

A mega-analysis using microbial prediction of individual performance across aquaculture species

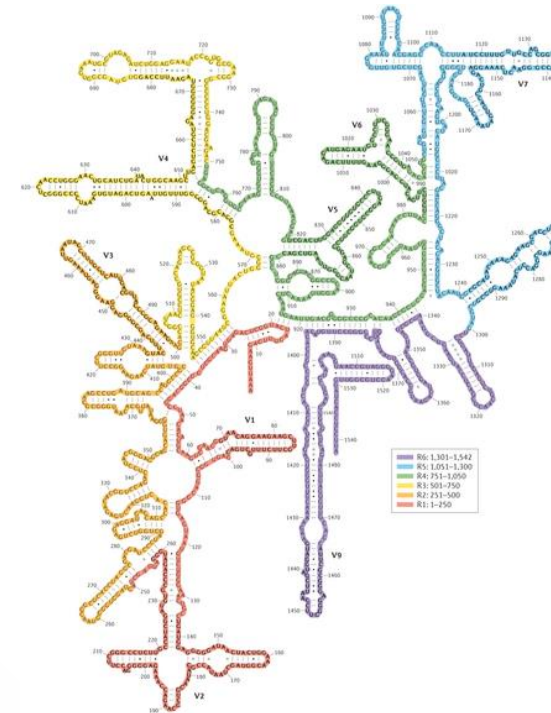
EAAP Gent 2019

Gareth Frank Difford & Erica Leder

Microbial Revolution



Culturable < Unculturable



Culture Independent methods 

