Impact of degradation and time of sampling on gut samples in wild-caught marine fish

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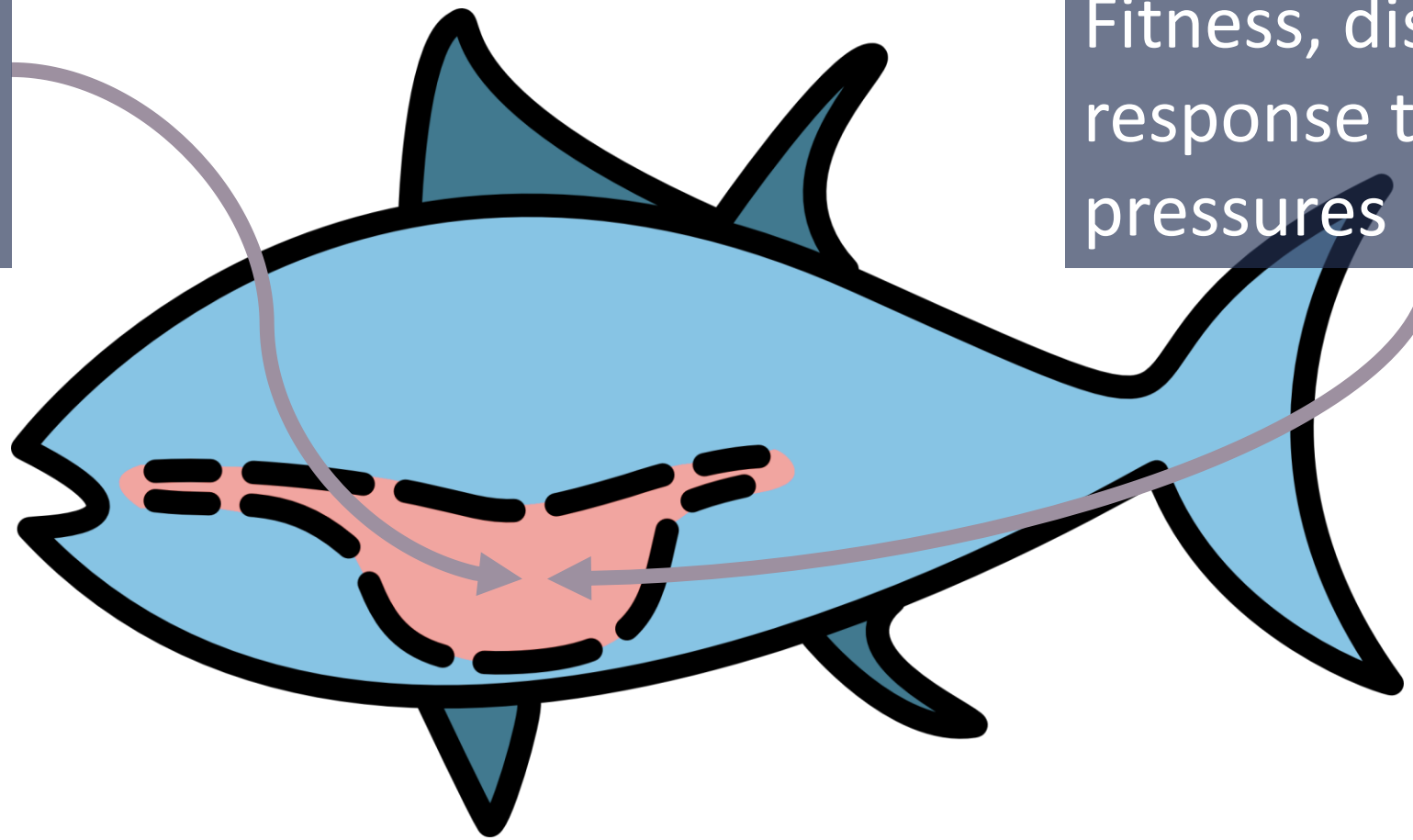
NATIONAL eDNA REFERENCE CENTRE

Gut of wild marine fish

Diet : ecosystem structure and interactions

(Siegenthaler et al., 2019; Clare et al., 2011)



Gut microbiome : Fitness, disease, response to external pressures

(Giatsis et al., 2015; Olmstead et al., 2023; Dvergedal et al., 2020)

