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Extent of genome-wide linkage disequilibrium in farmed Atlantic salmon (*Salmo salar* L.) using high density genotypes

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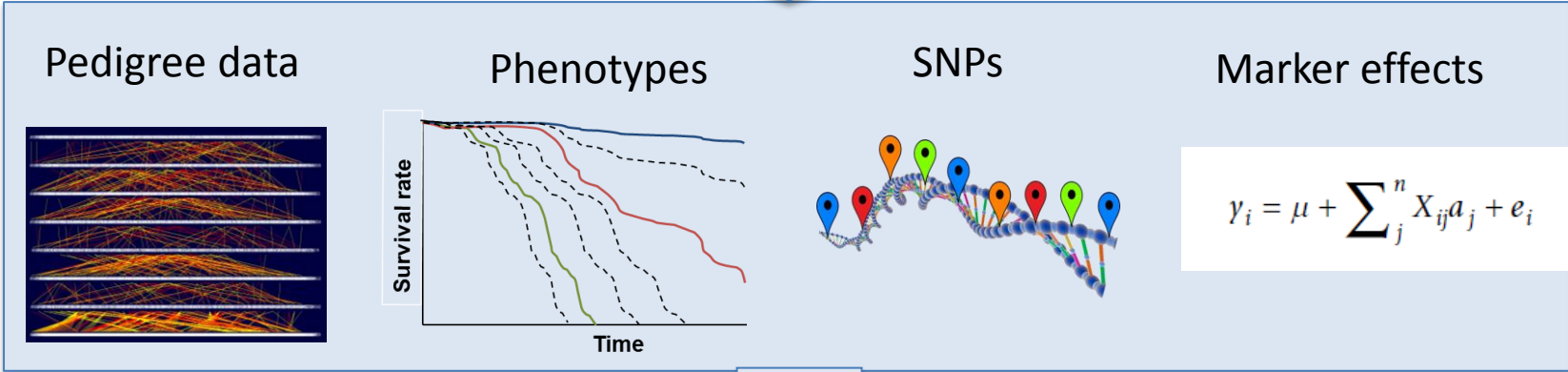
Traits that are difficult to measure...



Disease resistance

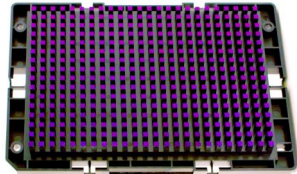
Carcass quality

Genomic Selection



↑ EBVs accuracies
 ↑ Response to selection
 Accelerates genetic progress

A routine SNP Genotyping platform is needed!



Development of a SNP array for Atlantic salmon

Phase 1 - SNP Discovery

- Whole genome sequencing (WGS) of **20 fish** from 7 commercial populations, including North American and European origin
- Bar-coded samples (100bp PE) Illumina HiSeq2000.
- Preliminary assembly from the ICSASG as a reference genome
- Pipeline to filter paramorphisms (Emrich et al., 2004): regions with excessive read counts and a high number of heterozygous were discarded

~10 million putative SNPs were discovered and after 6 filtering steps a definitive list of **~ 200K** SNPs were selected

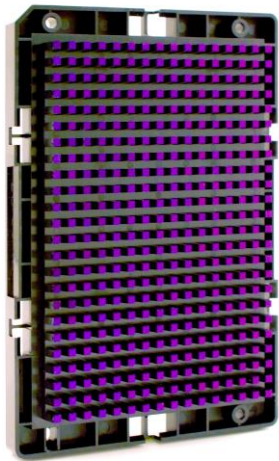
Development of a SNP array for Atlantic salmon

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Phase 2 - SNP Validation

affymetrix
Biology for a better world

- 200K SNPs Affymetrix Axiom® myDesign Custom Array
- We genotyped 480 fish from 8 different populations
- *Axiom Genotyping Console* (AGT, Affymetrix) and *SNPolar* for R



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200K SNP-CHIP

~79% (159,099) SNPs had probes belonging to good quality categories according to clustering properties.

Selection of 50K from 200K

159,099 probes (1 for each SNP)

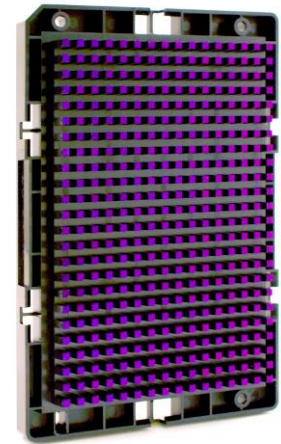
Filter By Mendelian error
137,712 retained

