NF = 100
Arctic charr	2n = 78-80	NF = 98-100



1. Hvordan oppnår et genom stabilitet via re-diploidisering?
2. Når og hvordan skjer det?
3. Er det samme mekanismer i ulike salmonider?

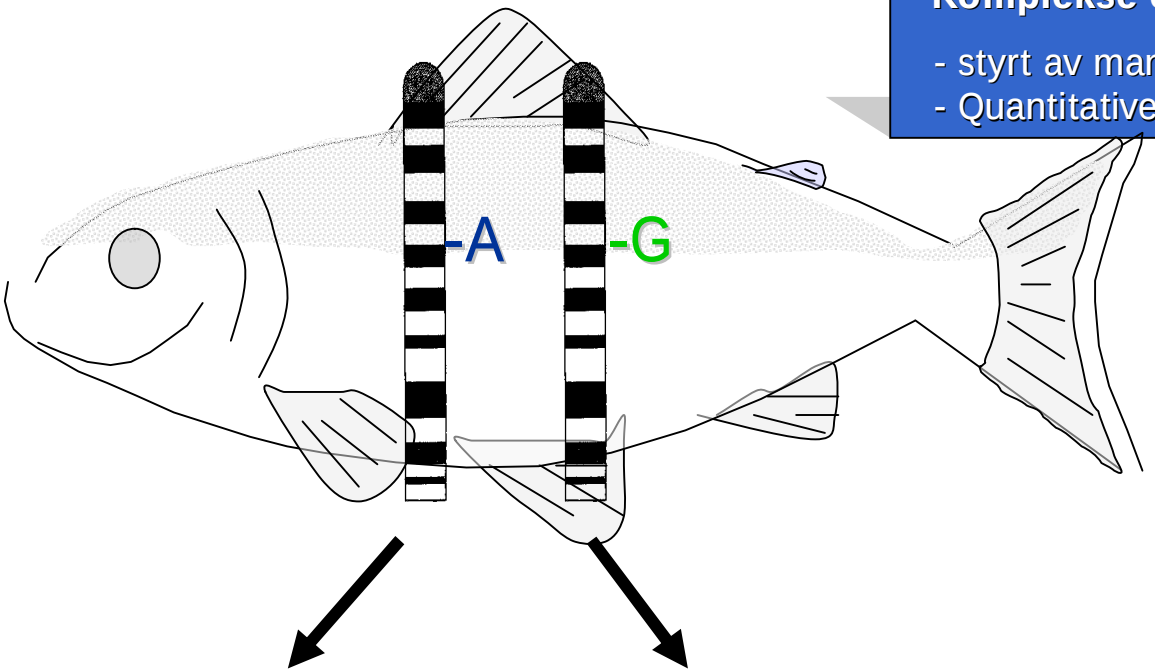
Anvendelser av SNP-chip (2)

- Bestemme LD og haplotype strukturer i laksepopulasjoner
- Finne områder i genomet (QTLer), gener og synteseveier som påvirker viktige økonomiske egenskaper
- Implementere genominformasjon i avl for forbedring av viktige egenskaper

QTL-kartlegging

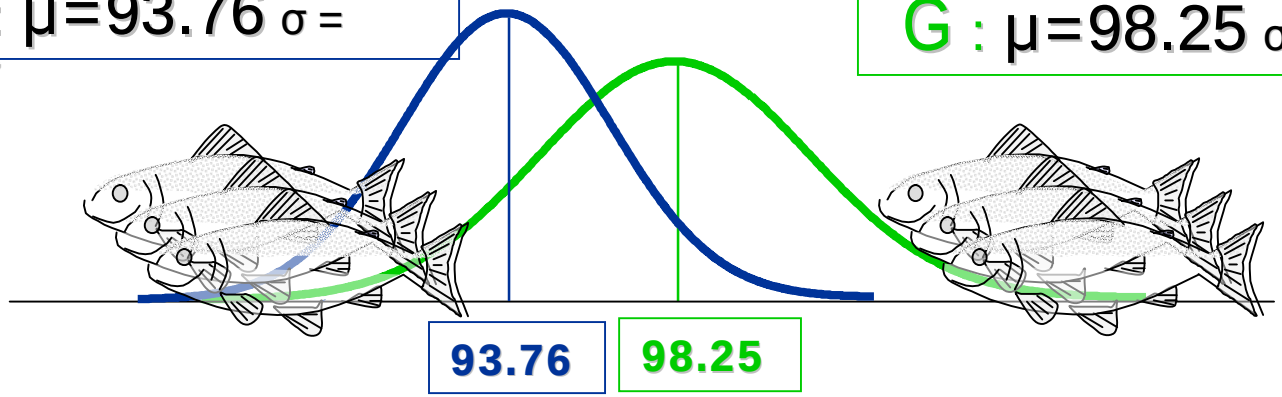
Komplekse egenskaper:

