Work Package 4
The influence of surrounding species on *Crassostrea gigas* disease risk in oyster farming

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Final VIVALDI Conference
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LEMAR

IHPE
Interactions-Hôtes-Pathogènes-Environnements

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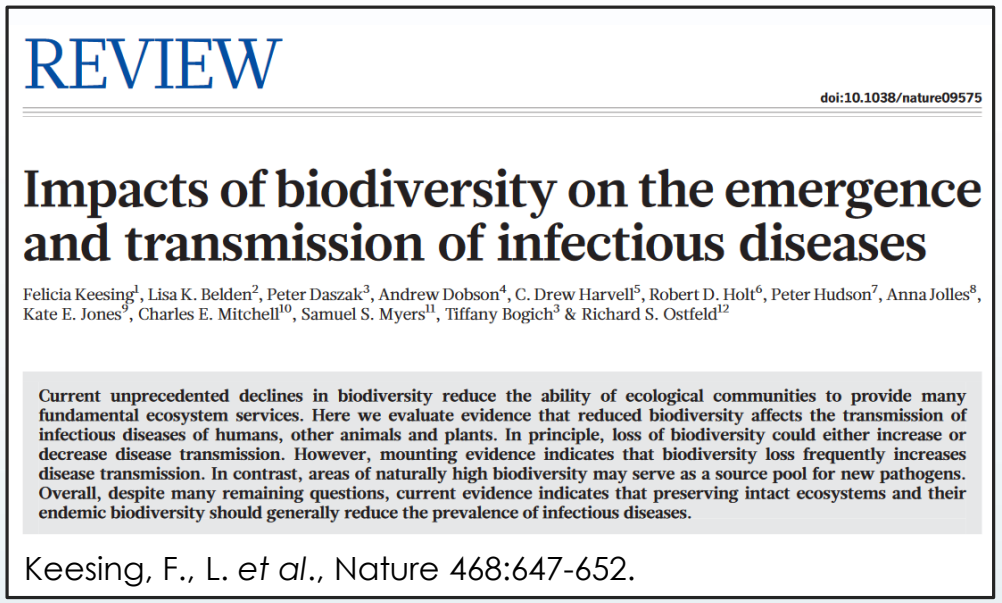
VIVALDI
Preventing and mitigating farmed bivalve diseases

Context

- Role of Biodiversity in mitigating disease
  - Known as mitigator of diseases in terrestrial area and integrated as part of ecosystems services (**Keesing et *al.*, 2010**)

  → Dilution effect: smaller proportion of vectors will infect competent hosts and so will spread less



REVIEW

doi:10.1038/nature09575

Impacts of biodiversity on the emergence and transmission of infectious diseases

Felicia Keesing[1], Lisa K. Belden[2], Peter Daszak[3], Andrew Dobson[4], C. Drew Harvell[5], Robert D. Holt[6], Peter Hudson[7], Anna Jolles[8], Kate E. Jones[9], Charles E. Mitchell[10], Samuel S. Myers[11], Tiffany Bogich[3] & Richard S. Ostfeld[12]

Current unprecedented declines in biodiversity reduce the ability of ecological communities to provide many fundamental ecosystem services. Here we evaluate evidence that reduced biodiversity affects the transmission of infectious diseases of humans, other animals and plants. In principle, loss of biodiversity could either increase or decrease disease transmission. However, mounting evidence indicates that biodiversity loss frequently increases disease transmission. In contrast, areas of naturally high biodiversity may serve as a source pool for new pathogens. Overall, despite many remaining questions, current evidence indicates that preserving intact ecosystems and their endemic biodiversity should generally reduce the prevalence of infectious diseases.

Keesing, F., L. *et al.*, Nature 468:647-652.

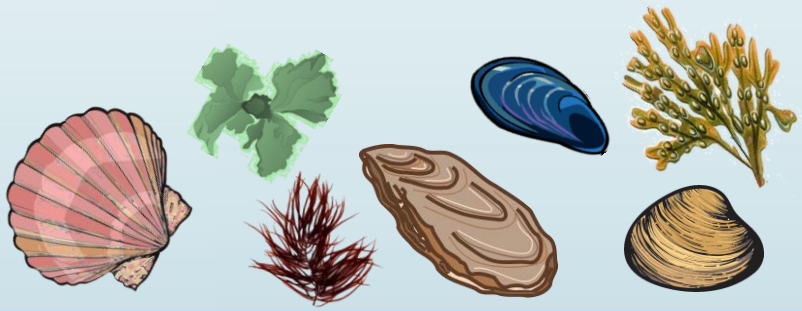
- Influence of abiotic parameters well known (such as temperature or salinity) (**Petton et *al.* (2013)** and **Fuhrmann et *al.* (2016)**)

- Influence of biotic parameters still to further decipher
  - Effects of other species in aquatic environments remain less studied (**Ben-Horin et *al.*, 2015**)

  → Recent observations seem to indicate a link between oyster resistance and surrounding species, with potential role of disease spreading regulator (**Burge et *al.*, 2016**)

Objective

To determine if biotic interactions influence disease risk in oysters and how ?



