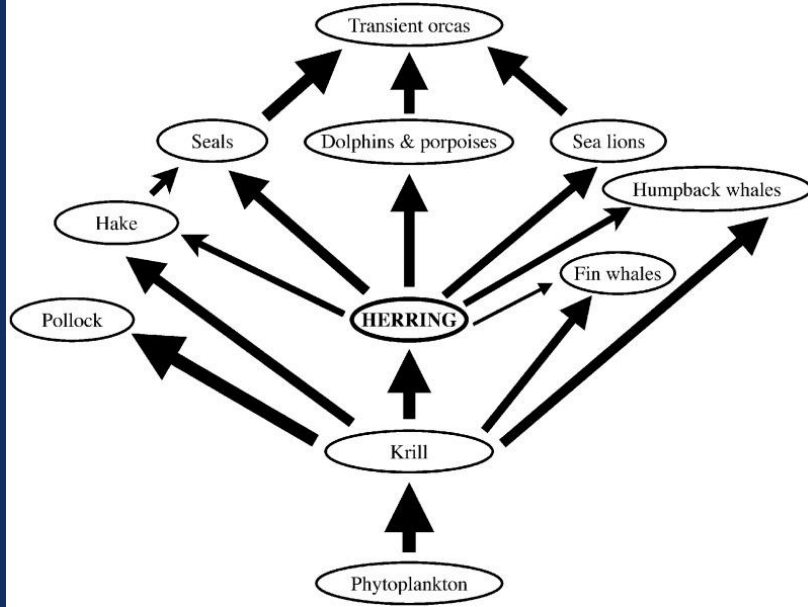


Seasonal differences of Pacific herring larval and embryo metrics are small, and proteomic analysis holds promise for uncovering subtle changes in physiology

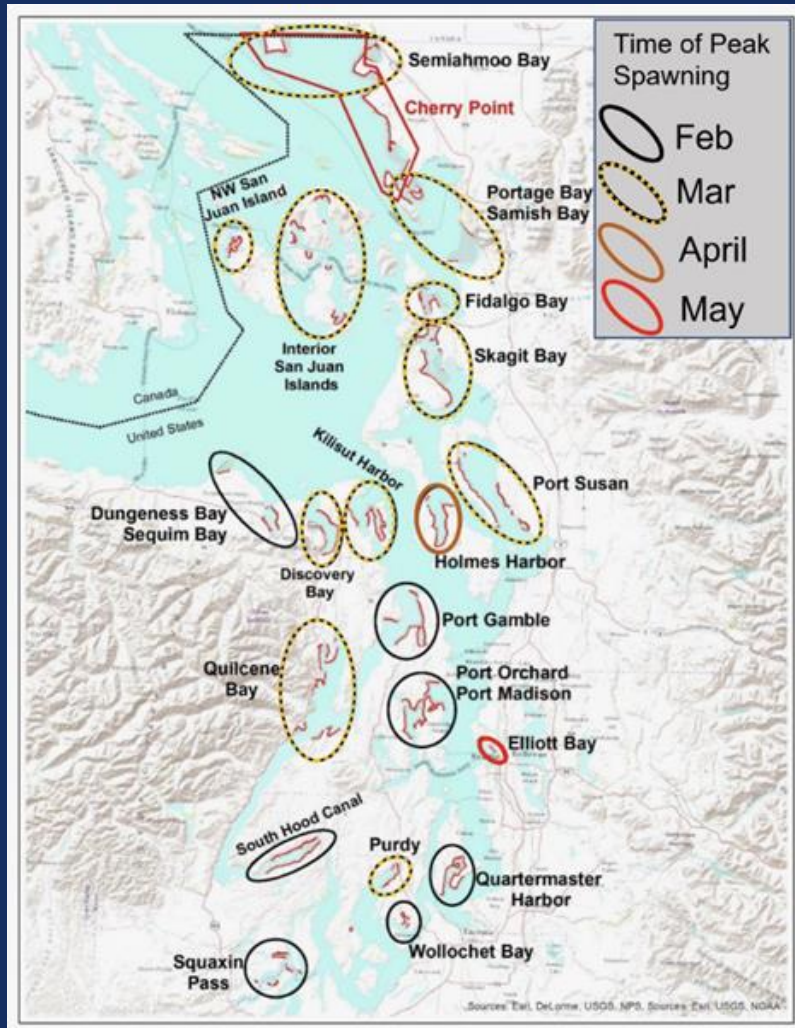
Ariel Shiley, Brooke Love, Emmanuel Keene, Lilia Vivaldo, Nic Benmam, Sabina Guzek



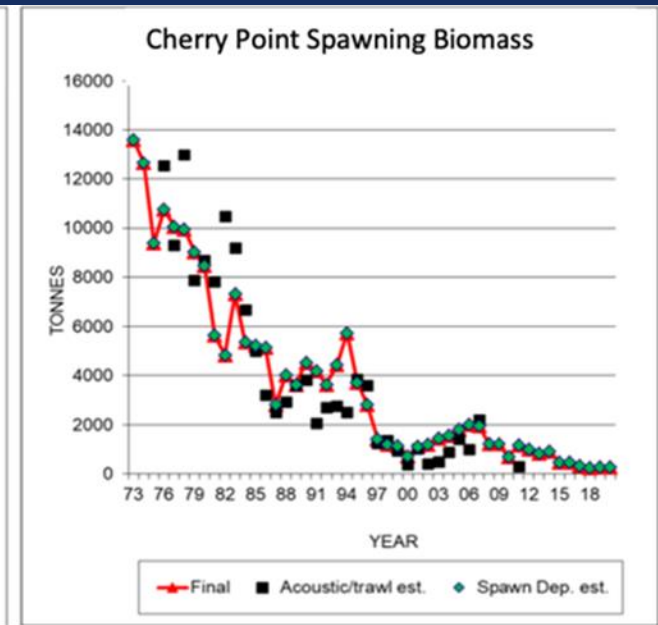
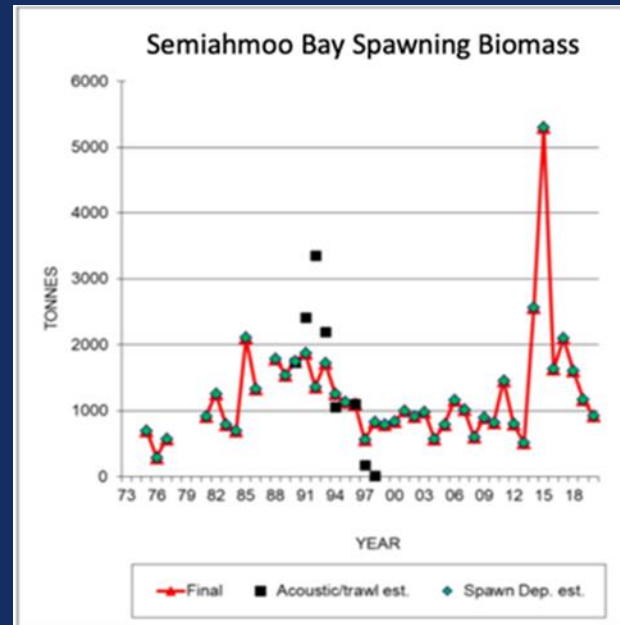
Pacific Herring are an important ecological, cultural, and economic resource