Host x Microbe interaction



Absence

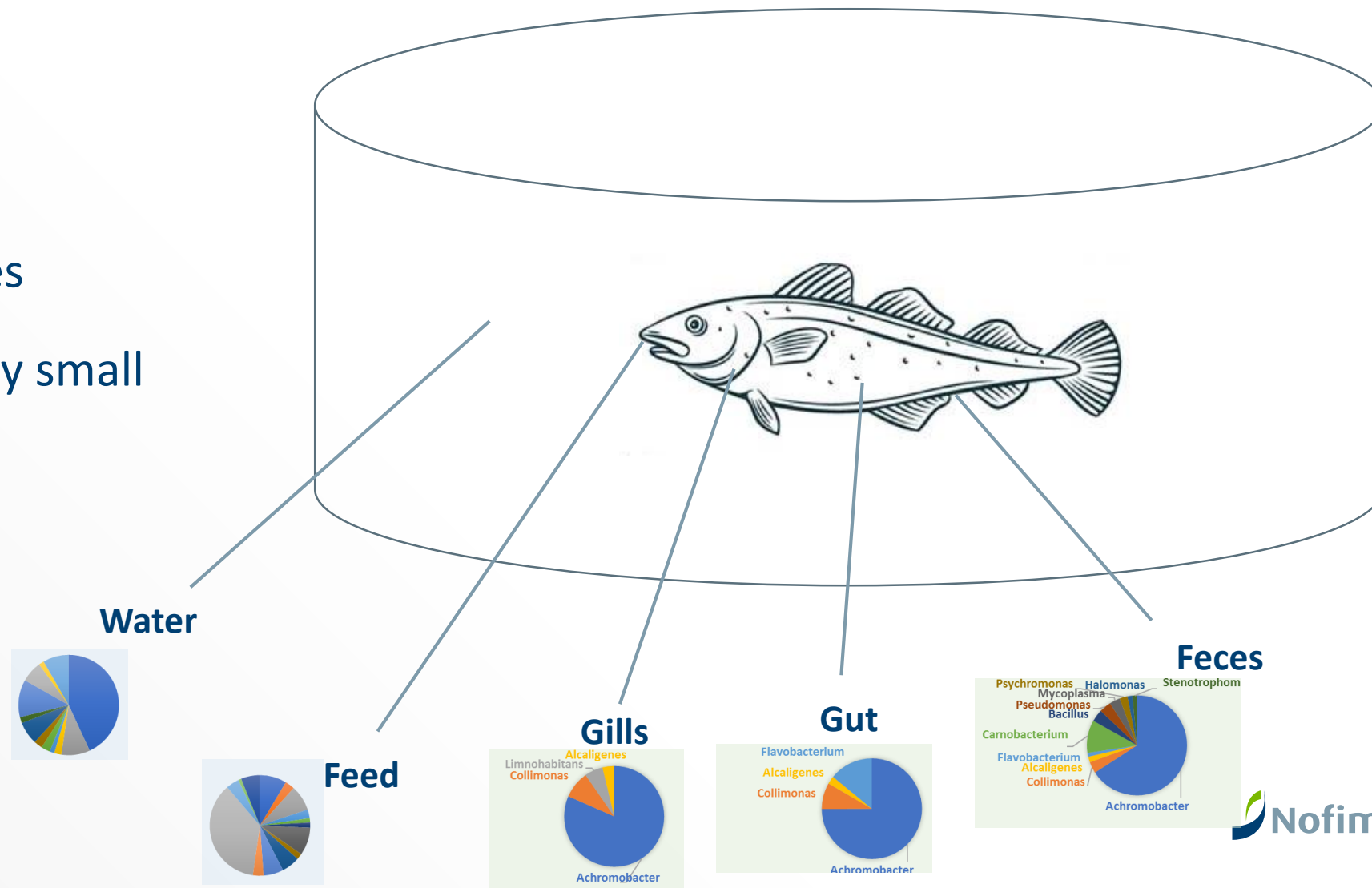


Presence

Host x Microbe interaction

Communities

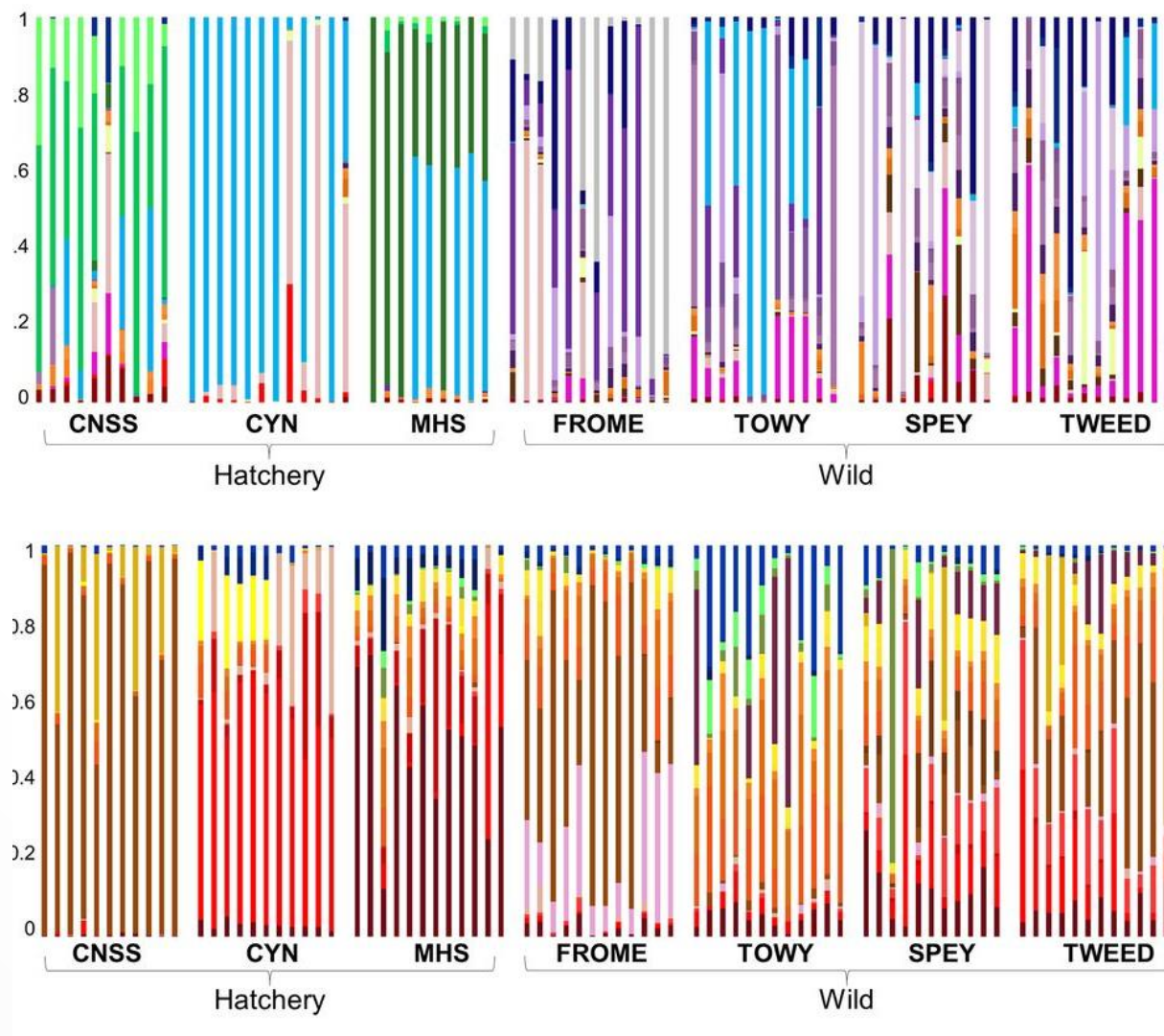
- Microbial communities
- Vital functions
- Many microbes / many small effects?
- + / -