Experimental manipulation

- Test the effect of macralgae and their associated communities on the disease risk of *Crassostrea gigas* facing OsHV-1

→ Algae are widely present in coastal ecosystems and particularly in oyster farming due to the sheltered areas

→ Their complex associated communities could interact with oysters

Experimental manipulation

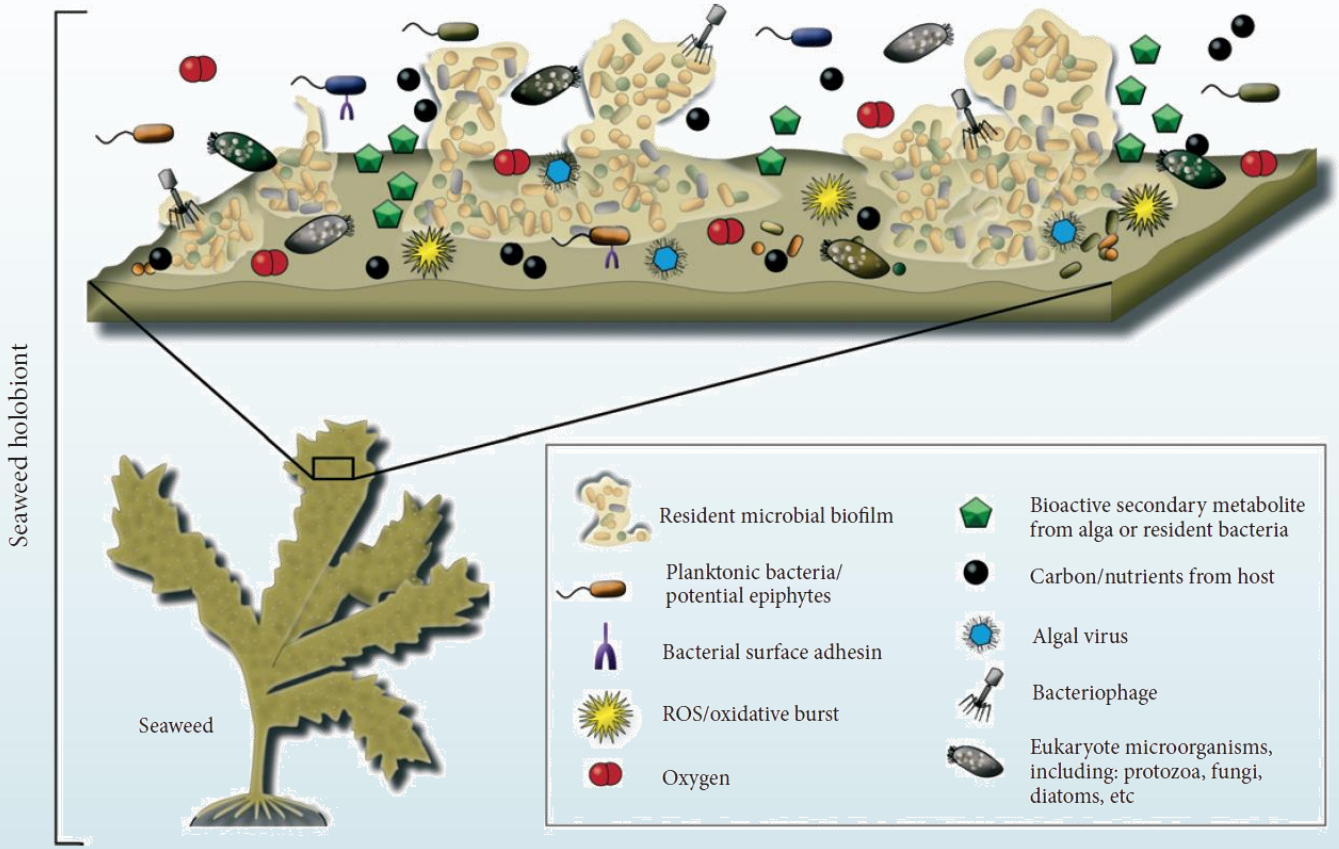
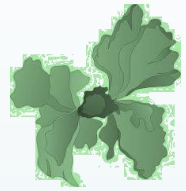
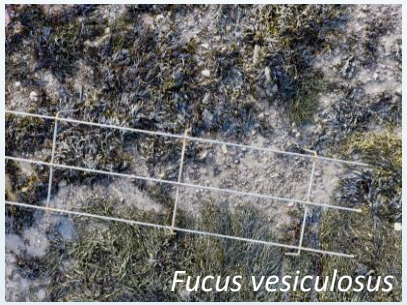


