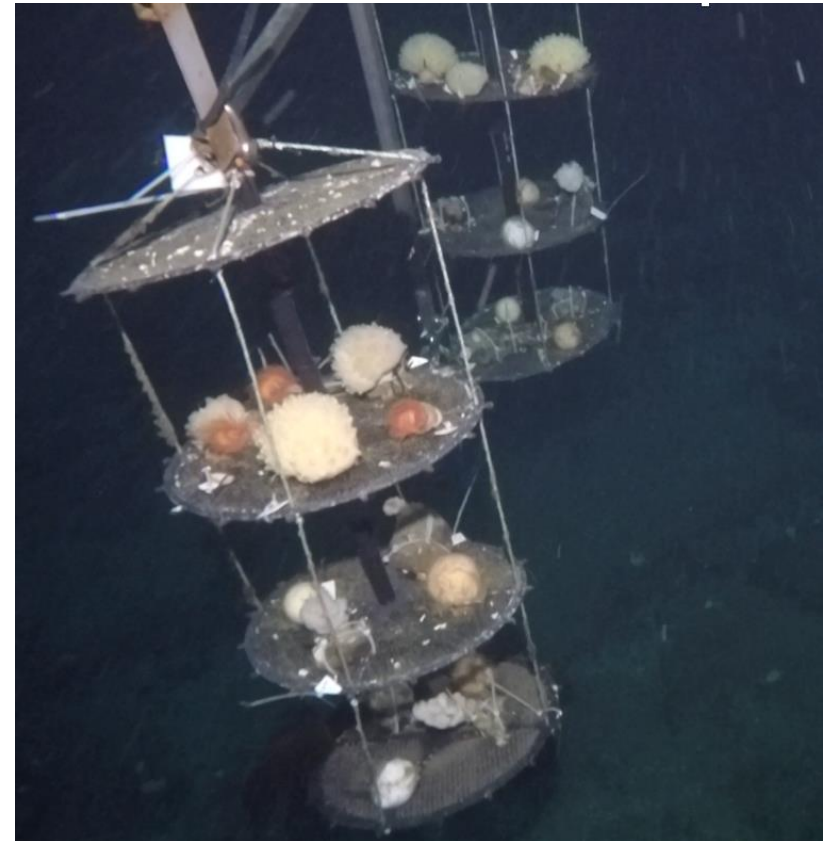# Benthic species' microbiomes and their response to salmon farming and associated environmental changes

By Olivier Laroche, Sonnich Meier, Astrid Harendza, Svein A. Mjøs, Raymond Bannister & Nigel Keeley

Polymastia sp.

