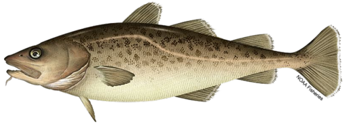
Molecular indicators of performance in Pacific cod exposed to climate stressors

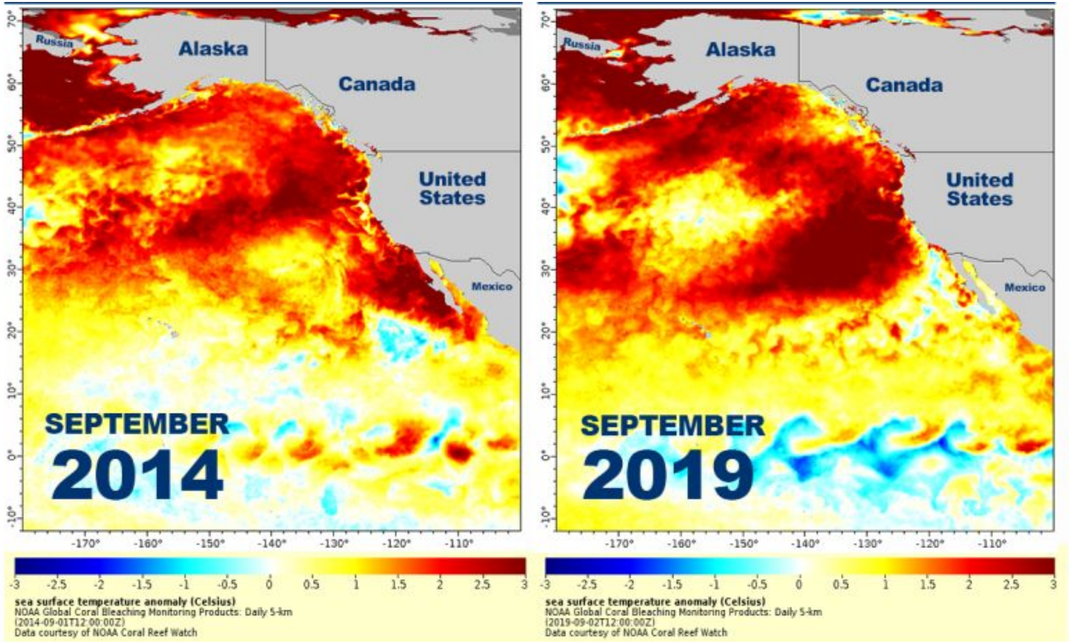


Laura Spencer[12], Ben Laurel[3], Emily Slesinger[3], Ingrid Spies[1], Mary Beth Rew Hicks[3], Louise Copeman[34], Sara Schaal[1,6], Laura Timm[1,5], Wes Larson[5], Michelle Stowell[4], Samantha Mundorff[3], Carlissa Salant[3], Kathleen Durkin[2], Tom Hurst[3], Steven Roberts[2]

[1]NOAA AFSC, Seattle
[2]University of Washington SAFS, Seattle
[3]NOAA AFSC, Newport
[4]Oregon State University
[5]NOAA AFSC, Juneau
[6]University of Oklahoma

NOAA OCEAN ACIDIFICATION PROGRAM

Gulf of Alaska cod fishery closed in 2020 after marine heatwaves



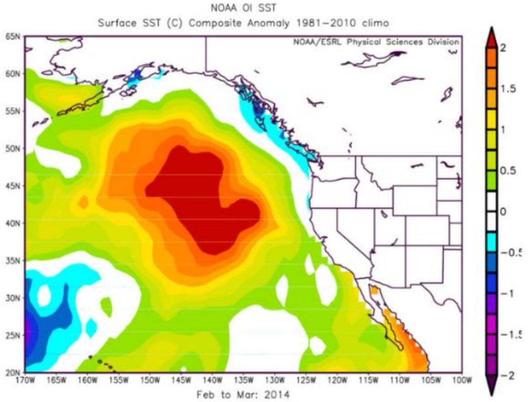
[NOAA feature story](), *September 05, 2019*

December 10, 2019

The Blob returns: Alaska cod fishery closes for 2020

by Jessica Hathaway in News, Alaska

SHARE



"The Blob" of 2014 severely depressed the Gulf of Alaska cod population. NOAA image.

FISH and FISHERIES

ORIGINAL ARTICLE | Open Access

Impact of the 2014–2016 marine heatwave on US and Canada West Coast fisheries: Surprises and lessons from key case studies

Correction(s) for this article

Christopher M. Free, Sean C. Anderson, Elizabeth A. Hellmers, Barbara A. Muhling, Michael O. Navarro, Kate Richerson, Lauren A. Rogers, William H. Satterthwaite, Andrew R. Thompson, Jenn M. Burt, Steven D. Gaines, Kristin N. Marshall, J. Wilson White, Lyall F. Bellquist ... See fewer authors

First published: 20 April 2023 | https://doi.org/10.1111/faf.12753 | Citations: 6

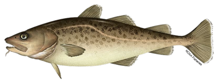
644

NRC Research Press

RAPID COMMUNICATION

Loss of spawning habitat and prerecruits of Pacific cod during a Gulf of Alaska heatwave

Benjamin J. Laurel and Lauren A. Rogers



FISH and FISHERIES

ORIGINAL ARTICLE | Open Access

Pacific cod in the Anthropocene: An early life history perspective under changing thermal habitats

Benjamin J. Laurel, Alisa Abookire, Steve J. Barbeaux, L. Zoe Almeida, Louise A. Copeman, Janet Duffy-Anderson, Thomas P. Hurst, Michael A. Litzow, Trond Kristiansen, Jessica A. Miller, Wayne Palsson, Sean Rooney, Hillary L. Thalmann, Lauren A. Rogers ... See fewer authors

First published: 27 July 2023 | https://doi.org/10.1111/faf.12779 | Citations: 1

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Article | Open access | Published: 27 June 2024

Marine heatwaves alter the nursery function of coastal habitats for juvenile Gulf of Alaska Pacific cod

Hillary L. Thalmann, Benjamin J. Laurel, L. Zoe Almeida, Kaitlyn E. Osborne, Kaylee Marshall & Jessica A. Miller

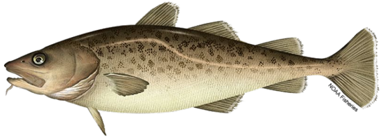
Scientific Reports **14**, Article number: 14018 (2024) | Cite this article

ORIGINAL RESEARCH article

Front. Mar. Sci., 19 August 2020
Sec. Marine Affairs and Policy
Volume 7 - 2020 | https://doi.org/10.3389/fmars.2020.00703

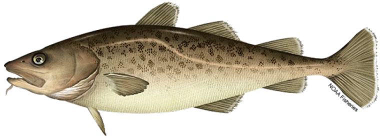
Marine Heatwave Stress Test of Ecosystem-Based Fisheries Management in the Gulf of Alaska Pacific Cod Fishery

Steven J. Barbeaux* Kirstin Holsman Stephani Zador



Pacific cod, *Gadus macrocephalus*

Hoff, Stevenson, & Orr 2015



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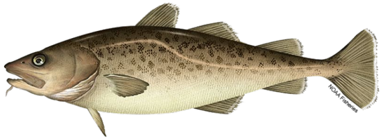

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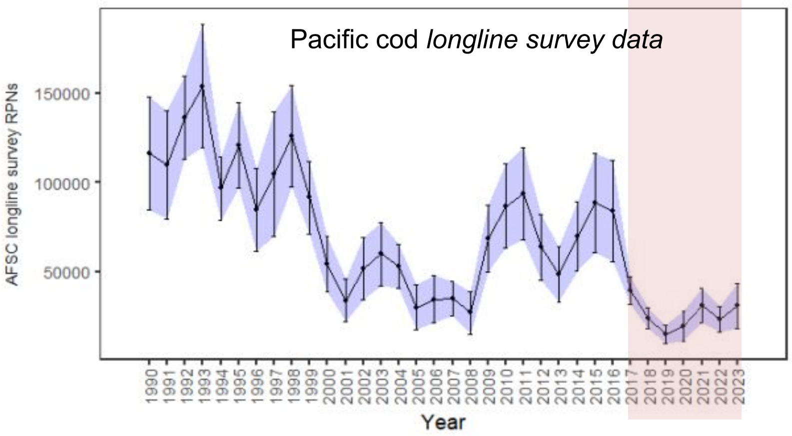
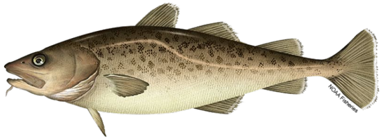


Stock Assessment Report, 2023, Gulf of Alaska,



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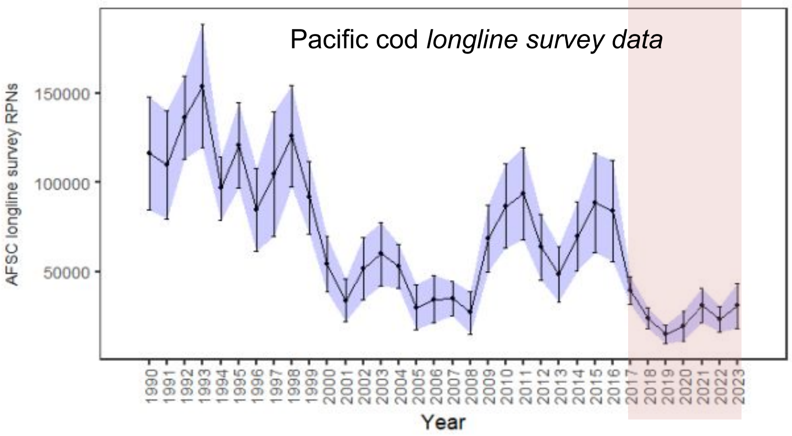
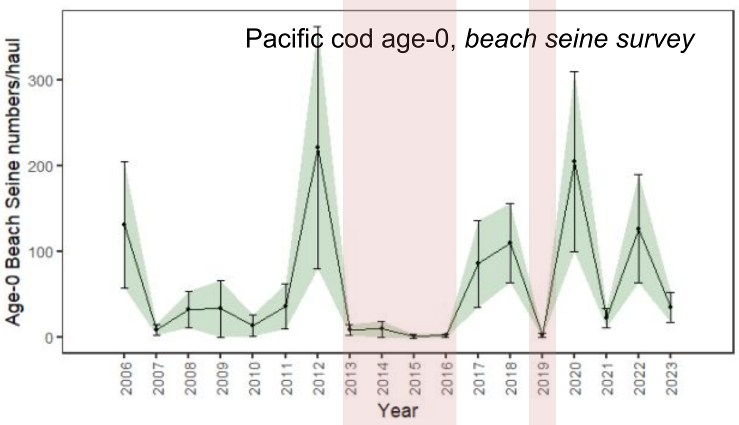
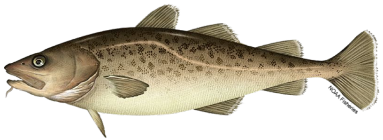




Stock Assessment Report, 2023, Gulf of Alaska,



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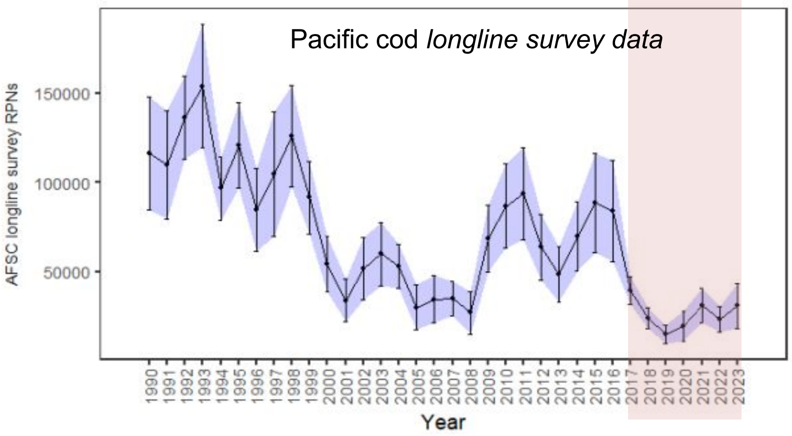
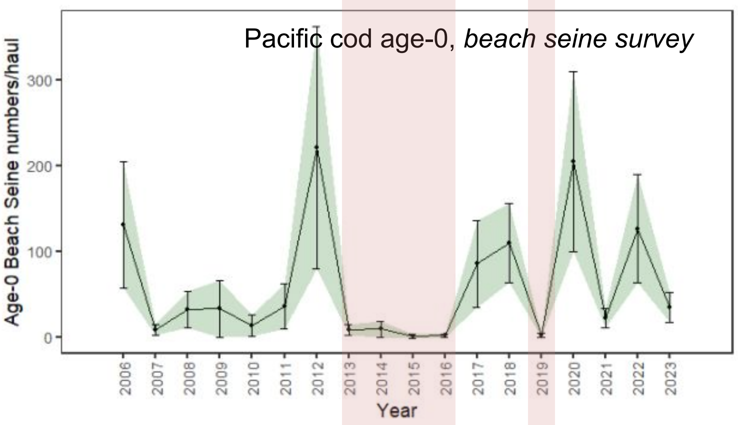
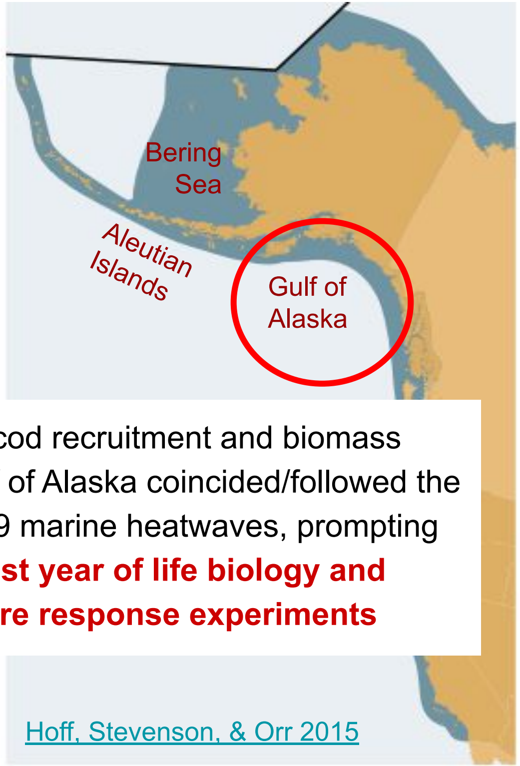


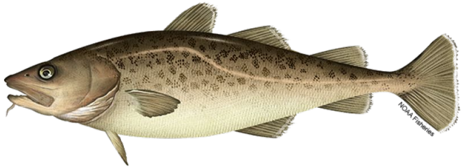


[Stock Assessment Report, 2023, Gulf of Alaska](),



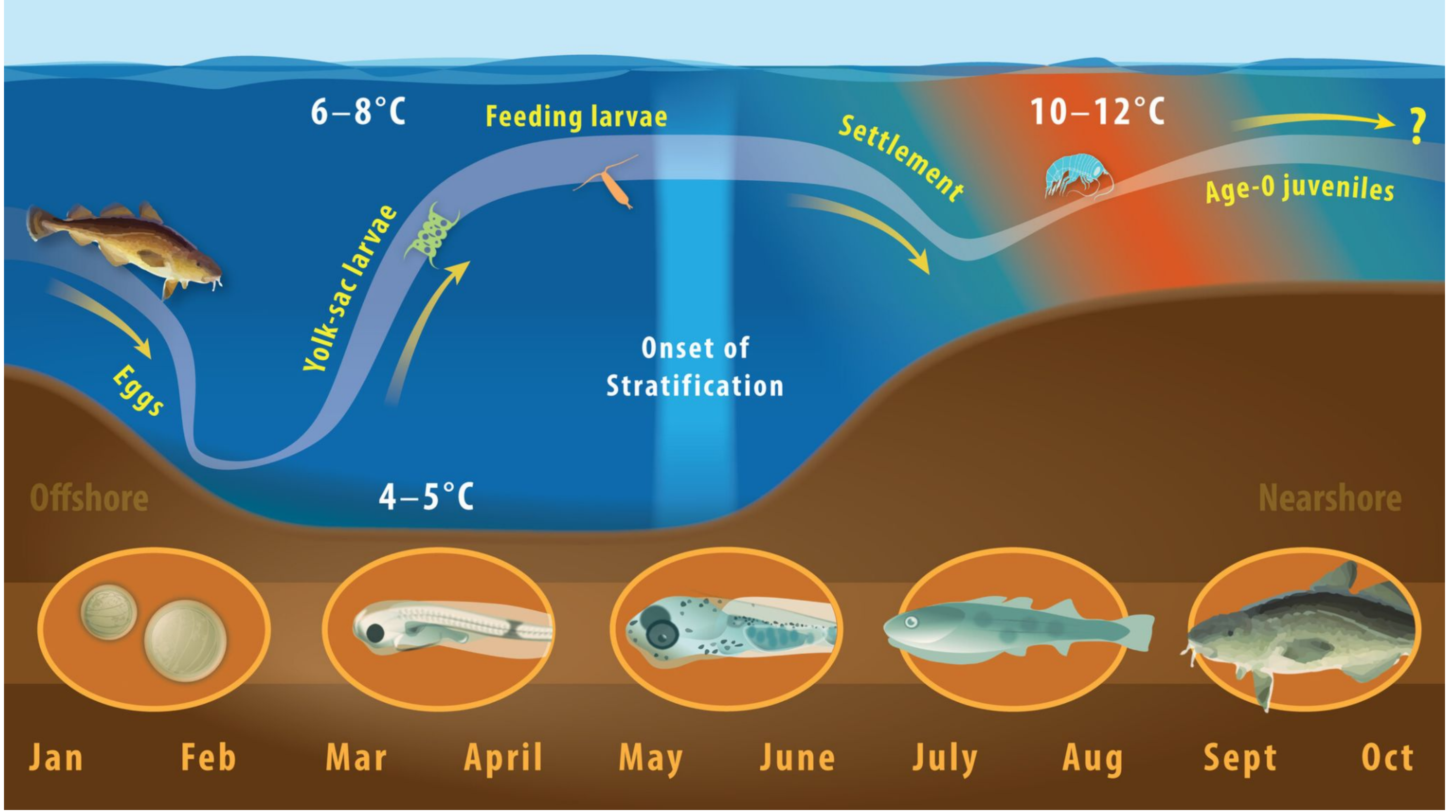
Low Pacific cod recruitment and biomass estimates in Gulf of Alaska coincided/followed the 2014-16 & 2019 marine heatwaves, prompting **review of 1st year of life biology and temperature response experiments**

[Hoff, Stevenson, & Orr 2015]()

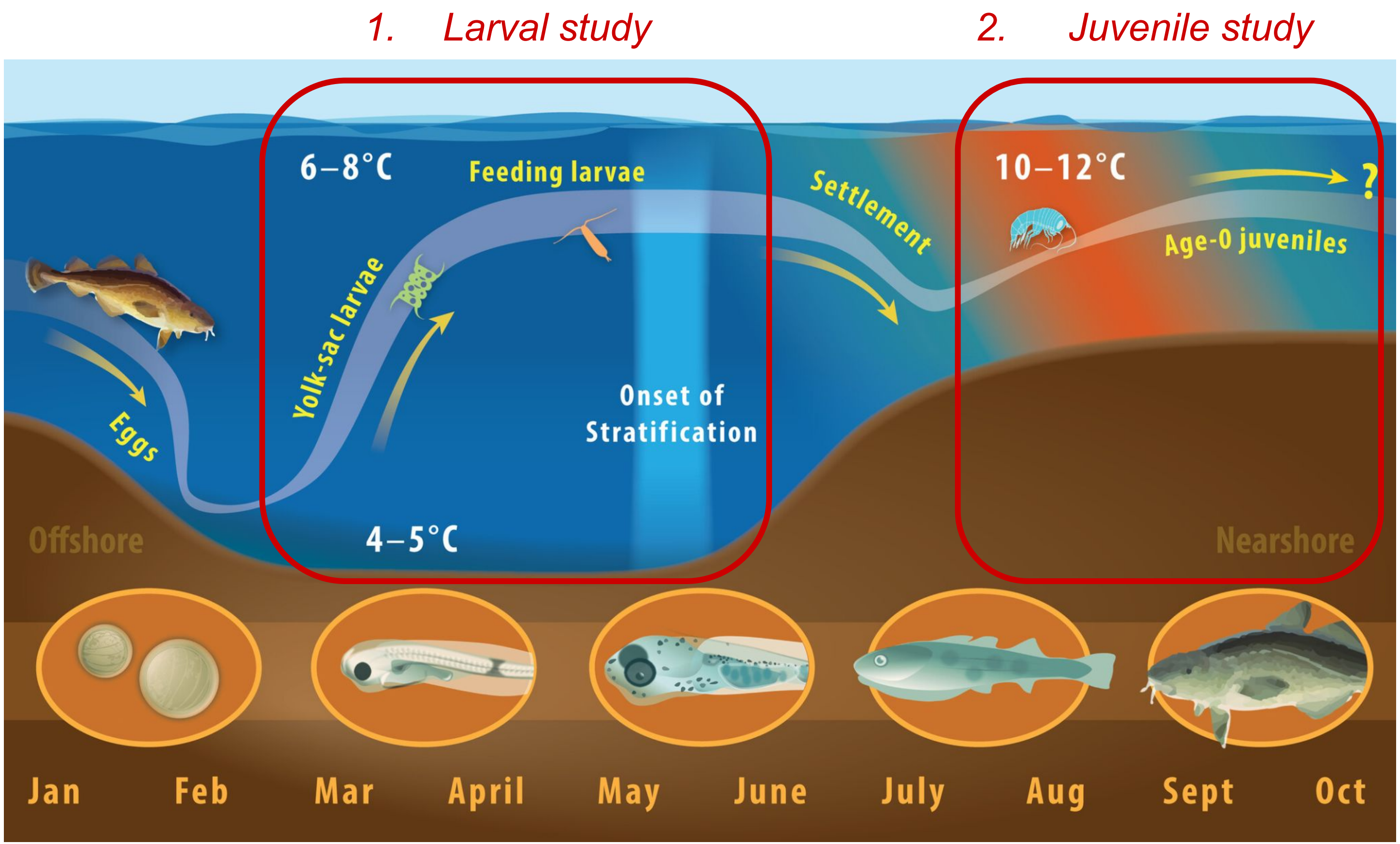


Big Questions

- Why & how does warming affect Pacific cod recruitment?
- Do biological reference points need to be updated in stock assessment models?
- How resilient are Pacific cod populations in Alaska to warming?