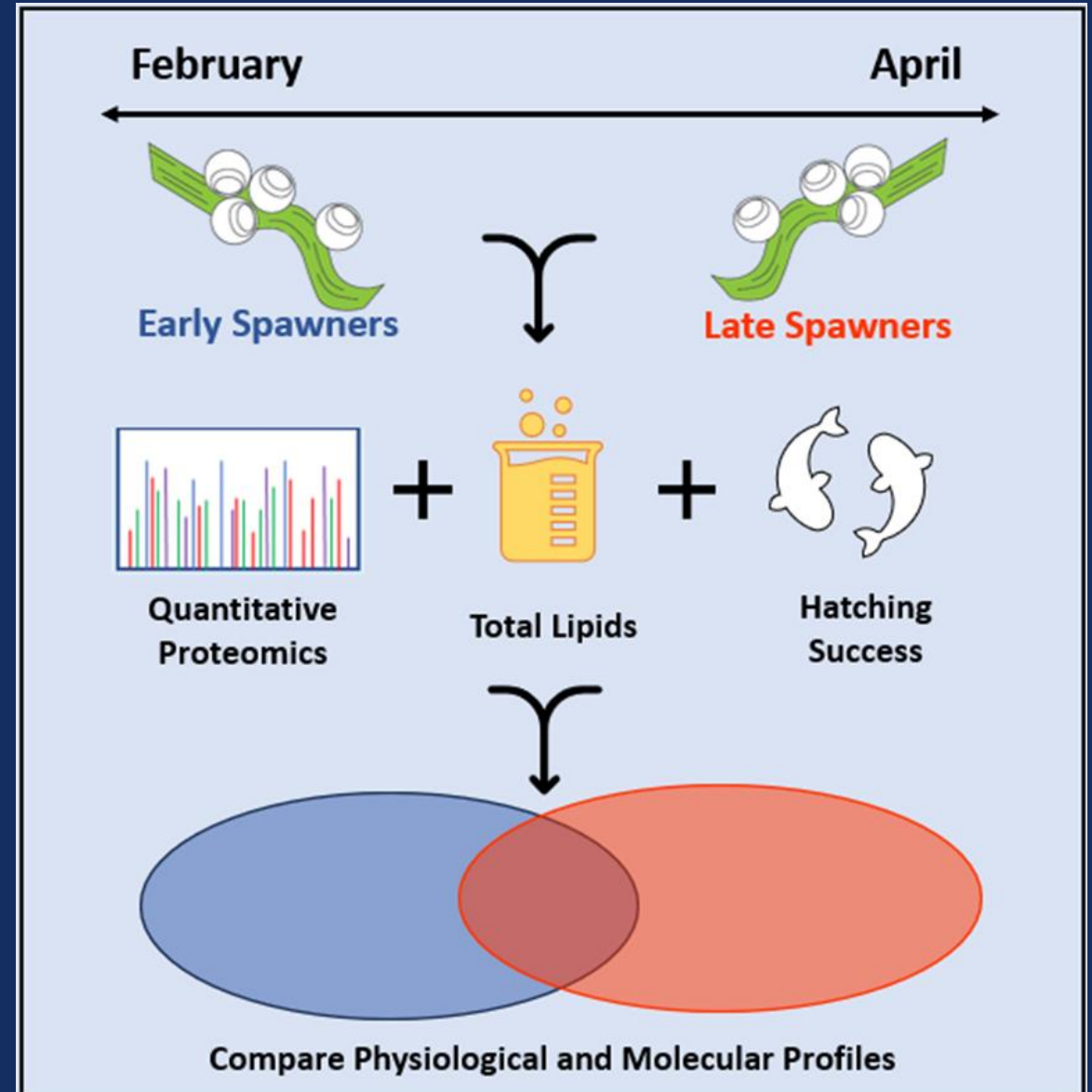
Failure of late spawning population required a change of plans



Population	Jan	Feb	Mar	April	May	June
Semiahmoo Bay (SB)						
Cherry Point (CP)						



The revised study compares early and late spawning cohorts within a single population.



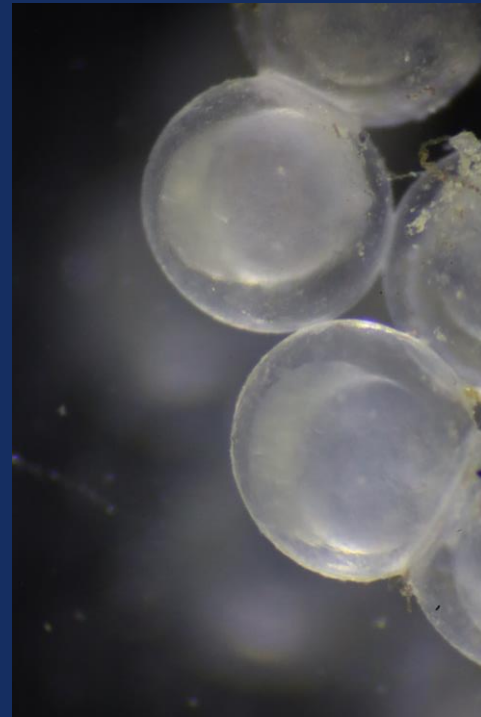
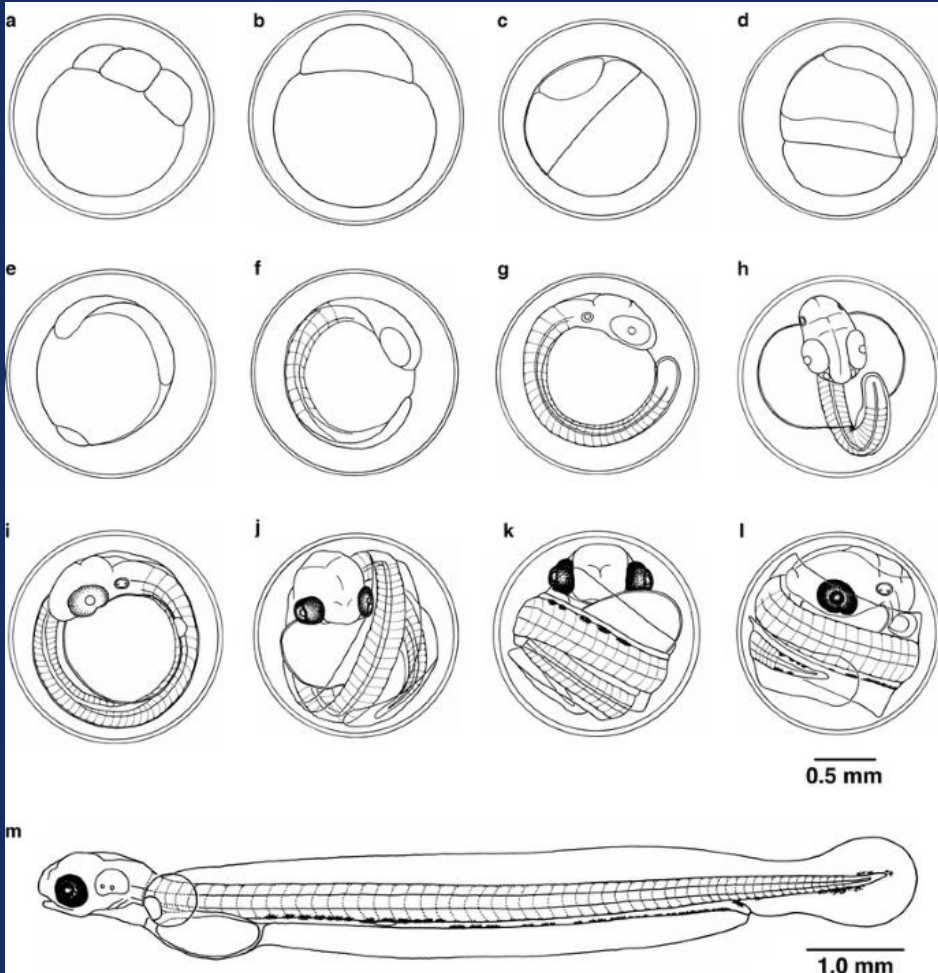
WDFW surveyed every 10-14 days during the spawning season, and we preserved each collection, culturing a cohort to hatch when possible.

