An in-depth coho salmon (Onchorhynchus kisutch) ovarian follicle proteome reveals coordinated changes across diverse cellular processes during the transition from primary to secondary growth

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September 25, 2024

Abstract

Teleost fishes are a highly diverse and ecologically essential group of aquatic vertebrates and include coho salmon, Onchorhynchus kisutch. Coho are semelparous and all ovarian follicles develop synchronously. Owing to their ubiquitous distribution, teleost provide critical sources of food worldwide through subsistence, commercial fisheries, and aquaculture. Enhancement of commercial hatchery practices requires a detailed knowledge of teleost reproductive physiology. Despite decades of research on teleost reproductive processes, an in-depth proteome of teleost ovarian development has yet to be generated. We describe a coho salmon ovarian proteome of over 5700 proteins, generated with data independent acquisition, revealing the suite of detectable proteins that change through the transition from primary to secondary ovarian follicle development. This transition is critical for puberty onset, egg quality, and further embryonic development. Primary ovarian follicle development was marked by differential abundances of proteins involved in carbohydrate metabolism, protein turnover, and the complement pathway, suggesting elevated metabolism as the oocytes enter maturation. The greatest proteomic shift occurred during the transition from primary to secondary follicle growth, with increased abundance of proteins underlying cortical alveoli formation, extracellular matrix reorganization, iron binding, and cell-cell signaling. This work provides a foundation for identifying biomarkers of salmon oocyte stage and quality.

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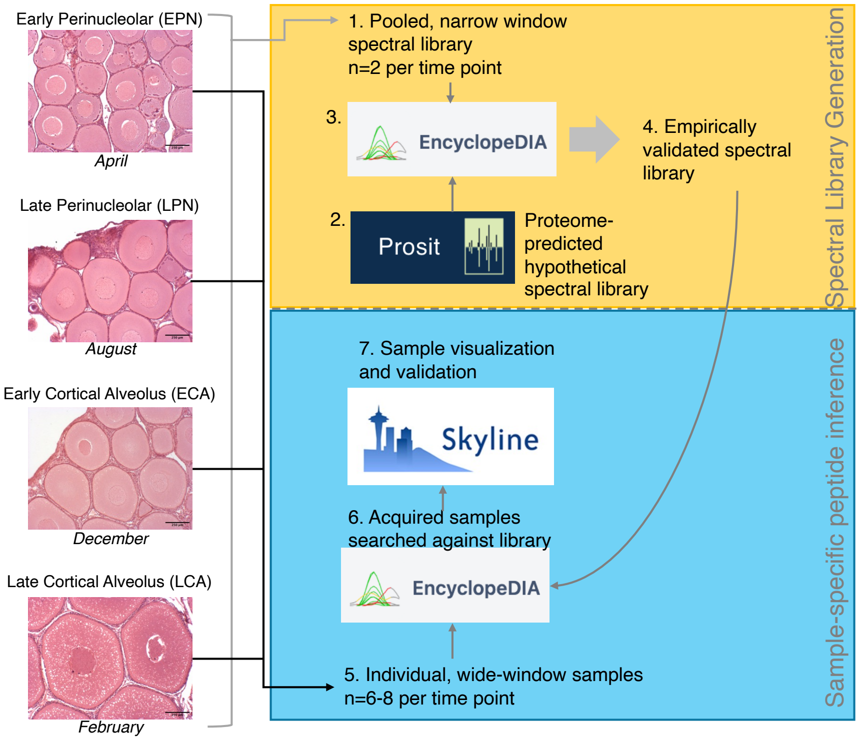
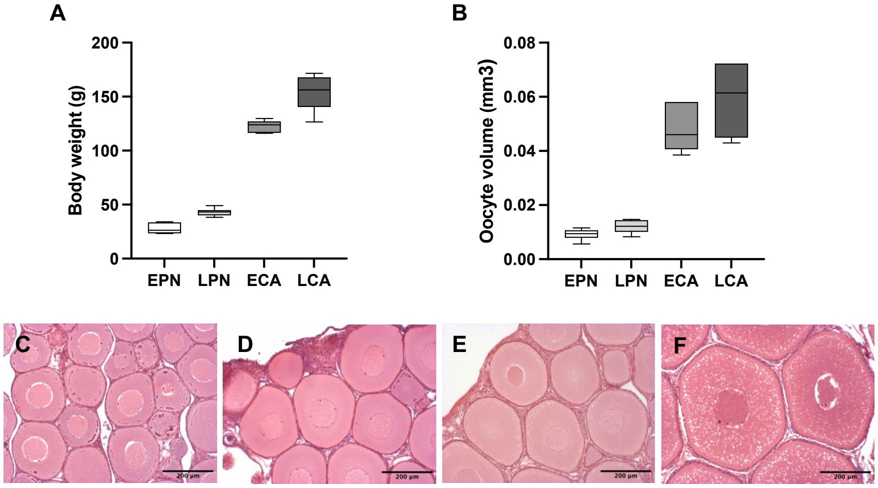
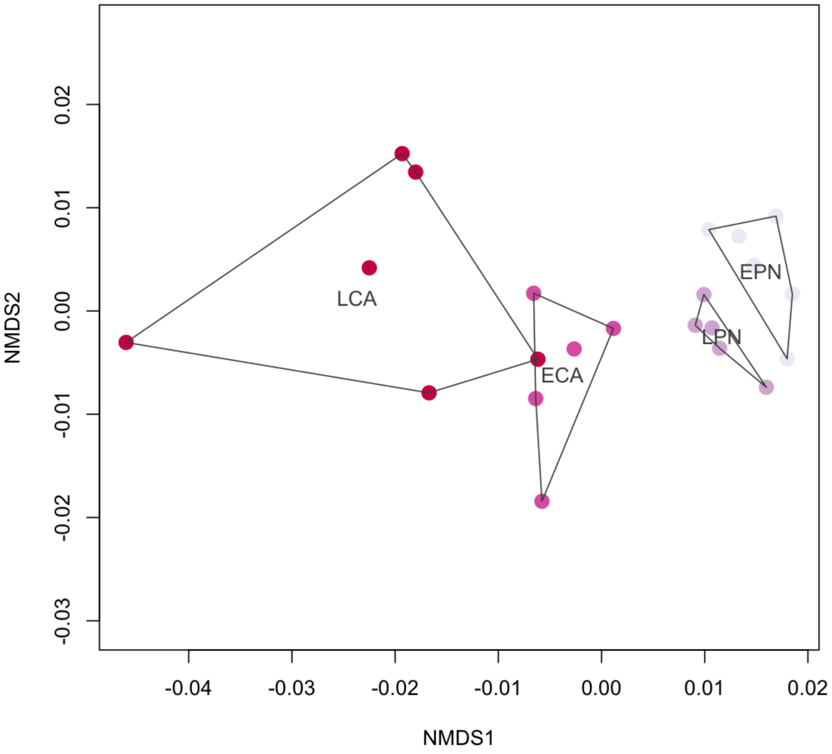
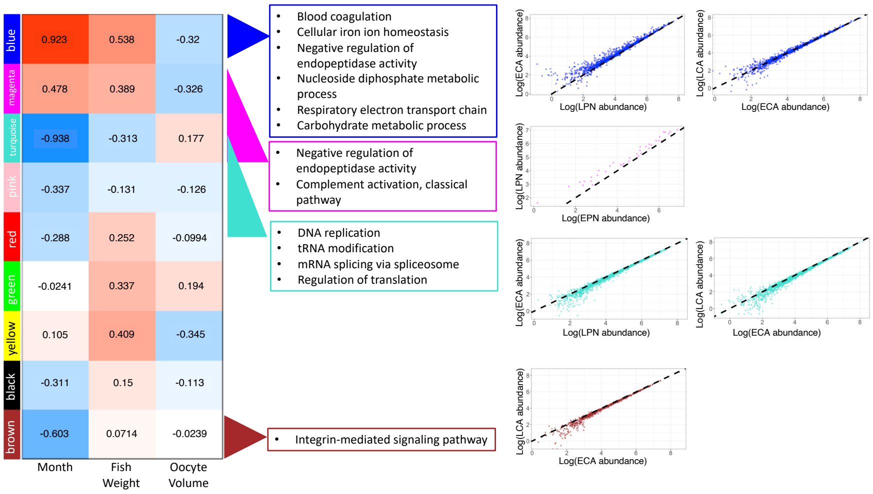
`Coho Proteomics manuscript for Proteomics.docx` available at https://authorea.com/users/499758/articles/1227965-an-in-depth-coho-salmon-onchorhynchus-kisutch-ovarian-follicle-proteome-reveals-coordinated-changes-across-diverse-cellular-processes-during-the-transition-from-primary-to-secondary-growth