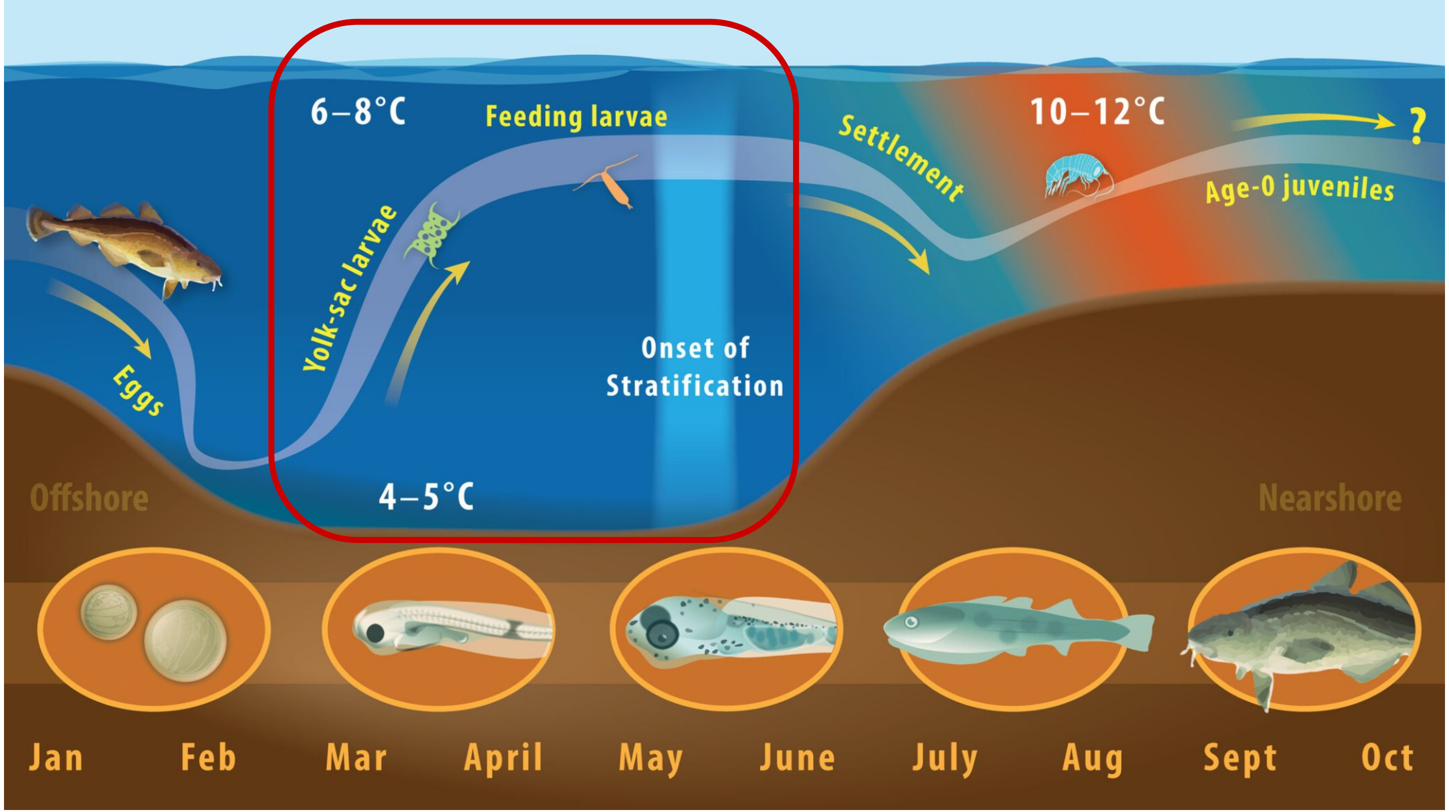


Laurel et al. 2023, in Fish & Fisheries



Laurel et al. 2023, in *Fish & Fisheries*

1. Larval study



Laurel et al. 2023, in Fish & Fisheries

Experimental Team

How does temperature and acidification affect **larval** Pacific cod **survival, growth, condition, & energy allocation**?

Gamete Finder

‘Omics Team

Experimental Team

Gamete Finder

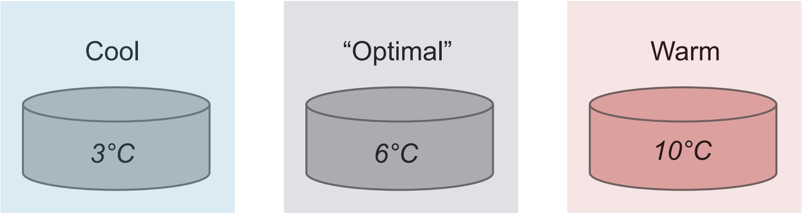
‘Omics Team

How does temperature and acidification affect **larval** Pacific cod **survival, growth, condition, & energy allocation**?

- Adults caught off Kodiak, AK to collect gametes

  1 female x 3 males

- Fertilized embryos transported to Newport, OR, reared through feeding stage in 3 temperatures



- Monitored growth & survival, ‘omics samples at end
- *Acidification treatment too!*

Experimental Team

Marine Biology (2024) 171:121
https://doi.org/10.1007/s00227-024-04439-w

ORIGINAL PAPER

The combined effects of ocean warming and ocean acidification on Pacific cod (*Gadus macrocephalus*) early life stages

Emily Slesinger[1,2] · Samantha Mundorff[1,3] · Benjamin J. Laurel[1] · Thomas P. Hurst[1]

Received: 23 June 2023 / Accepted: 11 April 2024 / Published online: 28 April 2024

How does temperature and acidification affect **larval** Pacific cod **survival, growth, condition, & energy allocation**?

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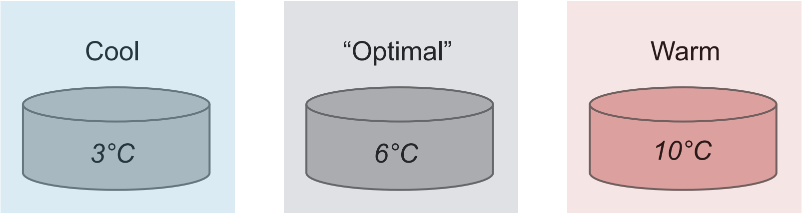


Monitored growth & survival, 'omics samples at end

Acidification treatment too!

High larval mortality in warming
(and Warm+Acidified)

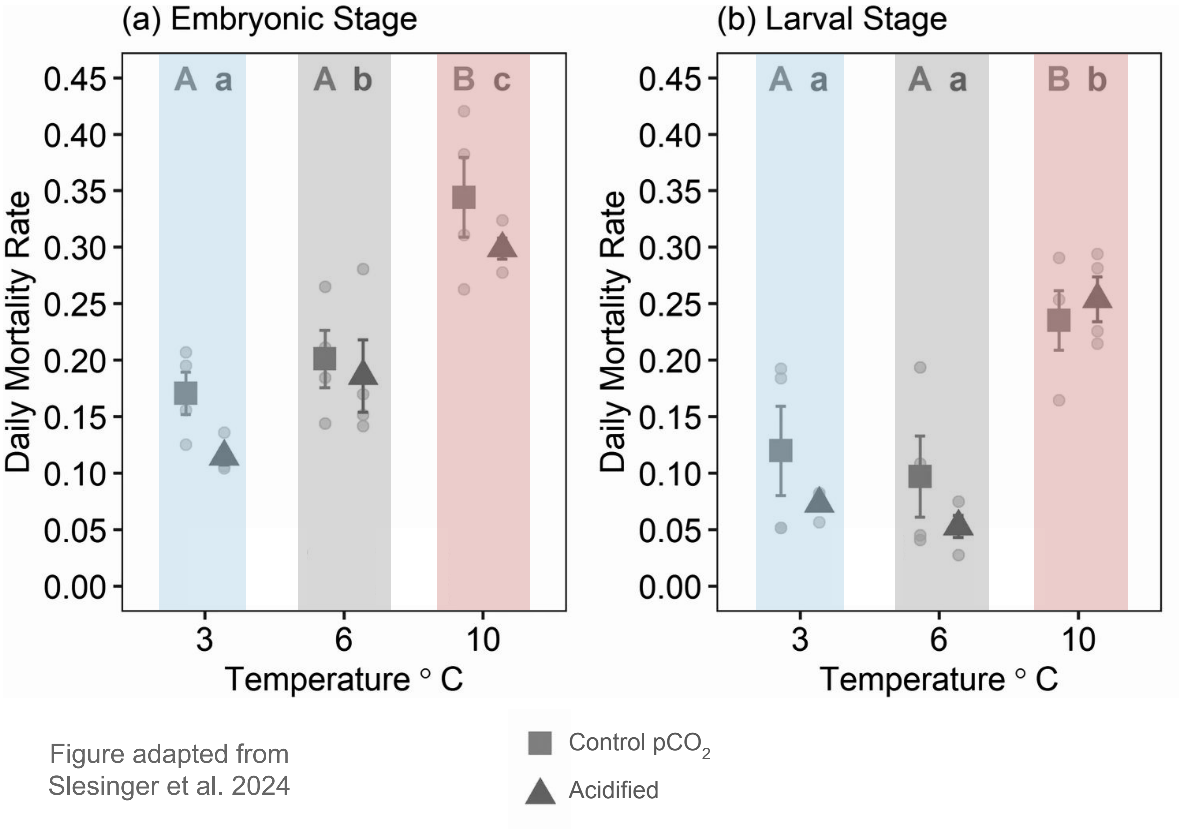
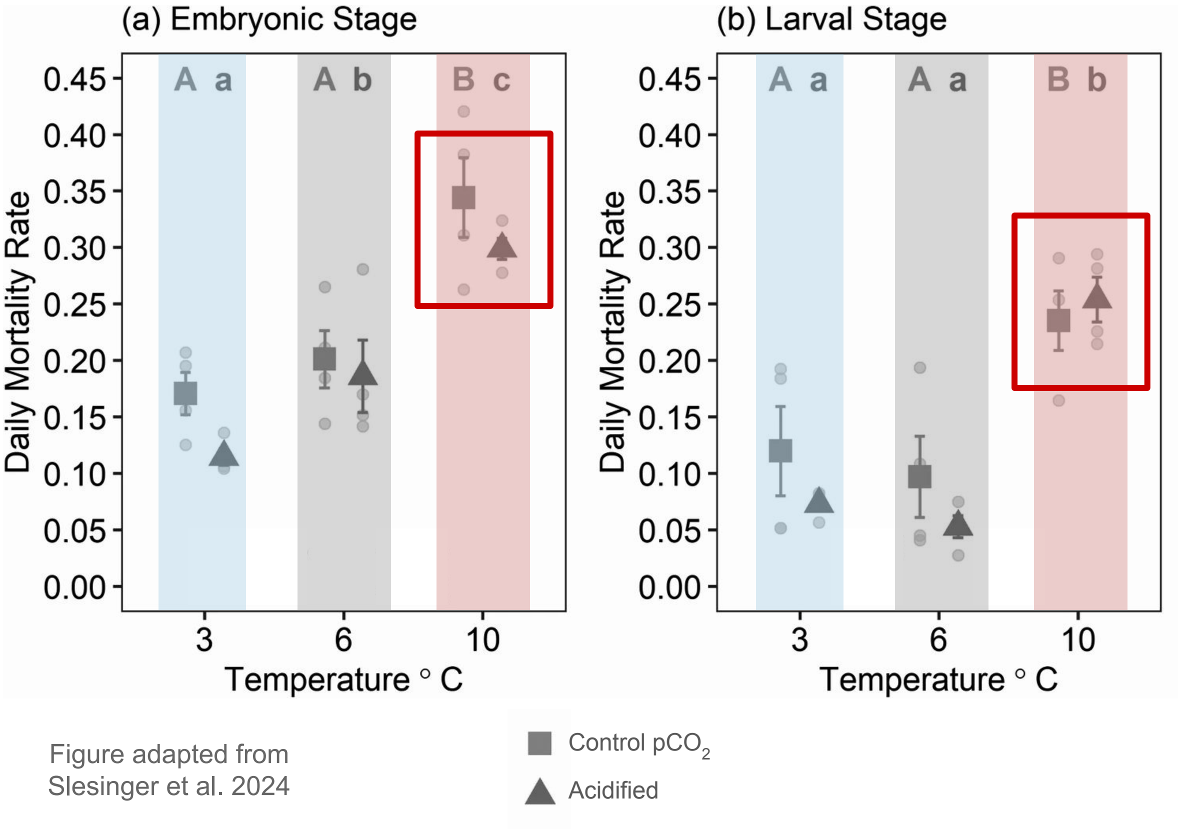


Figure adapted from
Slesinger et al. 2024

High larval mortality in warming - *Heat waves likely decreased recruitment due to low larval survival*
(and Warm+Acidified)



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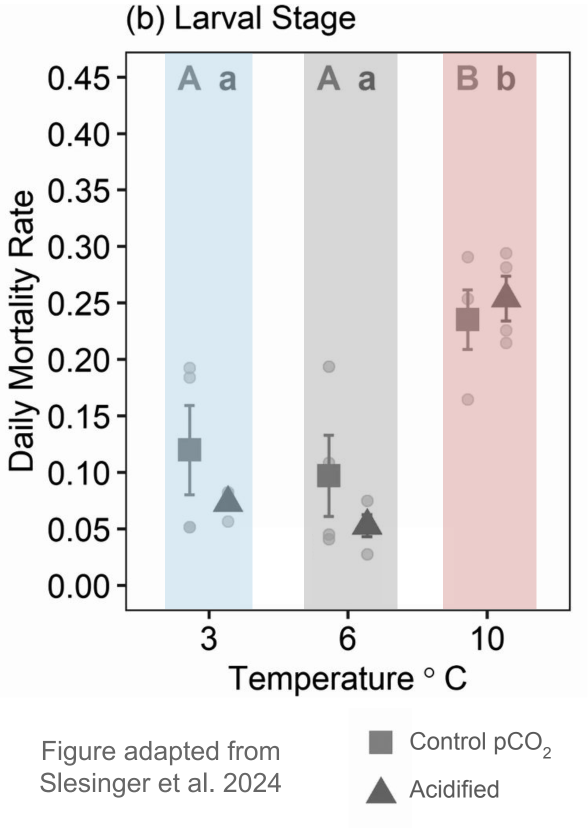


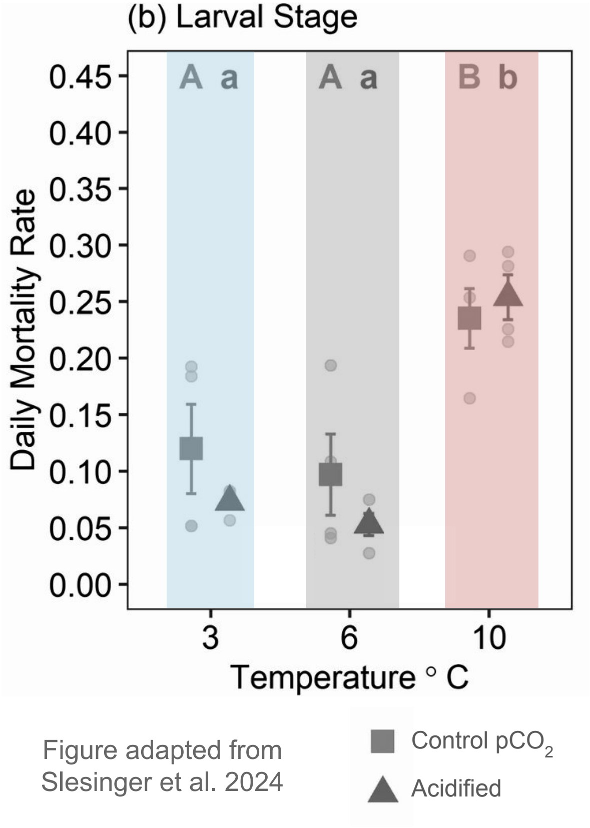
Figure adapted from Slesinger et al. 2024

But **why**?

- Gene expression analysis
- 73 larval cod individuals
- n=11-14 / treatment
- Whole-body tissue

***Goal**: Capture energy allocation, mechanisms of mortality in moribund larvae*

High larval mortality in warming
(and Warm+Acidified)



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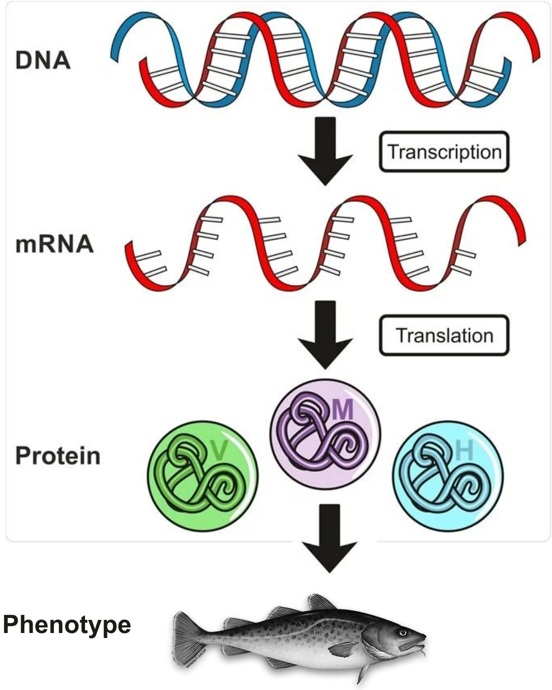

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High larval mortality in warming
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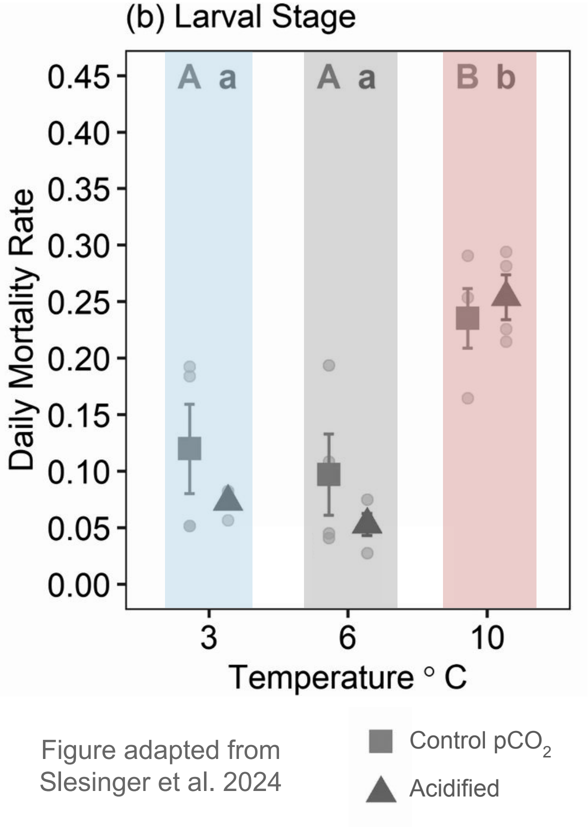

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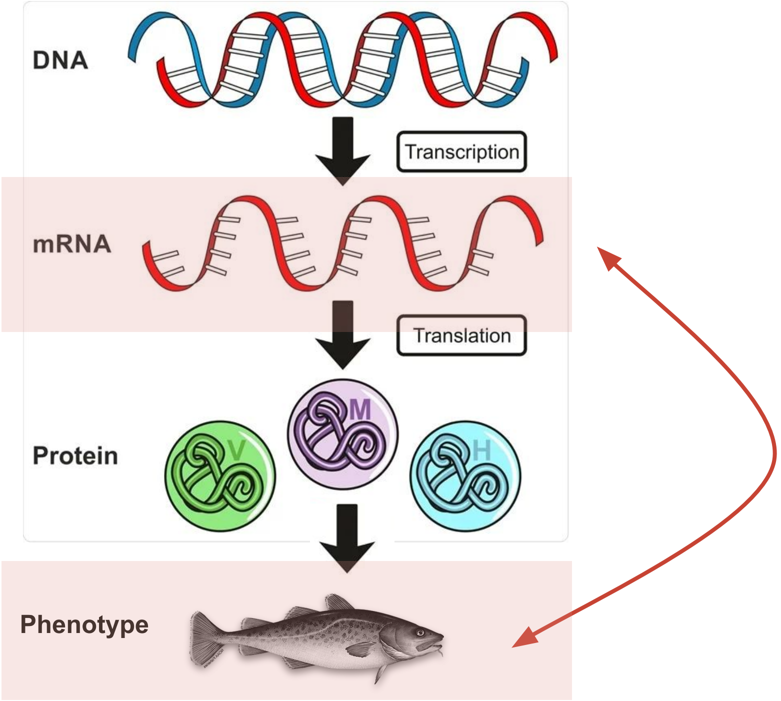

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Hypothesis: high mortality in warming is due to energetic limitations caused by lipid depletion paired with energy-demanding processes (inflammation, cell signaling / stability)