Year	Cohorts at Collection	Cohorts Hatched Out	Months	Temp Range
2023	5	3	Feb, Mar, April	7.1-8.4
2024	5	3	Feb, Mar, April	6-9

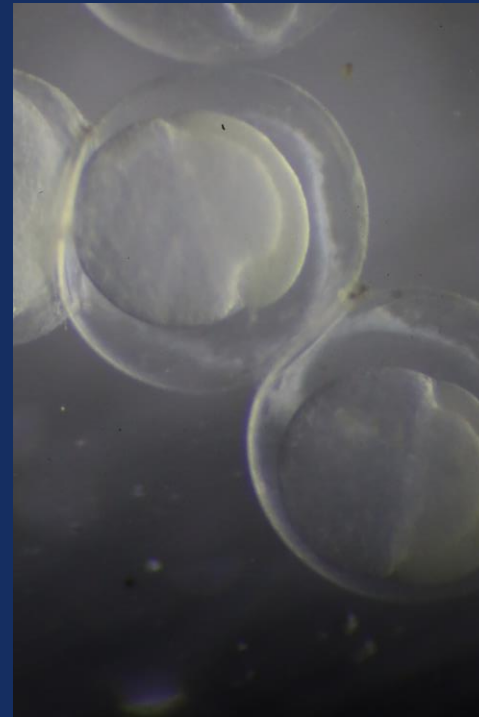
Lipids,
Proteomics

At hatch: Lipids,
Proteomics,
Morphology,
Hatching Success

Embryos had different developmental stages at time of collection



B/C
(5 cohorts)



E/F
(2 cohorts)

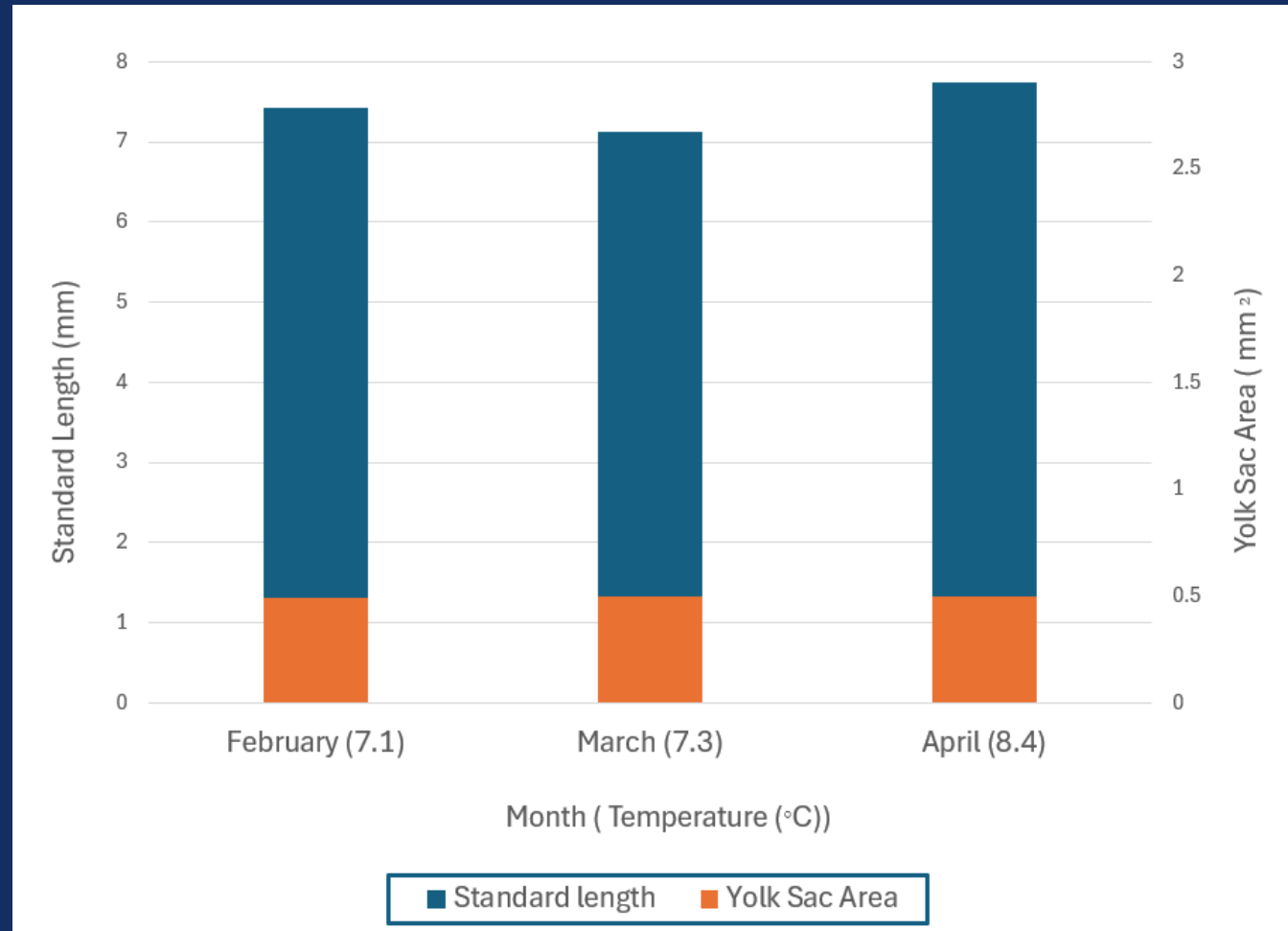


I/J
(3 cohorts)

Each cohort was maintained at the average field temperature at time of collection until hatch.

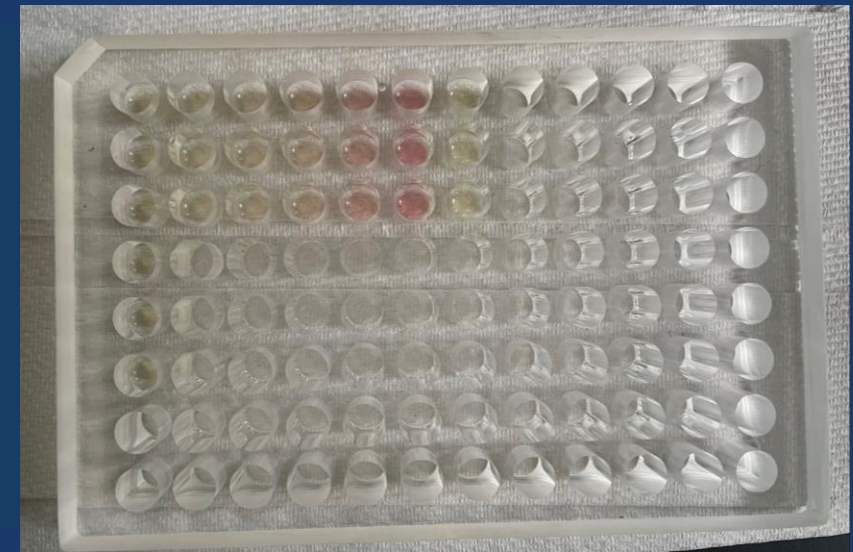
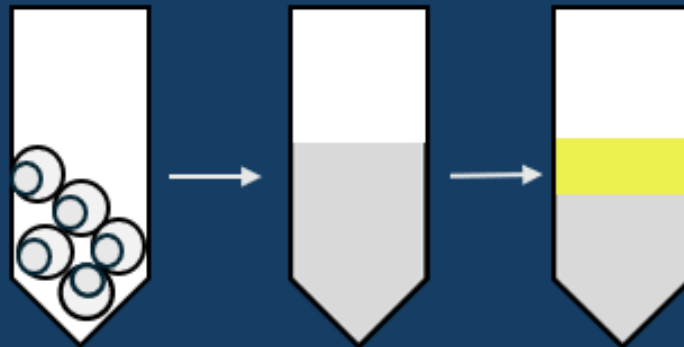