Filter By MAF > 0.05
112,241 retained

Filter by evenly spaced windows
55,591 retained

Filter By LD
53998 retained

Filter by distance (10K)
50K left

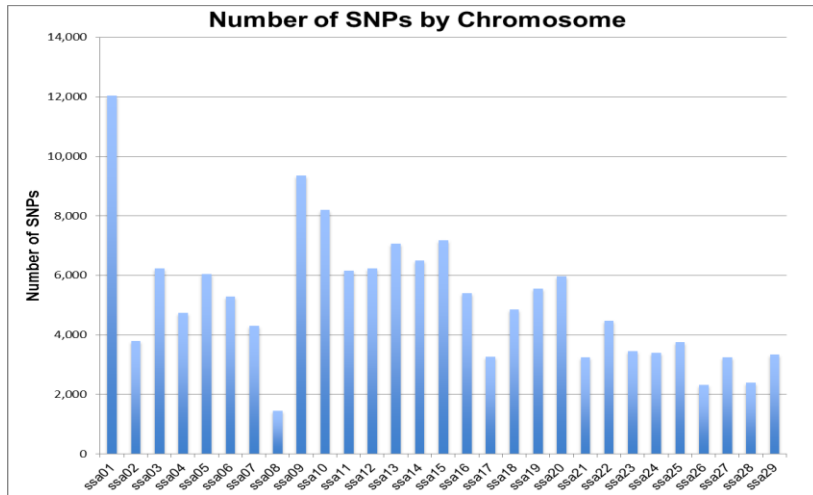


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50K SNP-CHIP

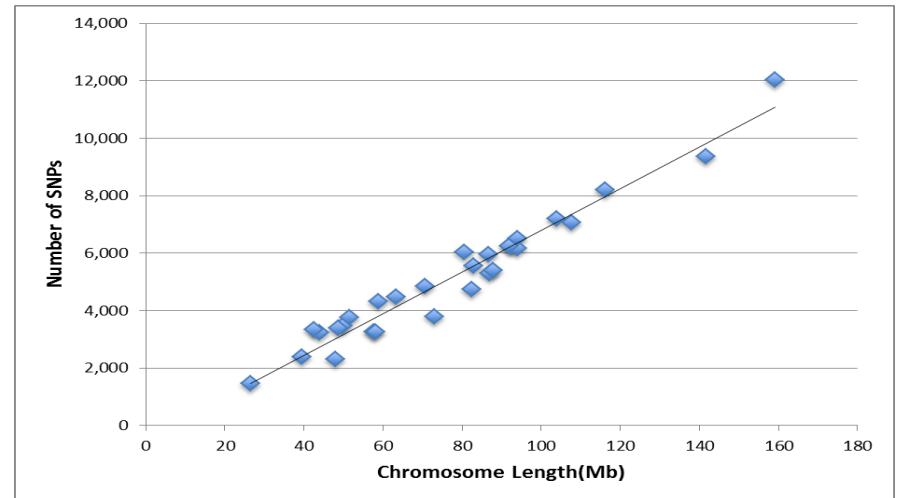
It is currently being used for Genome wide association studies and genomic selection in Atlantic salmon

Distribution of SNPs

Distribution of SNPs on the Atlantic salmon chromosomes



Relationship between the number of SNPs and chromosome length



... Other presentations related to these 200K and 50K SNP arrays

IDENTIFYING NON-PARALLEL GENOMIC CHANGES BETWEEN INDEPENDENT PAIRS OF WILD/DOMESTIC ATLANTIC SALMON POPULATIONS USING A HIGH DENSITY SNP ARRAY

López M.E., Correa K., Di Genova A., Moore J-S., Perrier C., Bernatchez L., Gilbey J., Soto C., Bassini L., Maass A., Neira R., Figueroa R., Lhorente J.P., Yáñez J.M.



María E. López

GENOME WIDE ASSOCIATION ANALYSIS FOR RESISTANCE TO *Caligus rogercresseyi* IN ATLANTIC SALMON (*Salmo Salar L.*)

Correa K.^{1,2} / Lhorente J.P.² / López M.E.^{2,3} / Figueroa, R.² / Bassini L.^{2,3} / Di Genova A.⁴ / Maass A.⁴ / Davidson W.⁵ / Yáñez, J.M.^{1,2}

GENOME WIDE ASSOCIATION ANALYSIS FOR RESISTANCE TO *Piscirickettsia salmonis* IN ATLANTIC SALMON (*Salmo Salar L.*)

Correa K.^{1,2} / Lhorente J.P.² / López M.E.^{2,3} / Figueroa, R.² / Bassini L.^{2,3} / Di Genova A.⁴ / Maass A.⁴ / Davidson W.⁵ / Yáñez, J.M.^{1,2}