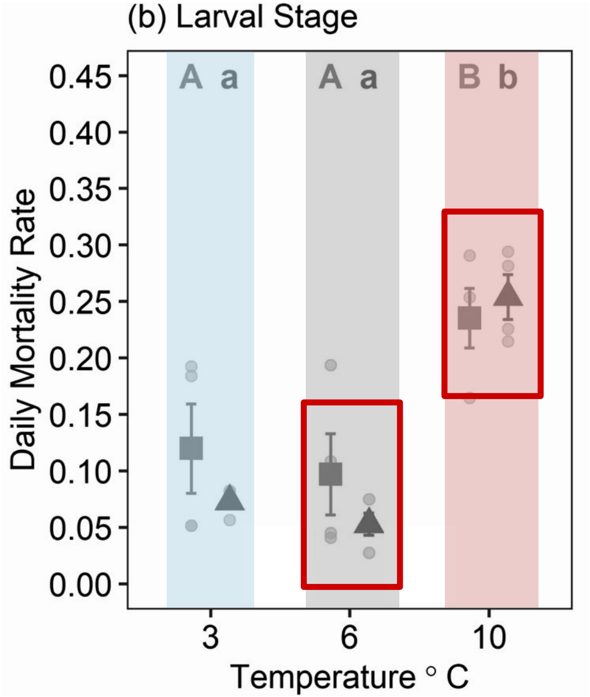
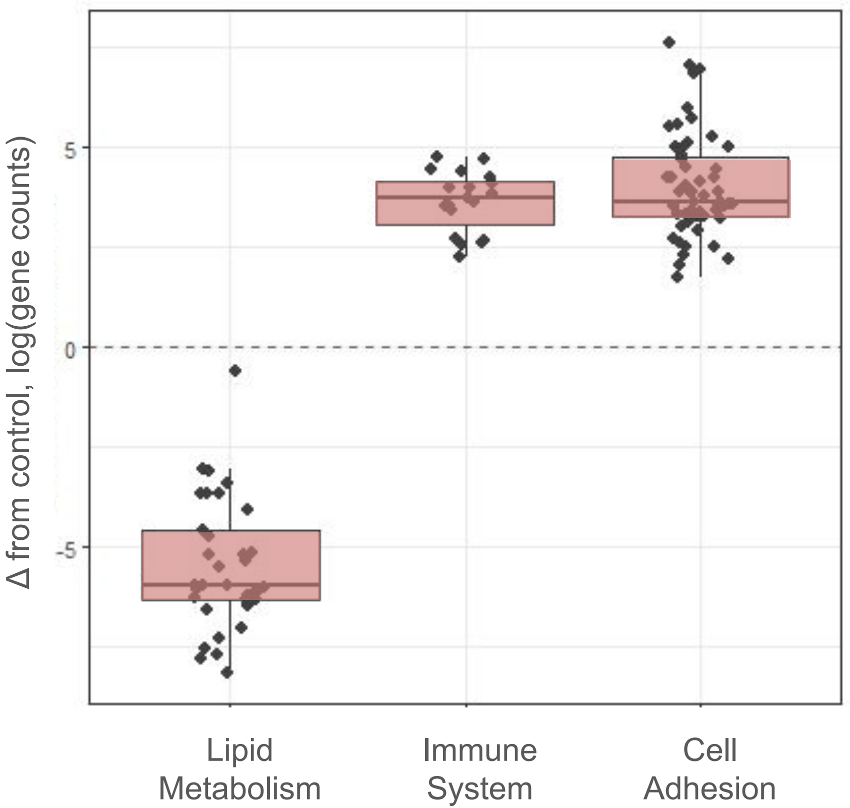


Figure adapted from Slesinger et al. 2024



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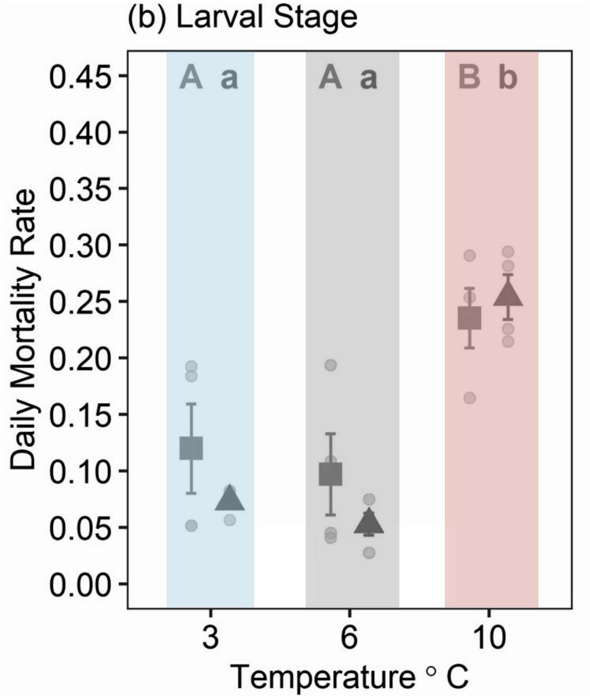


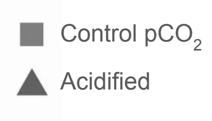
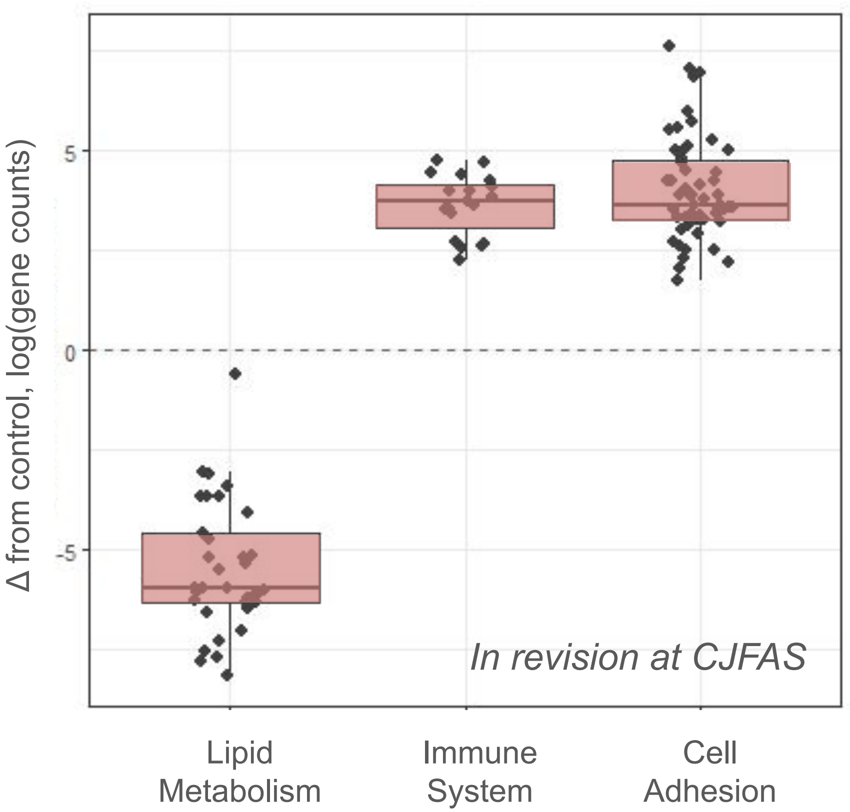


Figure adapted from Slesinger et al. 2024



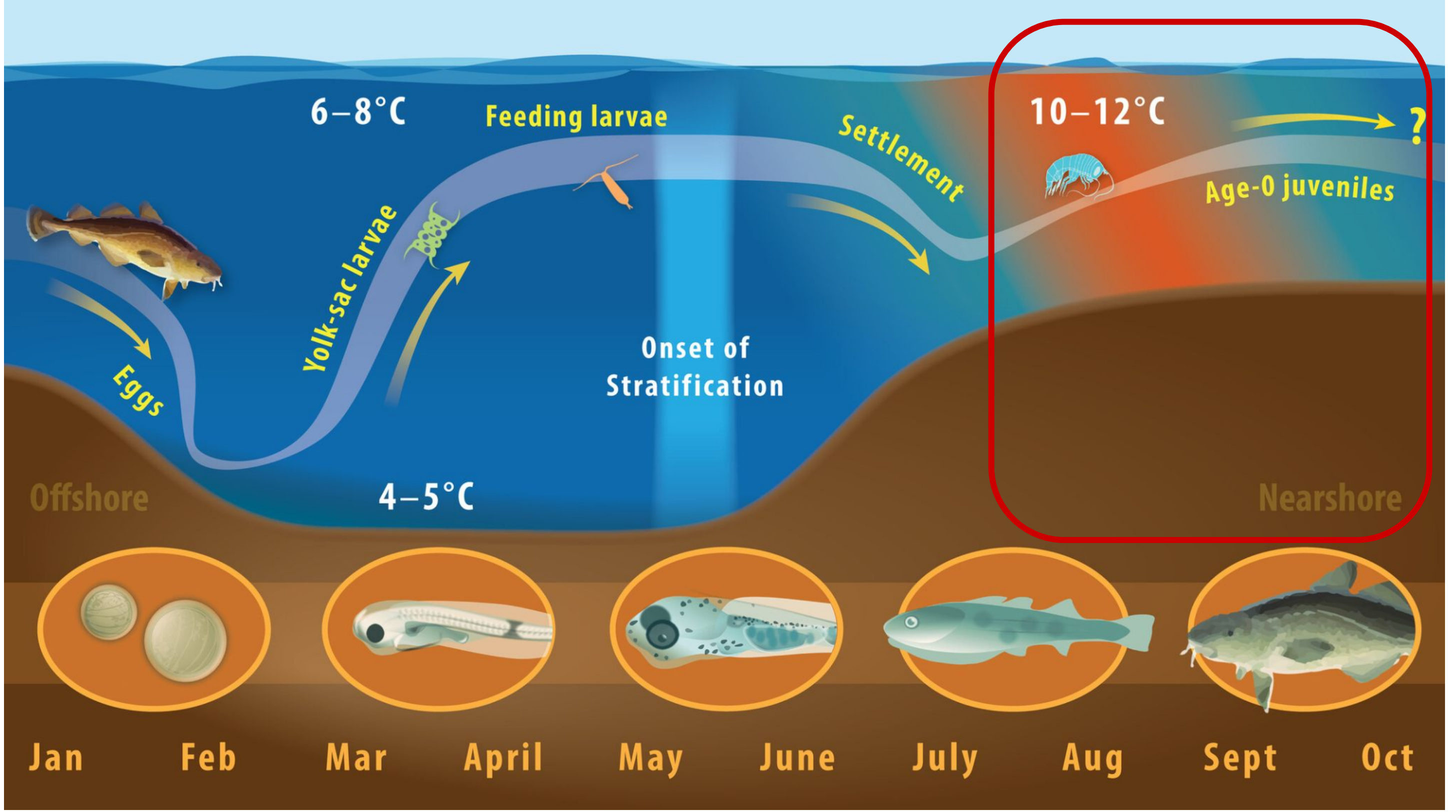
Warming increases larval mortality rates, which likely was a factor influencing recruitment during heatwave years.

Slesinger et al. 2024, Mar. Bio.

Mechanisms of larval mortality in warming could reflect energetic limitations paired with energy-demanding inflammation and cellular instability.

Spencer et al. In Revision, CJFAS

2. *Juvenile study*

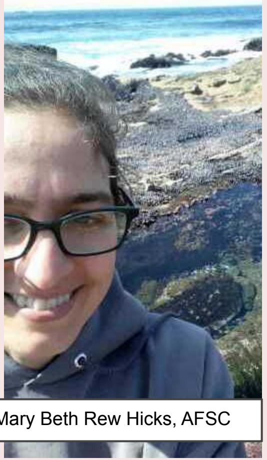


Laurel et al. 2023, in Fish & Fisheries

How does temperature affect **juvenile** Pacific cod **growth, survival, & energy allocation** in their first fall/winter?

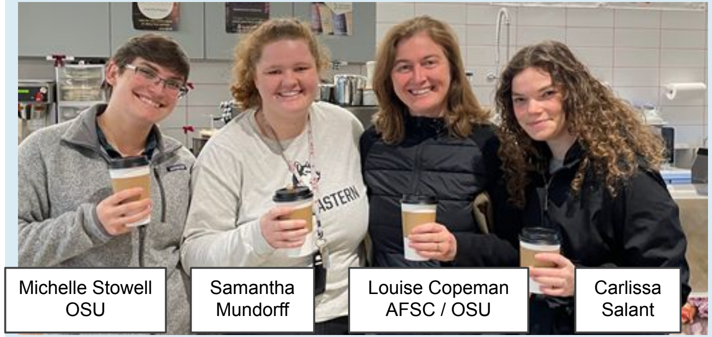
Experimental Team

Ben Laurel, AFSC



Mary Beth Rew Hicks, AFSC

Lipid Team



Michelle Stowell OSU

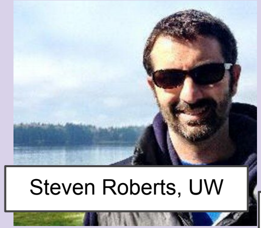
Samantha Mundorff

Louise Copeman AFSC / OSU

Carlissa Salant

‘Omics Team

Me



Steven Roberts, UW

Sara Schaal, AFSC & UO

Wes Larson, AFSC

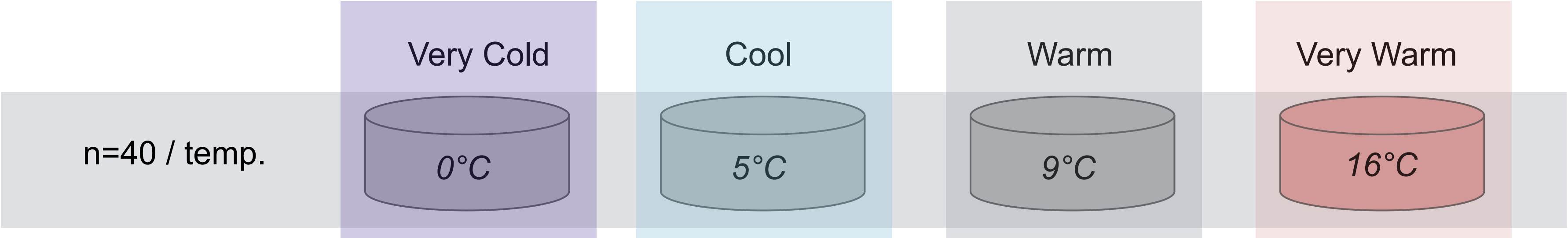
Ingrid Spies, AFSC

Laura Timm, AFSC

Kathleen Durkin, UW

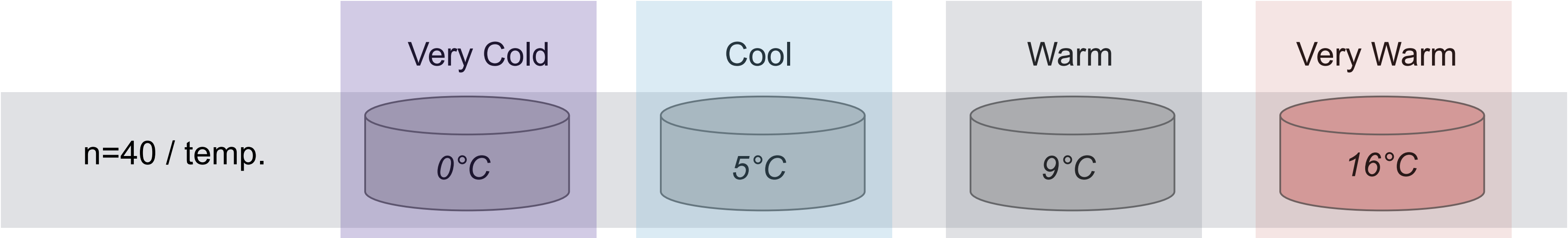
Juvenile temperature experiment

- Wild juveniles (age-0) caught off Kodiak, AK late summer
- Transported to Newport, OR wet lab
- Acclimated
- ~6 weeks experiment

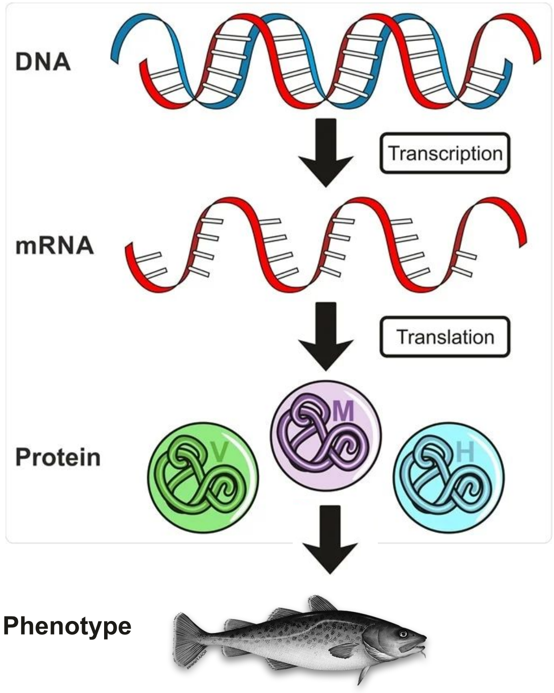


Individuals tagged, collected:

a. Genetics with fin clips, n=40/temp (lcWGS)
b. Growth rates (length & wet weight) during acclimation, treatment
c. Body condition (Kwet)
d. Liver condition (HSI)
e. Survival
f. Liver lipid components (n=25/temp)
g. Gene expression with liver, n=18/temp (RNASeq)



"Genome-to-Phenome" dataset, Pacific cod juvenile temperature response



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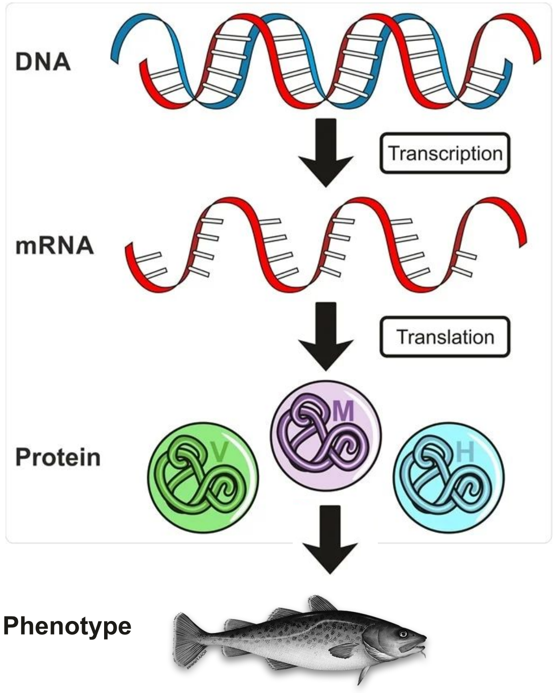
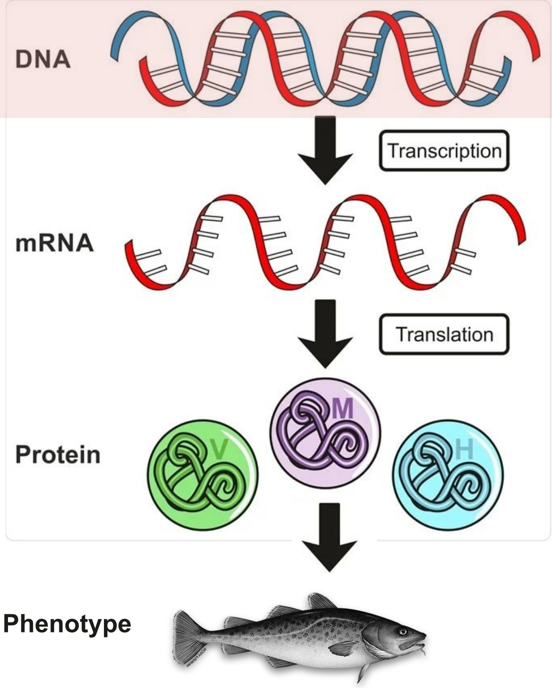


Adapted from: udaix/Shutterstock.com

1. Genetics –
   Who are they?
2. Phenotypes –
   How does warming affect key traits?
3. Integrate datasets –
   Why are some fish less sensitive?

“Genome-to-Phenome” dataset, Pacific cod juvenile temperature response

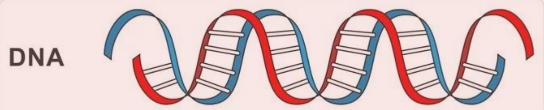
1. Genetics – Who are they (wild caught)?



Adapted from: udaix/Shutterstock.com

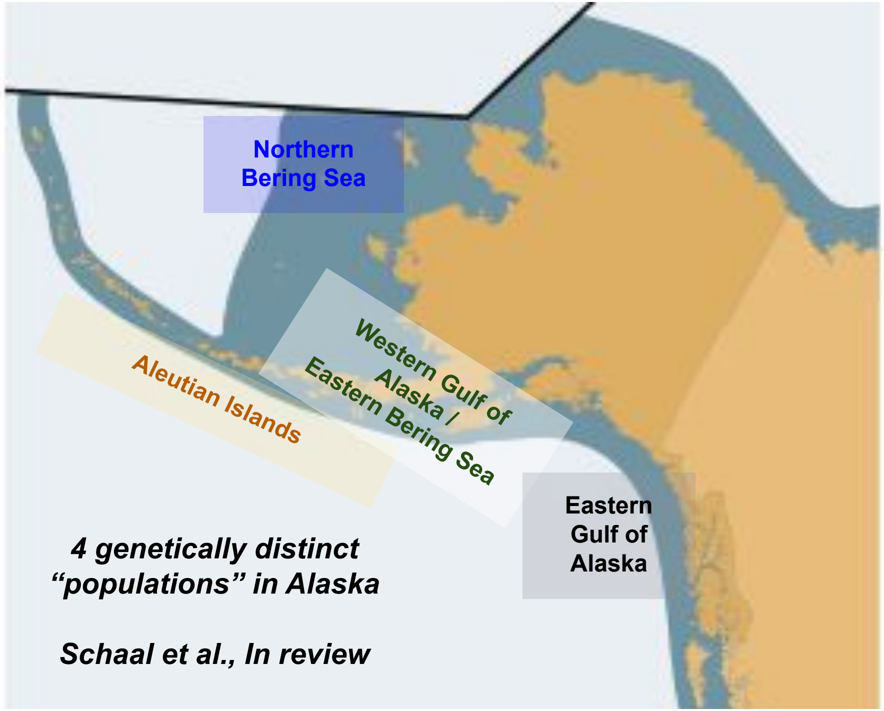
“Genome-to-Phenome” dataset, Pacific cod juvenile temperature response

1. Genetics – <u>Who</u> are they (wild caught)?



Tools used:

- Sequence whole genome ~3x (i.e. “low-coverage”), n=160
- High-quality reference genome for alignment & genotype probability data



What does genotype data look like?

Per-sample genotype

Genome location

Chromosome	Site	Sample 1	Sample 2
Chr1	**10,000,065**	**A/A**	**G/A**
Chr1	10.000,883	C/C	C/T
Chr1	10,001,961	G/G	A/T
Chr1	10,002,133	C/C	C/T
Chr1	10,002,294	G/A	G/A

~160 samples

~350,000 sites

Possible alleles: A,G,T,C
1 from each parent

What does genotype <u>probability</u> data look like?