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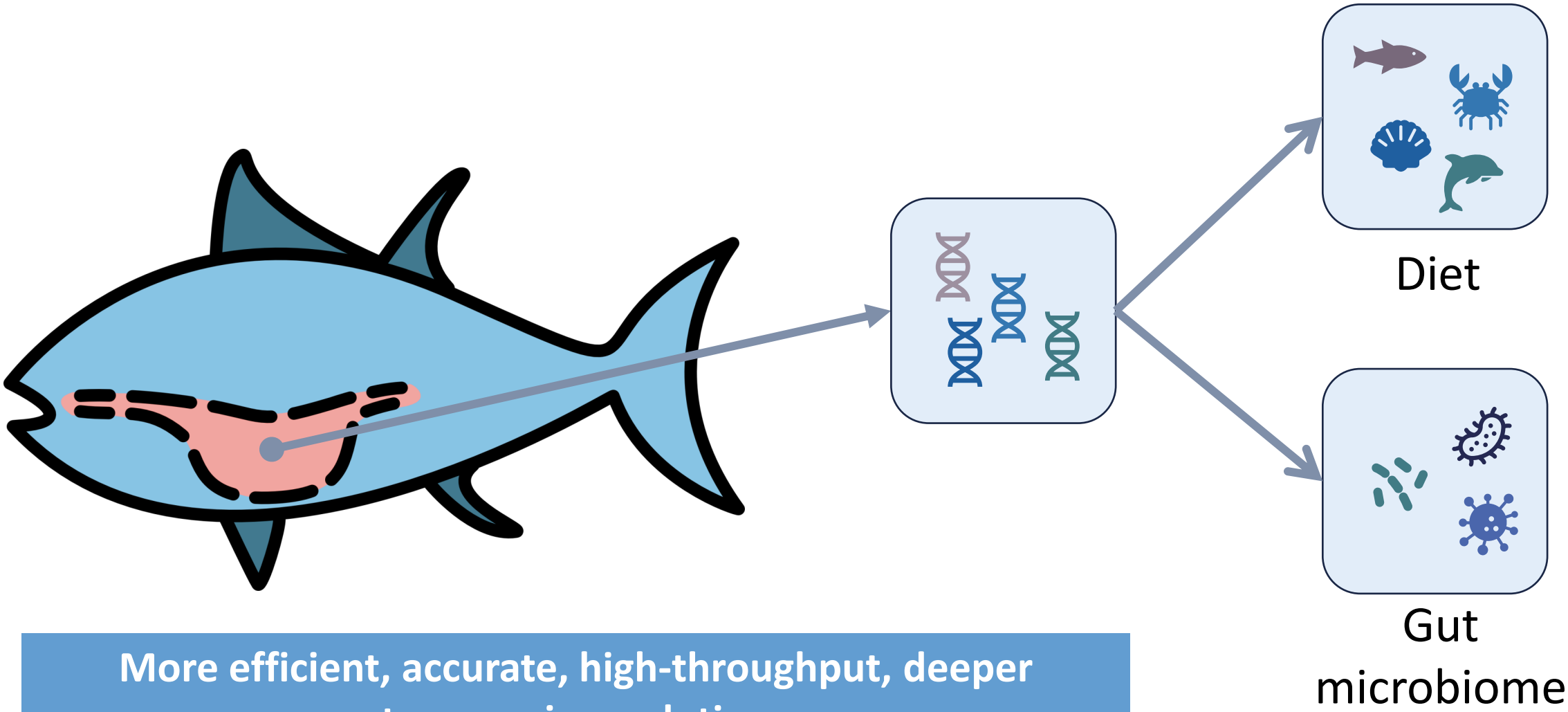
DNA metabarcoding



More efficient, accurate, high-throughput, deeper taxonomic resolution

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Challenge in wild marine fish

Can Stomach Content and Microbiomes of Tuna Provide Near Real-Time Detection of Ecosystem Composition in the Pacific Ocean?

Alejandro Trujillo-González[1], Teng Li[2,3], Joanne Potts[4], Simon Nicol[1,4], Valerie Allain[4], Sam C. Godwin[1], Elodie Vourey[4], Annie Portal[4], Brian Kumasi[5], Thomas Usu[5], Allen Rodrigo[2,3] and Dianne Gleeson[1]*

microorganisms MDPI

Article

Does the Composition of the Gut Bacteriome Change during the Growth of Tuna?