Early Perinucleolar (EPN)
April
Late Perinucleolar (LPN)
August
Early Cortical Alveolus (ECA)
December
Late Cortical Alveolus (LCA)
February
1. Pooled, narrow window spectral library n=2 per time point
3.
EncyclopeDIA
4. Empirically validated spectral library
2.
Prosit
Proteome-predicted hypothetical spectral library
Spectral Library Generation
7. Sample visualization and validation
Skyline
6. Acquired samples searched against library
EncyclopeDIA
5. Individual, wide-window samples n=6-8 per time point
Sample-specific peptide inference


A
Body weight (g)
200
150
100
50
0
EPN
LPN
ECA
LCA
B
Oocyte volume (mm3)
0.08
0.06
0.04
0.02
0.00
EPN
LPN
ECA
LCA
C
D
E
F
200 µm
200 µm
200 µm
200 µm





	Month	Fish Weight	Oocyte Volume
blue	0.923	0.538	-0.32
magenta	0.478	0.389	-0.326
turquoise	-0.938	-0.313	0.177
pink	-0.337	-0.131	-0.126
red	-0.288	0.252	-0.0994
green	-0.0241	0.337	0.194
yellow	0.105	0.409	-0.345
black	-0.311	0.15	-0.113
brown	-0.603	0.0714	-0.0239

- Blood coagulation
- Cellular iron ion homeostasis
- Negative regulation of endopeptidase activity
- Nucleoside diphosphate metabolic process
- Respiratory electron transport chain
- Carbohydrate metabolic process

- Negative regulation of endopeptidase activity
- Complement activation, classical pathway

- DNA replication
- tRNA modification
- mRNA splicing via spliceosome
- Regulation of translation

- Integrin-mediated signaling pathway