- styrt av mange gener
- Quantitative Trait Loci



A: μ=93.76 σ = 4.37

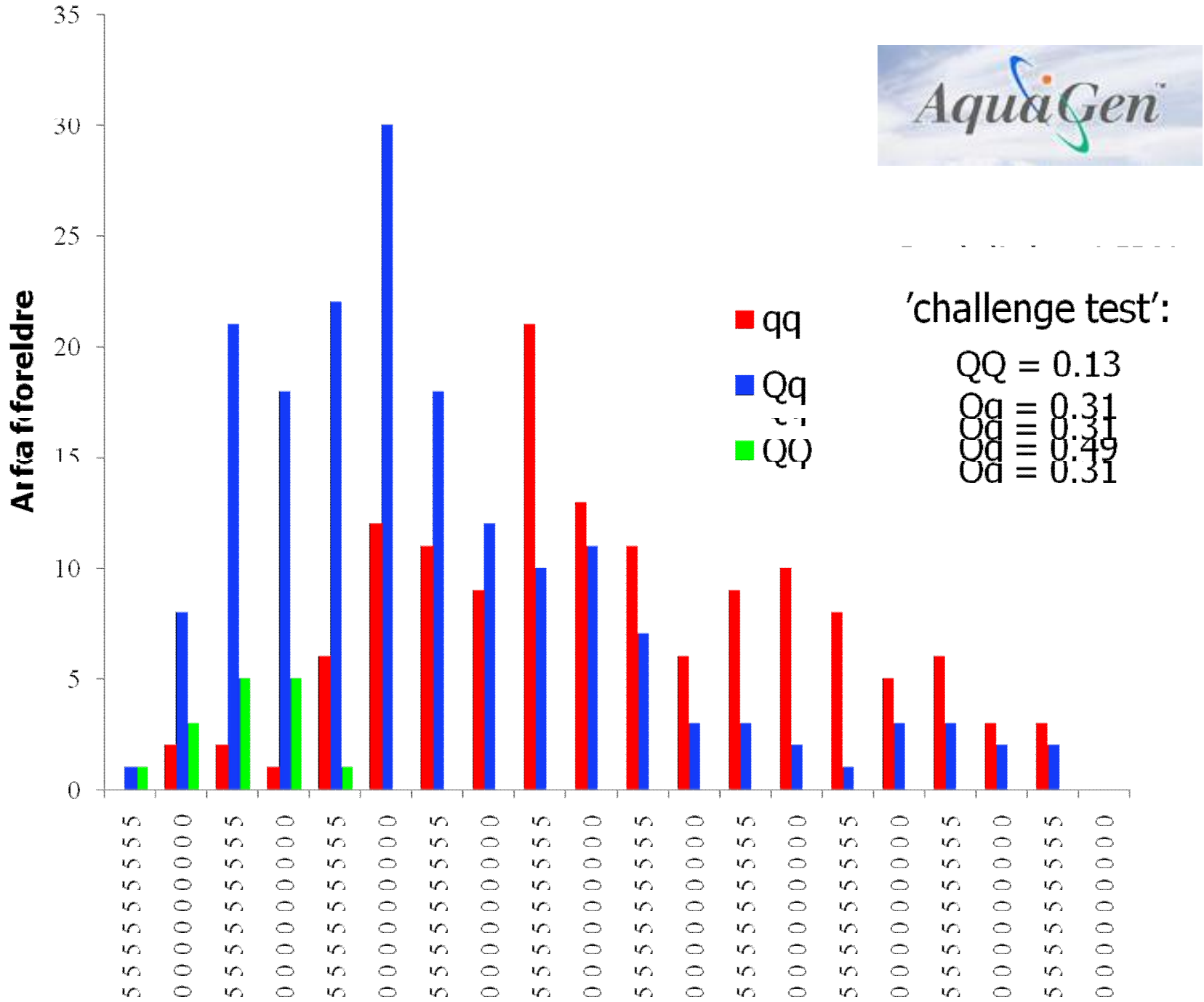
G : μ=98.25 σ = 7.17



25.06.2009

Aqua Gen lanserer gentestet lakserogn i førstkommende sesong

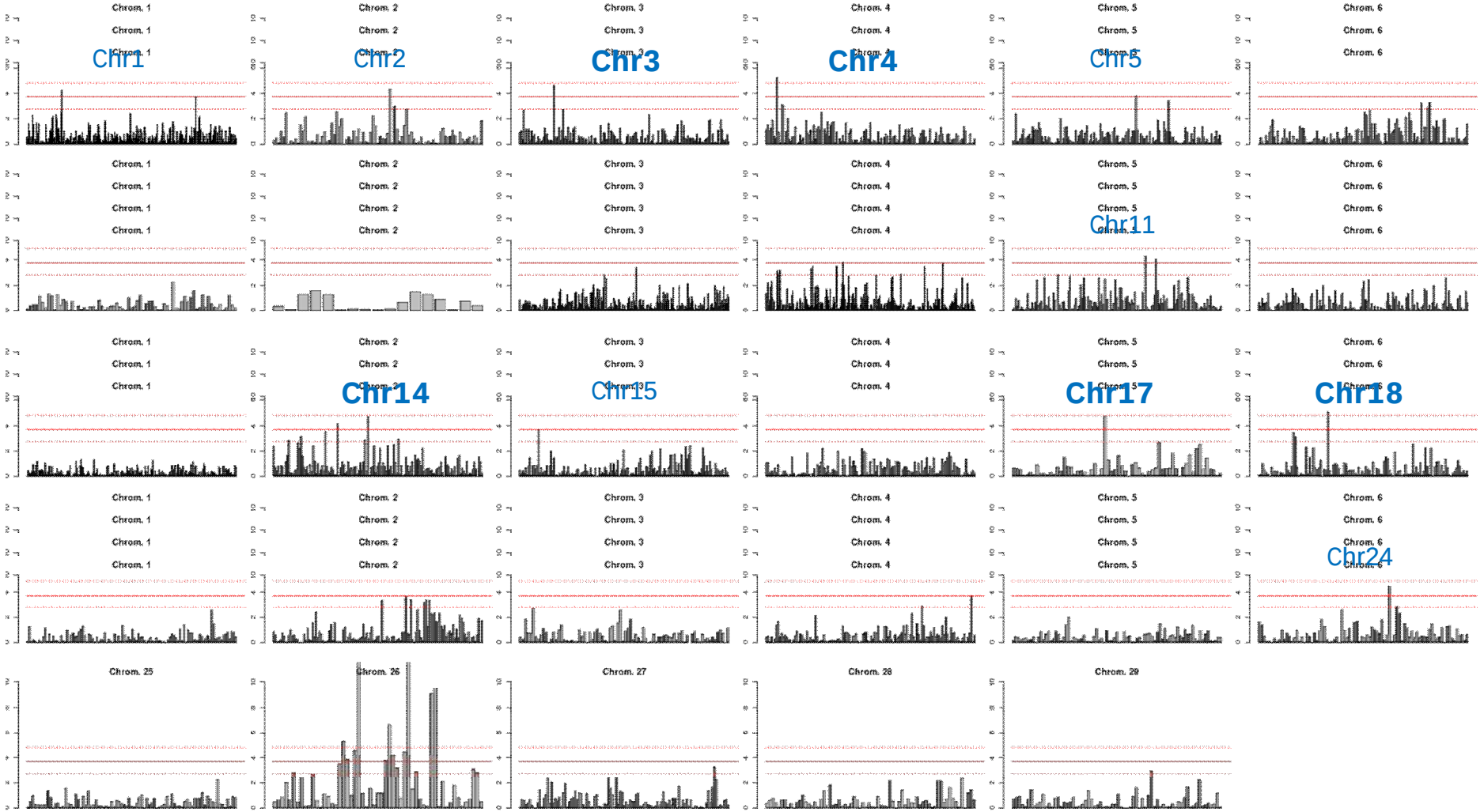
Som verdens første avlsselskap innen akvakultur vil det bli benyttet en genmarkør for å velge ut stamfisk som gir avkom med forutsigbar høy motstandsevne mot virussykdommen IPN. Ved å kombinere tradisjonell avlsmetode og gentesting vil avkommet få bedre egenskaper både for vekst og IPN-resistens samtidig i forhold til tidligere.


AquaGen
Antall foreldre
35
30
25
20
15
10
5
0
qq
Qq
QQ
'challenge test':
QQ = 0.13
Qq = 0.31
Qq = 0.31
Qq = 0.49
Qq = 0.31

Biobank materiale

- **Vekst, kjønn, produktkvaliteter:**
  - Vekt
  - Kjønn
  - Vaksineskader
  - Vekt og form på hjerte
  - Vekt og tykkelse på filet
  - Filletfarge og fettinnhold (Qvision NIR scanner)
  - Tekstur
- **Sykdommer:**
  - Infectious pancreatic necrosis (IPN)
  - Infectious salmon anemia (ISA)
  - Pancreas Disease (PD)
- **Lakselus**

