#### **Ocean warming shapes embryonic developmental**

#### prospects of the next generation in Atlantic cod?

#### Kaja H. Skjærven

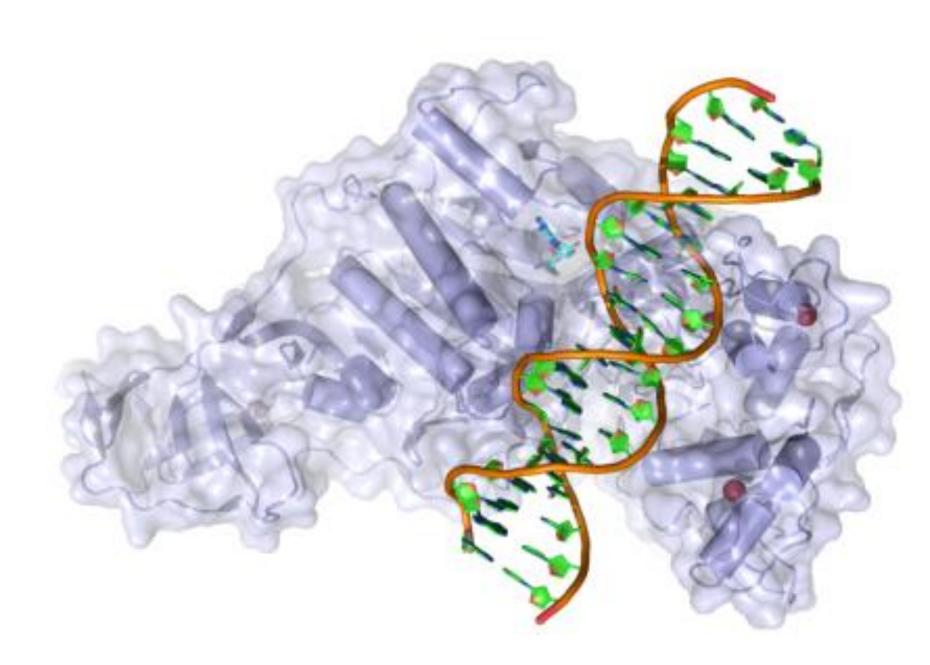
NWWAC webinar on climate change impacts on cod in the Celtic Sea, June 2024



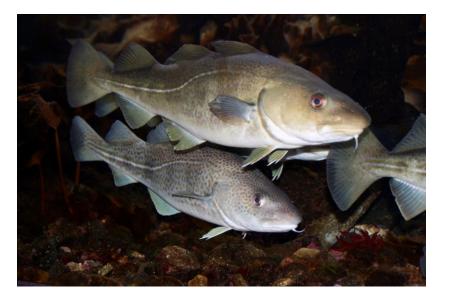






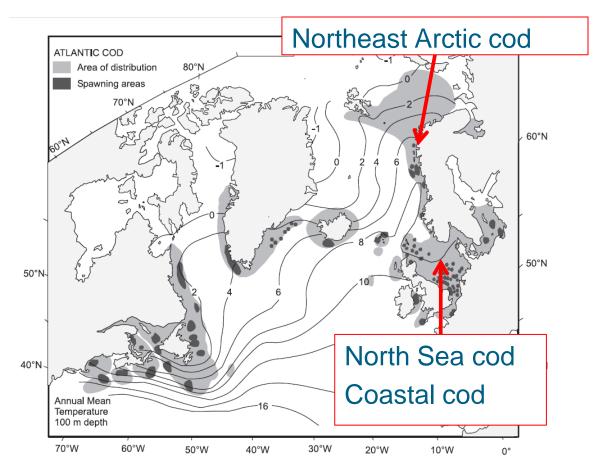


#### Atlantic cod (Gadus morhua)





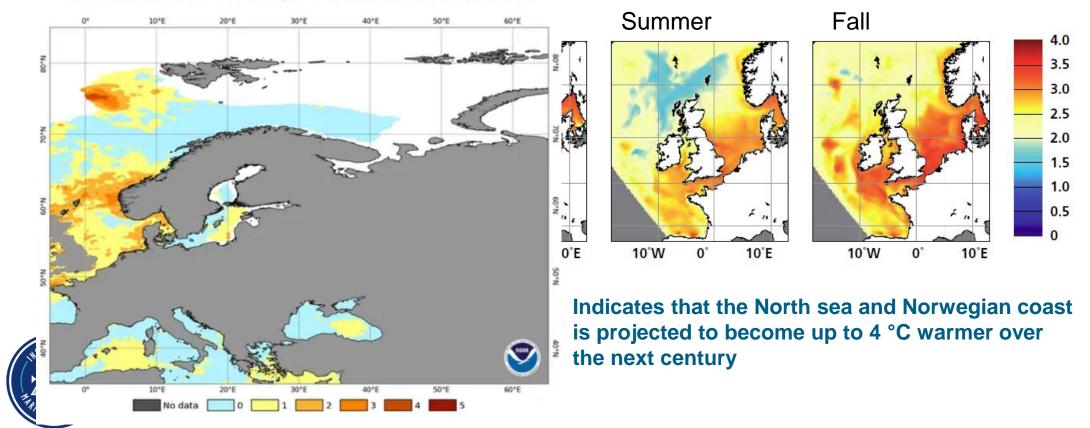
- Batch spawner
- Spawning pelagic eggs



Map: Sundby et. al 2000

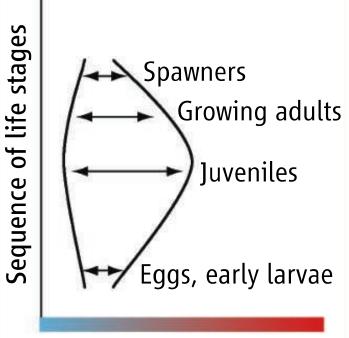
#### Simulated increase in sea surface temperature

NOAA Coral Reef Watch Daily 5km SST Anomaly Categories for Tracking Marine Heatwaves (v1.0.1) 22 May 2024



Embryonic egg stage is the thermal bottleneck

Thermal window widths across life stages (fishes)