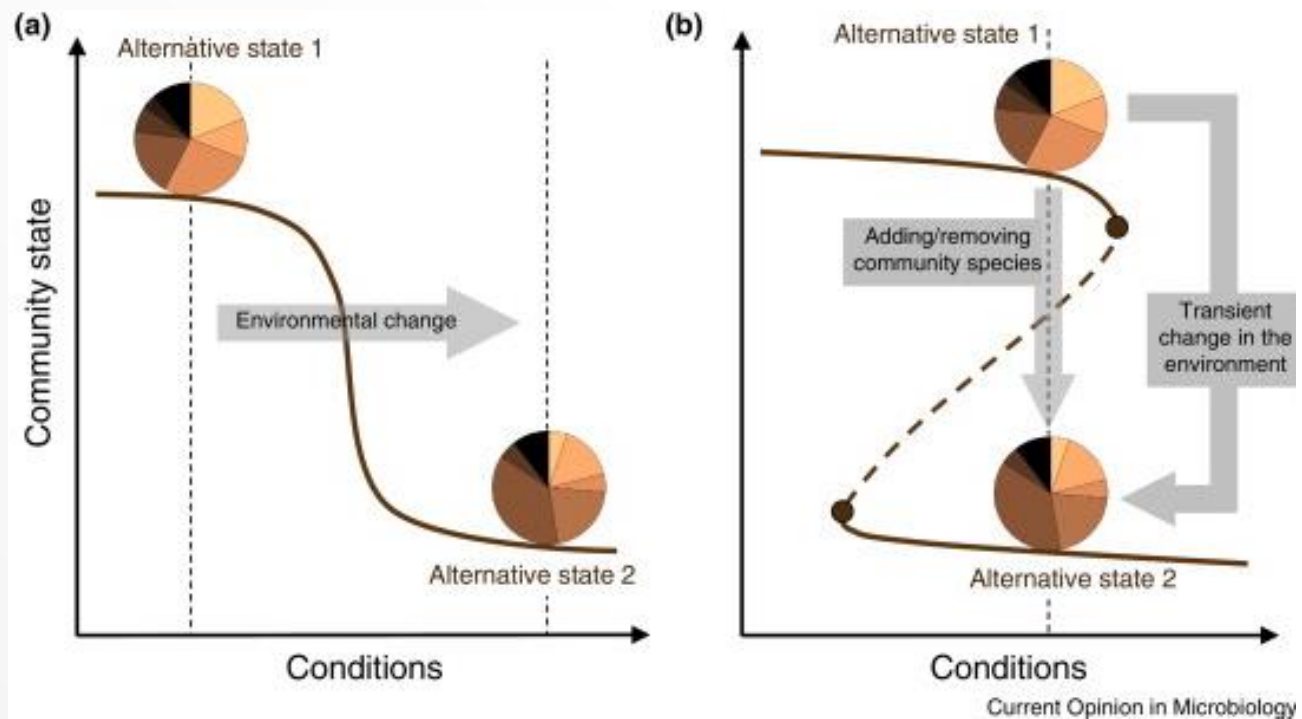
Microbial Communities

- Differ across Hatcheries
- Wild versus Captive
- Body sites

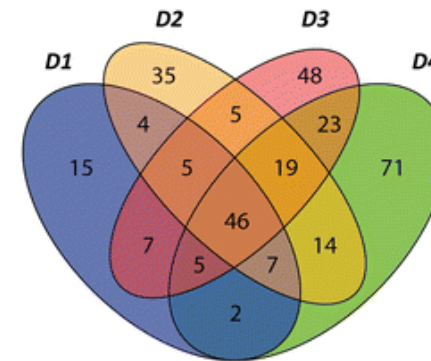
Highly redundant



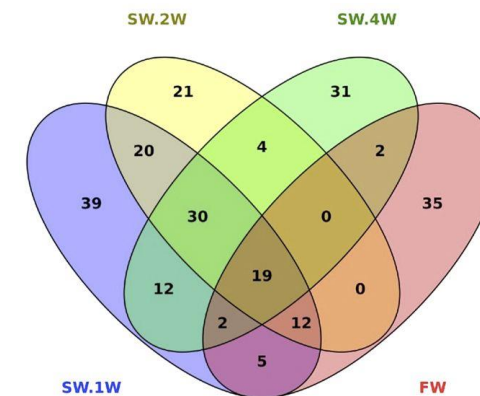
Community Perturbation



Faust et al., 2015



Diets
Piazzon et al. 2017



Freshwater – Saltwater
Lokesh & Kiron 2016

Publicly available Databases

54,992 “studies”

2,744,041

3,306,321 sequencing libraries

Smaller number are aquaculture species

Samples sizes are limited 5 – 300

Salmon dominates

Can we use this for anything?

SRA <https://www.ncbi.nlm.nih.gov/sra>

ENA <https://www.ebi.ac.uk/ena>

MGnify <https://www.ebi.ac.uk/metagenomics/>