Elsa Gadoin [1], Lucile Durand [1], Aurélie Guillou [1], Sandrine Crochemore [1], Thierry Bouvier [1], Emmanuelle Roque d'Orbcastel [1], Laurent Dagorn [1], Jean-Christophe Auguet [1], Antoinette Adingra [2], Christelle Desnues [3] and Yvan Bettarel [1,*]

Dvergedal *et al. Microbiome* (2020) 8:160
https://doi.org/10.1186/s40168-020-00938-2

Microbiome

RESEARCH Open Access

Association of gut microbiota with metabolism in juvenile Atlantic salmon

H. Dvergedal[1], S. R. Sandve[1*], I. L. Angell[2], G. Klemetsdal[1] and K. Rudi[2]

Catch **Transportation** ❄ **Lab**

weeks - months

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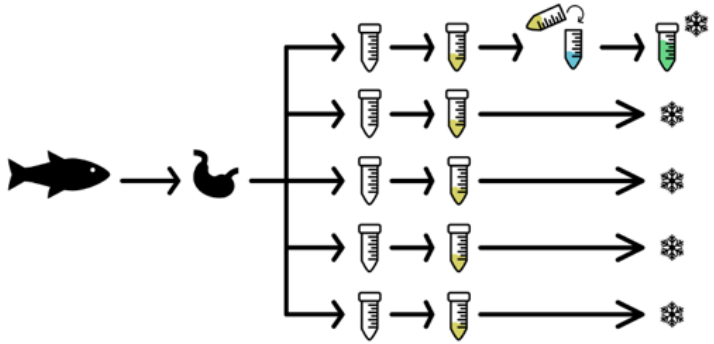
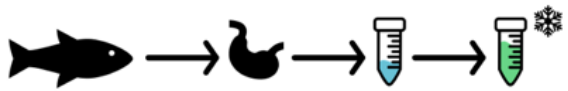
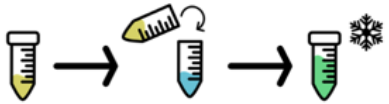
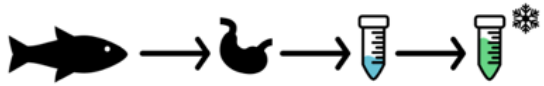
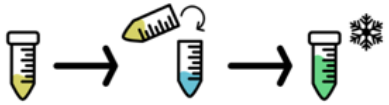
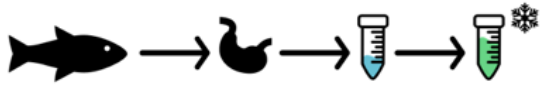
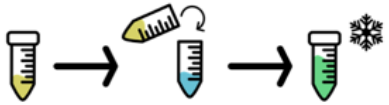
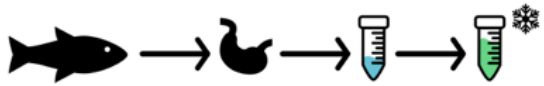
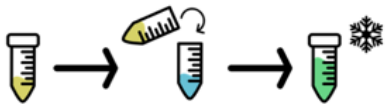
Intra- and inter-individual changes in wild-caught skipjack tuna (*Katsuwonus pelamis*)

Sampling time points	Experiment 1 Intra-individual gut microbiome degradation	Experiment 2 Inter-individual gut microbiome degradation
	× 10	× 50
0h		
2h		
24h		
288h		
576h		

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Methods

DNA extraction

Amplification

Library preparation

Sequencing

Bioinformatics & statistics

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16S rDNA V3-V4 region
(Pro341F - Pro805R)