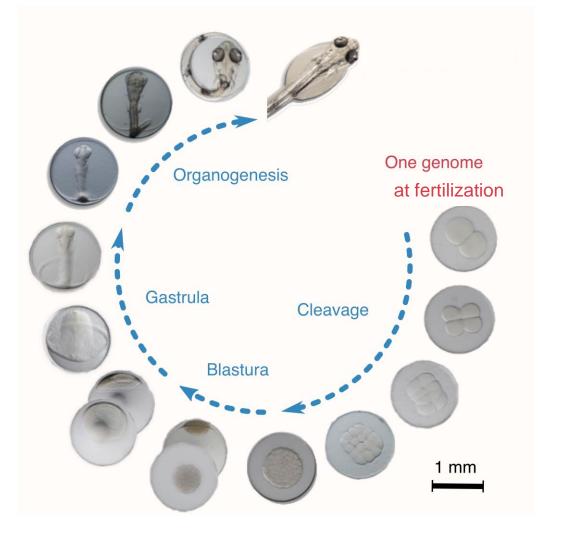


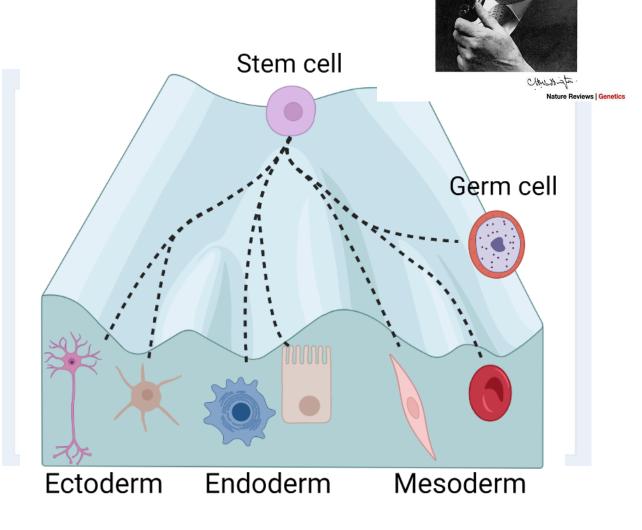


Pörtner & Farrell, 2008. Science

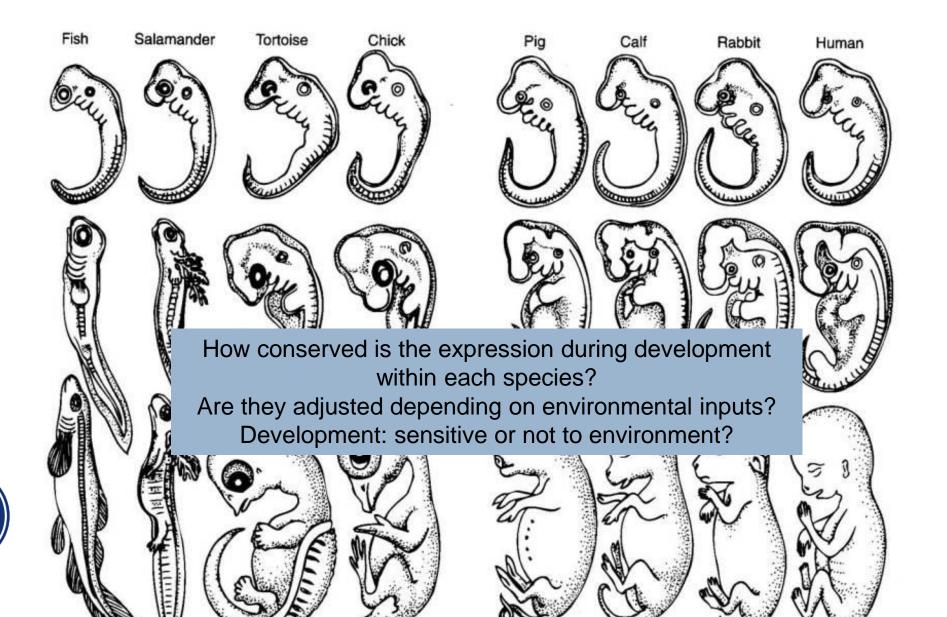


# Embryology

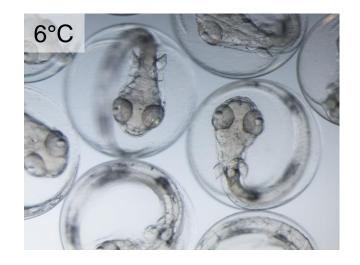


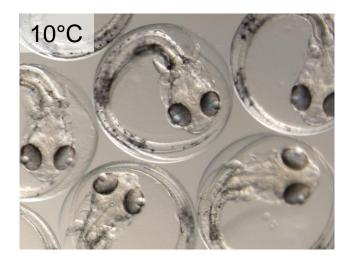


## Similarities among vertebrate embryos



THIS RESERVE







10°C incubation: Higher mortality Sensitive eggs Deformities





### Nutrition and Epigenetics Broodstock and Offspring





New Results

Altered spawning seasons of Atlantic salmon broodstock genetically and epigenetically influence cell cycle and lipid-mediated regulations in their offspring

D Takaya Saito, Marit Espe, Maren Mommens, D Christoph Bock, D Jorge M.O. Fernandes, Kaja H. Skjaerven **doi:** https://doi.org/10.1101/2024.02.03.578741