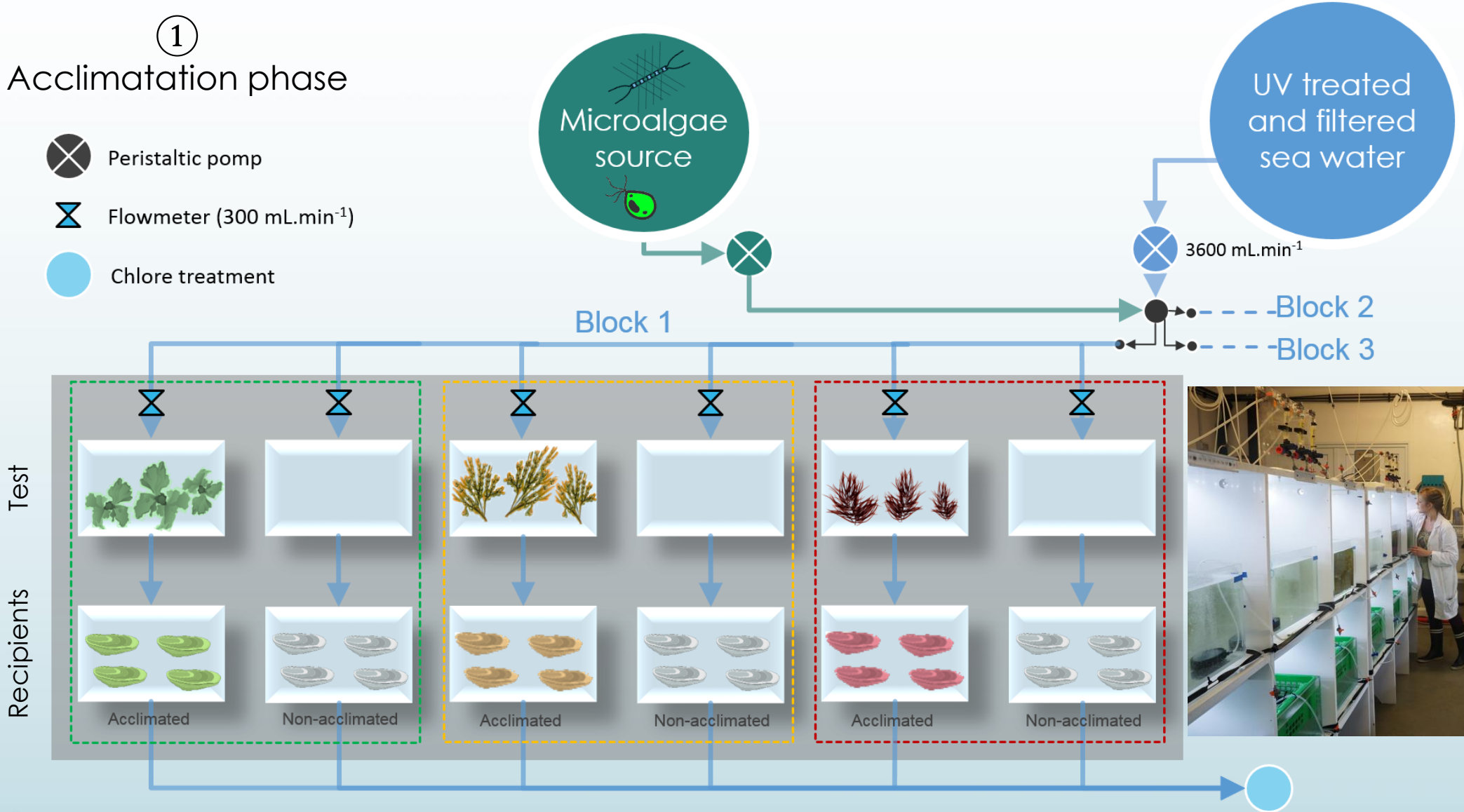
Fig. 2. The seaweed holobiont and the factors predicted to influence bacterial colonization on macroalgal hosts.
Egan *et al.*, FEMS Microbiology Reviews 37 (3), 462-476