- DADA2 (SILVA (138) ref db)
- phyloseq
- ggplot2

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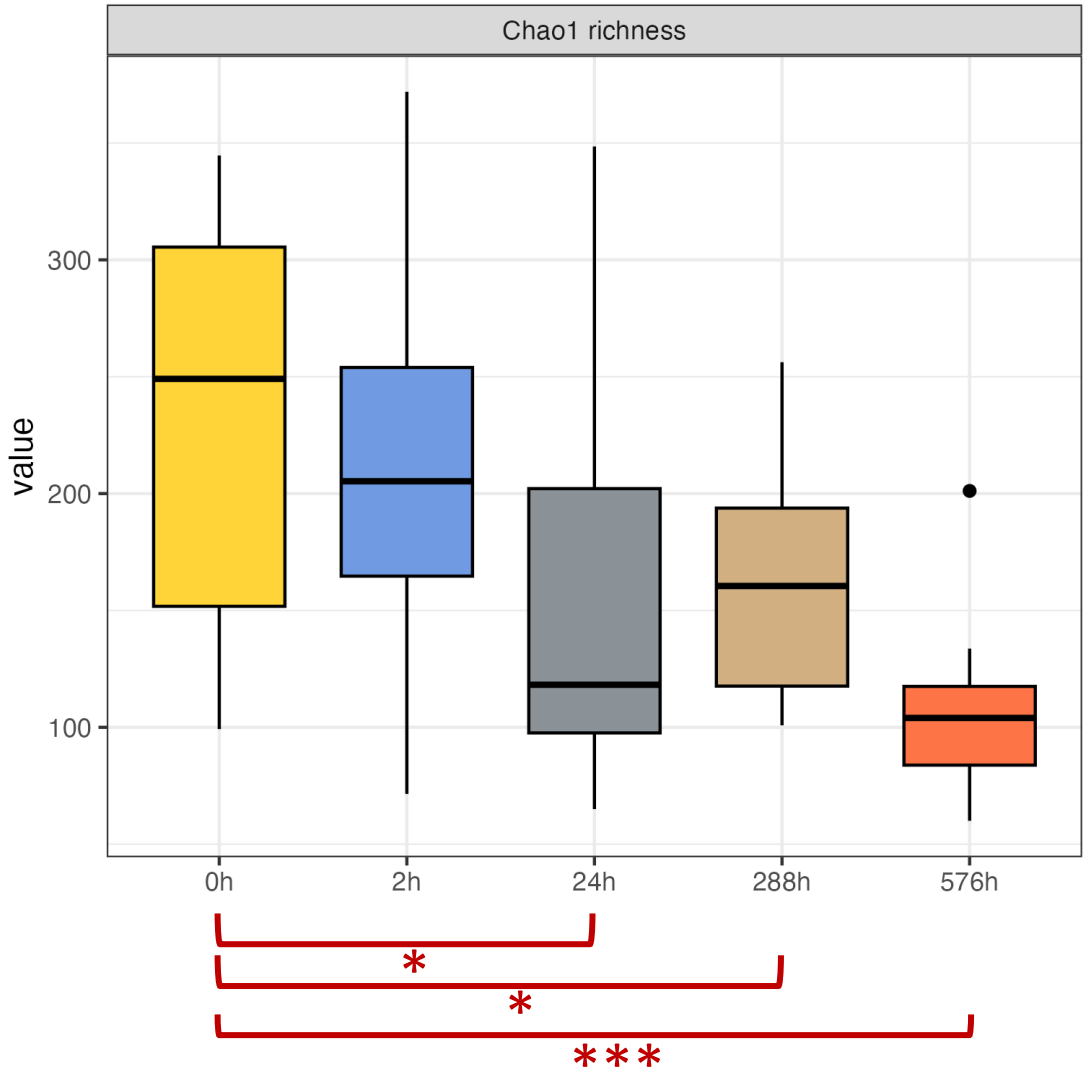
Results – intra-individual changes

ANCOVA: diversity ~ time + individual; Tukey's honestly significant difference (HSD) pair-wise test



Key finding: diversity changed in **2 hours**, significantly changed in **24 hours**