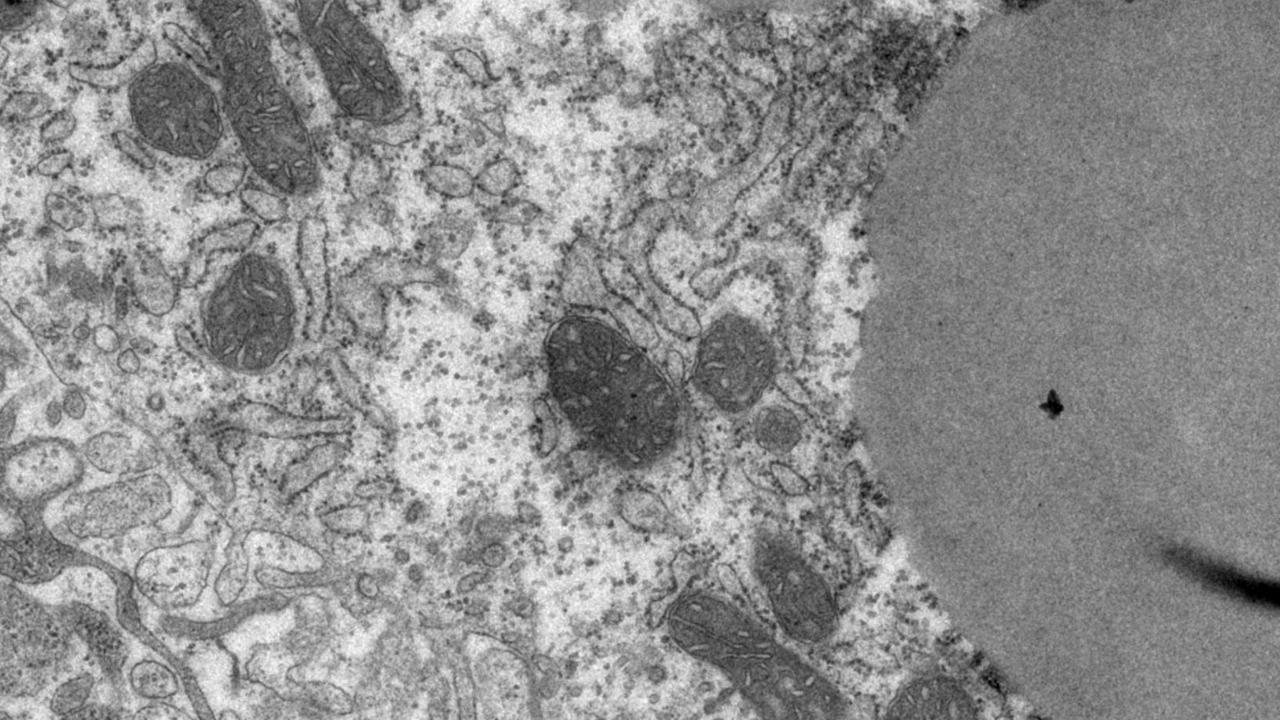
metanomicshealt BIOCRATES

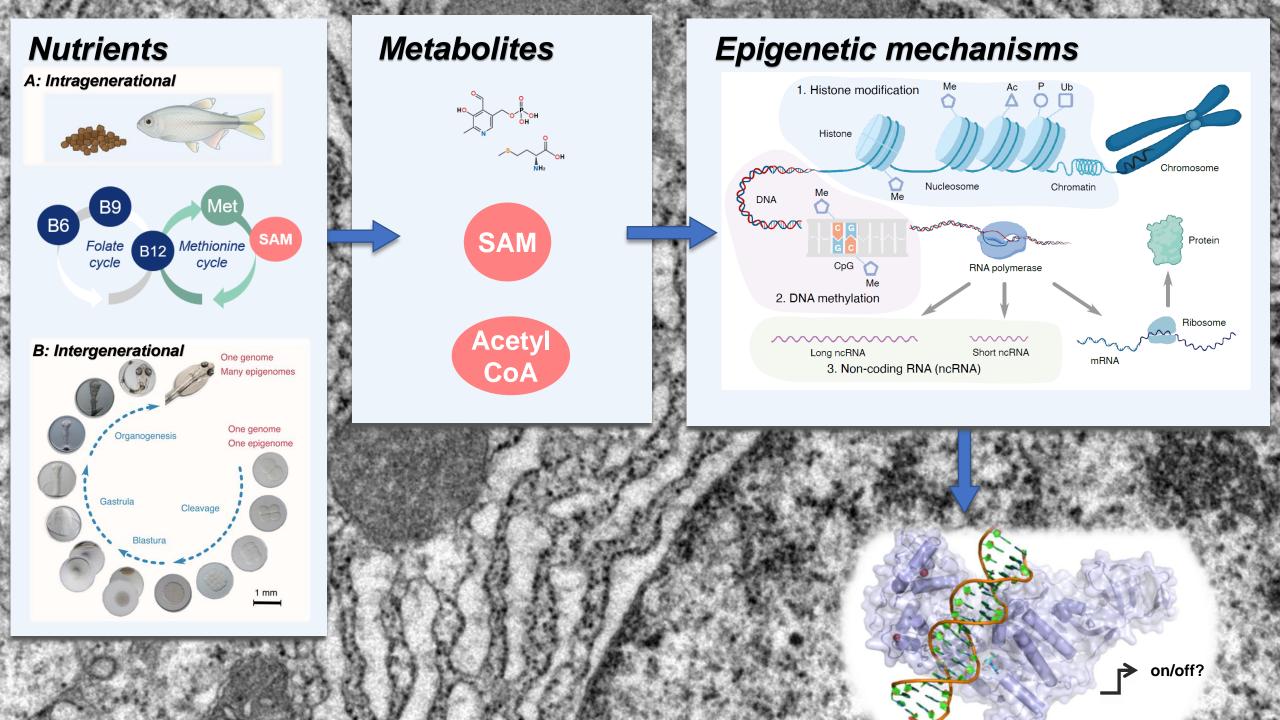
The Deep Phenotyping Compan





Ce-M-M-Research Center for Molecular Medicine of the Austrian Academy of Sciences







 Broodstock females are manipulated to spawn both earlier and later than the normal spawning season

**Why:** to produce offspring throughout the year-

**How:** can be controlled by regulation of feeding, light and temperature regimes

- Aim: to investigate if the spawning season differs in nutritional status, RNA seq and meDNA
- Help from Aqua Gen AS: Kyrksæterøra
- source broodfish <<< # offspring

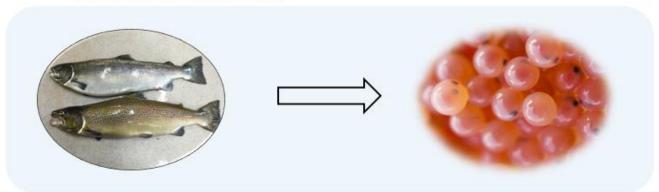




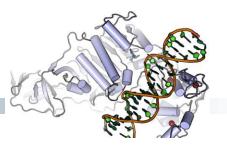
Denne ruggen av en stamfisk er med på å føre de beste genene videre, så den passes godt på av de ansatte i Aqua Gen.

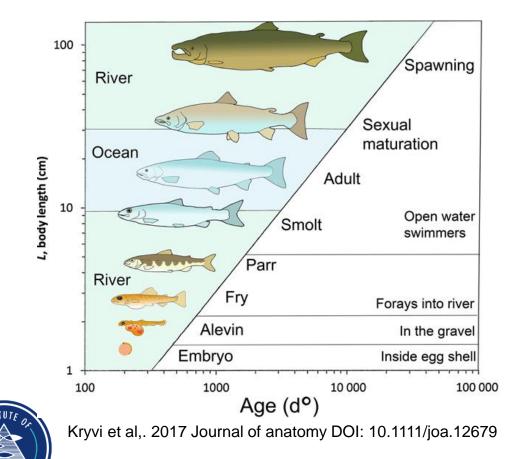


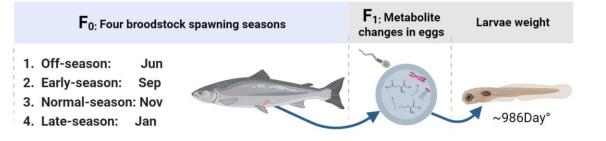




### Light and temperature to adjust time for spawning

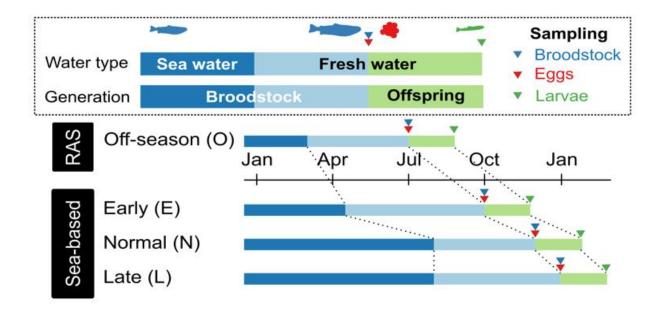






Season	Spawning	Starvation		
Off-season	June	109		
Early	Sept	163 120		
Normal	Nov			
Late	Jan	166		