No significant differences in hatching success, larval length, or yolk sac area at hatch seasonally

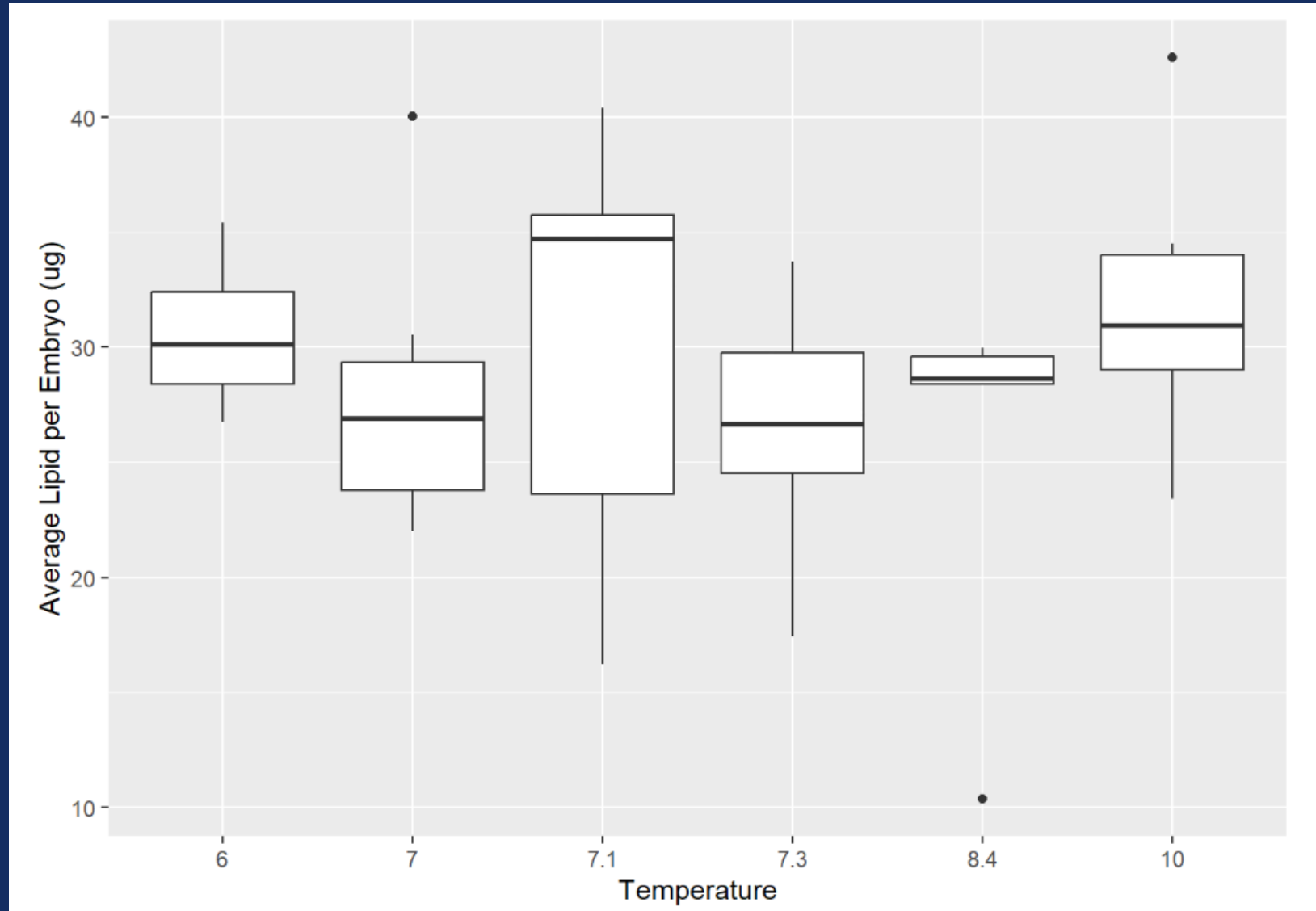


Total lipids were collected from embryos before and after culturing

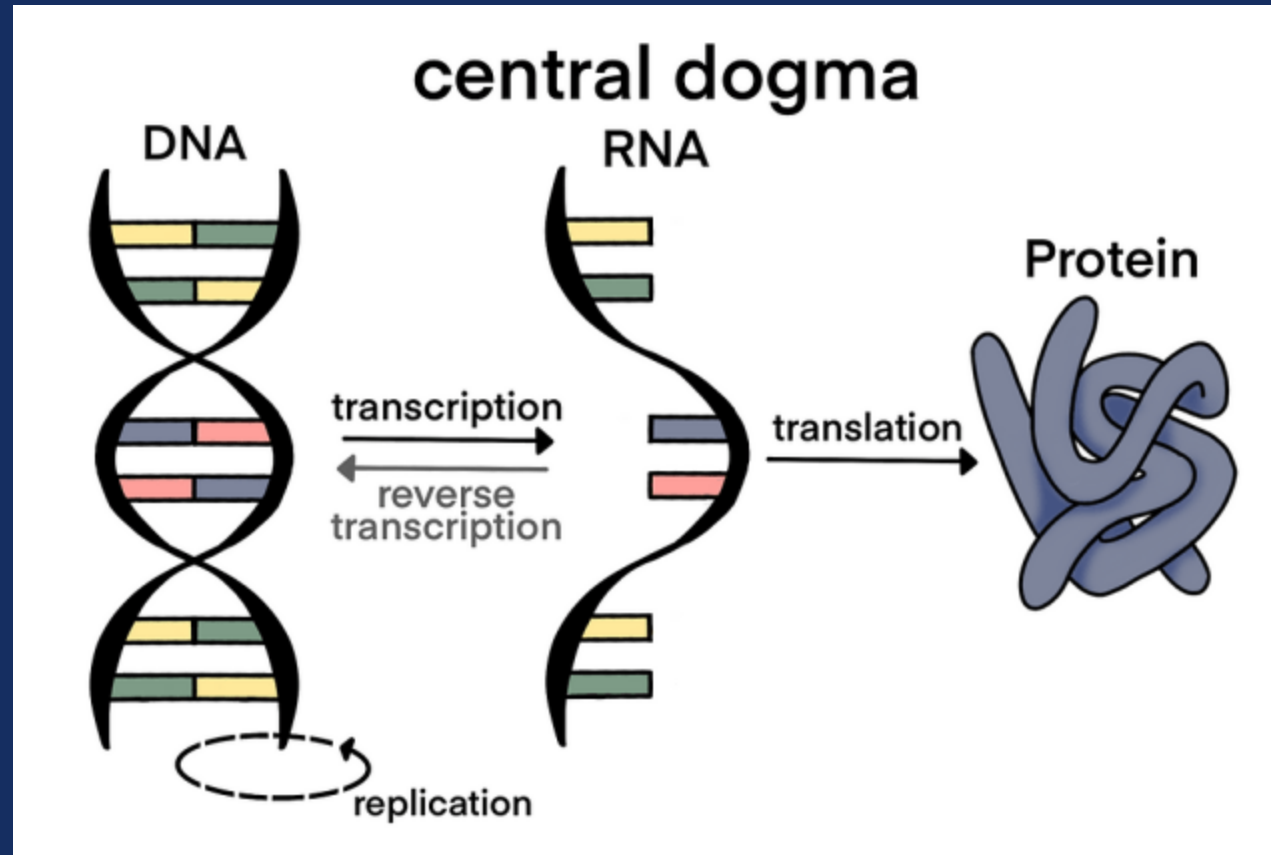
Homogenization → Extraction → Analysis



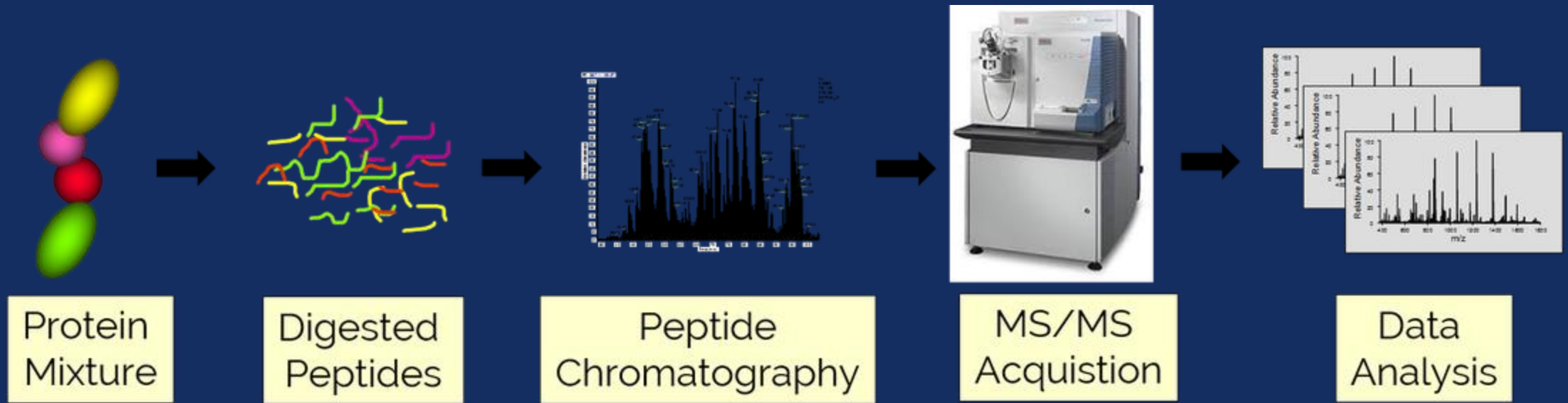
Total lipids were not significantly different between years, temperatures, or developmental stage



Proteomics is an emerging field in marine science



Samples were homogenized, digested, and analyzed to discover proteomic results

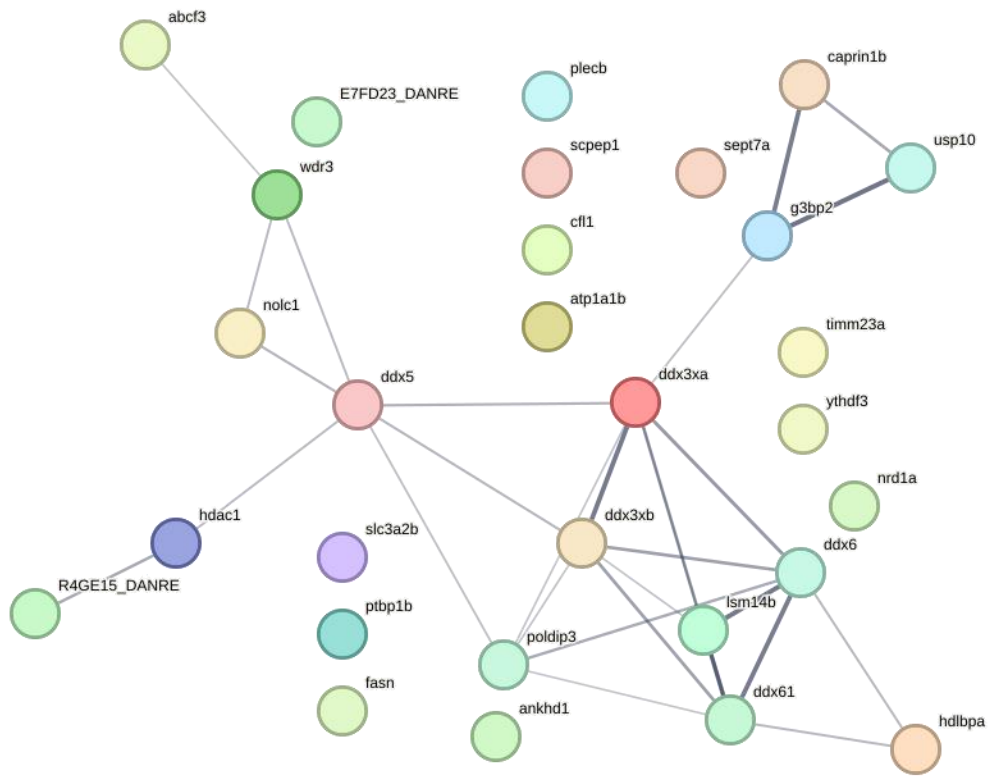


33 proteins in embryos of the same development had different relative abundance in Feb vs April

Protein names
Dihydrolipoyllysine-residue succinyltransferase
RNA helicase (EC 3.6.4.13)
Plectin isoform X9
Zgc:55673 protein
LSM family member 14B (Protein LSM14 homolog B)
RNA helicase (EC 3.6.4.13)
YTH domain-containing family protein
Septin
Uncharacterized protein C7orf57 homolog isoform X1
ATP-binding cassette sub-family F member 3 (Solute carrier family 3 member 2b) (Zgc:55813)
Mitochondrial import inner membrane translocase subunit TIM23 (EC 2.3.1.85) (EC 3.1.2.14) (EC 4.2.1.59)
Cofilin-1 (Muscle cofilin 2)
Sodium/potassium-transporting ATPase subunit alpha protein 1)
WD repeat domain 3 (WD repeat-containing protein 3)
RNA helicase (EC 3.6.4.13)
Polypyrimidine tract-binding protein 1
Nucleolar and coiled-body phosphoprotein 1
Histone deacetylase (EC 3.5.1.98)
Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)
GTPase activating protein (SH3 domain) binding protein
Polymerase delta-interacting protein 3 isoform X1
Carboxypeptidase (EC 3.4.16.-)
RNA helicase (EC 3.6.4.13)
Caprin-1 isoform X1
Nardilysin
Bromodomain adjacent to zinc finger domain protein 1A isoform X2
Histone H2B
RNA helicase (EC 3.6.4.13)
High density lipoprotein-binding protein a (Vigilin isoform X1)