Most common

Second most common

Per-sample genotype probabilities

Chrom.	Site	Major Allele	Minor Allele	Sample 1 G/G	Sample 1 G/A	**Sample 1 A/A**	Sample 2 G/G	**Sample 2 G/A**	Sample 2 A/A
Chr1	**10,000,065**	**G**	**A**	0.00	0.33	**0.67**	0.03	**0.97**	0.00
Chr1	10.000,883								
Chr1	10,001,961								
Chr1	10,002,133								
Chr1	10,002,294								

~160 samples

Genome location

Sample 1: 67% probability of A/A

Sample 2: 97% probability of G/A

~350,000 sites

Use genotype probability data to ***predict population of origin***

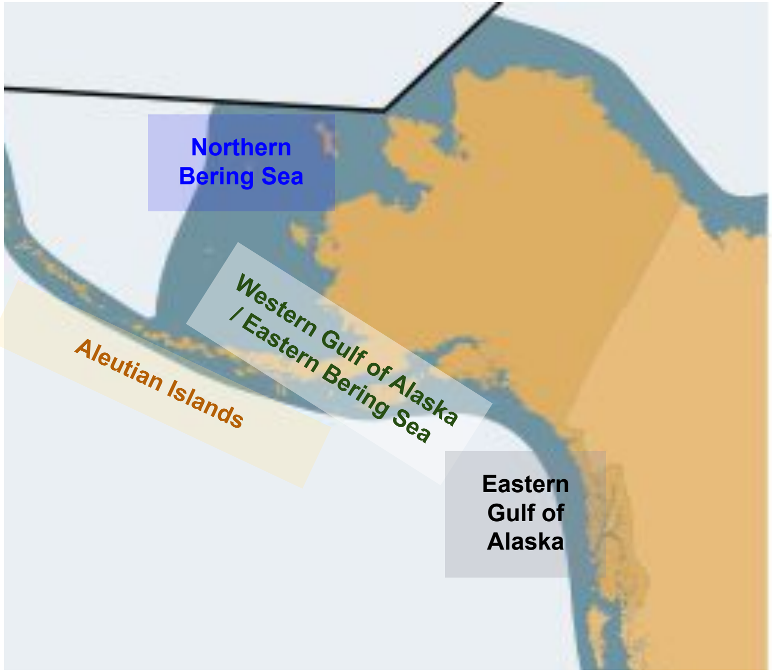
Used genotype probabilities from:

- 160 experimental fish
- <u>More</u> data: ~55 fish per population (Schaal et al. *In review),* “reference fish”

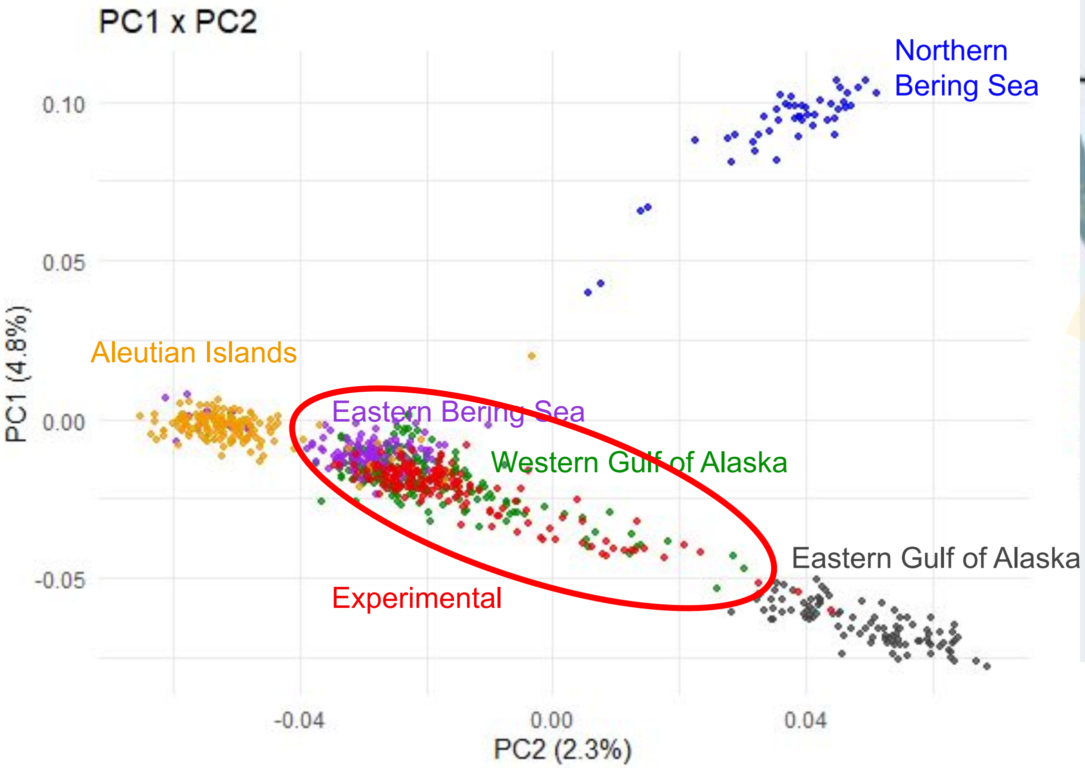
1. Identified sites associated with population differences (top Fst)

2. Identified best sites (n=6,101) that predict population, ~96% assignment accuracy in reference fish

3. **Predict population of origin for experimental fish** `(wgsassign)`



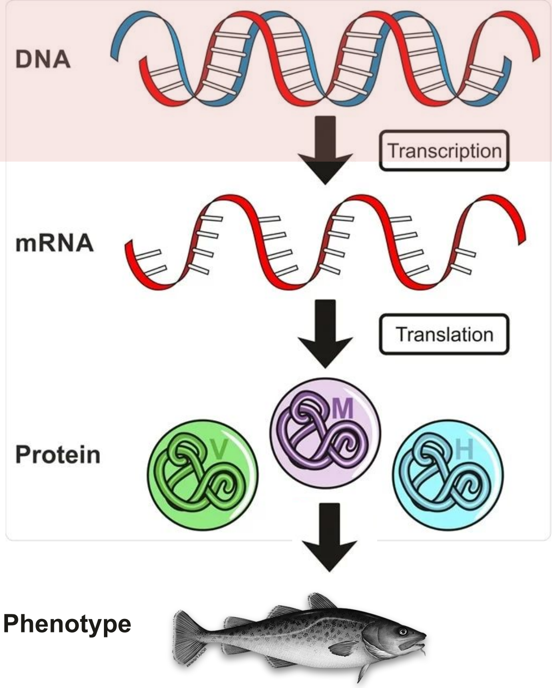
Predicted population of origin = ***Western GOA / Eastern Bering Sea group***



“Genome-to-Phenome” dataset, Pacific cod juvenile temperature response

✓ Genetics – **they are one population**

western Gulf of Alaska / Eastern Bering Sea



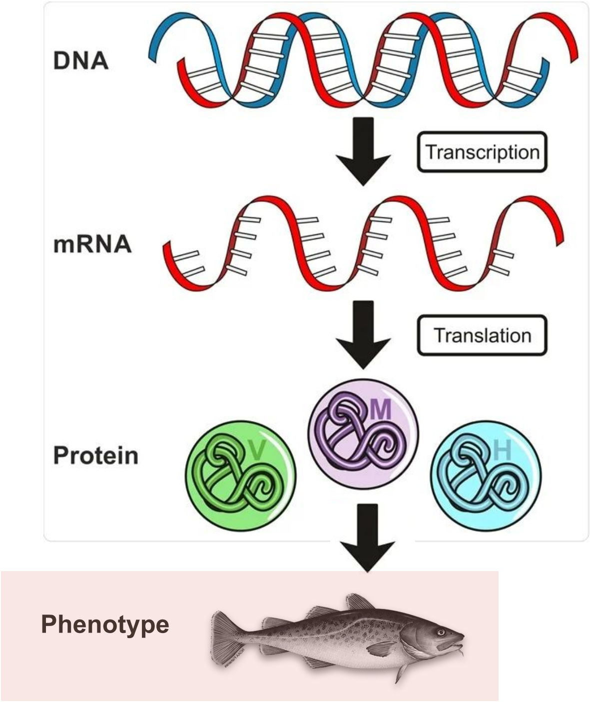
Adapted from: udaix/Shutterstock.com

“Genome-to-Phenome” dataset, Pacific cod juvenile temperature response

✓ Genetics – **they are one population**

western Gulf of Alaska / Eastern Bering Sea

\- Phenotypes – how are survival-associated traits affected?



Adapted from: udaix/Shutterstock.com

Phenotypes - growth rate, liver condition, lipid content

Growth Rate (weight)

Faster growth 👍

Hepatosomatic index (liver size)

Larger liver👍

Total Lipid Content in liver

More lipid 👍

Phenotypes - growth rate, liver condition, lipid content

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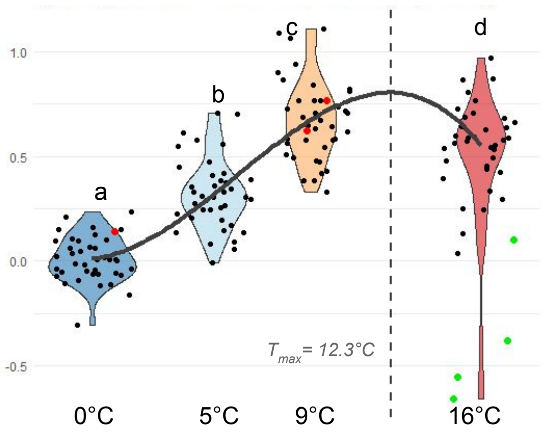

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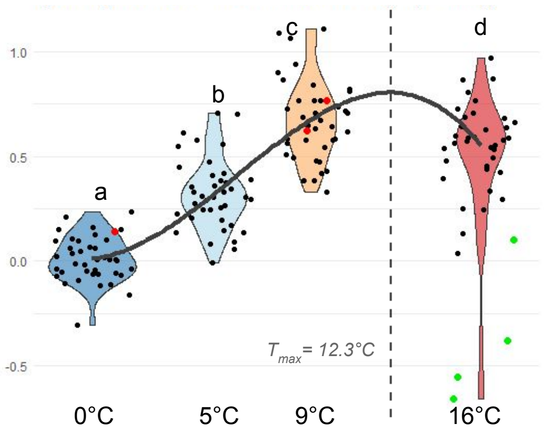

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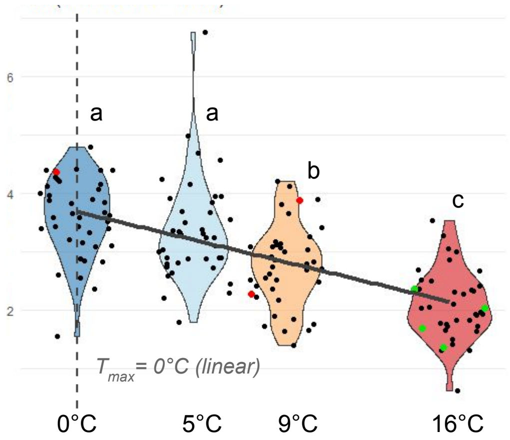

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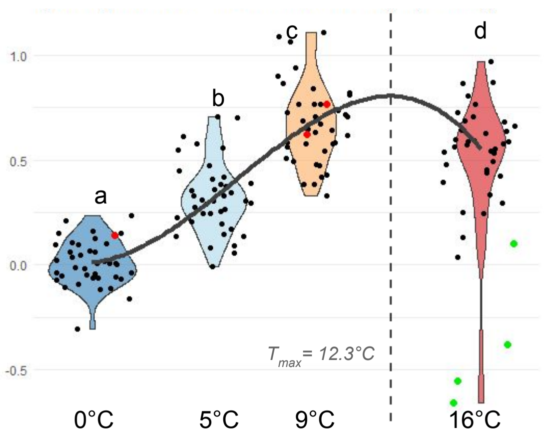

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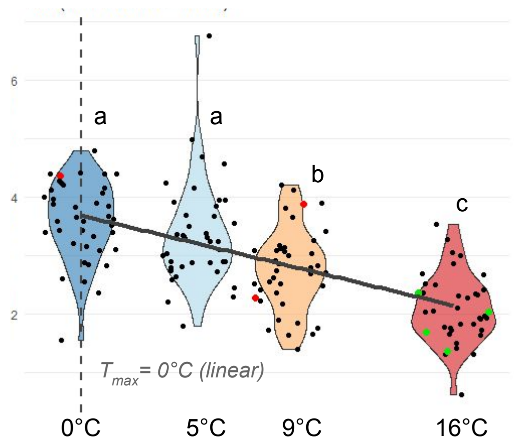

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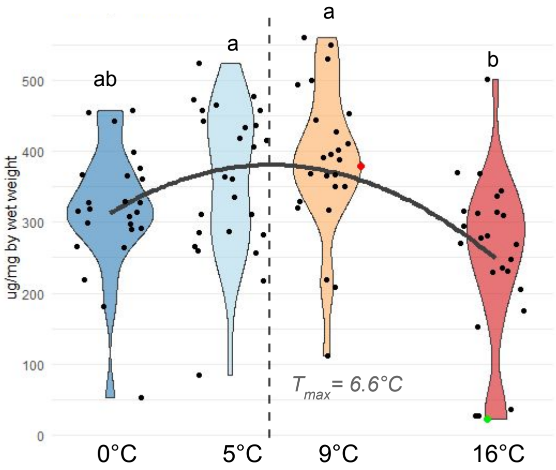
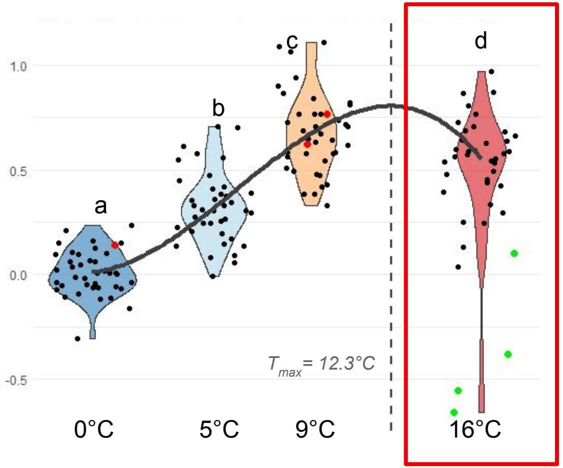


Warming decreased lipid reserves

<u>Growth Rate (weight)</u>

Faster growth 👍



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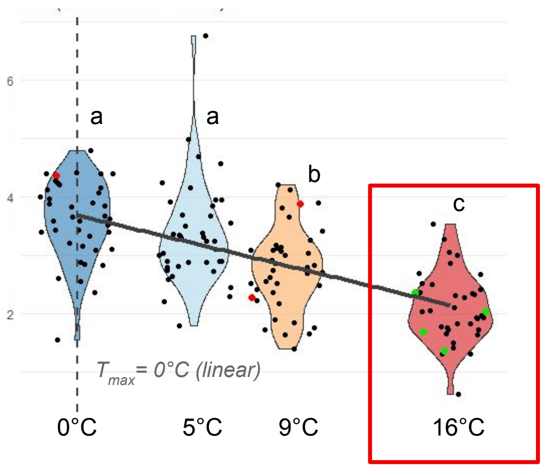

<u>Total Lipid Content in liver</u>

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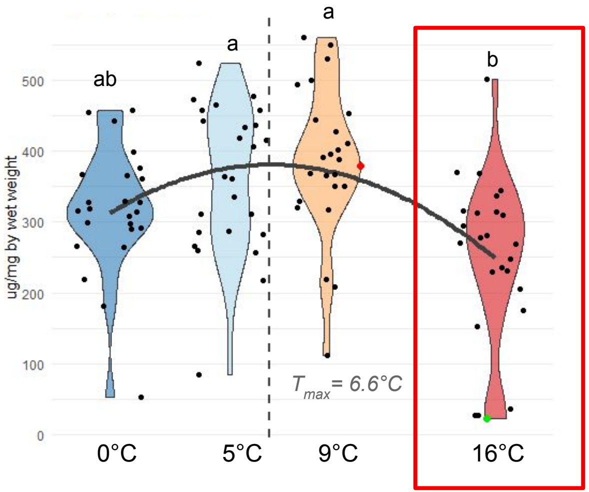

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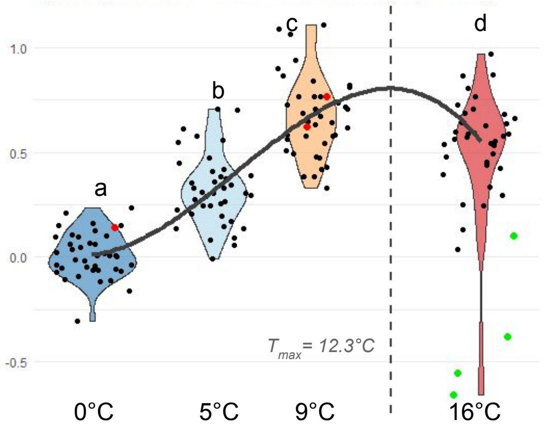

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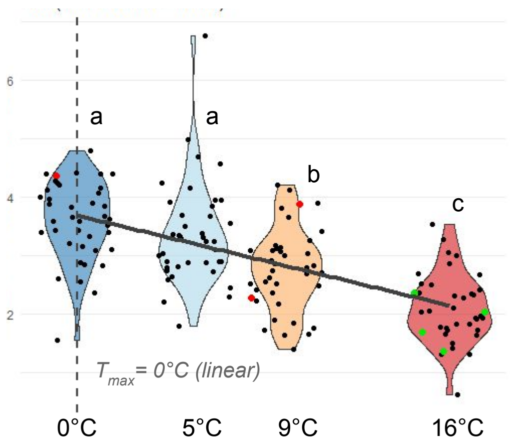

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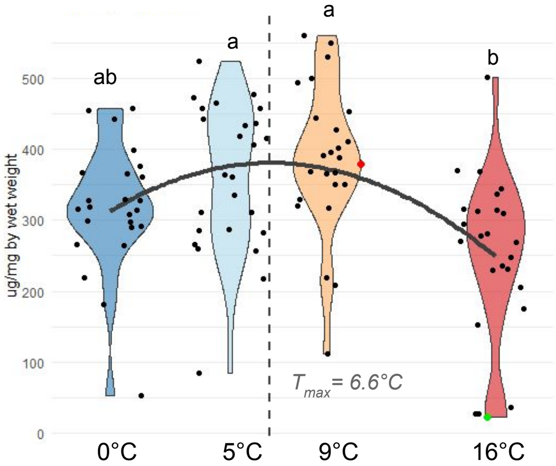


● Survived

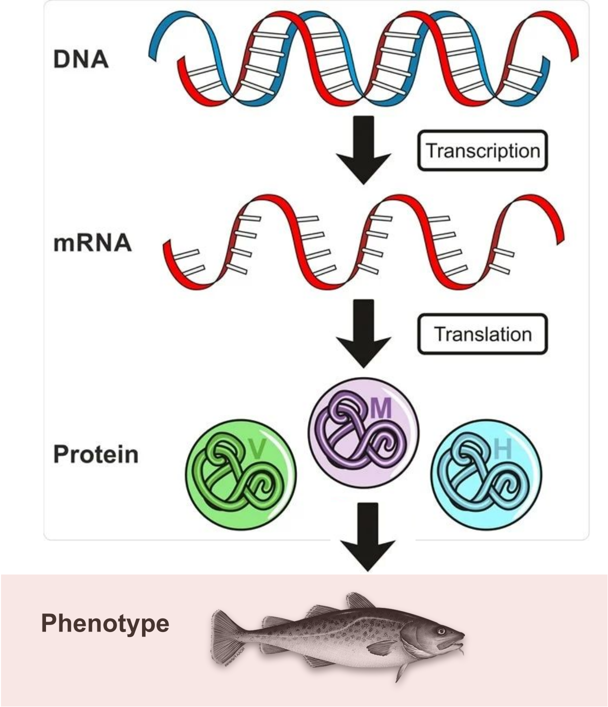
● Died

“Genome-to-Phenome” dataset for juvenile Pacific cod

✓ Genetics – **they are one population**

western Gulf of Alaska / Eastern Bering Sea

✓ Phenotypes – **Fewer lipid reserves in warming, slightly slower growth** - juvenile overwinter survival likely lower during heatwave years.