# Compared four spawning seasons:



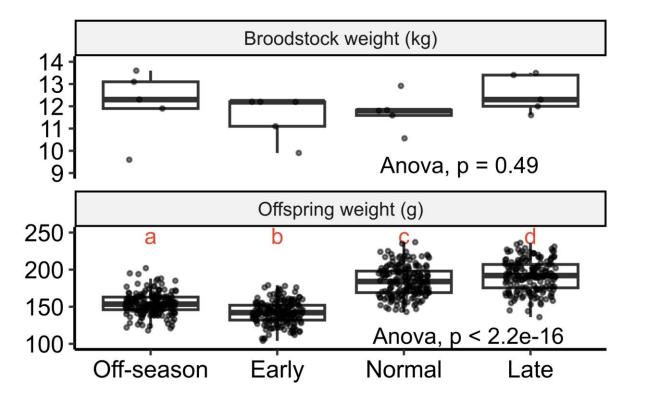




- Off: June (RAS)
- Early: Sept

- Normal: Nov
- Late: Jan

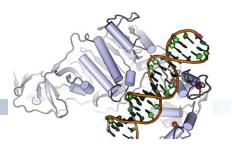
# Growth performance

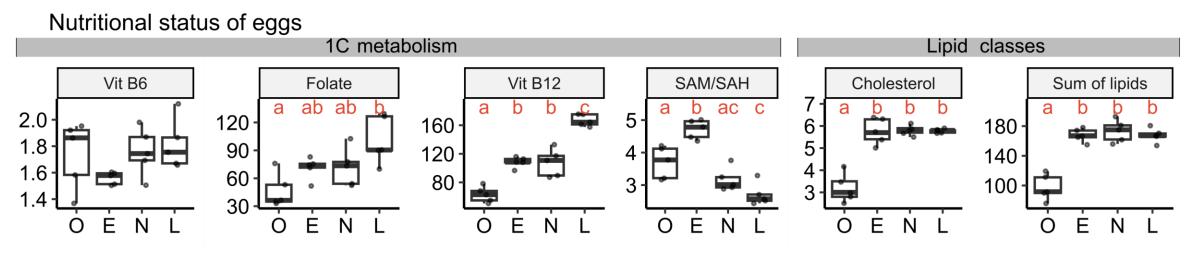


Egg/liter							
Off-season	6155						
Early	5835						
Normal	5082						
Late	4613						



### Spawning seasons: impact nutritional status of eggs







Aquaculture Volume 554, 30 May 2022, 738187



Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology Volume 247, September 2020, 110717



Out-of-season spawning affects the nutritional status and gene expression in both Atlantic salmon female broodstock and their offspring

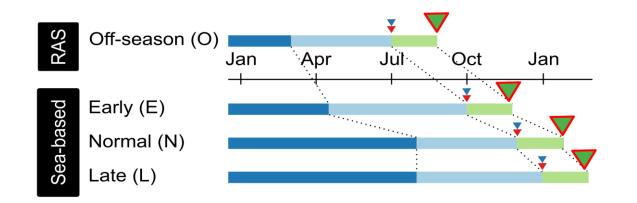
<u>Kaja H. Skjærven</u> <sup>a</sup> A ⊠, <u>Eystein Oveland</u> <sup>a</sup>, <u>Maren Mommens</u><sup>b</sup>, <u>Elisa Samori</u><sup>a</sup>, <u>Takaya Saito</u><sup>a</sup>, <u>Anne-Catrin Adam</u><sup>a</sup>, <u>Marit Espe</u><sup>a</sup>



Earlier or delayed seasonal broodstock spawning changes nutritional status and metabolic programming of growth for nextgeneration Atlantic salmon

<u>Kaja H. Skjærven</u><sup>a</sup> ∧ <u>Maren Mommens</u><sup>b</sup>, <u>Anne-Catrin Adam</u><sup>a</sup>, <u>Takaya Saito</u><sup>a</sup>, <u>Eystein Oveland</u><sup>a</sup>, <u>Marit Espe</u><sup>a</sup>

# **Omics analysis**

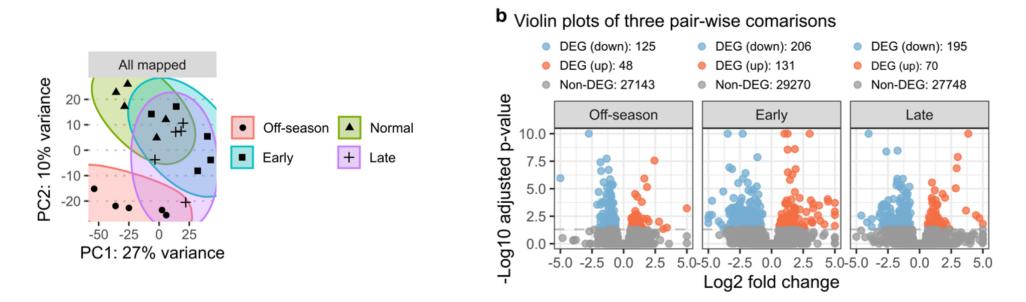


- Larvae liver samples
- Gene expression with RNA-seq
- DNA methylation with bisulfite sequencing





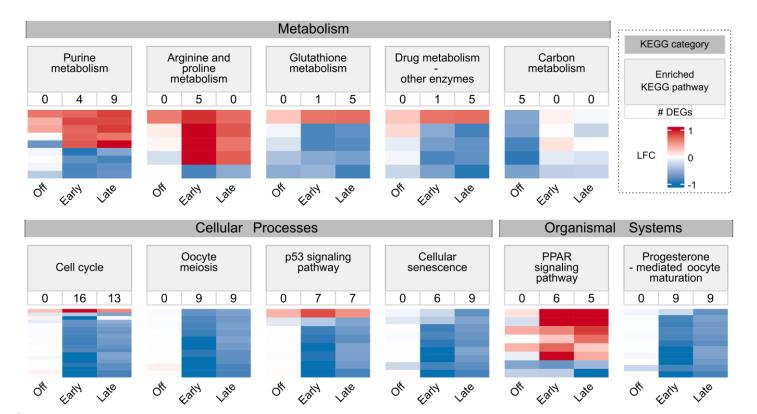
# Results of gene expression analysis



- Off-season is different: Broodstock from RAS
- Similarity between early and late seasons
- More downregulation of mRNA expression compared to normal season
- Off: 173 Early: 337 Late: 265 DEGs