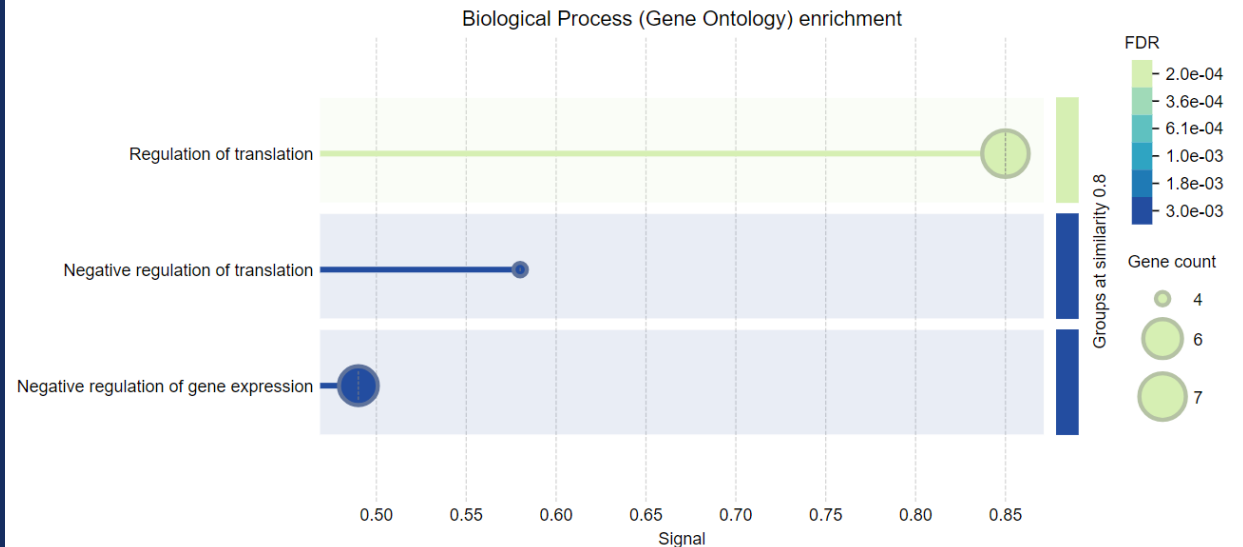
More abundant
April vs. February

Less abundant
April vs. February

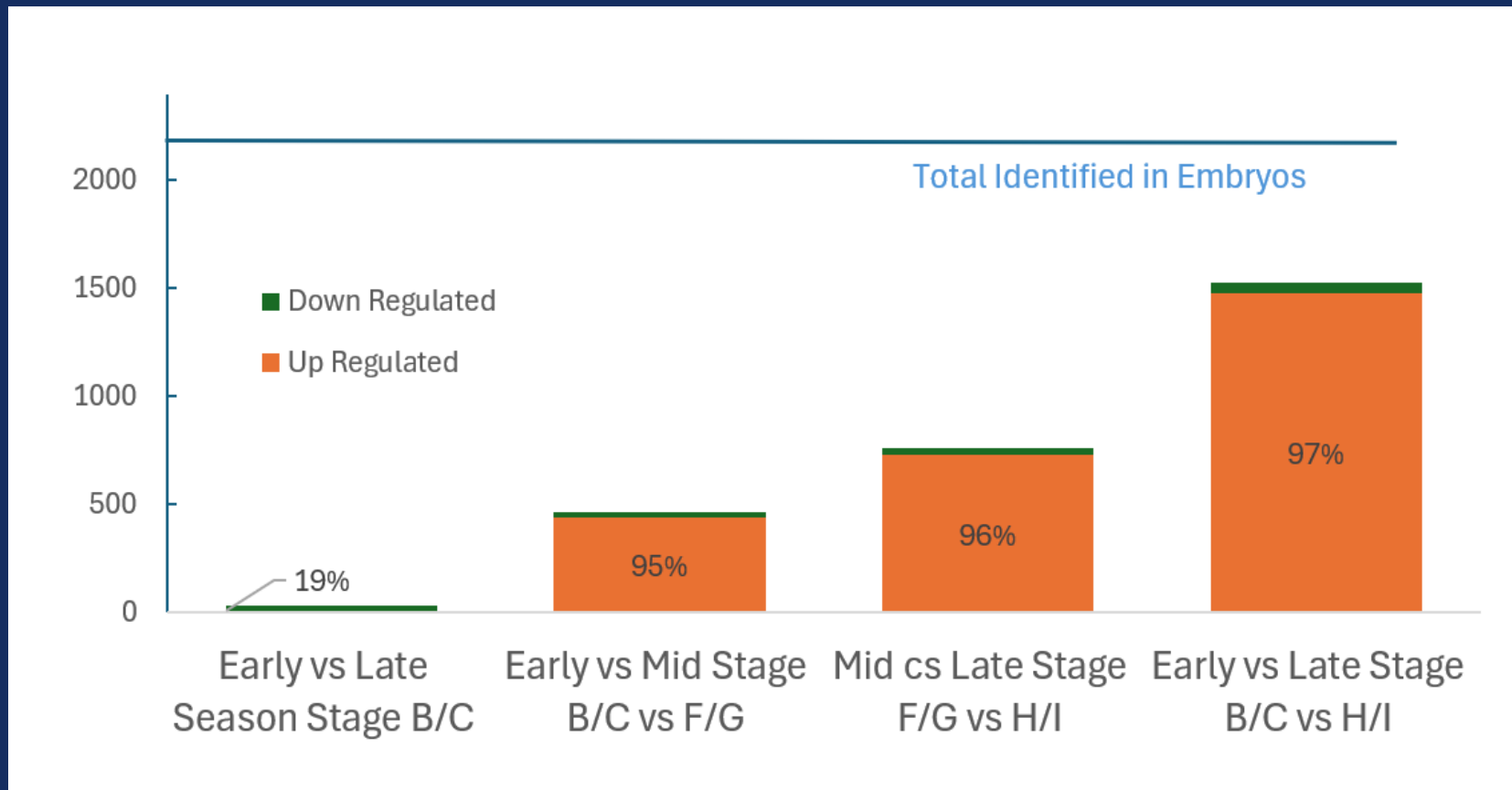


STRING analysis helps identify relationships between proteins that differ between seasons, and assesses the likelihood that this is a random set of proteins from the whole set in the genome.

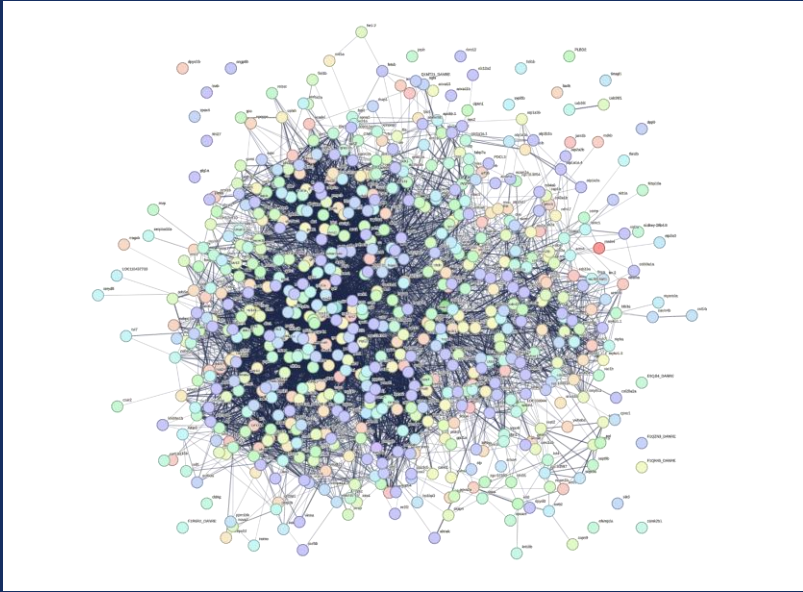
Seasonal differences in proteome may be related to subtle temperature driven changes in growth rate