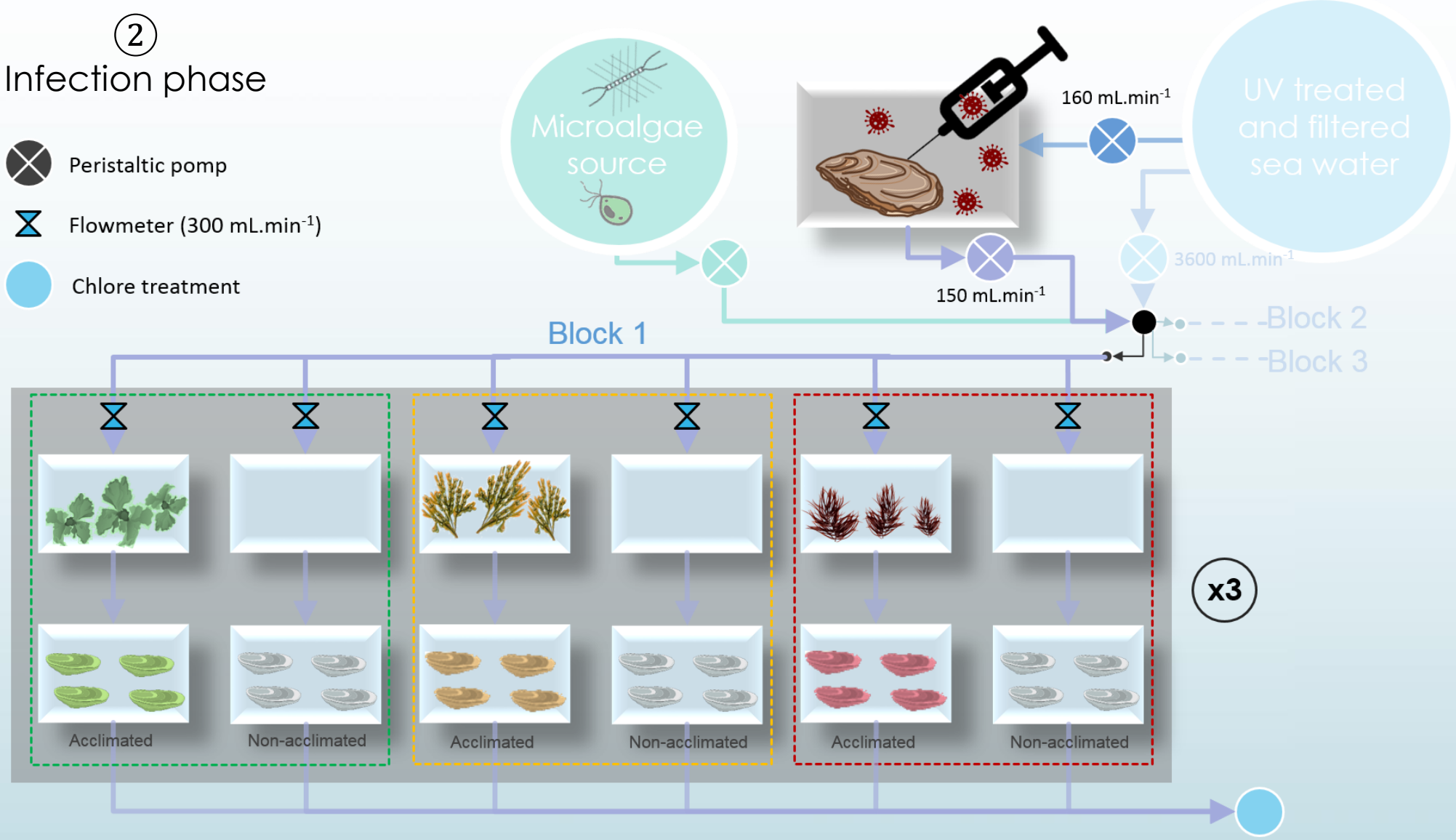
Experimental manipulation

① Acclimatation phase

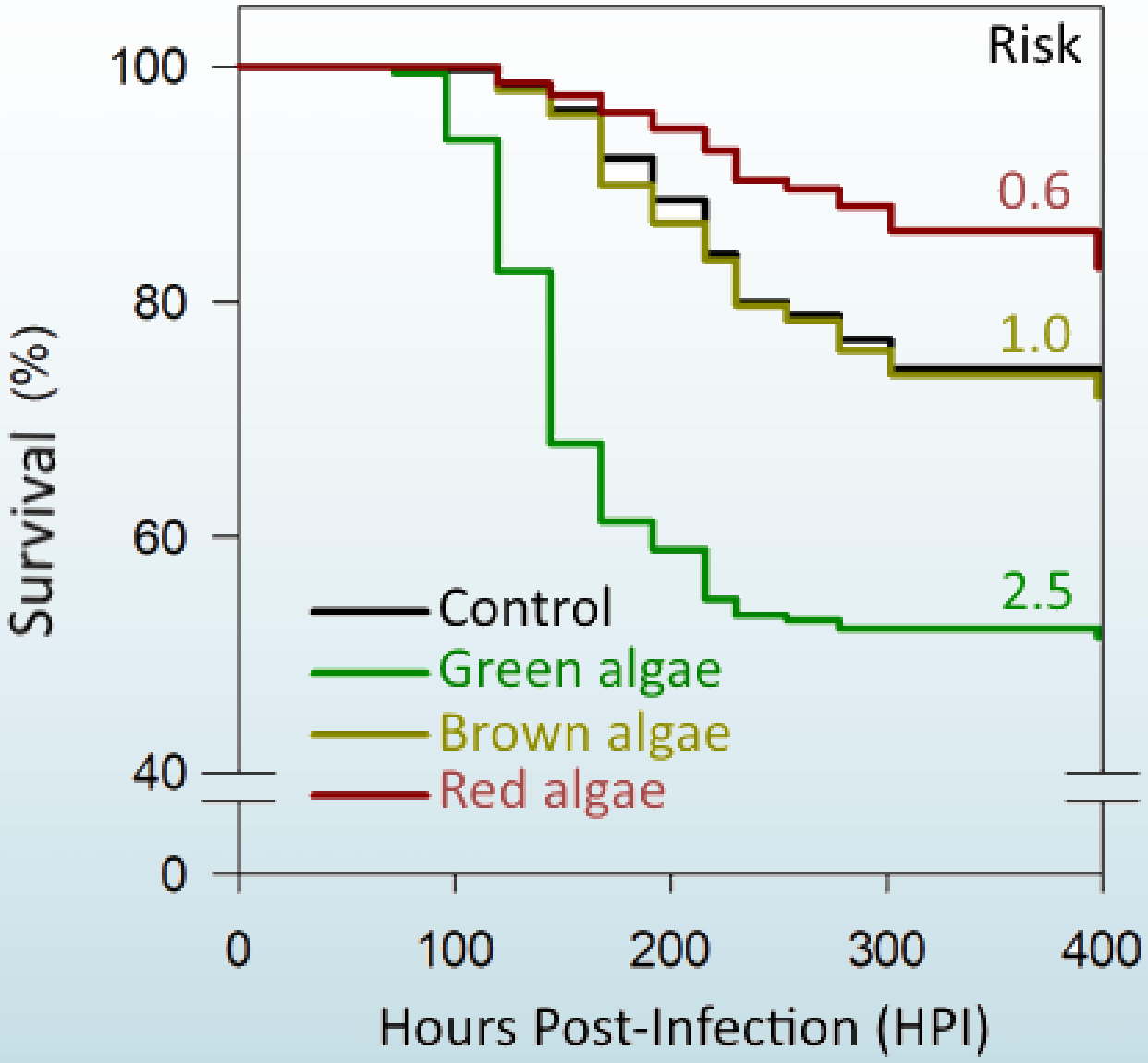


Experimental manipulation

② Infection phase

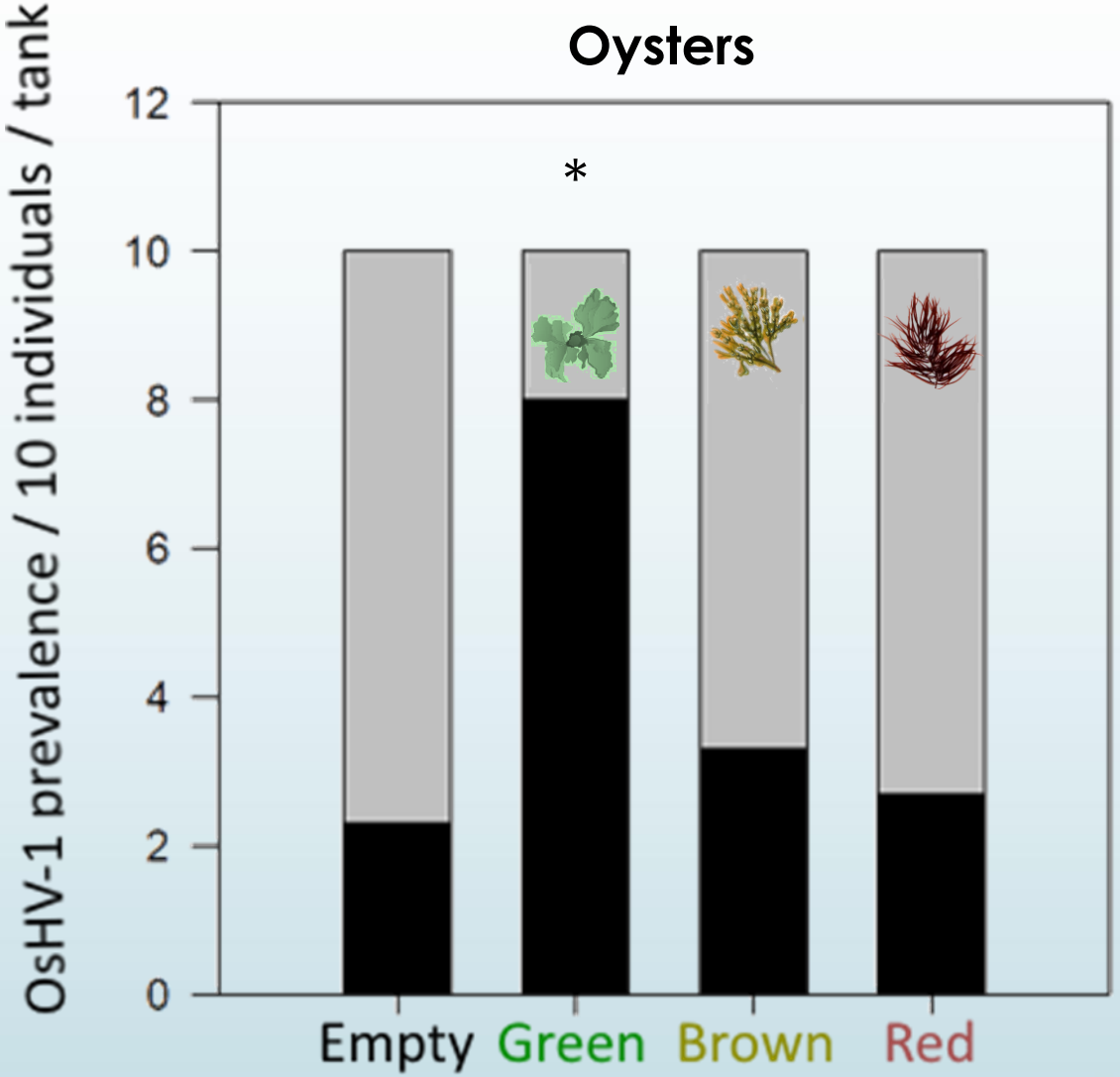


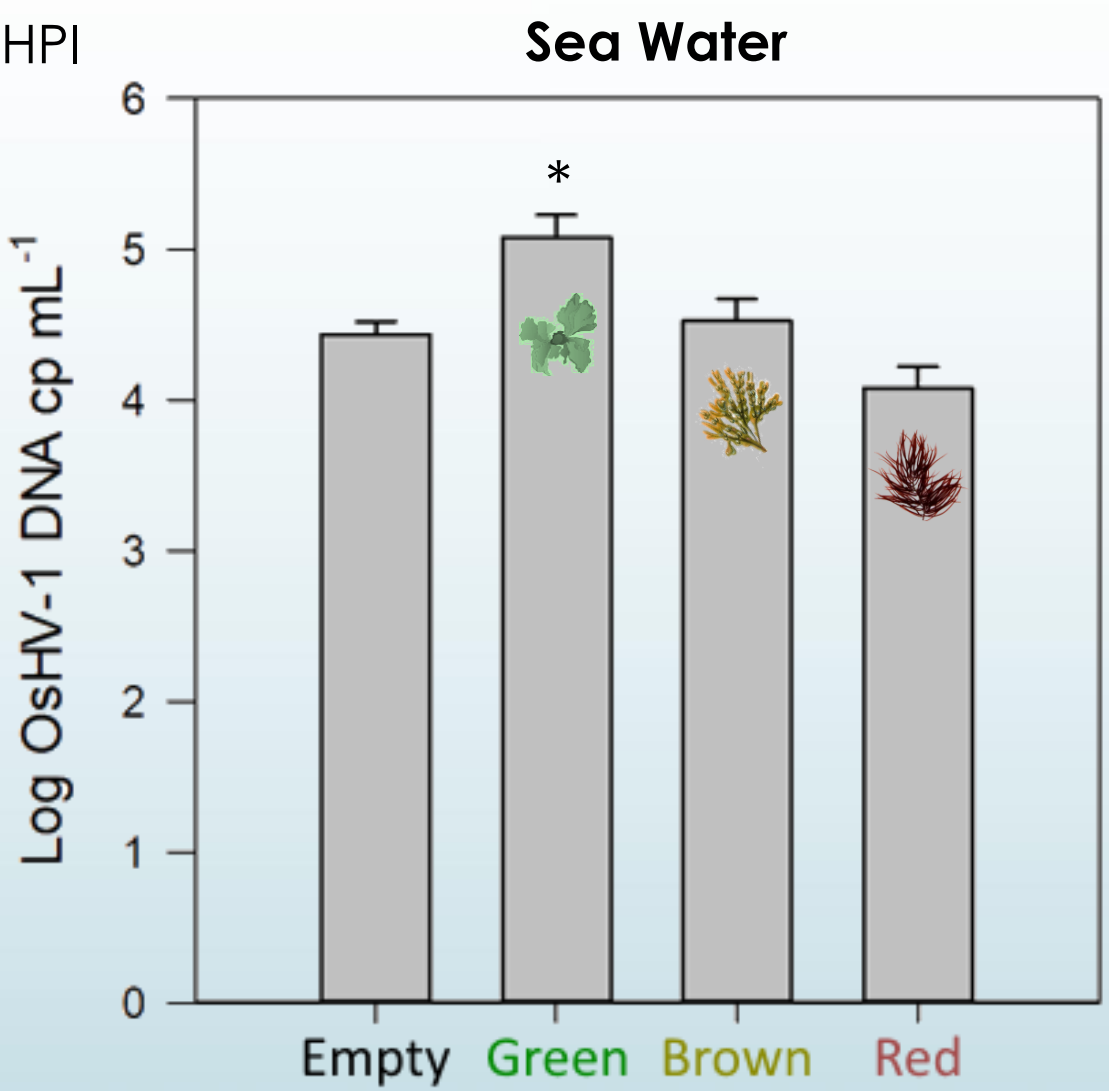
Survival


Risk
0.6
1.0
2.5
Control
Green algae
Brown algae
Red algae
Survival (%)
100
80
60
40
0
0
100
200
300
400
Hours Post-Infection (HPI)

OsHV-1 DNA detection

72 HPI





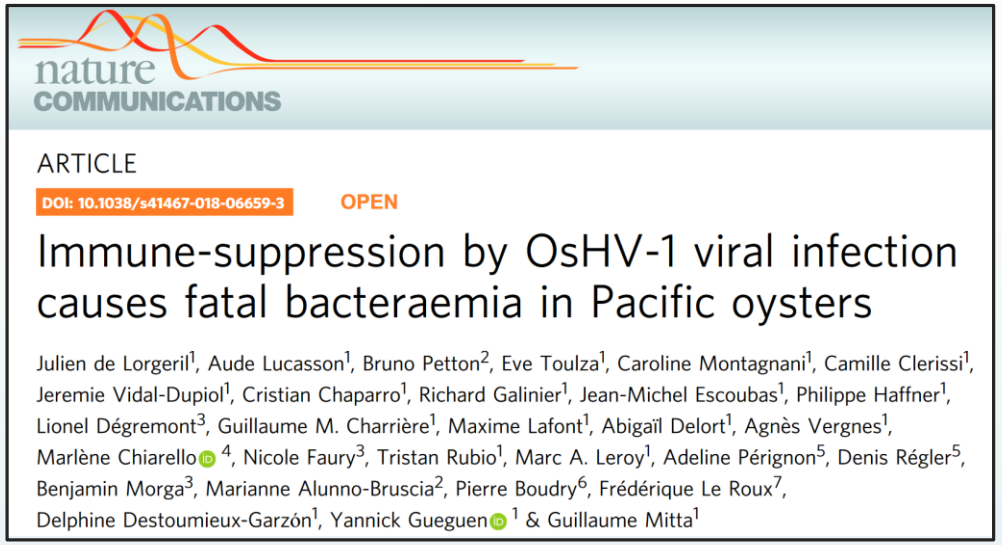