### 11 biological pathways changed in offspring liver



**Off:** the carbon metabolism. All five DEGs associated with carbon metabolism showed down-regulation

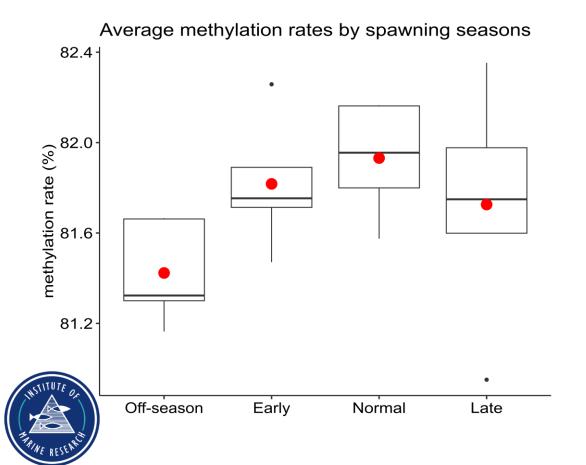
#### Early and late:

- consistent expression patterns in terms of up- and down-regulation
- cellular processes: strong downregulation

These findings may be linked to variations in the nutritional status of the eggs.



# **DNA** methylation analysis





# Correlation DMC with DEGs: Cell cycle genes are regulated

Gene ID	Symbol	DMC <sup>1</sup>			DEG <sup>2</sup>			Gene name	Function
		Off- season	Early	Late	Off- season	Early	Late		
106562317	caprin-1	Нуро	(Hypo)	(Hypo)	Down	(Down)	(Down)	caprin-1	Cell cycle
106599887	cyp8b1	Нуро	-	-	Down	-	-	5-beta-cholestane-3-alpha,7-alpha-diol 12-alpha-hydroxylase	Metabolism, cytochrome P450
106588407	kifc1	-	Нуро	Нуро	-	Down	Down	carboxy-terminal kinesin 2	Cell cycle, Meiosis
106582038	adrenodoxin	-	Нуро		-	Down	-	adrenodoxin	Metabolism, cytochrome P450
106604665	slc43a1a	-	Нуро	-	-	Up	(Up)	solute carrier family 43 member 1a	Transporter
106561604	aurkb	(Hyper)	Hyper	Hyper	-	Down	Down	aurora kinase B	Cell cycle
106570052	lpin1	-	Hyper	-	-	Up	-	phosphatidate phosphatase LPIN1	Metabolism

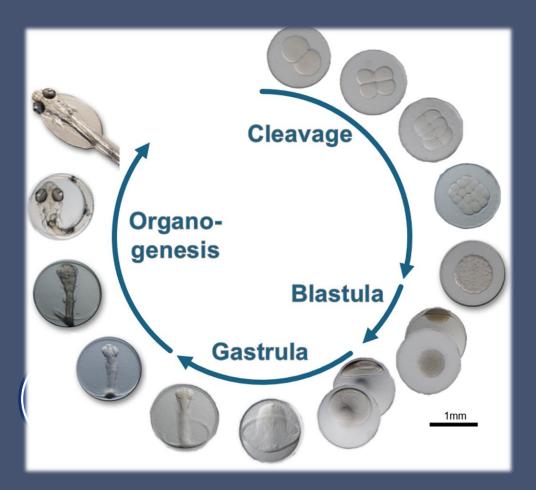


Correlating methylation differences with corresponding LFCs, we found 11 DMCs:

4 DMCs in P250, 7 DMCs in P1K associated with DEGs.

*caprin-1* and *kifc1:* hypo-methylated CpG sites, *aurkb:* hyper-methylated CpG sites; all three: Downreg. CpG methylation differences greater than 30% lacked clear association with DEGs in the liver

### Climate change and adaptation via maternal mRNA? Broodstock and Offspring



*ICES Journal of Marine Science*, 2024, Vol. 0, Issue 0, 1–15 https://doi.org/10.1093/icesjms/fsae025 **Received:** 14 November 2023; **revised:** 15 February 2024; **accepted:** 16 February 2024 **Original Article** 



### Ocean warming shapes embryonic developmental prospects of the next generation in Atlantic cod

Kaja H. Skjærven <sup>[b],†</sup>, Maud Alix <sup>[b2,†</sup>, Lene Kleppe <sup>[b],†</sup>, Jorge M.O. Fernandes <sup>[b]</sup>, Paul Whatmore <sup>[b]</sup>, Artem Nedoluzhko <sup>[b]</sup>, Eva Andersson <sup>[b]</sup>, Olav Sigurd Kjesbu <sup>[b],\*</sup>

<sup>1</sup>Institute of Marine Research, P.O. Box 1870 Nordnes, 5817 Bergen, Norway <sup>2</sup>Institute of Marine Research, Austevoll Research Station, 5392 Storebø, Norway <sup>3</sup>Faculty of Biosciences and Aquaculture, Nord University, 8049 Bodø, Norway

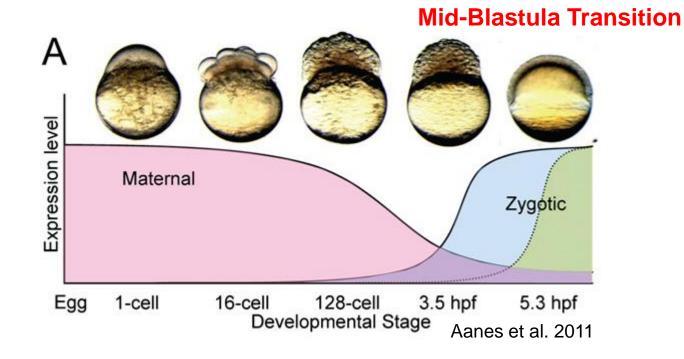




## Research questions:

- Changes in broodstock incubation temperature: change the maternal mRNA in the newly fertilized eggs?
- Can the differences be detected in the ovarian tissue several months before spawning?