Drifa glomerata

Craniella zetlandica

Hormathia digitata

Main objective

Fill knowledge gap on common coastal benthic sessile organisms living on mixed or hard-substrate habitats and how they respond to the effects of salmon farming.
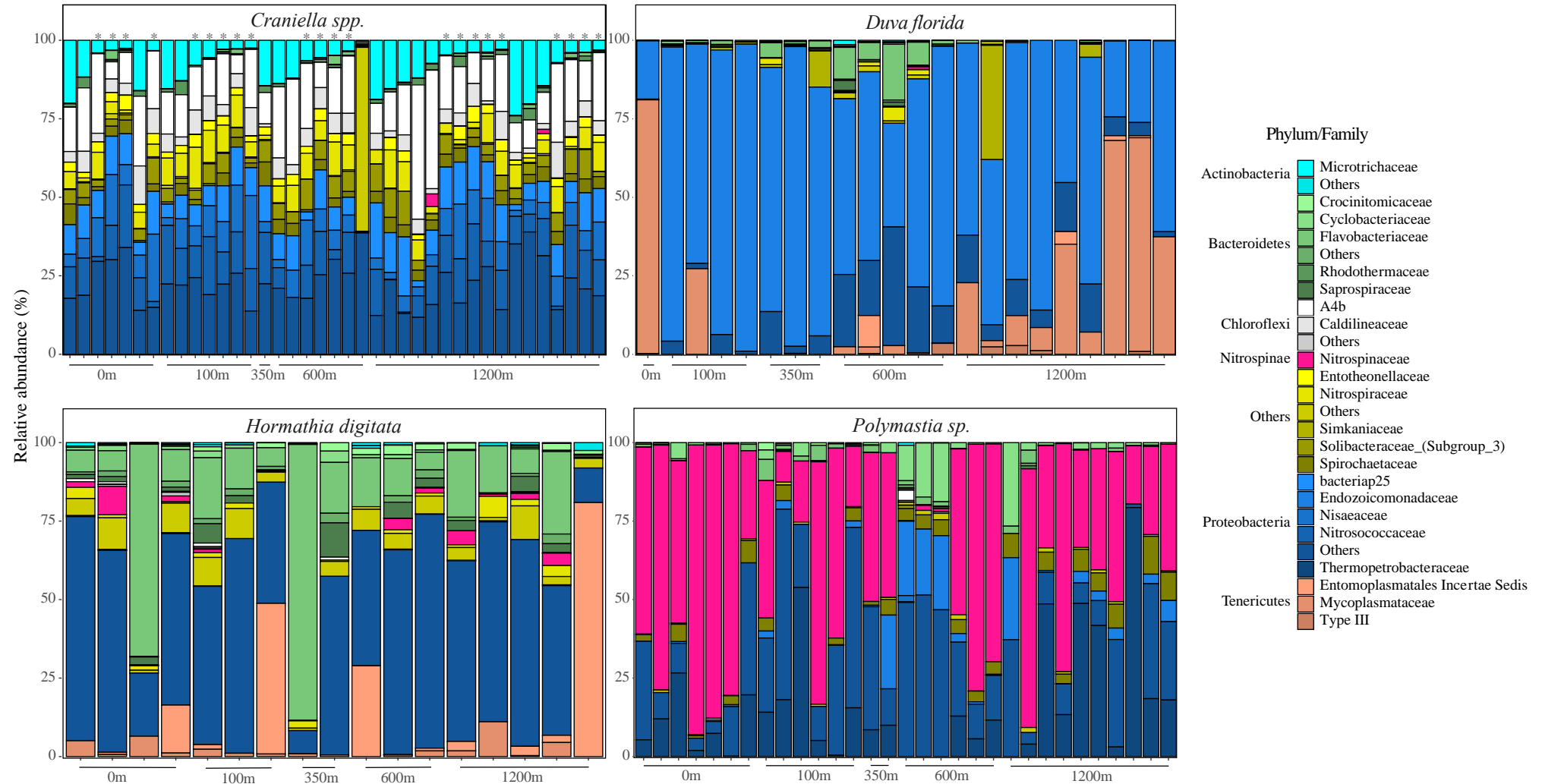
Specific objectives

Compare benthic species' taxonomic and functional microbiome diversity;