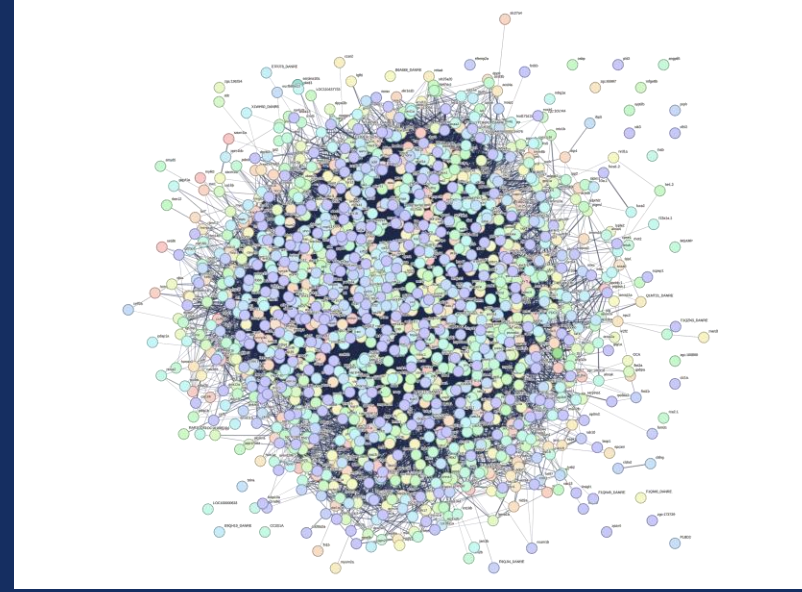
Proteins increased in relative abundance during embryonic development



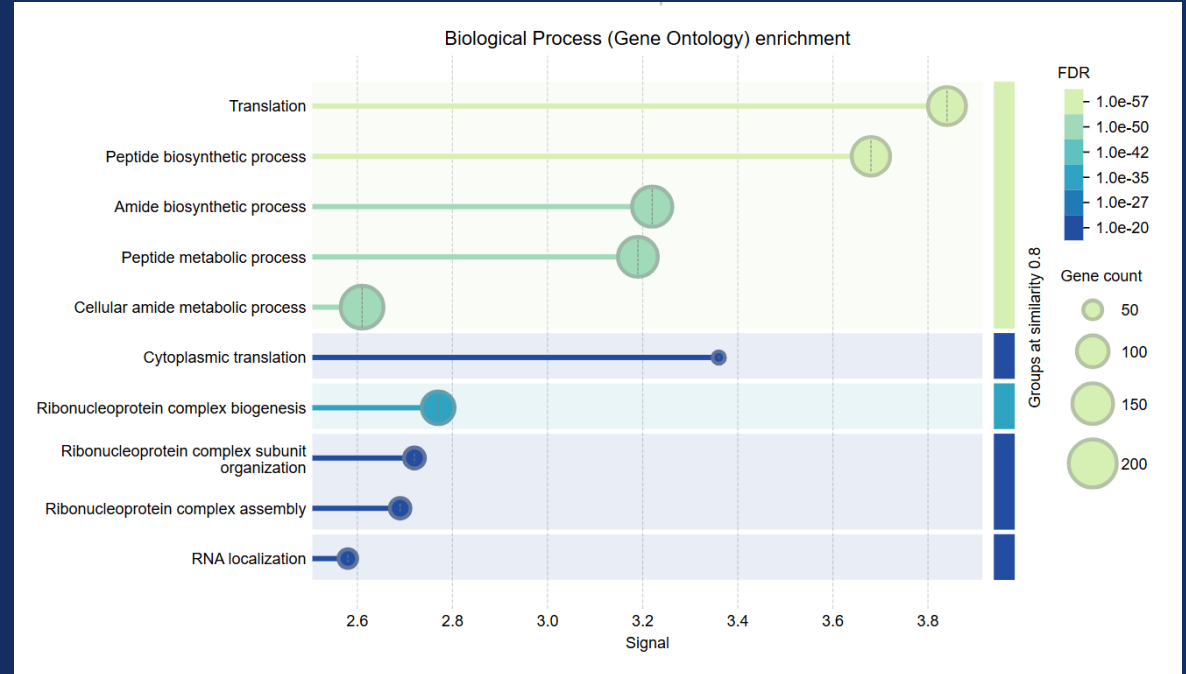
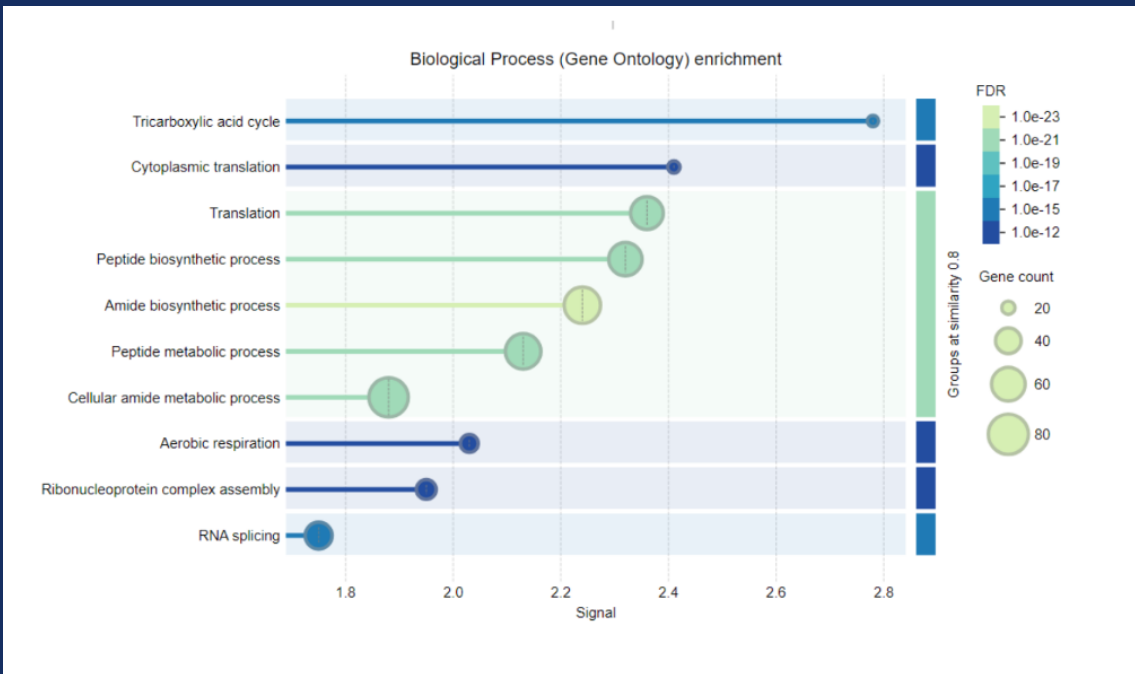
To understand environmentally driven changes in the proteome, we must first map developmental changes