Adapted from: udaix/Shutterstock.com

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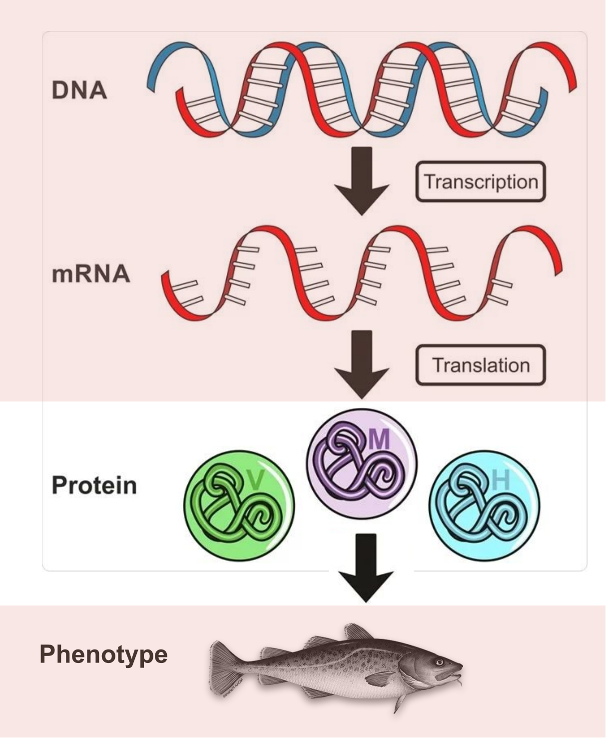
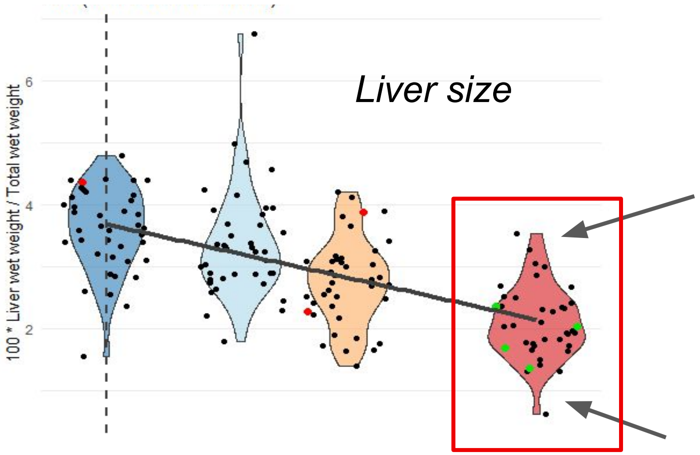
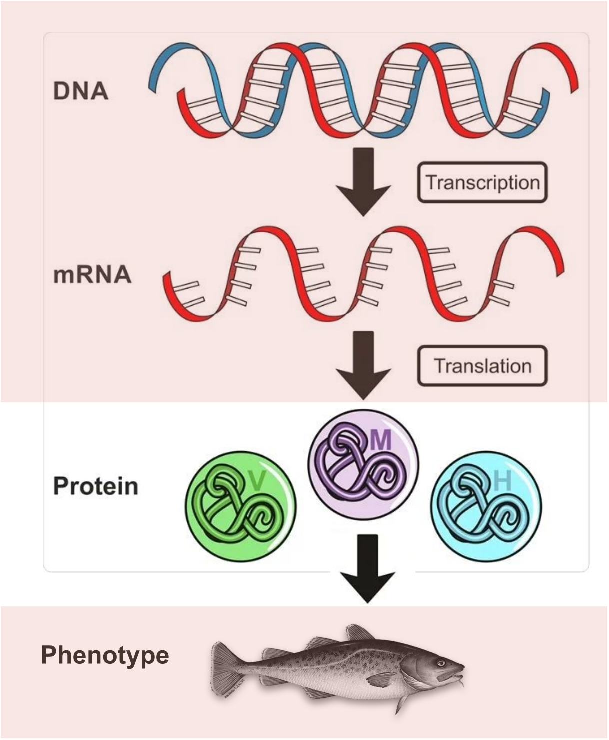
- Integrate datasets – Performance indicators!
  a. Genetic variants
  b. Expression patterns



Adapted from: udaix/Shutterstock.com

Variation within each temperature - opportunity!





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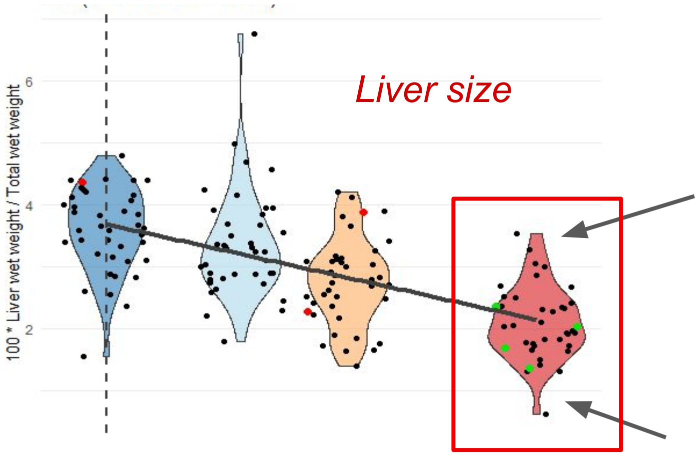
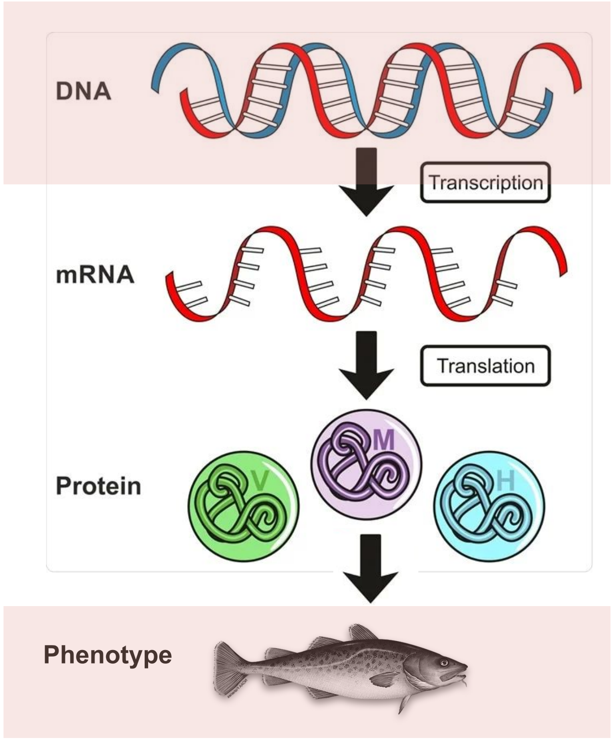


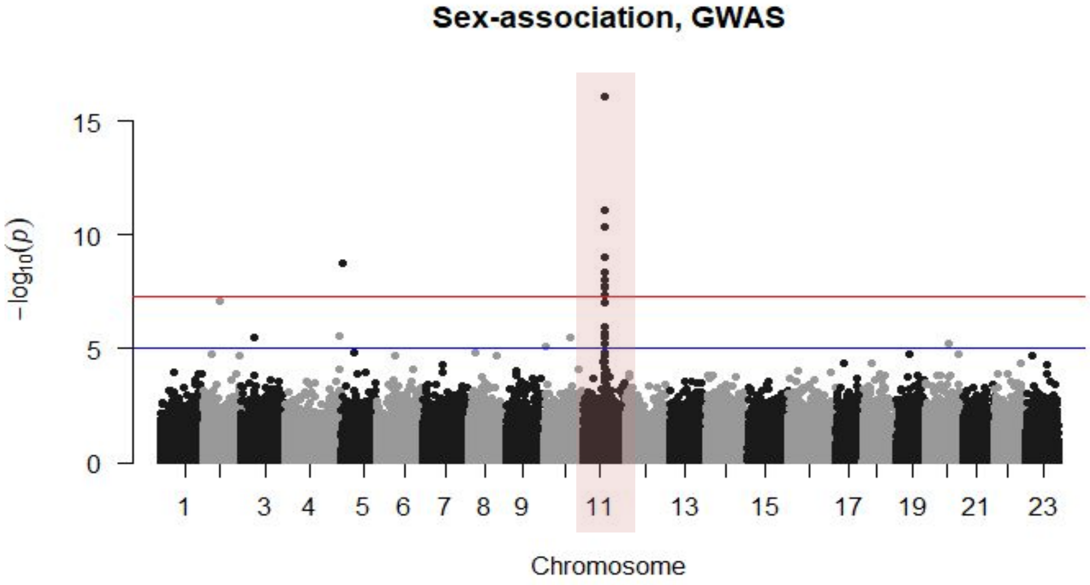
Identified **sites on genome** associated with **liver size**, lipid content, & growth in warming

Genome-Wide Association Studies (GWAS) within each treatment



Adapted from: udaix/Shutterstock.com

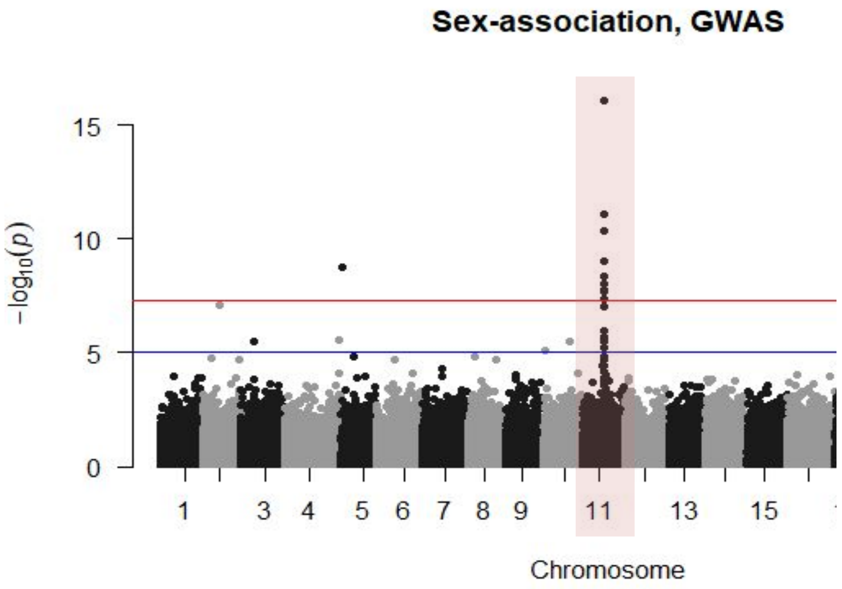
Tangent – using GWAS to identify sex markers (preliminary)



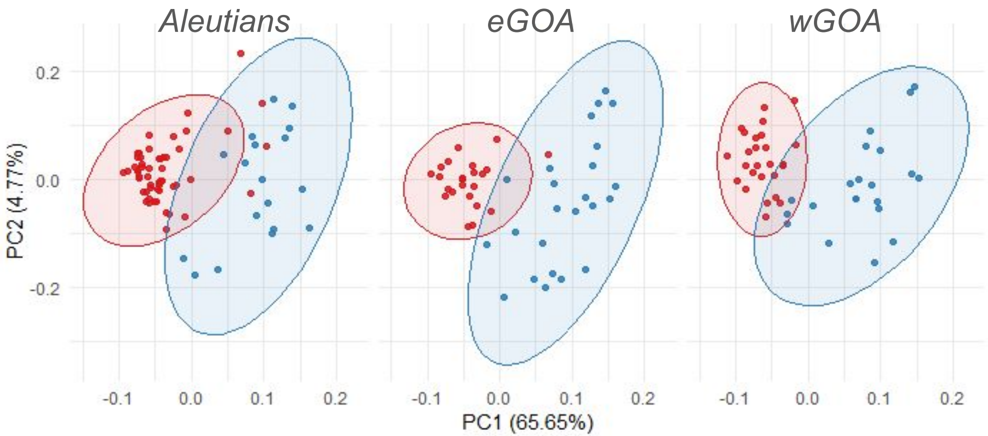
Leveraged genetic data from ~60 females & ~100 males

Data from Schaal et al. In review

Tangent – using GWAS to identify sex markers (preliminary)



PCAs with ~50 sex-associated sites



Female = Male

Tangent – using GWAS to identify sex markers (preliminary)

Sex marker in same Chromosome 11 region in Atlantic cod

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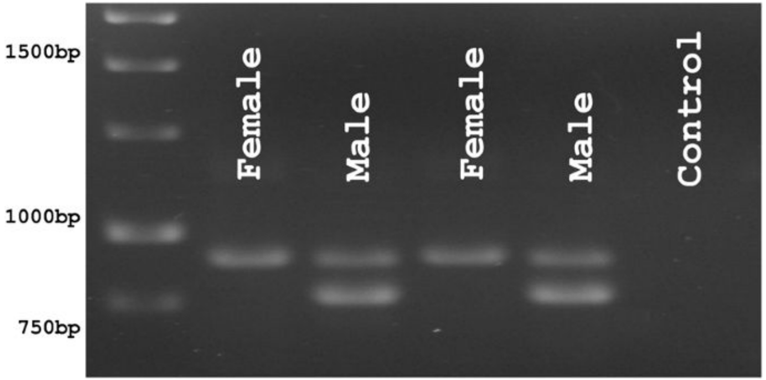
Article | Open access | Published: 15 January 2019

Characterization of a male specific region containing a candidate sex determining gene in Atlantic cod

Tina Graceline Kirubakaran, Øivind Andersen, Maria Cristina De Rosa, Terese Andersstuen, Kristina Hallan, Matthew Peter Kent & Sigbjørn Lien

Scientific Reports **9**, Article number: 116 (2019) | Cite this article

Benchtop sex assay in Atlantic cod



Tangent – using GWAS to identify sex markers (preliminary)

American Genetic Association

Journal of Heredity, 2018, 326–332
doi:10.1093/jhered/esx102
Brief communication
Advance Access publication 9 November 2017

Brief communication

Identification of Genomic Regions Associated With Sex in Pacific Halibut

Daniel P. Drinan, Timothy Loher, and Lorenz Hauser

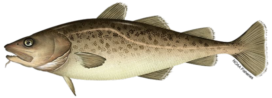
From the University of Washington, School of Aquatic and Fishery Sciences, Seattle, Washington (Drinan); International Pacific Halibut Commission, Seattle, Washington (Loher); University of Washington, School of Aquatic and Fishery Sciences, Seattle, Washington (Hauser).

International Pacific Halibut Commission

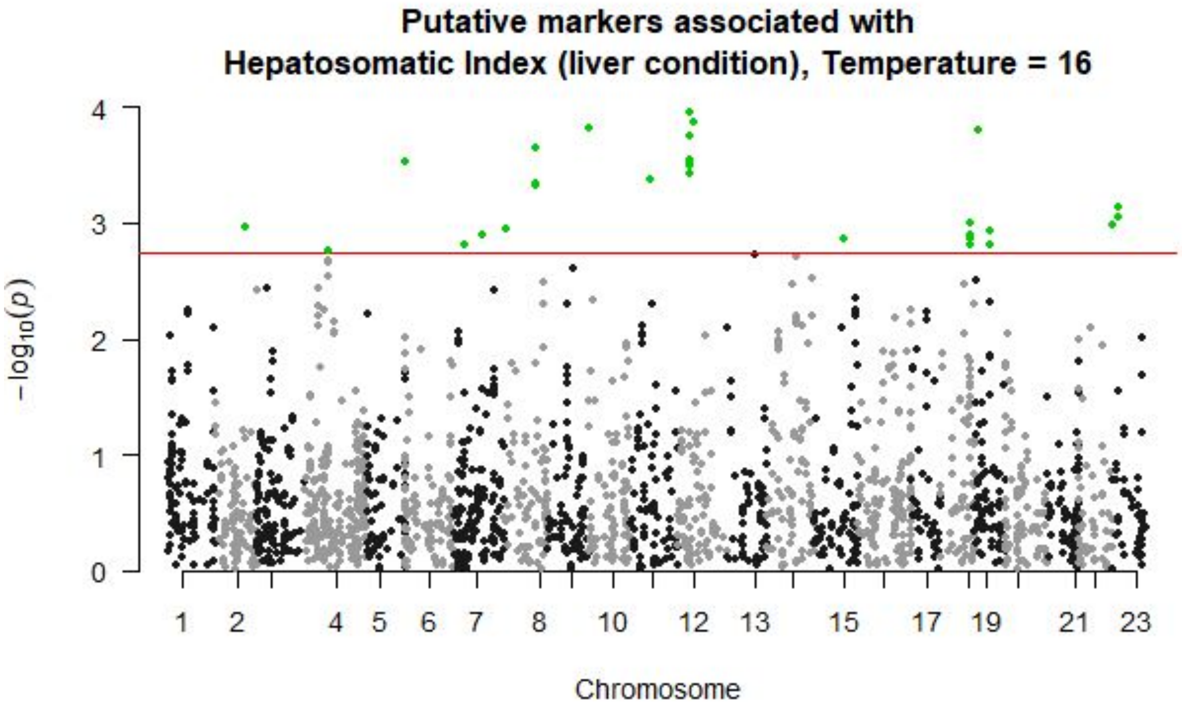
Genetic Markers (SNPs) For Sex Identification

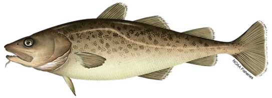
The sex ratio of the commercial fishery catch represents an extremely important source of uncertainty in the annual stock assessment (Stewart and Hicks, 2020). The IPHC has generated sex information of the entire set of aged commercial fishery samples on an annual basis since 2017 (>10,000 fin clips per year). Sex information is obtained using genetic techniques based on the identification of sex-specific single nucleotide polymorphisms (SNPs) (Drinan et al., 2018) using TaqMan qPCR assays conducted at the IPHC's Biological Laboratory. Therefore, direct estimates of the sex-ratio at age for the directed commercial fishery are now available for stock assessment. Sex-ratio information of the commercial catch is likely to further inform selectivity parameters and cumulatively reduce uncertainty in future estimates of stock size, in addition to improving simulation of spawning biomass in the MSE Operating Model.

Genetic markers add sex data from commercially caught halibut to assessment



~100 markers putatively associated with liver size in Pacific cod juveniles exposed to warming





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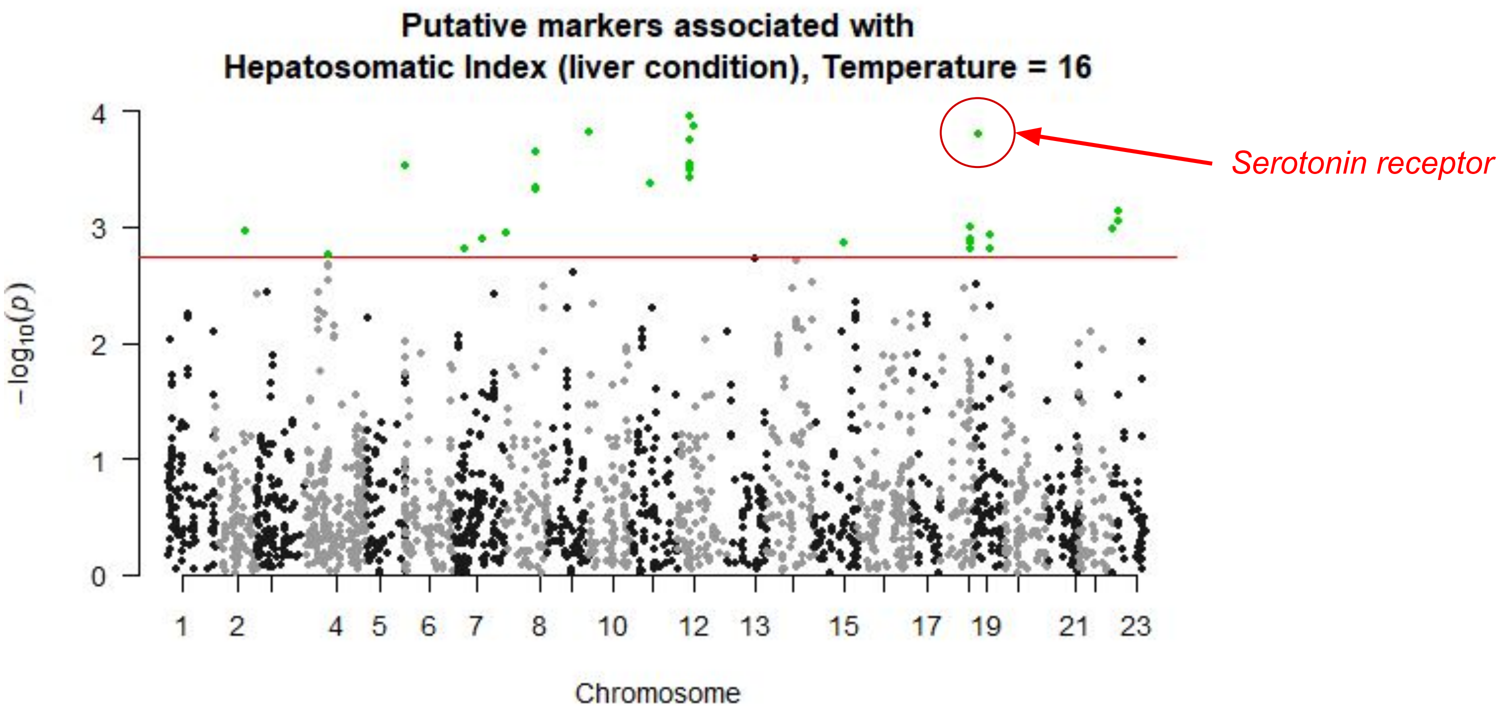

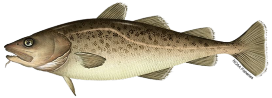

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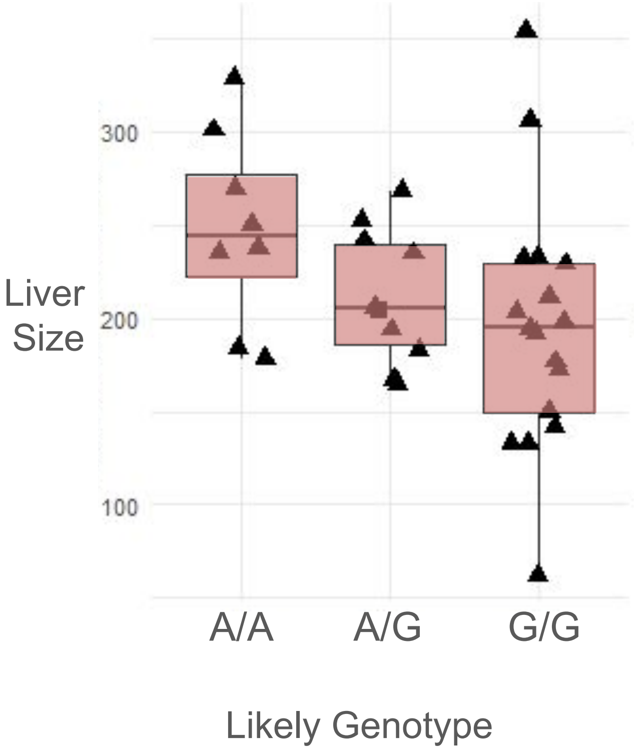


Marker in a gene coding for a ***receptor for serotonin*** *(5-HT4) which regulates appetite*

“Genome-to-Phenome” dataset for juvenile Pacific cod

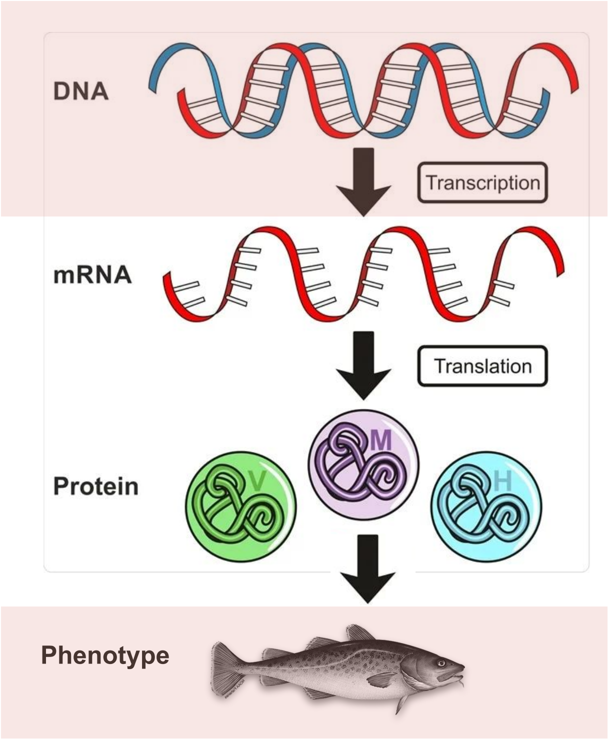
- ✓ Genetics – **they are one population**

  western Gulf of Alaska / Eastern Bering Sea

- ✓ Phenotypes – **Fewer lipid reserves in warming, slightly slower growth**

- ✓ Gene expression – **Lipid usage, immune activity, & damage control may deplete energy reserves**

1. Integrate datasets – Performance indicators!
   - ✓ **~100 genetic markers** of liver size in warming
   - a. Expression patterns



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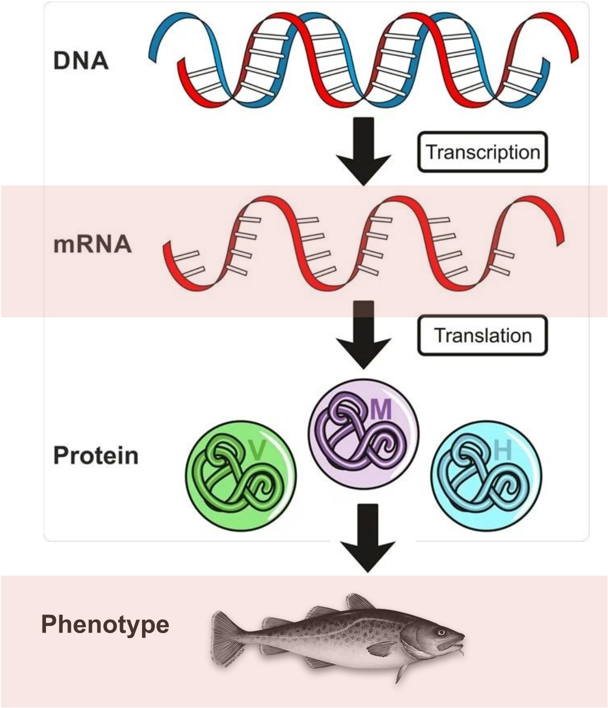


Adapted from: udaix/Shutterstock.com

What does my gene expression data look like?