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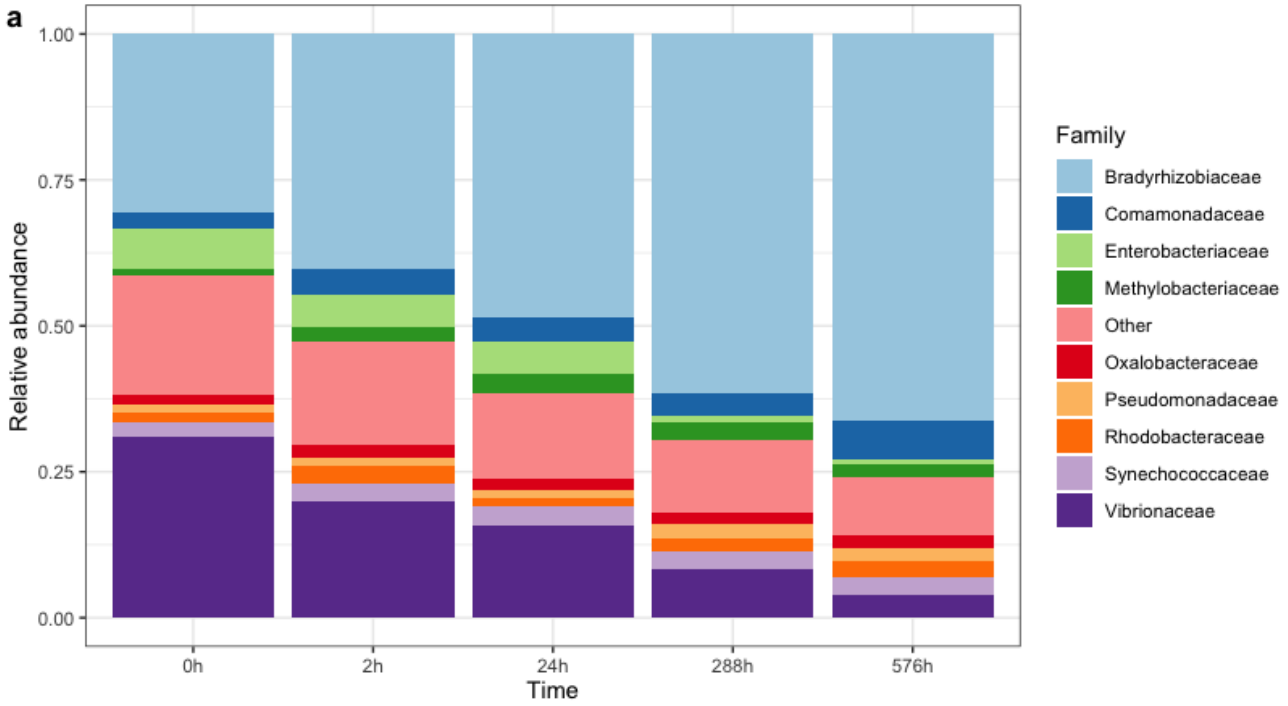
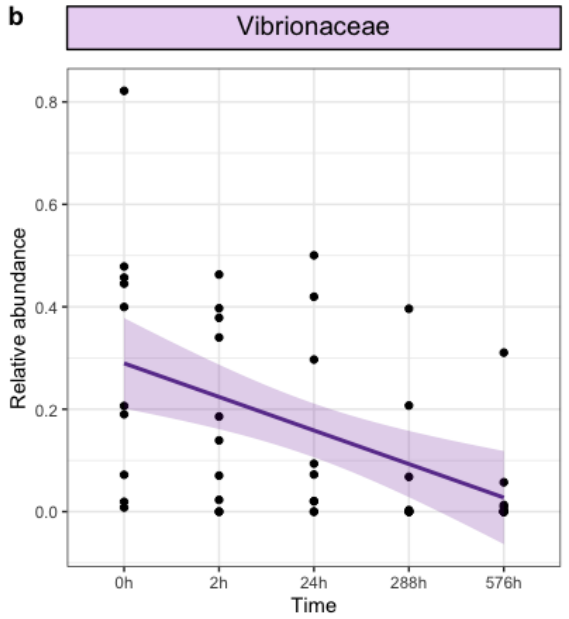
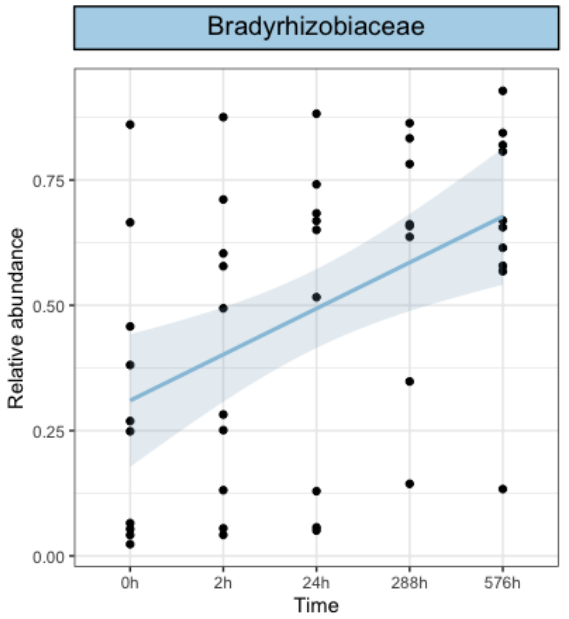
Results – intra-individual changes



GLM: $p < 0.01$



GLM: $p < 0.01$



Key finding: **Bradyrhizobiaceae** and **Vibrionaceae** changed significantly

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Results – intra-individual changes

Key finding: changes in **Bradyrhizobiaceae** and **Vibrionaceae** were consistent across individuals