MG-RAST <https://www.mg-rast.org>

IMG <https://img.jgi.doe.gov/>

iMicrobe <https://www.imicrobe.us>

National Microbiome Data Collaborative <https://microbiomedata.org/>

Human Microbiome Project <https://portal.hmpdacc.org/>

GOLD <https://gold.jgi.doe.gov>

Microbiome DB <https://www.microbiomeDB.org>

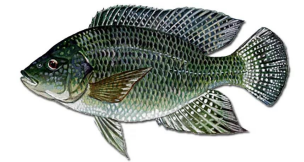
QIITA <https://qiita.ucsd.edu>

GigaDB <http://gigadb.org>

curatedMicrobiomeData <https://waldronlab.io/curatedMetagenomicData>

Aims

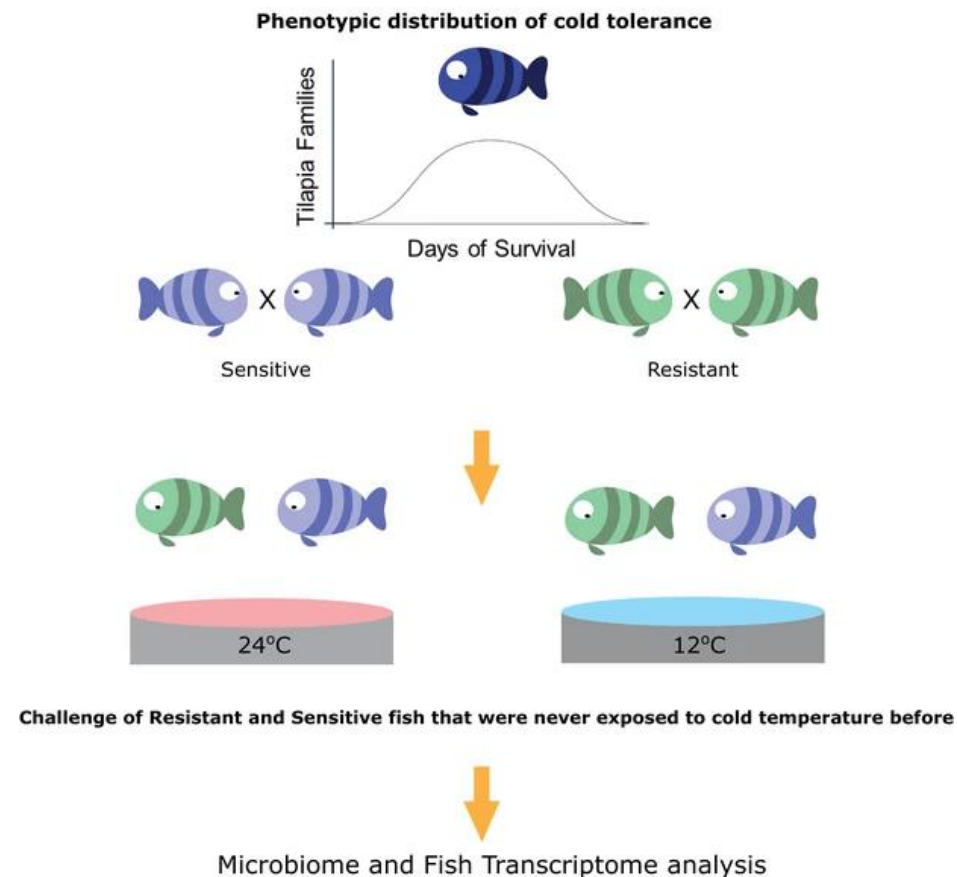
- Extract and curate aquaculture microbiome data
 - Investigate association microbial communities and host phenotypes
1. Detailed example
 2. Overview