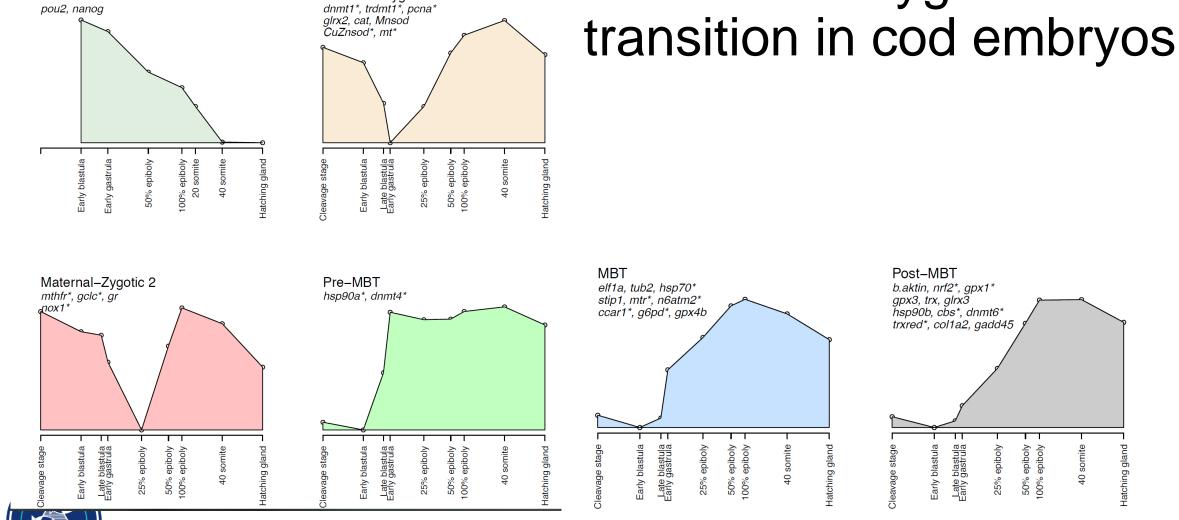




- Early embryonic development is controlled by maternal mRNA
- Zygotic transcription is initiated



Maternal-to-zygotic transition



Maternal-Zygotic 1



Maternal

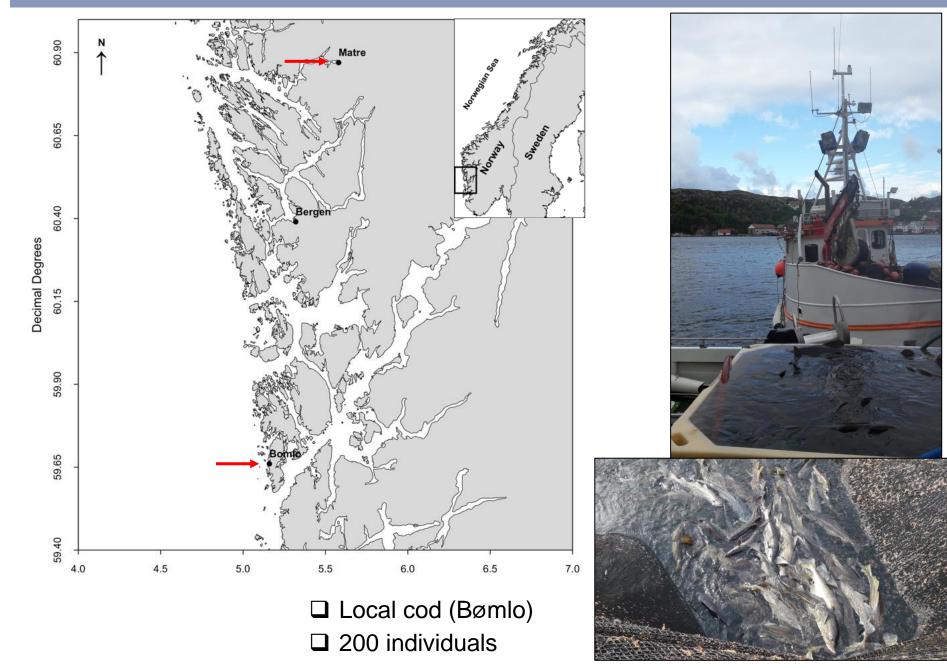
Redrawn from Skjaerven et al., 2010, 2011, 2014

40 somite

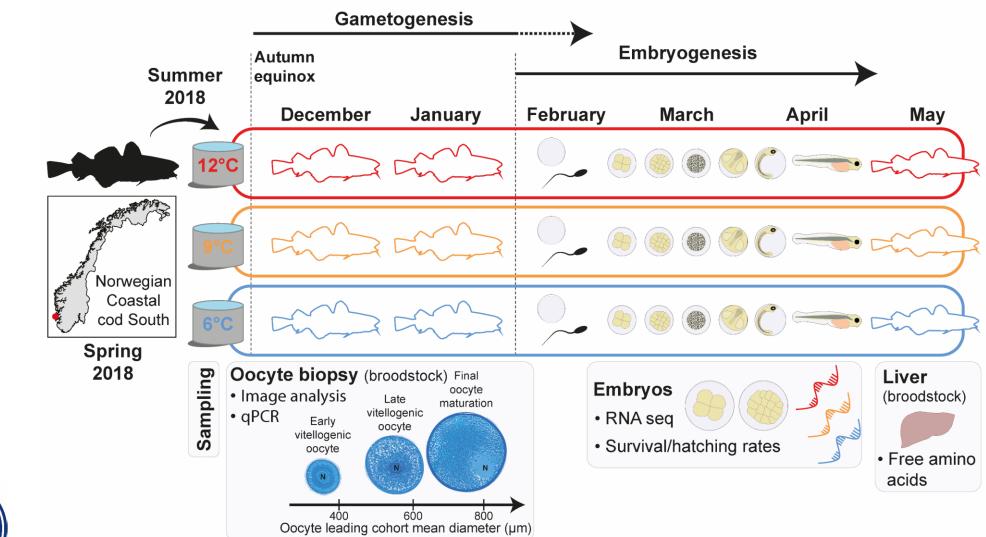
Hatching gland

Maternal-to zygotic

#### **Fish collection**



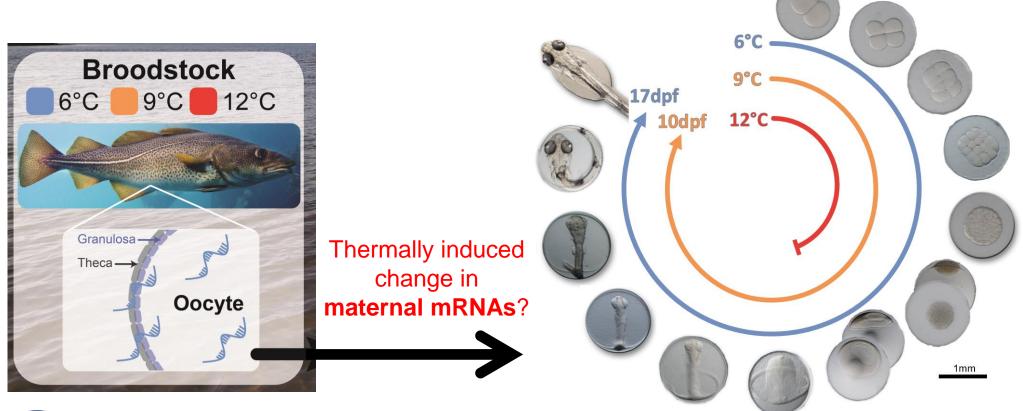
### **Experimental design**





## Broodstock temperature

Early embryoninc protein production relies exclusively on maternal molecules like messenger mRNAs incorporated into the ovarian follicles