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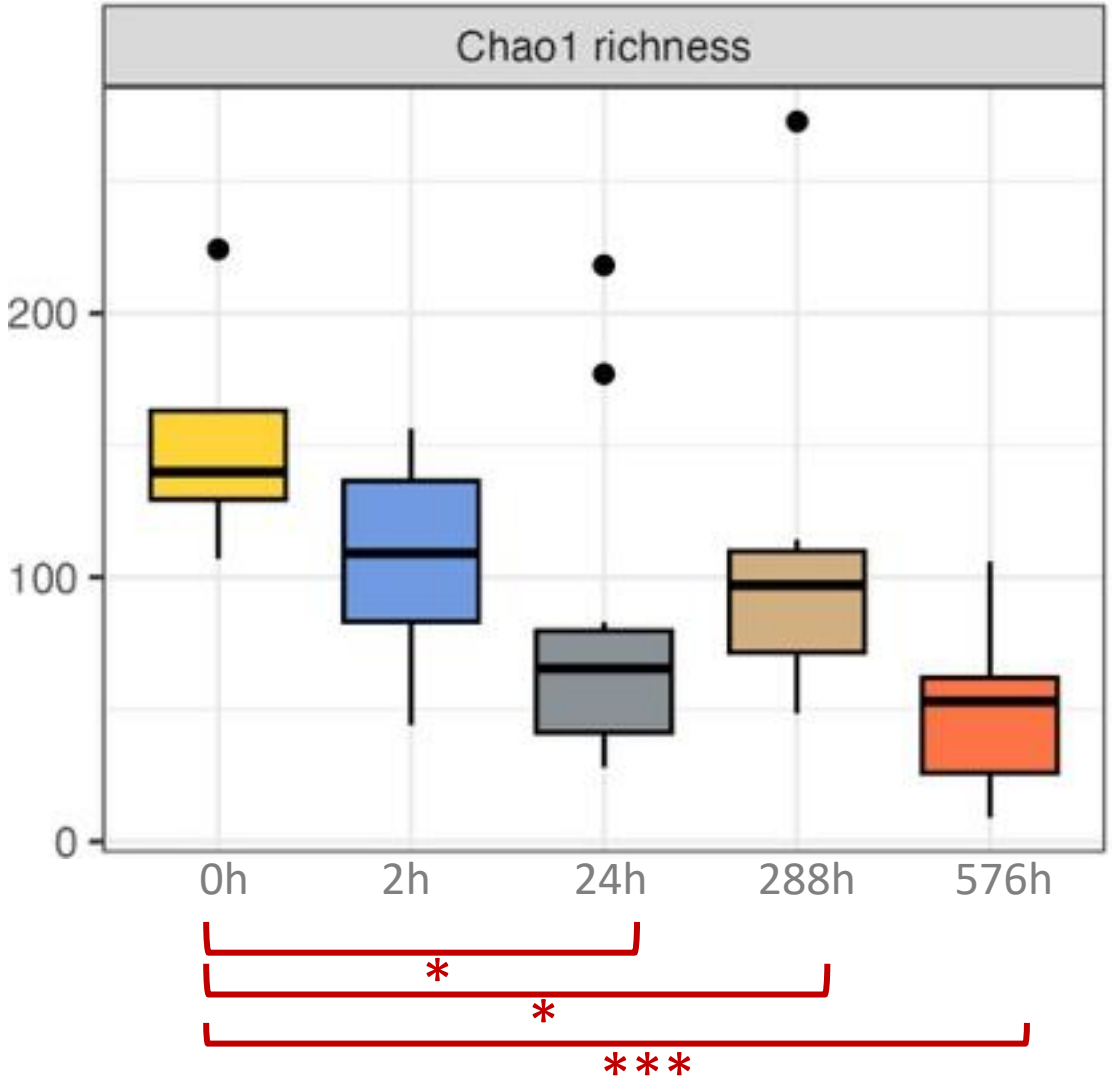
Results – inter-individual changes

Kruskal-Wallis rank sum test; Wilcoxon rank sum pair-wise test



Key finding: diversity changed in **2 hours**, significantly changed in **24 hours**