Gene ID in genome

Samples

gene_gadmor	PCG001	PCG004	PCG011	PCG015	PCG017	PCG020	PCG029	PCG035
ND1	8276	8202	8327	7750	5508	4351	5673	6385
ND2	39142	43297	57032	31681	33489	30275	38921	36460
COX1	555463	631876	917827	551062	378628	403956	438595	455514
COX2	315625	309958	493176	294979	189346	229132	227614	219894
ATP6	82892	105415	89100	73253	77770	58061	86703	78859
COX3	165275	189321	235193	135559	112870	81377	135462	126615
ND3	10710	13595	10404	7013	10244	2567	9792	8231
ND4L	19364	31196	42855	16261	20566	17877	21021	16269
ND4	37081	42648	67118	30275	29274	37939	35681	34155
ND5	16299	21803	[illegible]	[illegible]	[illegible]	19960	19262	18187
ND6	4102	3787	[illegible]	[illegible]	[illegible]	1774	3772	3391
CYTB	176843	211635	[illegible]	[illegible]	[illegible]	114784	137070	144369
LOC115539476	260	228	333	219	270	266	312	266
LOC115539709	890	849	919	777	561	461	945	1000
LOC115538781	586	596	576	630	417	450	704	730
abhd14a	1197	1381	1629	1031	774	757	1158	1108
acy1	1626	1244	1670	1245	1224	1386	1566	1642
LOC115537228	2106	2402	2555	2008	1845	2826	2127	2235
LOC115537019	659	544	911	564	505	611	696	444
LOC115538651	727	674	630	564	479	599	554	523
LOC115538267	57	192	81	153	104	137	110	104
kbtbd12	1003	743	646	766	715	875	301	216

Gene counts

What does my gene expression data look like?

Gene ID in genome

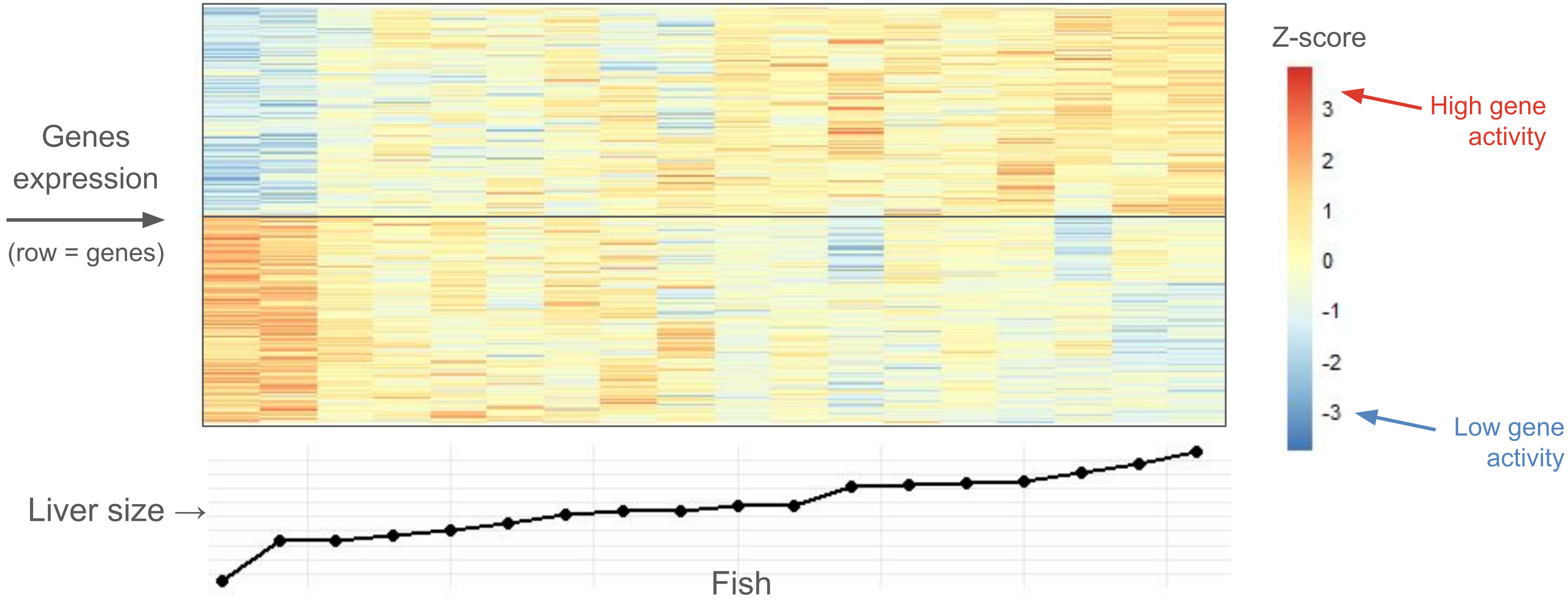
Samples

functional info for many gene

Gene counts

gene_gadmor	PCG001	PCG004	PCG011	PCG015	PCG017	PCG020	PCG029	PCG035	spid	species	evalue	protein_names
ND1	8276	8202	8327	7750	5508	4351	5673	6385	P55779	GADMO	0.00e+00	NADH-ubiquinone oxidoreductase chain 1 (EC 7.1.1.2) (NA
ND2	39142	43297	57032	31681	33489	30275	38921	36460	P55780	GADMO	2.40e-158	NADH-ubiquinone oxidoreductase chain 2 (EC 7.1.1.2) (NA
COX1	555463	631876	917827	551062	378628	403956	438595	455514	Q36775	GADMO	0.00e+00	Cytochrome c oxidase subunit 1 (EC 7.1.1.9) (Cytochrome c
COX2	315625	309958	493176	294979	189346	229132	227614	219894	Q37741	GADMO	1.12e-132	Cytochrome c oxidase subunit 2 (EC 7.1.1.9) (Cytochrome c
ATP6	82892	105415	89100	73253	77770	58061	86703	78859	P55778	GADMO	2.60e-104	ATP synthase subunit a (F-ATPase protein 6)
COX3	165275	189321	235193	135559	112870	81377	135462	126615	P55777	GADMO	5.84e-152	Cytochrome c oxidase subunit 3 (EC 7.1.1.9) (Cytochrome c
ND3	10710	13595	10404	7013	10244	2567	9792	8231	P15957	GADMO	1.48e-32	NADH-ubiquinone oxidoreductase chain 3 (EC 7.1.1.2) (NA
ND4L	19364	31196	42855	16261	20566	17877	21021	16269	P23633	GADMO	1.08e-41	NADH-ubiquinone oxidoreductase chain 4L (EC 7.1.1.2) (N
ND4	37081	42648	67118	30275	29274	37939	35681	34155	P55781	GADMO	0.00e+00	NADH-ubiquinone oxidoreductase chain 4 (EC 7.1.1.2) (NA
ND5	16299	21803	2823[illegible]	[illegible]	[illegible]	19960	19262	18187	P55782	GADMO	0.00e+00	NADH-ubiquinone oxidoreductase chain 5 (EC 7.1.1.2) (NA
ND6	4102	3787	3181	[illegible]	[illegible]	1774	3772	3391	P55783	GADMO	1.86e-42	NADH-ubiquinone oxidoreductase chain 6 (EC 7.1.1.2) (NA
CYTB	176843	211635	277395	[illegible]	[illegible]	114784	137070	144369	Q37080	GADMO	0.00e+00	Cytochrome b (Complex III subunit 3) (Complex III subunit
LOC115539476	260	228	333	219	270	266	312	266	Q99MK9	MOUSE	1.66e-27	Ras association domain-containing protein 1 (Protein 123F
LOC115539709	890	849	919	777	561	461	945	1000	Q9WVF8	MOUSE	5.41e-27	Tumor suppressor candidate 2 (Fusion 1 protein) (Fus-1 pr
LOC115538781	586	596	576	630	417	450	704	730	Q12891	HUMAN	3.51e-104	Hyaluronidase-2 (Hyal-2) (EC 3.2.1.35) (Hyaluronoglucosam
abhd14a	1197	1381	1629	1031	774	757	1158	1108	Q1LV46	DANRE	4.34e-34	Protein ABHD14A (EC 3.-.-.-) (Alpha/beta hydrolase domai
acy1	1626	1244	1670	1245	1224	1386	1566	1642	Q6PTT0	RAT	2.57e-16	Aminoacylase-1B (ACY-1B) (EC 3.5.1.14) (ACY IB) (N-acyl-L-
LOC115537228	2106	2402	2555	2008	1845	2826	2127	2235	Q6PHS9	MOUSE	1.07e-34	Voltage-dependent calcium channel subunit alpha-2/delta
LOC115537019	659	544	911	564	505	611	696	444	Q90339	CYPCA	1.94e-172	Myosin heavy chain, fast skeletal muscle
LOC115538651	727	674	630	564	479	599	554	523	Q9NXG6	HUMAN	5.61e-20	Transmembrane prolyl 4-hydroxylase (P4H-TM) (EC 1.14.11
LOC115538267	57	192	81	153	104	137	110	104	Q8CIW6	MOUSE	3.91e-23	Solute carrier family 26 member 6 (Anion exchange transp
kbtbd12	1003	743	646	766	715	875	301	216	Q3ZB90	DANRE	0.00e+00	Kelch repeat and BTB domain-containing protein 12 (Kelch

~ 1,600 genes with expression associated with liver size in warming



Liver size performance indicators in **warming**, both GENETICS and EXPRESSION

	Chromosome	# of markers	Gene ID	Protein Name	Function
Cell adhesion	4	3	LOC132456135	Netrin receptor UNC5D	Cell adhesion, apoptosis in response to DNA damage
Calcium transport	12	2	tmco1	Calcium load-activated calcium channel	Calcium transport, endoplasmic reticulum calcium homeostasis
	10	1	LOC132466560	TBC1 domain family member 9B	Membrane trafficking, calcium transport
Immune system	2	1	LOC132453053	Stonustoxin subunit beta	May be related immune system function. From stonefish, toxic/fatal to mammals.
	5	1	LOC132457513	Stonustoxin subunit beta	May be related immune system function. From stonefish, toxic/fatal to mammals.
	23	1	LOC132452628	NLR family CARD domain-containing protein 3	Negative regulator of the innate immune response
	23	1	LOC132452644	HERV-H LTR-associating protein 2	Enhances T-cell proliferation and cytokine production
	17	2	LOC132445594	Unknown	Unknown

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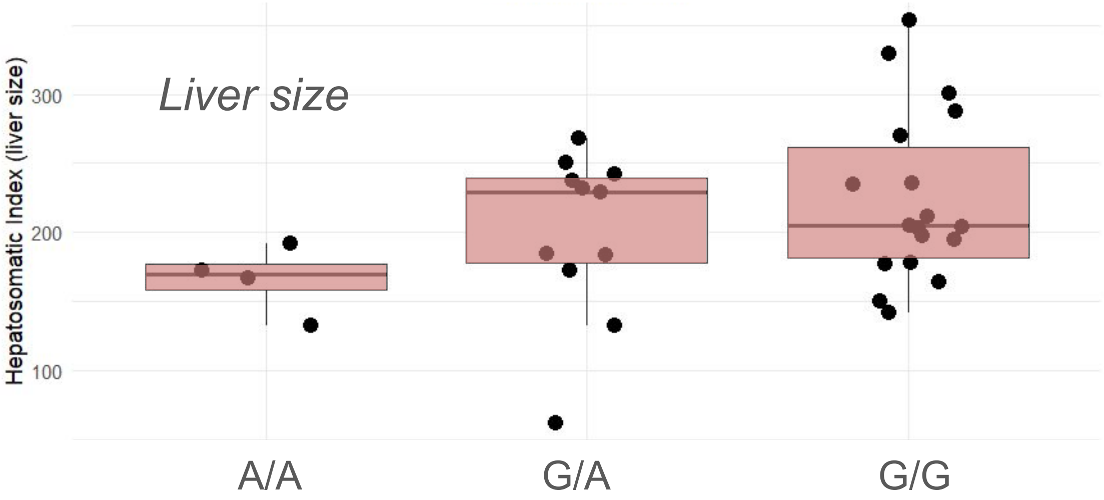
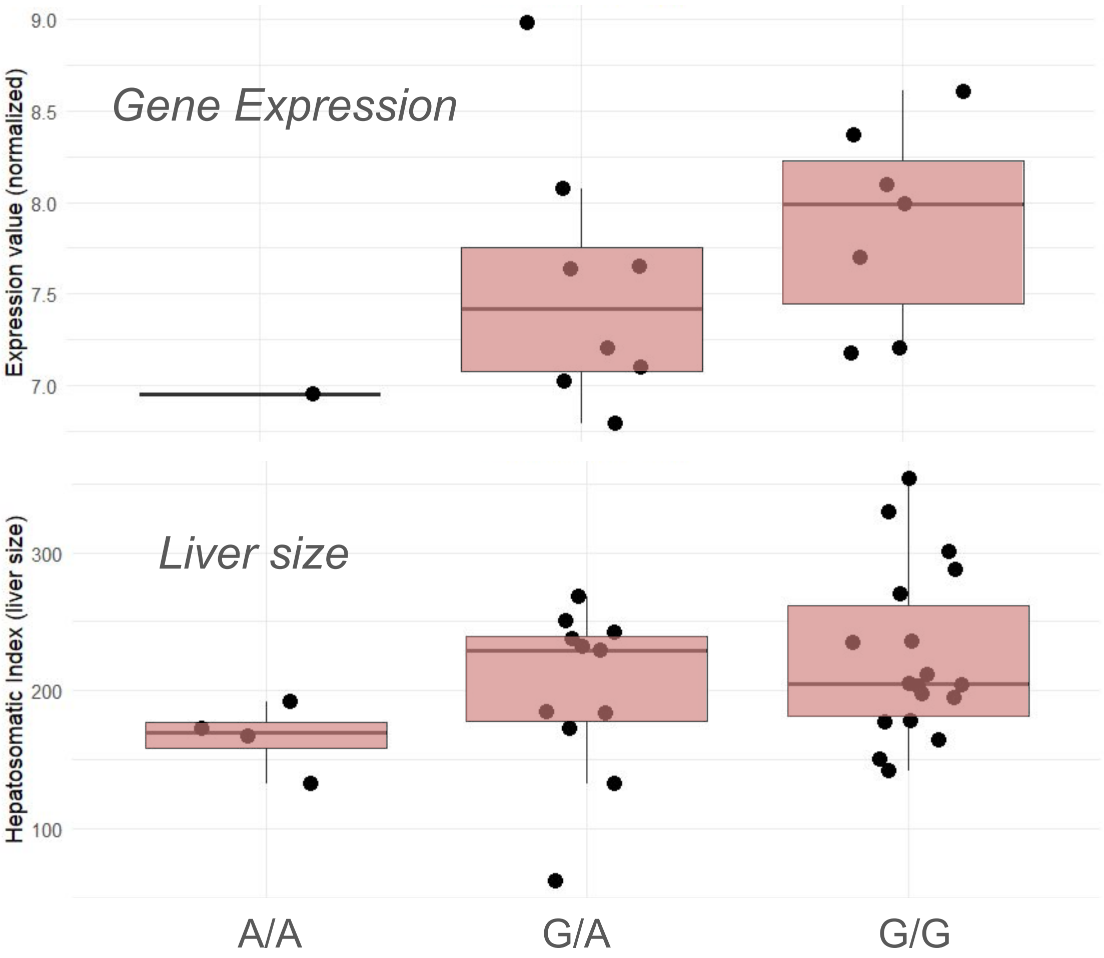
	23	1	LOC132452628	NLR family CARD domain-containing protein 3	Negative regulator of the innate immune response
	23	1	LOC132452644	HERV-H LTR-associating protein 2	Enhances T-cell proliferation and cytokine production
	17	2	LOC132445594	Unknown	Unknown



NLR family CARD domain-containing protein 3

Negatively regulates immune system



NLR family CARD domain-containing protein 3

Negatively regulates immune system

This marker found in all four temperature treatments

“Genome-to-Phenome” dataset for juvenile Pacific cod

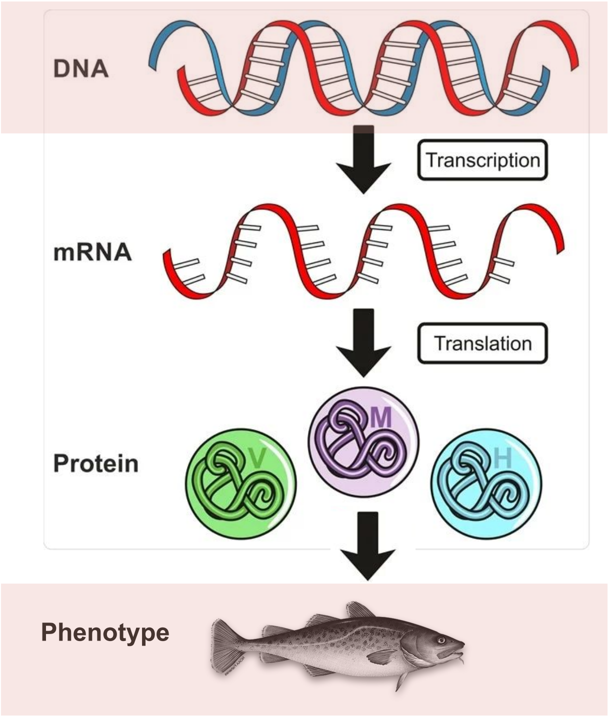
- ✓ Genetics – **they are one population**

  western Gulf of Alaska / Eastern Bering Sea

- ✓ Phenotypes – **Fewer lipid reserves in warming, slightly slower growth**

- ✓ Gene expression – **Lipid usage, immune activity, & damage control may deplete energy reserves**

- ✓ Markers of juvenile performance in warming
  - ✓ **~100 genetic markers**
  - ✓ **~1,600 gene expression indicators**



Adapted from: udaix/Shutterstock.com

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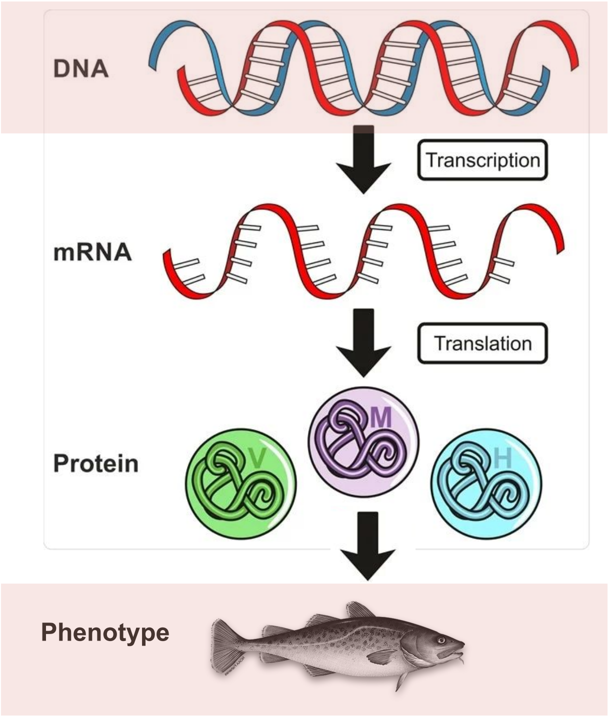
  - ✓ **~100 genetic markers**
  - ✓ **~1,600 gene expression indicators**

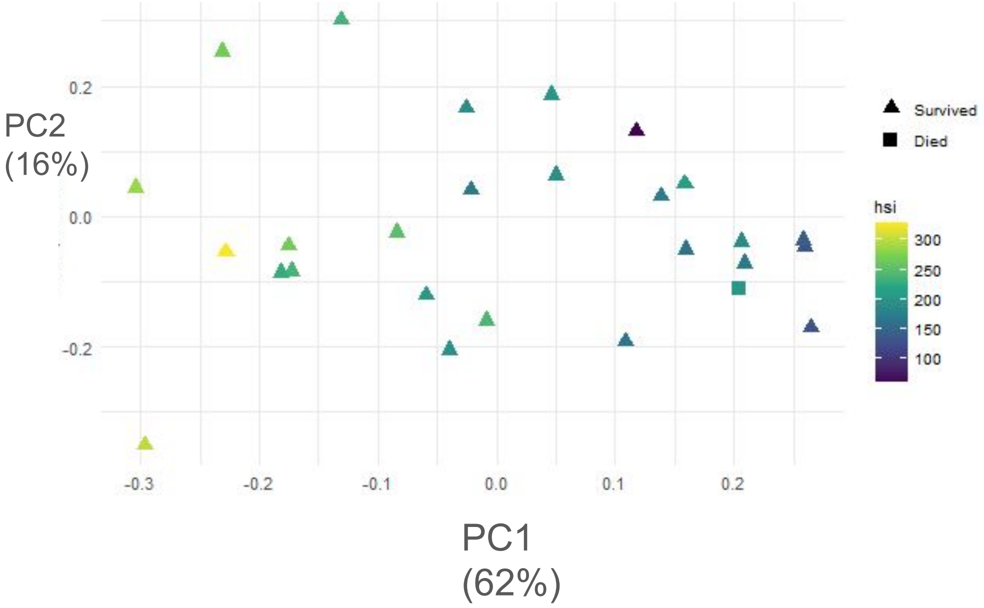
- Can we predict “performance” or “resilience” of other cod groups using our markers?