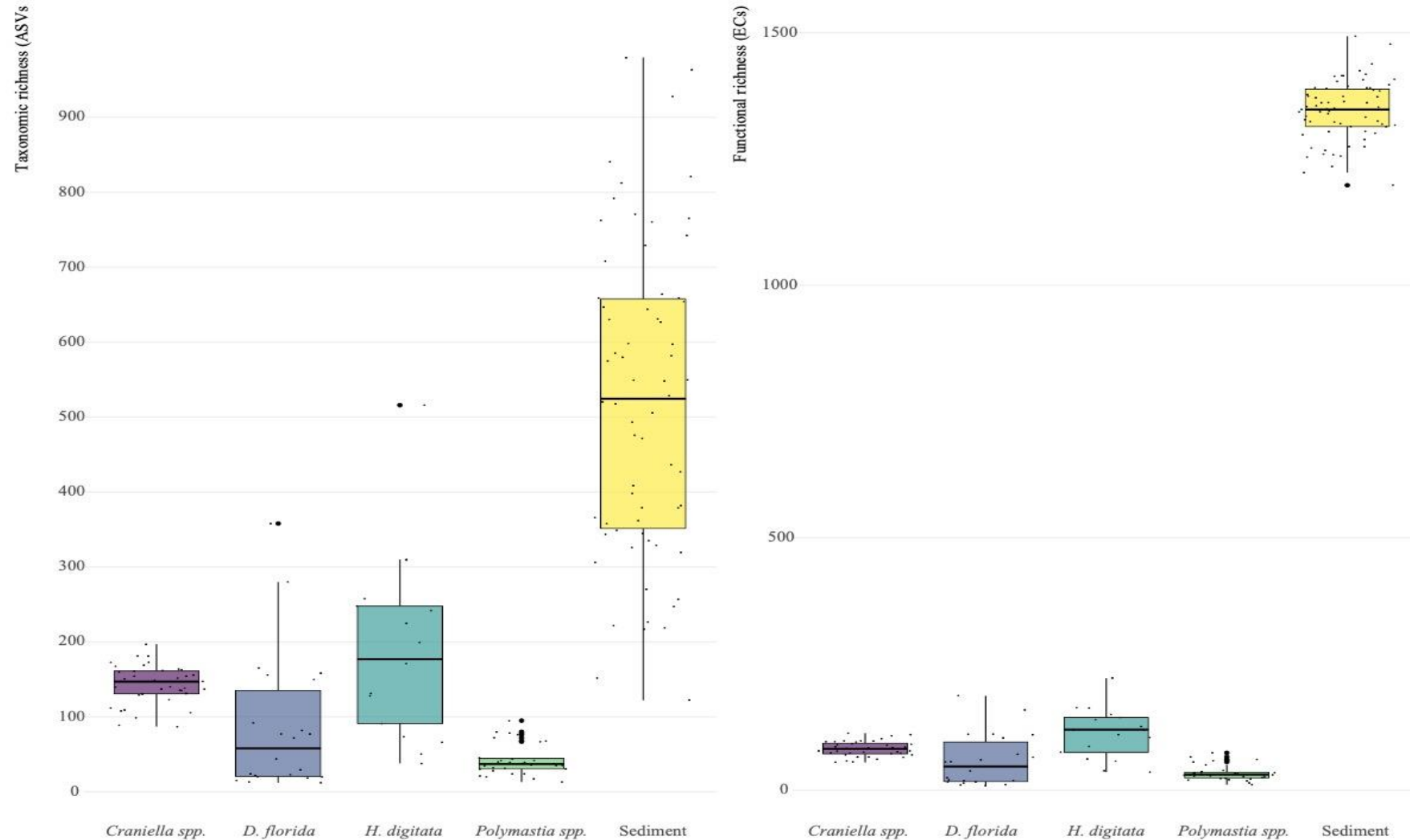Assess sensitivity of the microbiome of each taxa towards