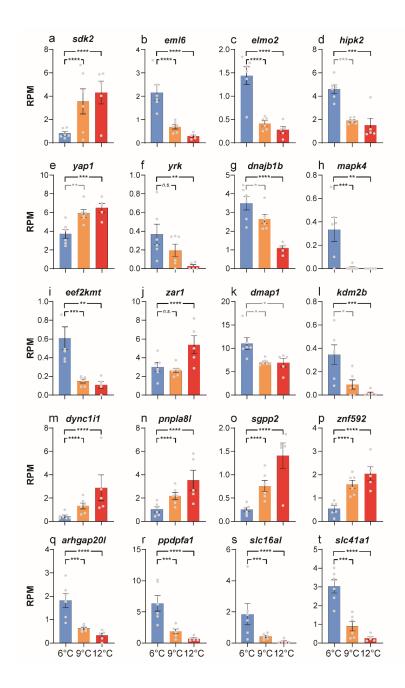


Elevated temperatures (9°C and 12°C vs. 6°C) during oogenesis Influenced the next generation?

Targeting maternal mRNAs embryos, in view of up- and down-regulated genes in ovarian follicles of pre-spawning adults

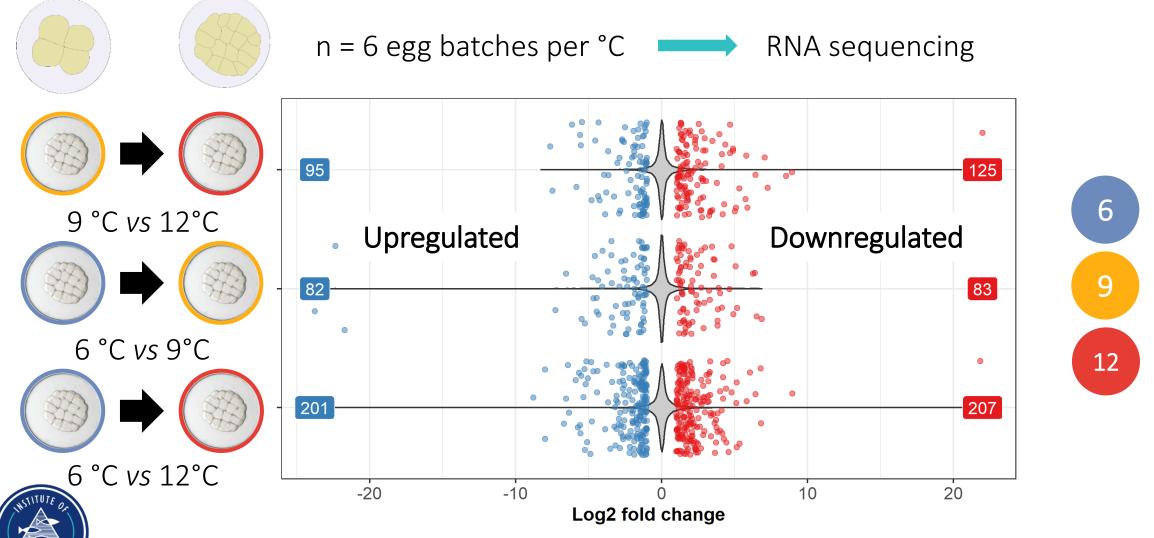
# Broodstock temperature modulates maternal mRNA in offspring

 mRNAs functions in embryonic development: cytoskeleton assembly: sdk2, eml6, elmo2 cell fate: hipk2, yap1, and yrk folding of proteins: dnajb1b transcriptional regulator and mitosis: mapk4 protein methylation: eef2kmt translation: zar1 chromatin configuration: smarce1 and kdm2b



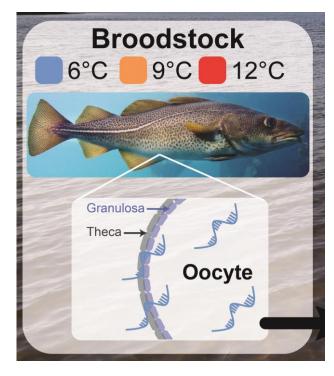


### Temperature-induced maternal mRNAs adjustments in embryos

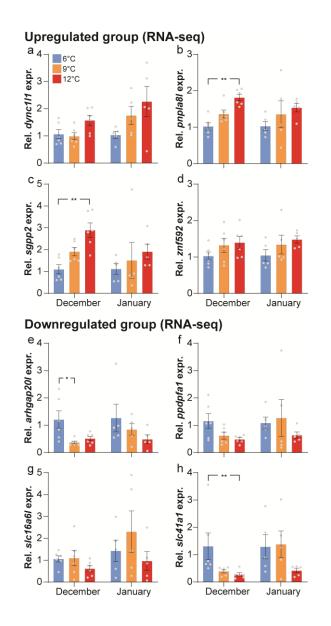


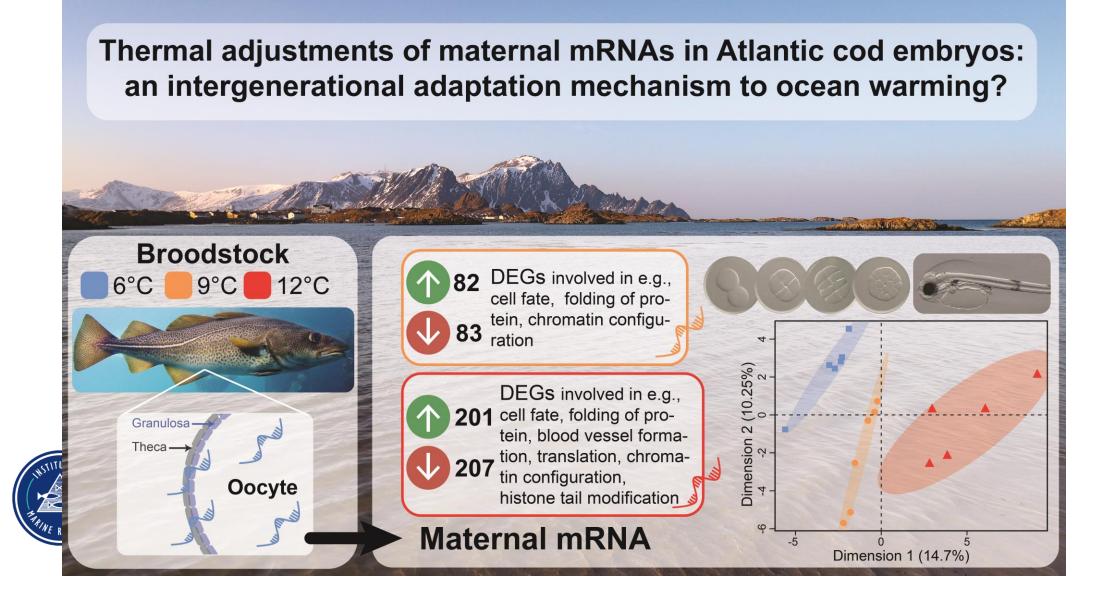
Number of **Differentially expressed genes** is proportional to temperature difference