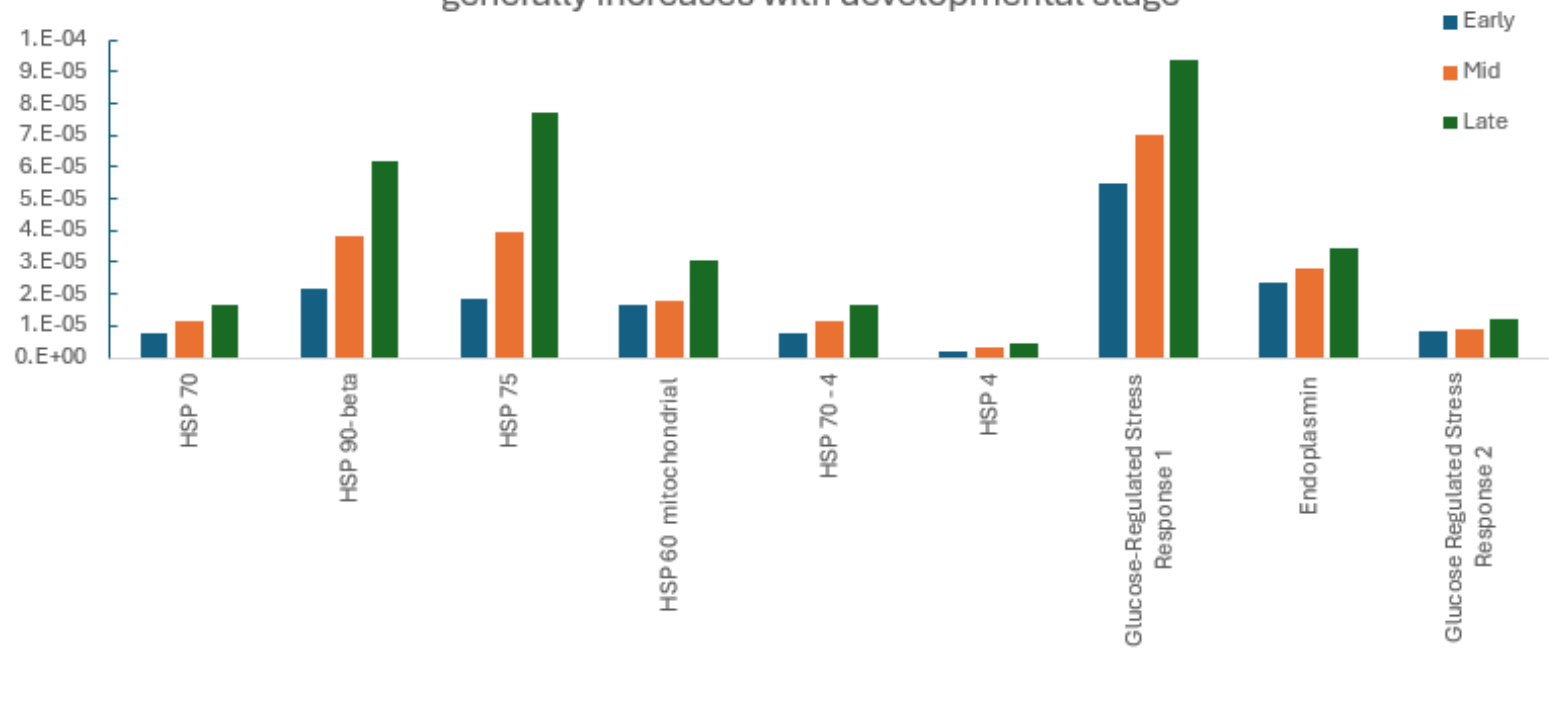
f/g
v.
h/i

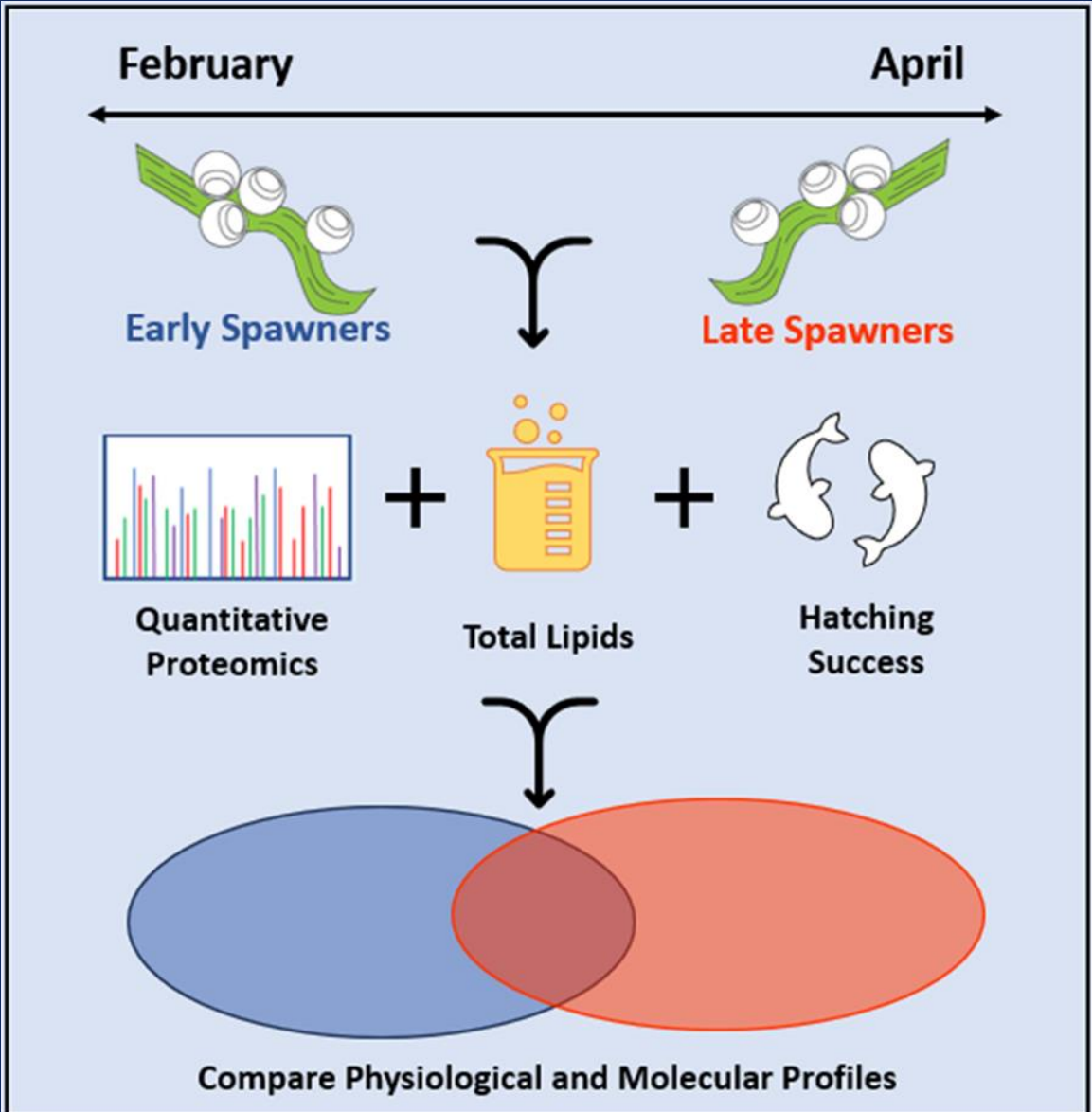


b/c
v.
h/i



Relative abundance of heat shock and other stress response proteins generally increases with developmental stage





We did not discover significant differences in pacific herring physiology and their biological pathways only had subtle differences.

Future research can use the baseline of proteomes from different developmental stages to distinguish developmental and external influences on proteomics.