Adapted from: udaix/Shutterstock.com

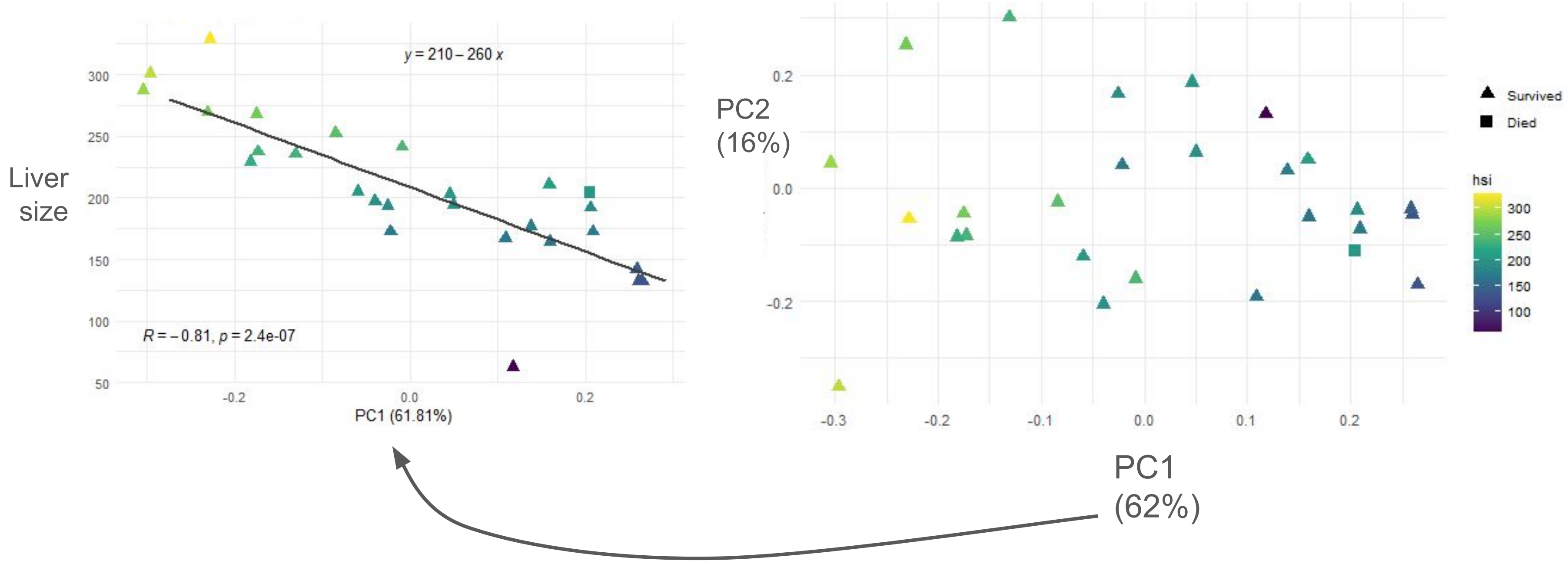
Exploratory analysis: predicting liver size

PCA from genotype probabilities, liver size markers in warm fish only



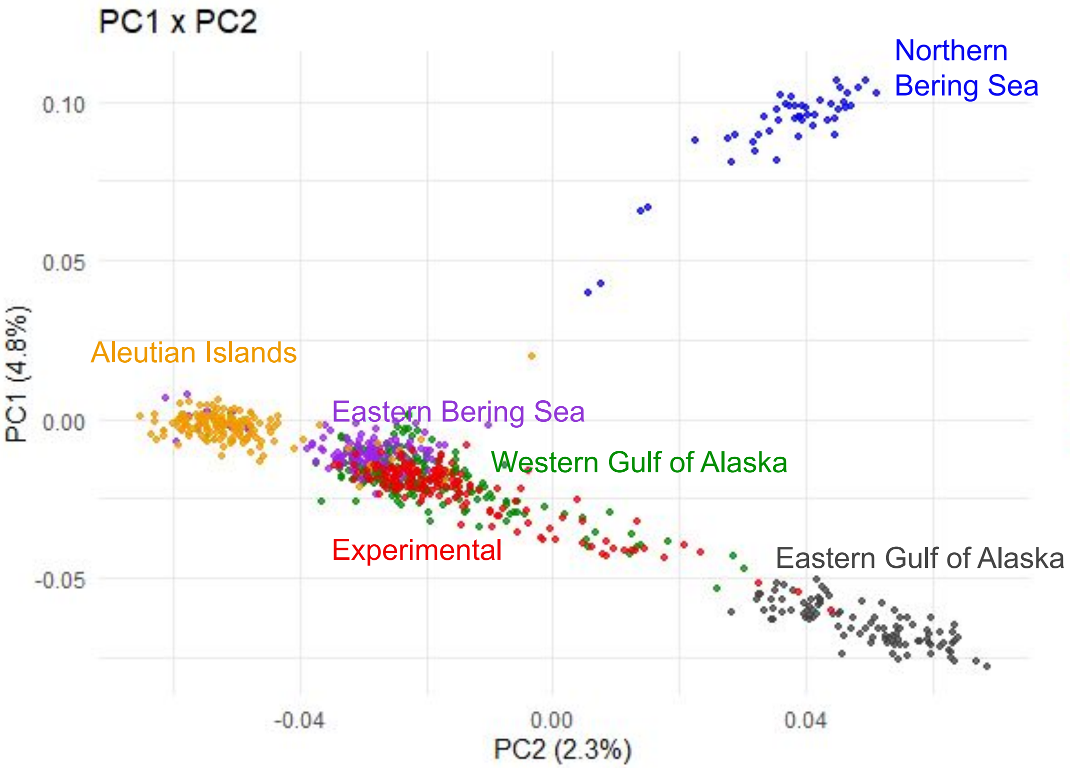
Exploratory analysis: predicting liver size

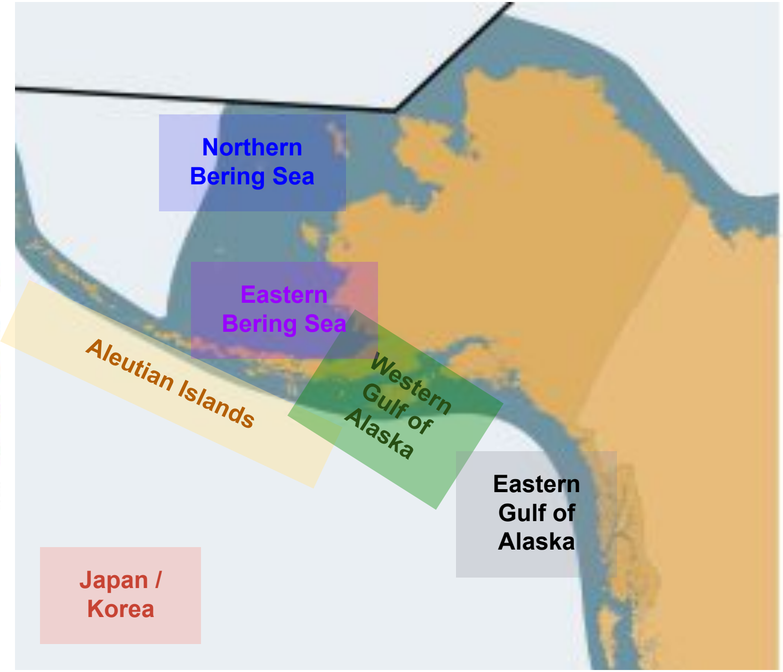
PCA from genotype probabilities @ 32 top liver size markers, warm fish only



Exploratory analysis:

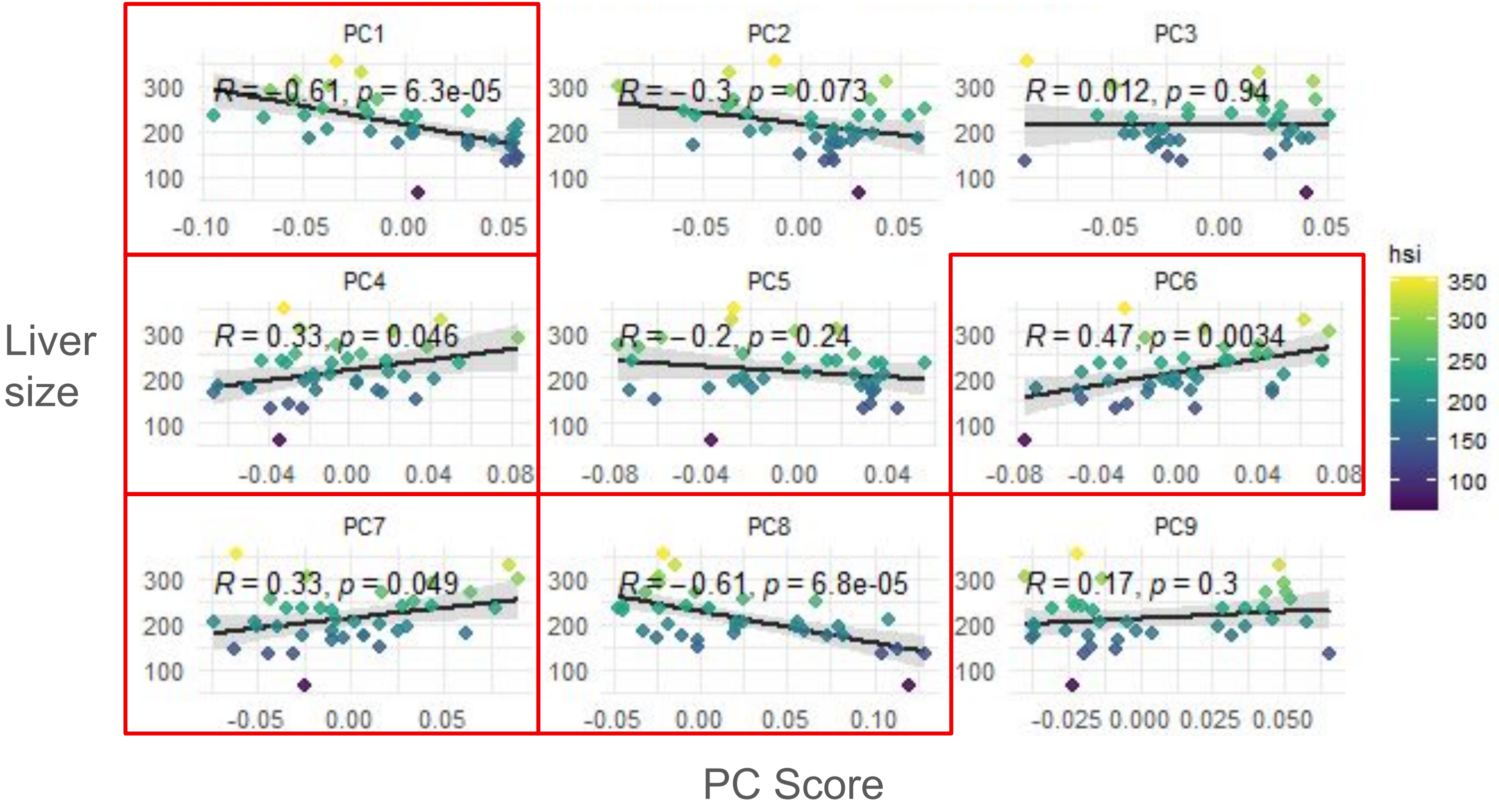
Which populations would we predict to have largest livers in warm conditions?





Exploratory analysis: predicting liver size

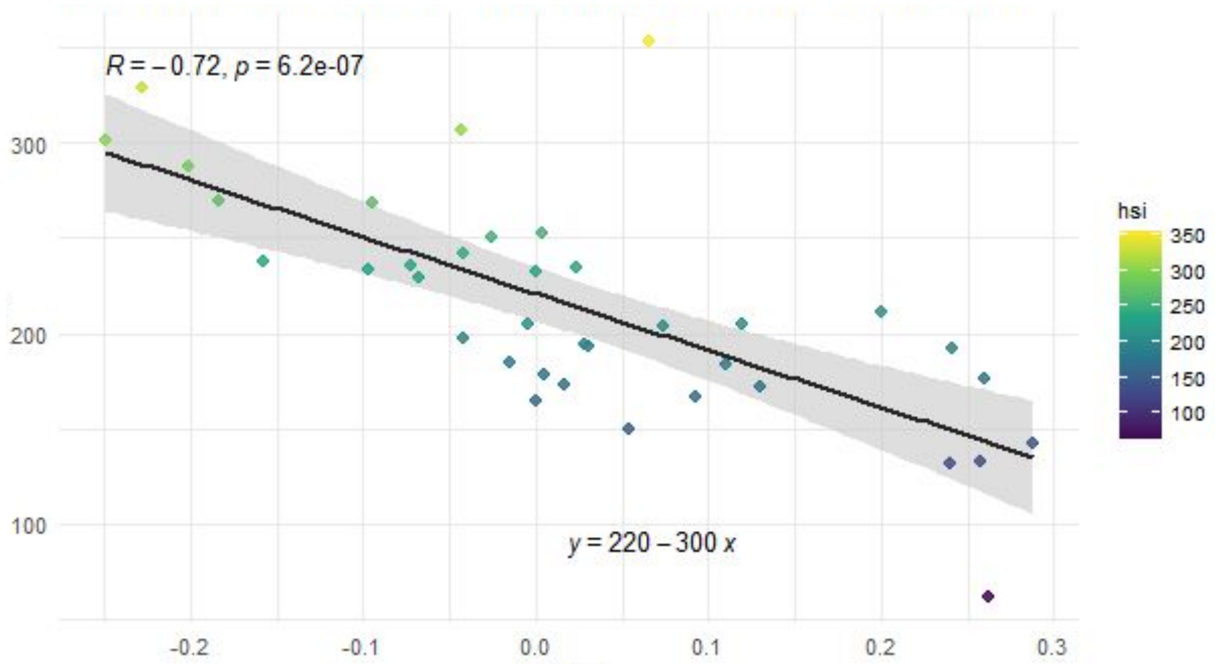
Step 1. PCA from genotype probabilities @ 32 top liver size markers



Exploratory analysis: predicting liver size

Step 2. Model liver size ~ PC scores in experimental fish

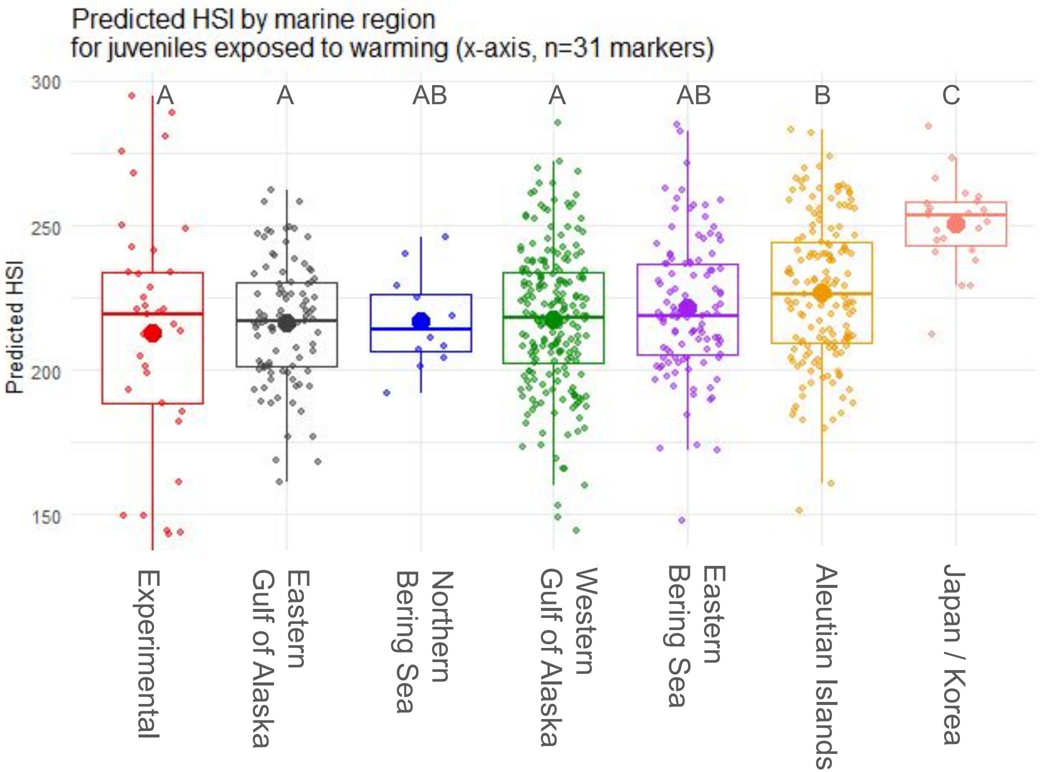
Liver size,
fish exposed to
warming

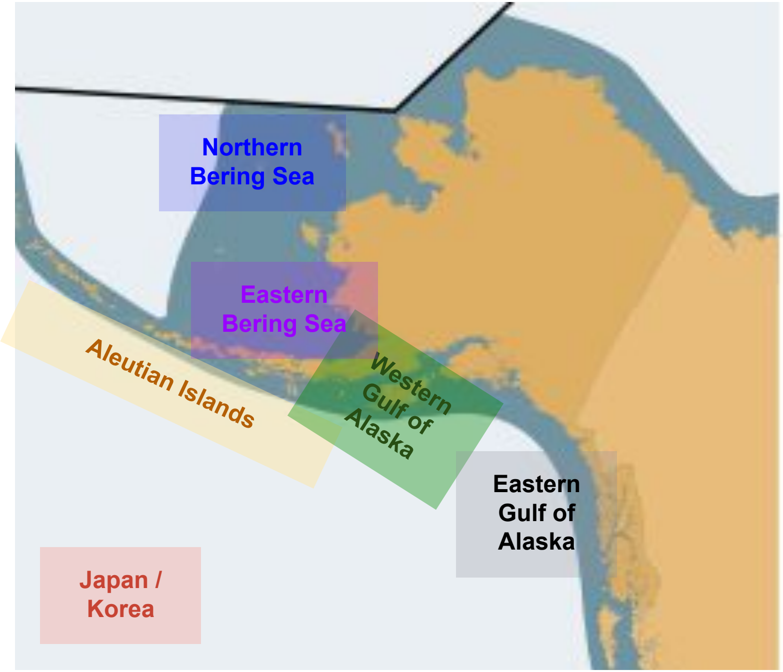


PC scores (summed)
55% total variation

Exploratory analysis: predicting liver size

Step 3. Use PC-based model to predict liver size in other populations





Exploratory analysis: predicting liver size

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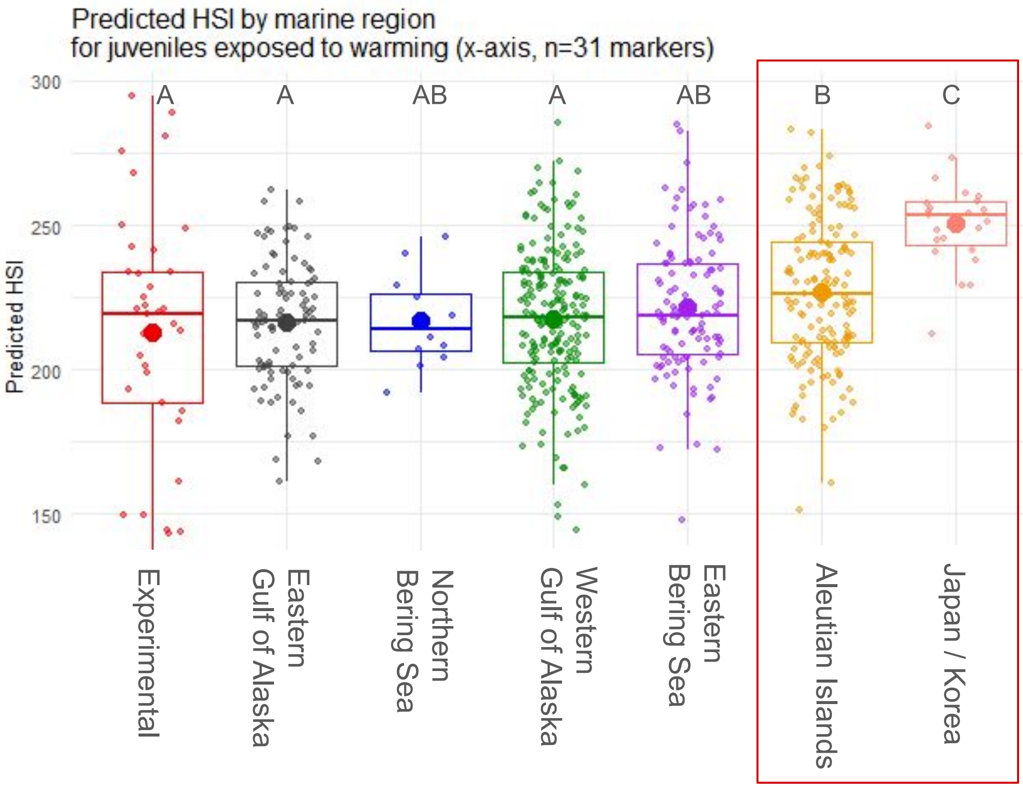
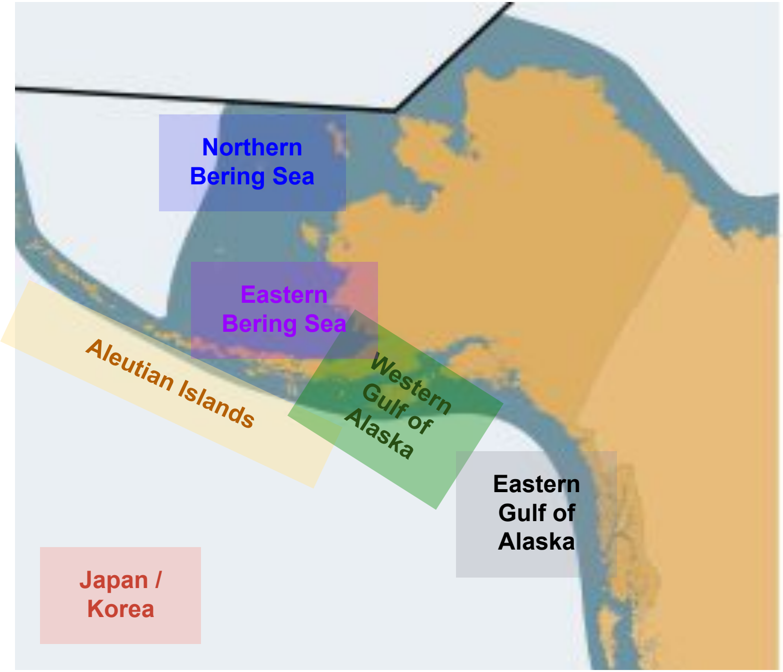