Katharina Correa

BIO-ECONOMIC MODELING: A KEY TOOL TO EVALUATE THE BENEFITS OF GENOMIC SELECTION IN ATLANTIC SALMON

Araneda M.E.¹ / Yáñez J.M.^{1,2} / Lhorente J.P.¹ / Moreno J.M.¹



Marcelo Araneda

The extent of LD has implications for both GWAS and the delivery of accurate genomic predictions

Objective

To determine levels and extent of linkage disequilibrium in three farmed Atlantic salmon populations (*Salmo salar*) using high density genotypes

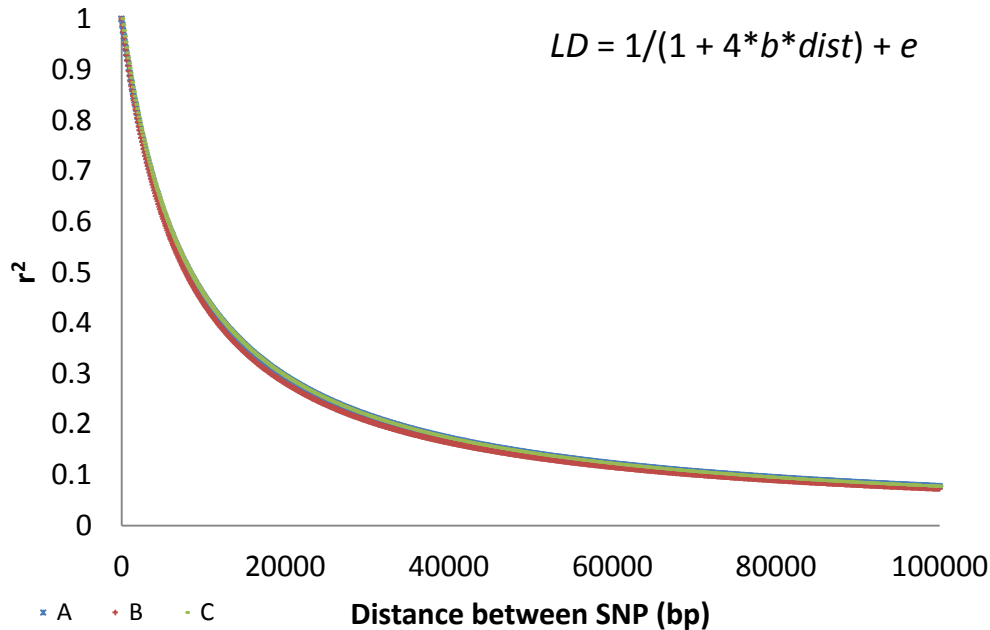
Genotyped fish

Descriptive results of population genetic estimates and statistics for the three different farmed populations genotyped with the 200K SNP Array (159,099 SNPs validated)

Population	n_G	n_{QC}^1	HWE ²		MAF > 0.05 ³		MAF > 0.01 ⁴		H_0^6	H_E^7
			n	% ⁵	n	% ⁵	n	% ⁵		
Farmed A	93	91	151,248	95	140,202	88	148,116	93	0.3910	0.3832
Farmed B	86	85	151,261	95	141,685	89	149,220	94	0.3866	0.3828
Farmed C	78	74	121,827	77	132,798	83	142,793	90	0.4604	0.3817

LD decay in three populations of farmed Atlantic salmon

Decay of average LD (r^2) over distance in three Atlantic salmon populations



Average r^2 at various distances in three populations of Atlantic salmon

Distance (kb)	LD (r^2)
10	0.38
50	0.21
100	0.16
500	0.11

Average LD dropped below 0.2 at marker distances above 60 kb

Conclusion

- The **200K** and **50K** SNP panels developed in this study provide a platform for:
 - the genetic dissection of economically important traits through **Genome Wide Association studies (GWAs)**,
 - assisting breeding programs through **genomic selection** and
 - **population genetics** studies in wild populations using genome-wide information
- **40,000** to **50,000** SNPs are necessary to perform genome-wide association studies with a desirable power and accurate genomic-enabled predictions on these populations.

Future Directions

To implement a **cost-effective genomic selection strategy** to improve disease resistance and carcass quality traits in Chilean Atlantic salmon populations by means of using **lower density SNP panels** and **efficient imputation** approaches



Dorian Garrick
Iowa State University

Future directions in other species...



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- Developing genomic resources in **coho salmon** for determining genomic basis of disease resistance traits



GenomeCanada



FONDEF
Fondo de Fomento al Desarrollo Científico y Tecnológico

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William Davidson
Simon Fraser University
Canada



Louis Bernatchez
Université Laval
Canada



Ross Houston
The Roslin Institute
Scotland

- Developing **200K** and **50K** SNP arrays for **Nile tilapia** to incorporate genomic information into the genetic evaluations for disease resistance and carcass quality traits

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Muchas gracias!



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Facultad de Ciencias Veterinarias y Pecuarias

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