QTL-kartlegging filet farge



CRV AmBreed NZ

Your Choice, Your Profit

illumina

Bovine 50K SNP-chip

News > Genomic Selection launched

Genomic Selection launched

Situations Vacant | News Archives | Fertilty Express Packs

AmBreed launches world first in genetics

inSire

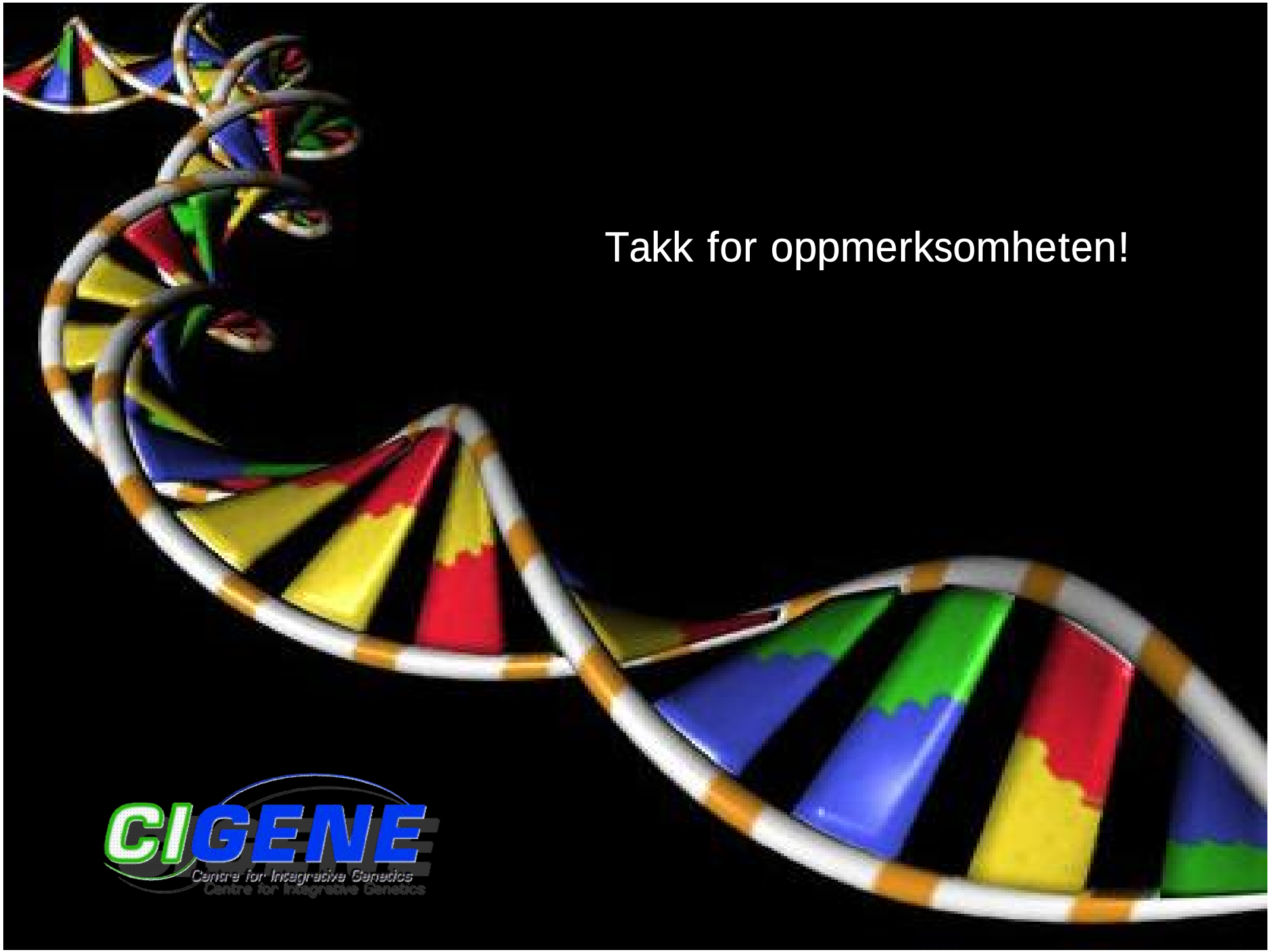
Genomic Selection by AmBreed

June marks not only the start of a new farming year, but the launch of new breeding technology that New Zealand farmers are the first in the world to benefit from.

The first ever teams of bulls proven through genome-wide mapping technology is now available through AmBreed New Zealand.

Known as inSire the genomic technology provides farmers with faster genetic gains than progeny testing, and may even replace the traditional sire proving schemes long the mainstay of dairy production genetics.

The ability to compare a bull's DNA pattern to the pattern of known desirable traits is at the heart of inSire Genomic Selection technology. It improves the reliability of predicted breeding values to 50%-65% depending on the trait, up from 35% using parent averages.


Takk for oppmerksomheten!
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