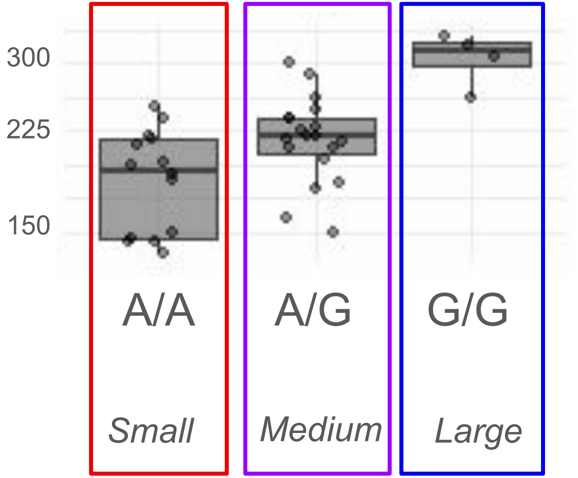


Example marker in gene **GalNAc-T2**

- *Cell signaling, cell adhesion, and protecting the mucosal surfaces in various tissues*
- *Glygoprotein / glycolipid biosynthesis*

Actual liver size ~ likely genotype

Warm-exposed fish



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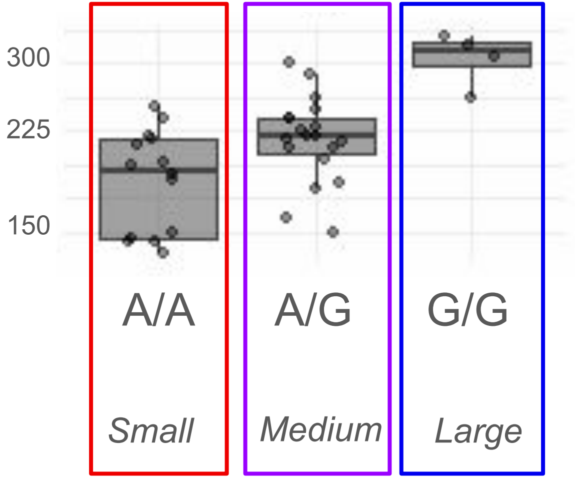
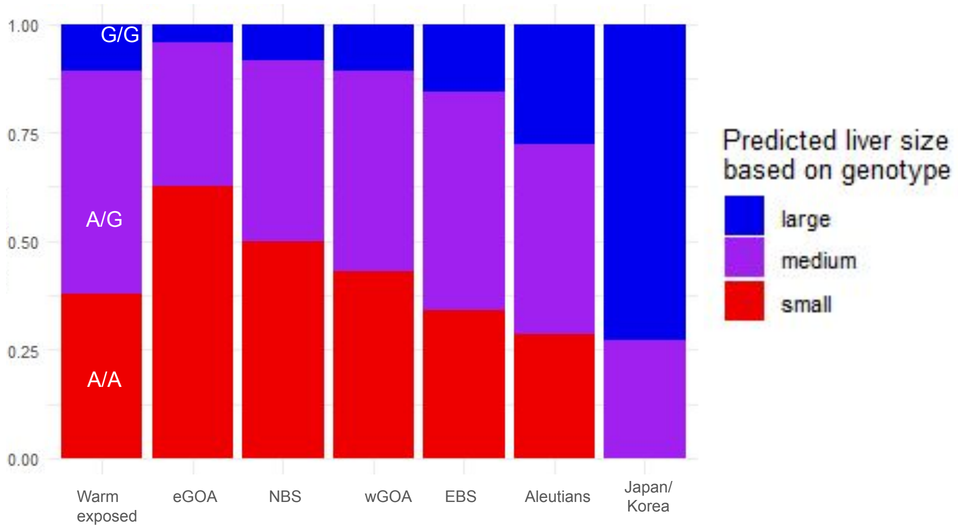
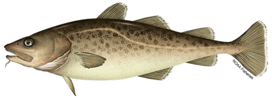


Predicted liver size based on likely genotype
Reference fish & warm-exposed fish





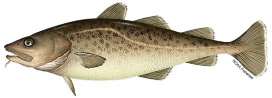
Broad Conclusions (preliminary)

- **Low recruitment in GoA during heatwaves** is likely related to **high larval mortality** and **low juvenile overwintering survival,** both related to *lipid metabolism, inflammation, and cell adhesion effects*.

- Stock assessments may need to **adjust reference points** in heat wave years

- **Genetic variability related to adaptive traits** may enable selection for juveniles **more capable of allocating lipid reserves, more resilient populations**

- Other Pacific cod groups could be screened for **putative markers of performance**
  - Through time – before/during/after heat waves (future project!) - is selection happening?
  - Distinct Pacific cod groups – are some groups more resilient than others?
    - Juveniles using different nursery habitat (onshore vs. offshore, Laurel study)



Applications of genomic resources in fisheries management

Building Genomics Database – Sequence data + metadata = opportunities for integration!

Sex identification – for sex data from fisheries or surveys, benchtop assay for experiments, surveys using DNA

Tagging studies – identify sex, population of origin, other markers (e.g. climate resilience) using fin clips

Ancient DNA studies – have genotypes at temperature-sensitive / performance markers changed through time?

Aging tools – “Epigenetic clock”, if developed, to estimate ages from DNA

Assay development – Expression data in lieu of more invasive / costly measurements (e.g. lipid components)

eDNA – Collected during surveys to estimate species presence, quantify relative abundance

Collaborators & Funders

NOAA FISHERIES

Newport

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Emily Slesinger
Louise Copeman
MaryBeth Hicks
Tom Hurst

Seattle

Ingrid Spies
Sara Schaal

Juneau

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SCHOOL OF AQUATIC & FISHERY SCIENCES

University of Washington

Steven Roberts
Kathleen Durkin

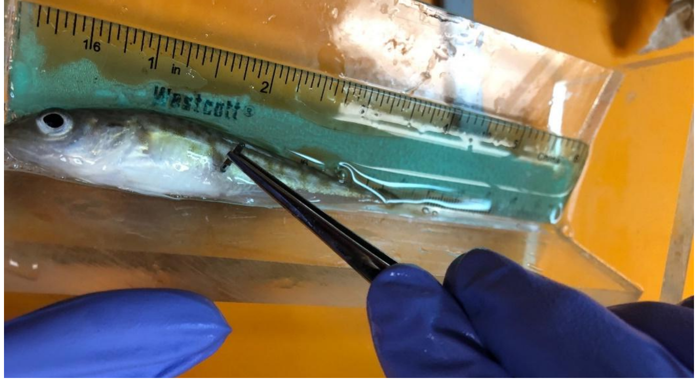
CICOES

NOAA OCEAN ACIDIFICATION PROGRAM

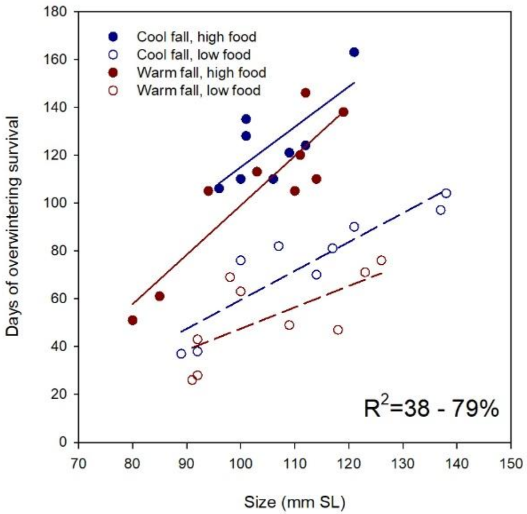
IDAHO • OREGON • ALASKA
PACIFIC STATES MARINE FISHERIES COMMISSION
WASHINGTON • CALIFORNIA

Questions?

Extra slides



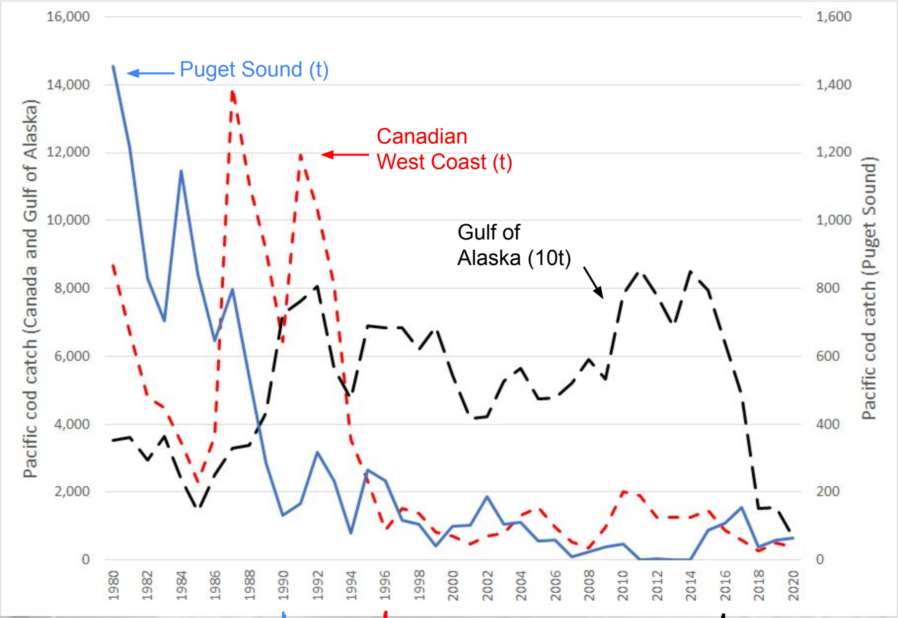
Juvenile cod overwintering survival depends on size, lipid reserves, and both are temperature-dependent



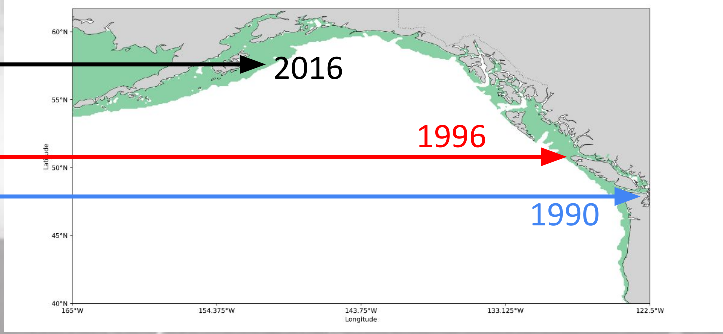
*Overwintering survival is **higher** after **cooler** autumns*

Laurel et al., in review at CJFAS

A latitudinal progression of population decline…



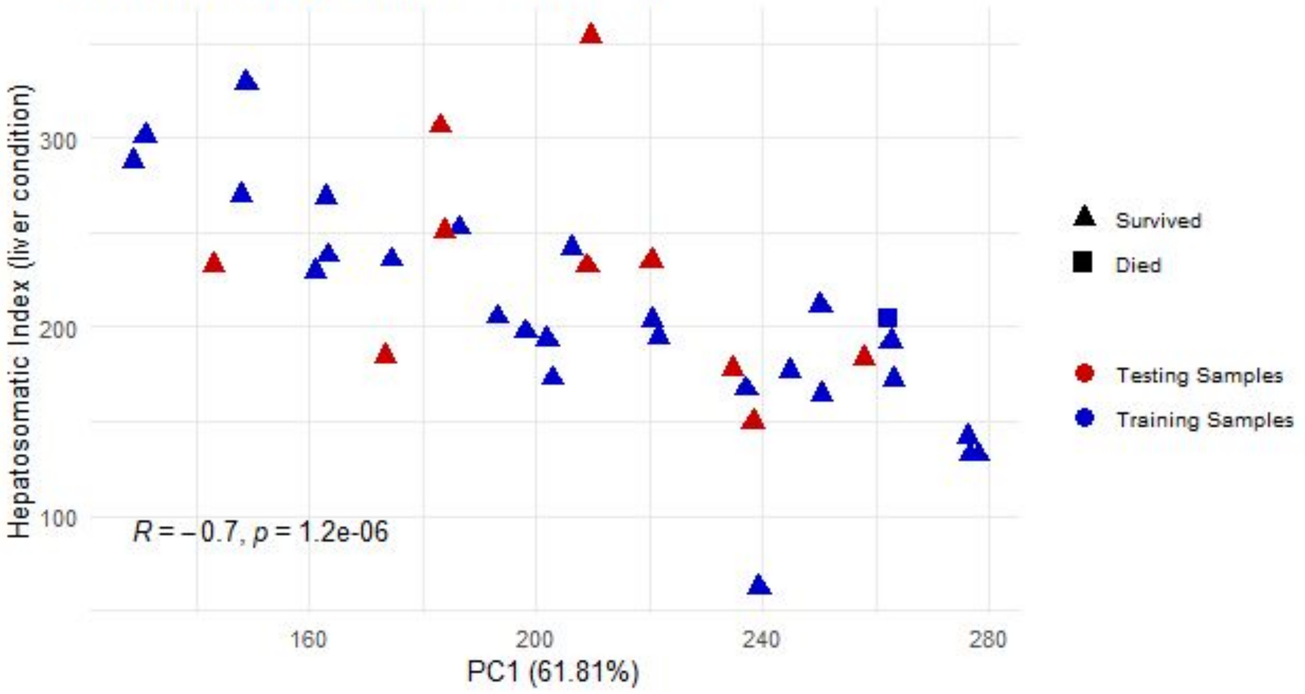
Low Pacific cod recruitment and biomass estimates in Gulf of Alaska coincided/followed the 2014-16 marine heatwaves, prompting review of 1st year of life biology and temperature response experiments

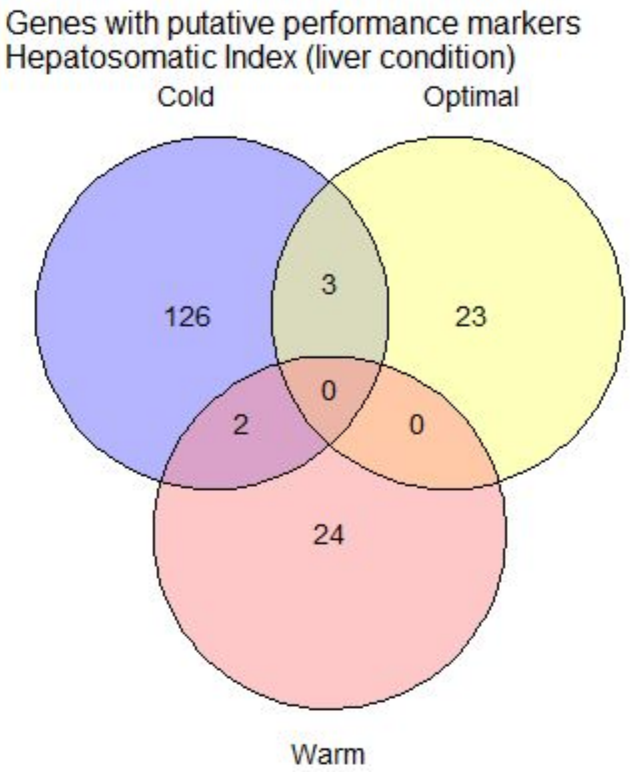


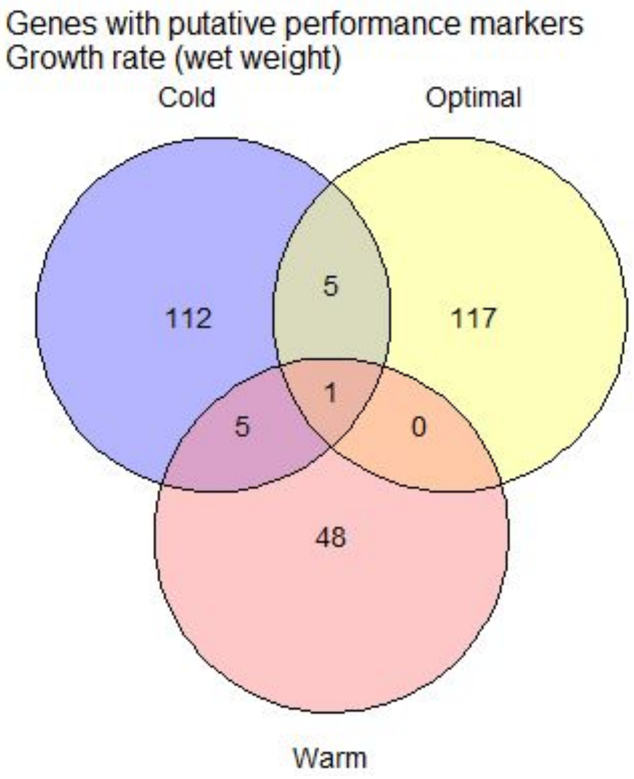
Slide from Ben Laurel

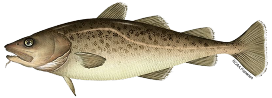
Exploratory analysis: predicting liver size

PCA from genotype probabilities @ 32 top liver size markers, warm fish only

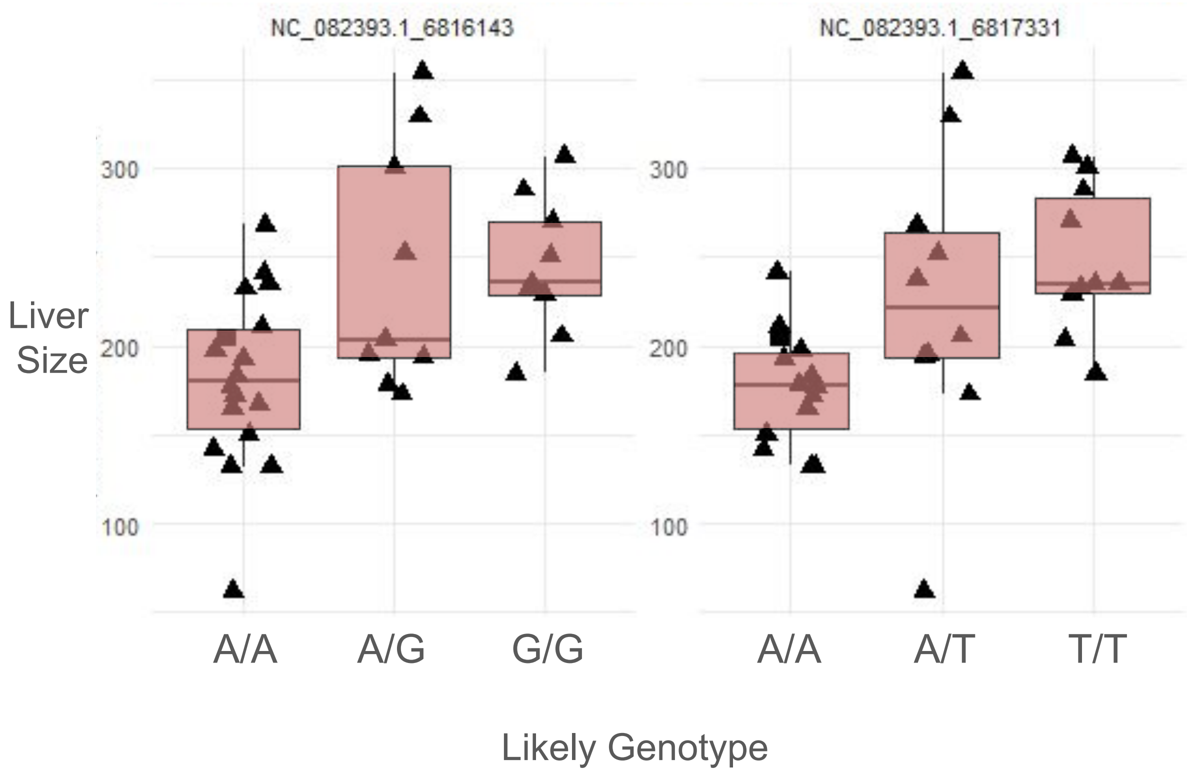



Genes with putative performance markers
Hepatosomatic Index (liver condition)
Cold
Optimal
126
3
23
0
2
0
24
Warm


Genes with putative performance markers
Growth rate (wet weight)
Cold
Optimal
112
5
117
1
5
0
48
Warm



~100 markers putatively associated with liver size in Pacific cod juveniles exposed to warming



One markers in a gene coding for a ***calcium channel*** *involved in calcium homeostasis, metabolic regulation*