Cold tolerance

Israeli Tilapia

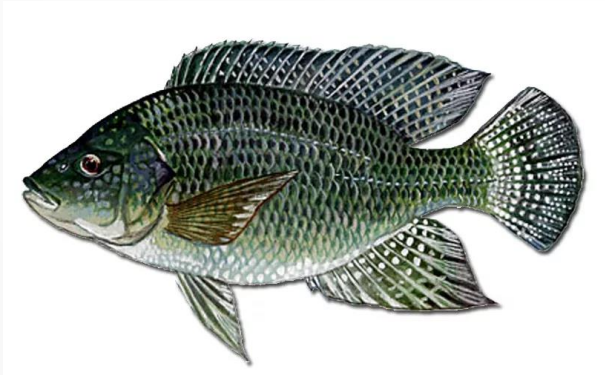
- Selected offspring
- 3 cold resistant, 3 cold sensitive families
- N = 168
- 2 tank temperature treatments
- Gut microbiota



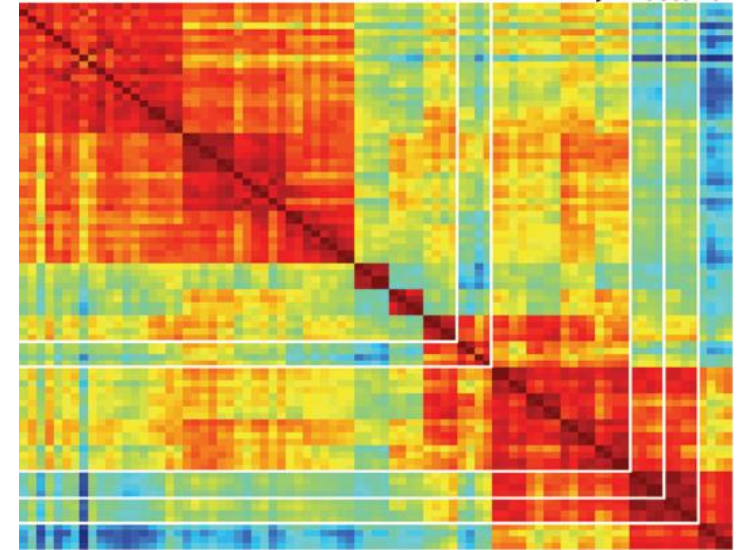
Kokou et al., 2018

Cold tolerance

Israeli Tilapia



$$Y = U + Xb + Mz + e$$



Training data

Validation data

Prediction Accuracy
R2validation
65%

Across Species

$$Y = U + Xb + Mz + e$$

Binary traits



Cold adaptation

Gut

R2 = 65%



Fresh vs Salt

Skin

R2 = 77%

Quantitative traits



Length (Wild)

Gut

R2 = 7%



Length (Farmed)

Gut

R2 = 33%

Environmental Trait



Tank

Skin

R2 = 93%

Conclusion

Freely available microbial data is extremely valuable

Microbiota as predictive tools are very promising

Covariance \neq Causation

Challenges

Are there microbes common across species?

Can we make an aquaculture host microbe reference database

Thank you!

Any questions?