### Change in transcripts in oocytes for embryo development months ahead of spawning









### Maternal temperature history

 maternal temperature history: contributes to egg quality and embryogenesis via maternal mRNAs

#### • mRNAs functions in embryonic development:

cytoskeleton assembly: *sdk2*, *eml6*, *elmo2* cell fate: *hipk2*, *yap1*, and *yrk* folding of proteins: *dnajb1b* transcriptional regulator and mitosis: *mapk4* protein methylation: *eef2kmt* translation: *zar1* chromatin configuration: *smarce1* and *kdm2b* 

 mRNAs: may change developmental gene regulatory networks, causing a 'domino effect' through subsequent embryonic tissue

chitecture, growth, and development?

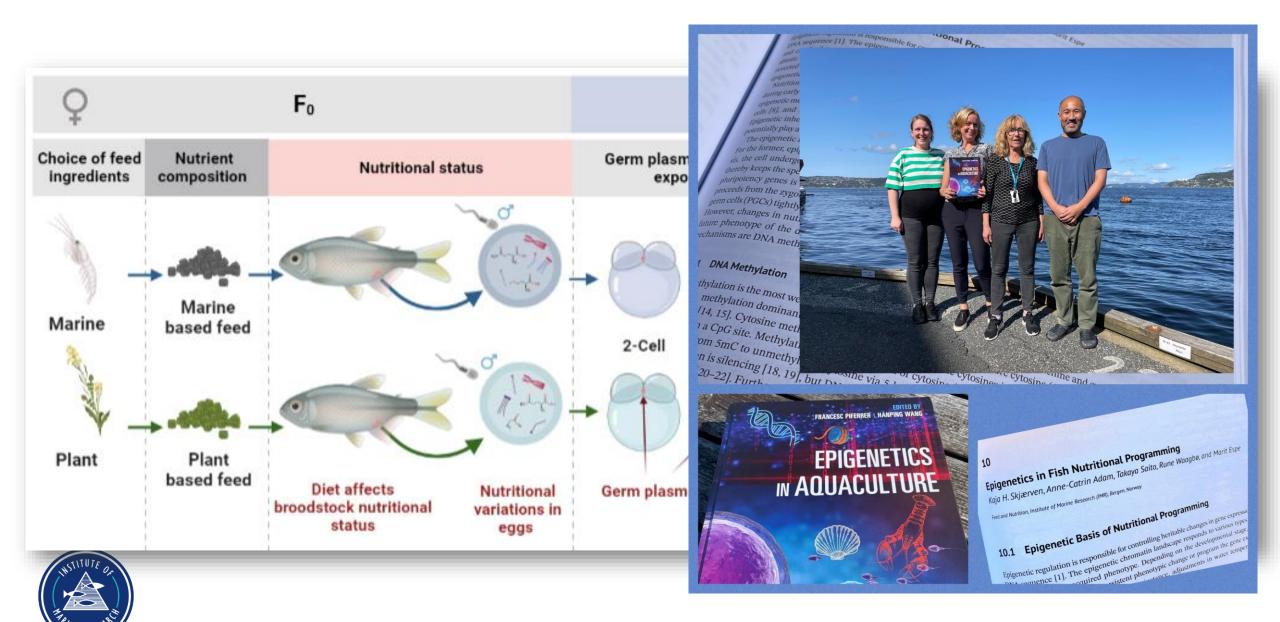
#### NEWS

Editor's Choice- Atlantic cod adaptation: Genetic insights into climate resilience

The latest Editor's Choice in ICES Journal explores climate adaptation in fish. The study looked at genetic adaptation of Atlantic cod to rising sea temperatures, providing a deeper understanding of marine species' response to climate change.

Published: 19 March 2024





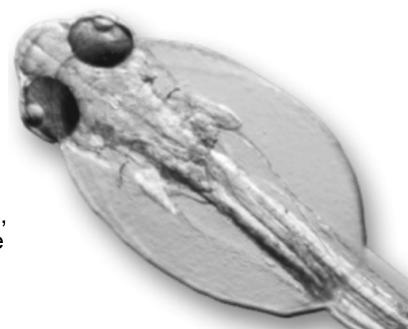
Epigenetics in aquaculture. Skjærven et al., 2023

# Summary:

- The metabolism interacts with the (epi-)gene regulation
- Broodstock handling affects the nutrient status of eggs- like SAM –, is needed for DNA methylation
- Atlantic salmon:
  - Broodstock spawning season manipulation changes the nutritional status of broodstock, and their offspring (Skjærven et al., 2020 and 2022). Altered spawning seasons transcriptionally and epigenetically influence cell cycle and lipid mediated regulations in their offspring (Saito et al., in review)
- Atlantic cod:
  - Temperature (Ocean warming) shapes embryonic developmental prospects of the next generation in Atlantic cod by altering maternal mRNA in offspring, these where regulated months earlier in the ovarian tissue (Skjærven, Maud, Kleppe et al.,Kjesbu 2024)
    - Further studies:

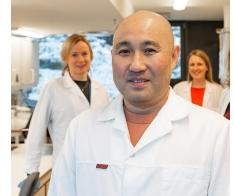


 mRNAs: may change developmental gene regulatory networks, causing a 'domino effect' through subsequent embryonic tissue architecture, growth, and development?











267787 (NutrEpi) 295118 (EpiFishGrowth)

#### **Co-workers and collaborators:**

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Olav Kjesbu, Lene Kleppe and Maud Alix

Cambridge: Audrey Putman, Erik Miska Nord Uni: Jorge M.O. Fernandes CeMM: Christoph Bock









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The Deep Phenotyping Compan

**Ce–M–M–** Research Center for Molecular Medicine of the Austrian Academy of Sciences