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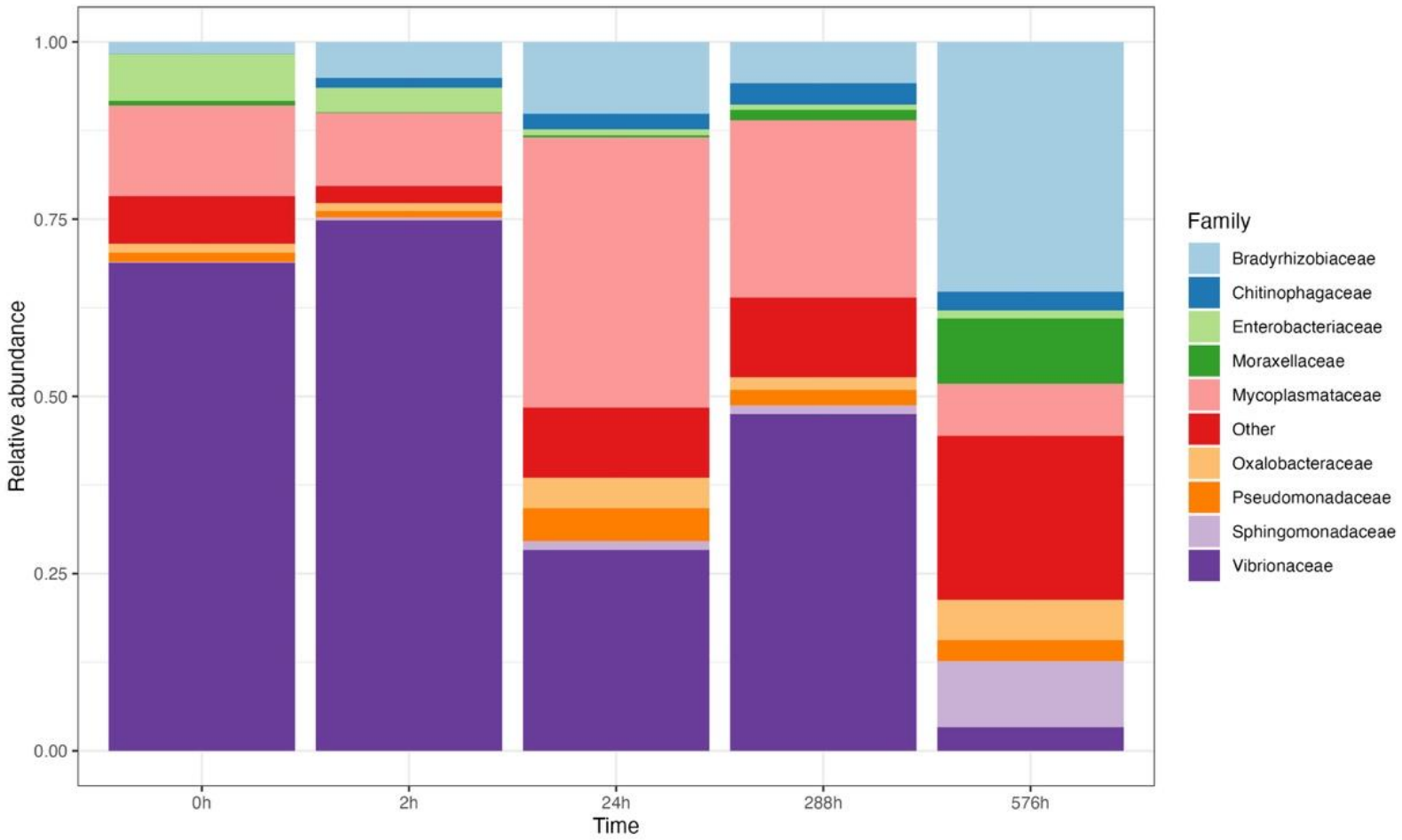
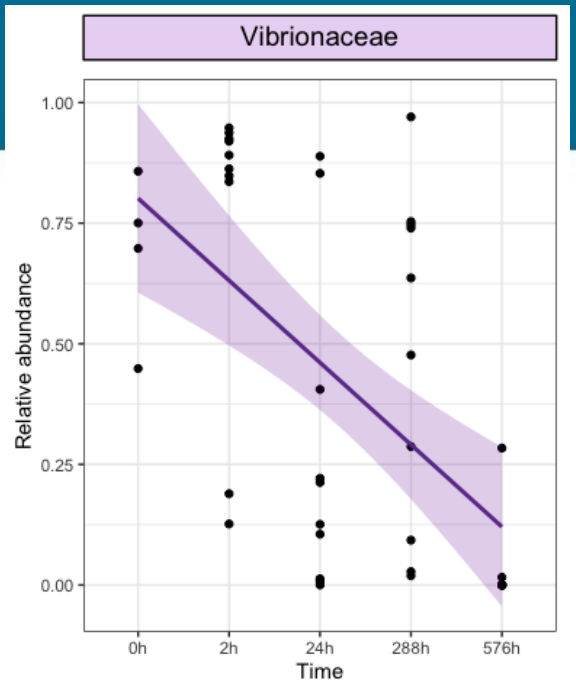
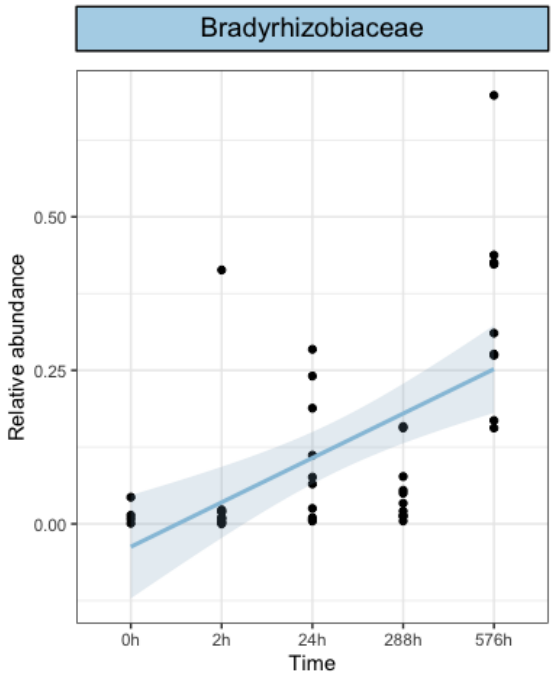
Results – inter-individual changes