aquaculture activities.
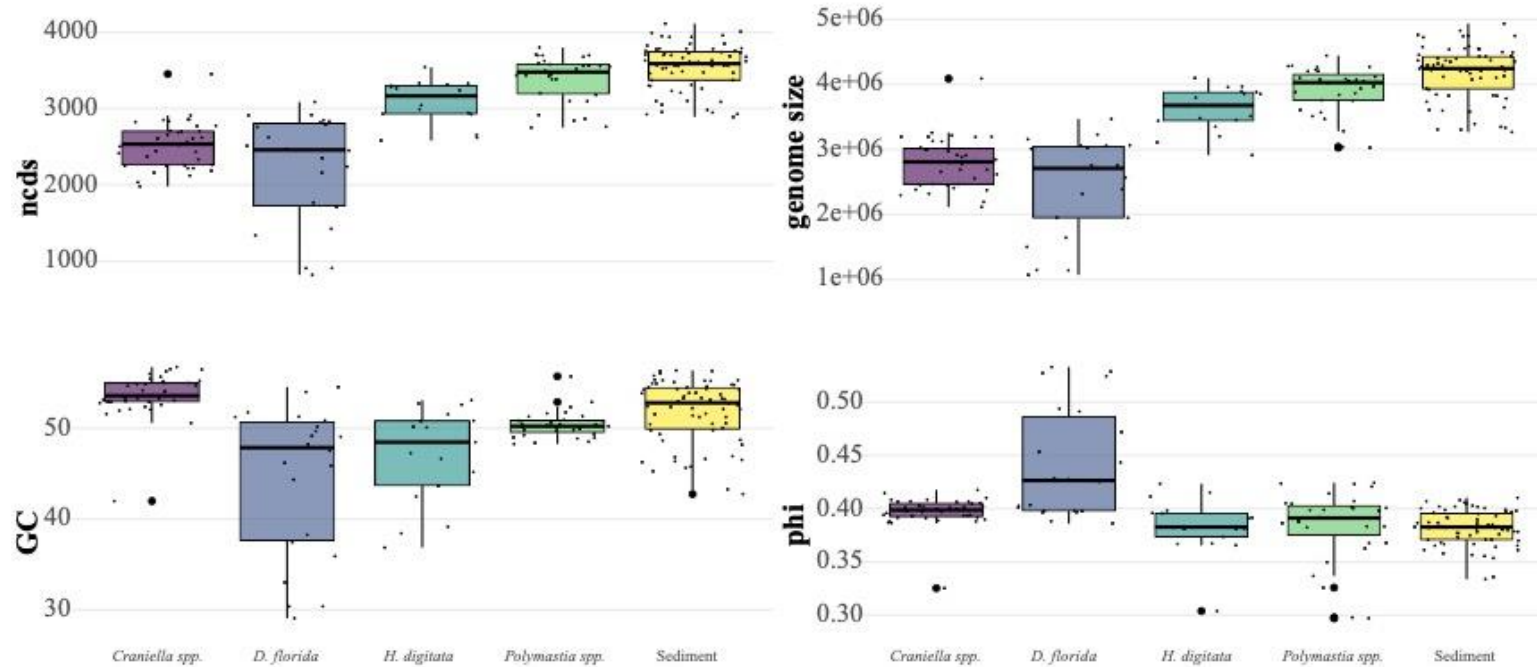
Microbiome
taxonomic profile