Host physiology

- Differences observed in survival rate are not due to an altered host physiology
  - Microalgae consumption of oysters have been daily followed and was constant
  - Energetic reserves and food quality were the same among the treatments

↳ Host physiology was unaltered by macroalgae

New perspectives

- A destabilized microbiota could explain the differences observed in oyster survival
  - A repression of antibacterial defenses is caused by OsHV-1
  - Observed changes in oyster-associated microbiota followed by bacteraemia and mortalities (**de Lorgeril et *al.*, 2018**)



nature COMMUNICATIONS

ARTICLE

DOI: 10.1038/s41467-018-06659-3 OPEN

Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters

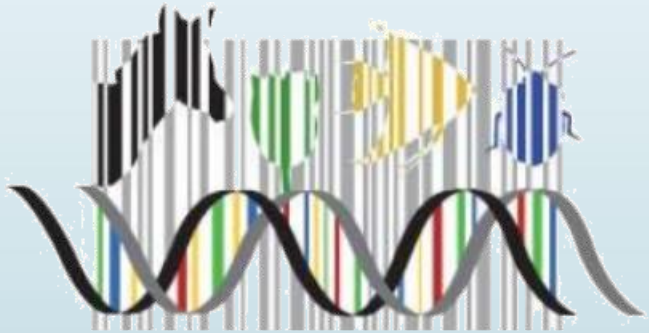
Julien de Lorgeril[1], Aude Lucasson[1], Bruno Petton[2], Eve Toulza[1], Caroline Montagnani[1], Camille Clerissi[1], Jeremie Vidal-Dupiol[1], Cristian Chaparro[1], Richard Galinier[1], Jean-Michel Escoubas[1], Philippe Haffner[1], Lionel Dégremont[3], Guillaume M. Charrière[1], Maxime Lafont[1], Abigaïl Delort[1], Agnès Vergnes[1], Marlène Chiarello[4], Nicole Faury[3], Tristan Rubio[1], Marc A. Leroy[1], Adeline Pérignon[5], Denis Régler[5], Benjamin Morga[3], Marianne Alunno-Bruscia[2], Pierre Boudry[6], Frédérique Le Roux[7], Delphine Destoumieux-Garzón[1], Yannick Gueguen[1] & Guillaume Mitta[1]