GLM:
$p < 0.01$



GLM:
$p < 0.01$

Key finding: **Bradyrhizobiaceae** and **Vibrionaceae** changed significantly (consistent with intra-individual results)

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Implications

Catch

Transportation

Lab

Preserve gut samples in 2 hours
(no more than 24 hours)

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Implications

Species	Storage method	% Vibrionaceae	Source
Katsuwonus pelamis	Immediate sampling **(5h)**	~ 30%	(Gadoin et al., 2023)
Thunnus albacares		~ 45%	
Katsuwonus pelamis	-80 ℃, sampling **after 40 days**	~ 1%	(Gadoin et al., 2021)
Thunnus albacares		~ 10%	
Katsuwonus pelamis	-20 ℃, sampling **after landing**	~ 5%	(Trujillo-González et al., 2022)

? True gut microbiome composition

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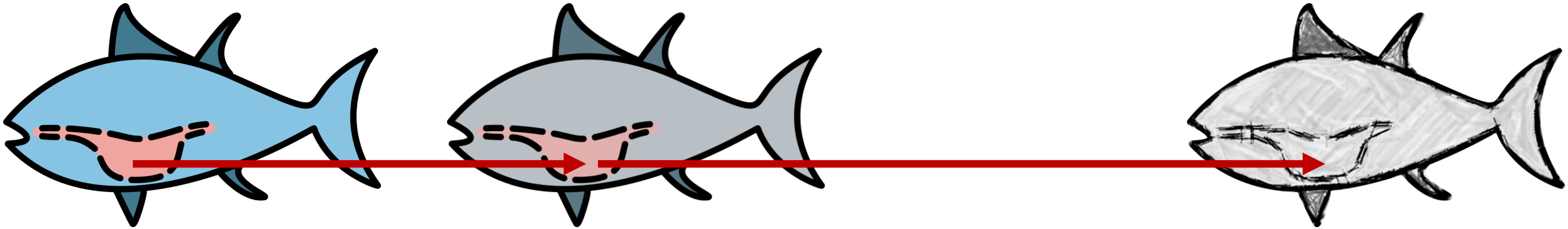
Conclusions



2h

24h

Bradyrhizobiaceae + **Vibrionaceae -**

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Acknowledgements

- Fisheries Research and Development Corporation
- University of Canberra
- The Pacific Community

- Prof. Dianne Gleeson
- Prof. Stephen Sarre
- Dr. Alejandro Trujillo-González
- Dr. Simon Nicol (the Pacific Community, SPC)
- Dr. Roger Huerlimann (Okinawa Institute of Science and Technology, OIST)

- EcoDNA group
- SPC staff: Marion Boutigny, Aurelie Guillou, Bruno Leroy, Joe Scutt Phillips
- Marine Climate Change Unit at OIST

Pacific Community
Communauté du Pacifique

UNIVERSITY OF CANBERRA

FRDC

Thank you

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