Microbiome
taxonomic and functional richness

Microbiome

Genetic properties

Beta-diversity

A) Taxonomic community

ASV richness
- 100
- 200
- 300
- 400
- 500

PC2 [9%]

PC1 [25.3%]

B) Functional community

KEEG richness
- 3000
- 3500
- 4000
- 4500
- 5000

PC2 [14.8%]

PC1 [27.4%]

C) Genetic properties

PC2 [23.7%]

PC1 [41.5%]

Species: ● *Craniella spp.* ● *Duva florida* ● *Hormathia digitata* ● *Polymastia spp.*
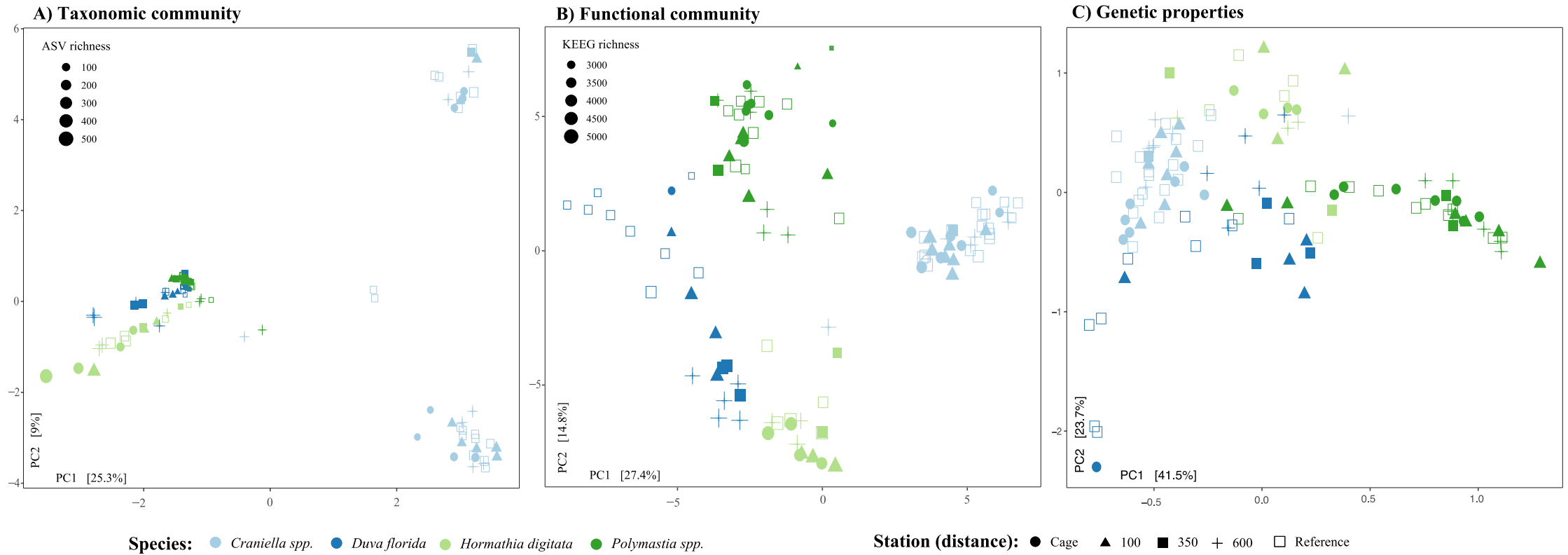
Station (distance): ● Cage ▲ 100 ■ 350 + 600 □ Reference

Significant differences between species for all data types;

Distance is not a strong factor;

Species-Distance interaction significant for functional diversity and genetic properties.

Dataset	Terms	PERMANOVA	
		R2	P.value
ASVs	Species	0.35	**<0.001**
	Distance	0.01	0.39
	Species:Distance	0.02	0.11
	Residual	0.62	
ECs	Species	0.46	**<0.001**
	Distance	0.01	0.07
	Species:Distance	0.02	**0.01**
	Residual	0.51	
GPs	Species	0.58	**<0.001**
	Distance	0.01	0.13
	Species:Distance	0.04	**0.002**
	Residual	0.37	

Permutational analysis of variance per data source across the fourth root of distance from the pen

Species	Terms	Df	Taxonomic		Functional		Genetic properties	
			R2	P.value	R2	P.value	R2	P.value
H. digitata	Distance	1	0.112	**<0.001**	0.098	**0.015**	0.025	0.881
	Residuals	15	0.888		0.902		0.975	
D. florida	Distance	1	0.024	0.972	0.097	**0.024**	0.107	0.095
	Residuals	20	0.976		0.903		0.823	
Polymastia spp.	Distance	1	0.041	0.172	0.054	0.056	0.033	0.372
	Residuals	29	0.959		0.946		0.967	
Craniella spp.	Distance	1	0.021	0.553	0.052	**0.020**	0.054	0.089
	Residuals	37	0.979		0.948		0.946	
Sediment	Distance	1	0.056	**<0.001**	0.084	**<0.001**	0.103	**<0.001**
	Residuals	65	0.944		0.916		0.897	

Take home message

(Preliminary results)

- Microbiomes highly specific to each benthic taxa in terms of taxa and functions;

- Looking at microbiomes can help identify/detect different species, even when closely related.

- Hosts' microbiome taxonomic & functional richness, and GPs not affected by fish farm activities;

- Microbial functional community composition more sensitive in detecting fish farm impact on hosts.