- Potential negative effect of green algae in influencing this polymicrobial disease process
  - Is oyster microbiota modified by macroalgae due to cohabitation ?
  - In this case, does it influence oyster susceptibility to pathogens ?

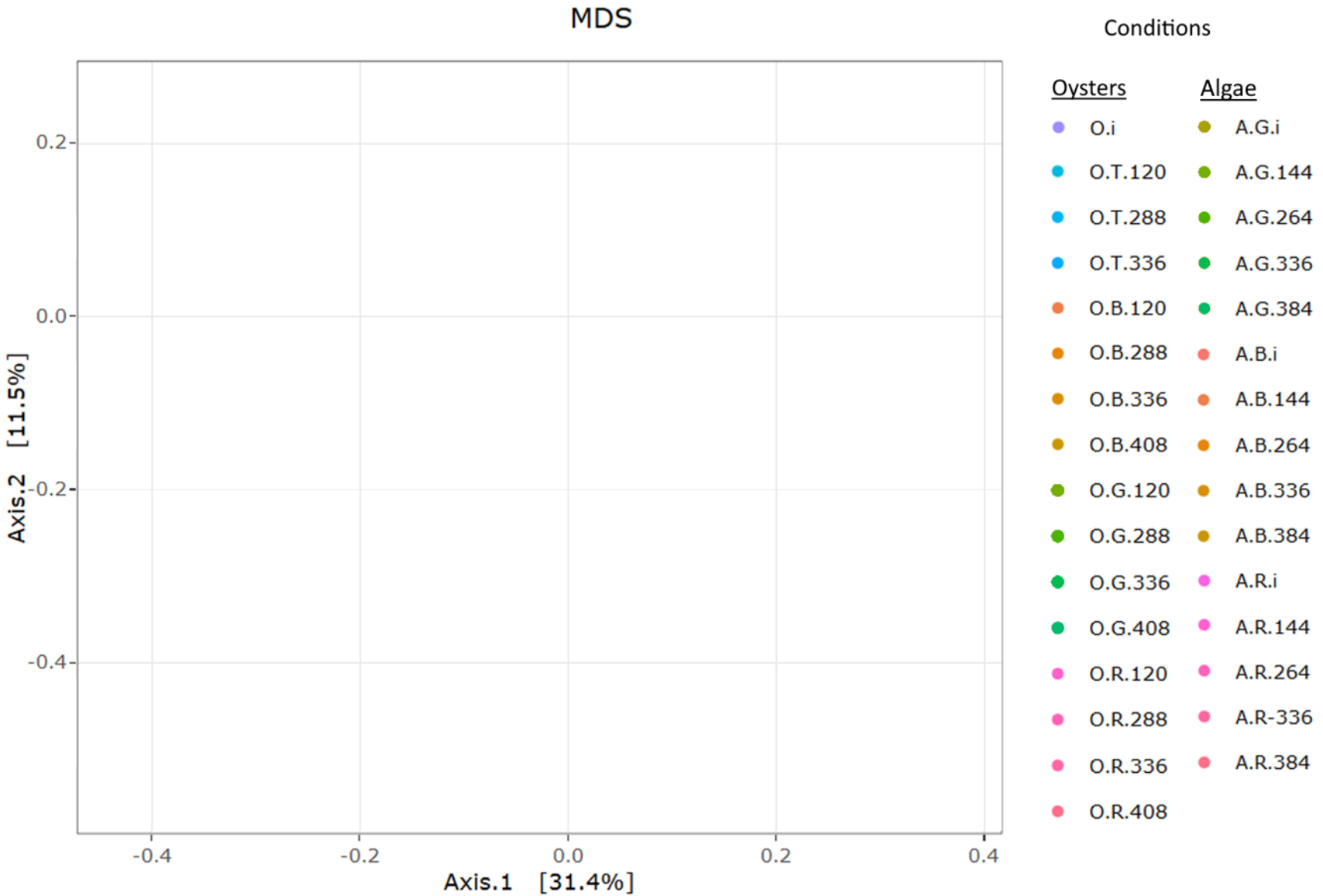
Metabarcoding analysis

- Use of Metabarcoding analysis methods focusing on Bacteria

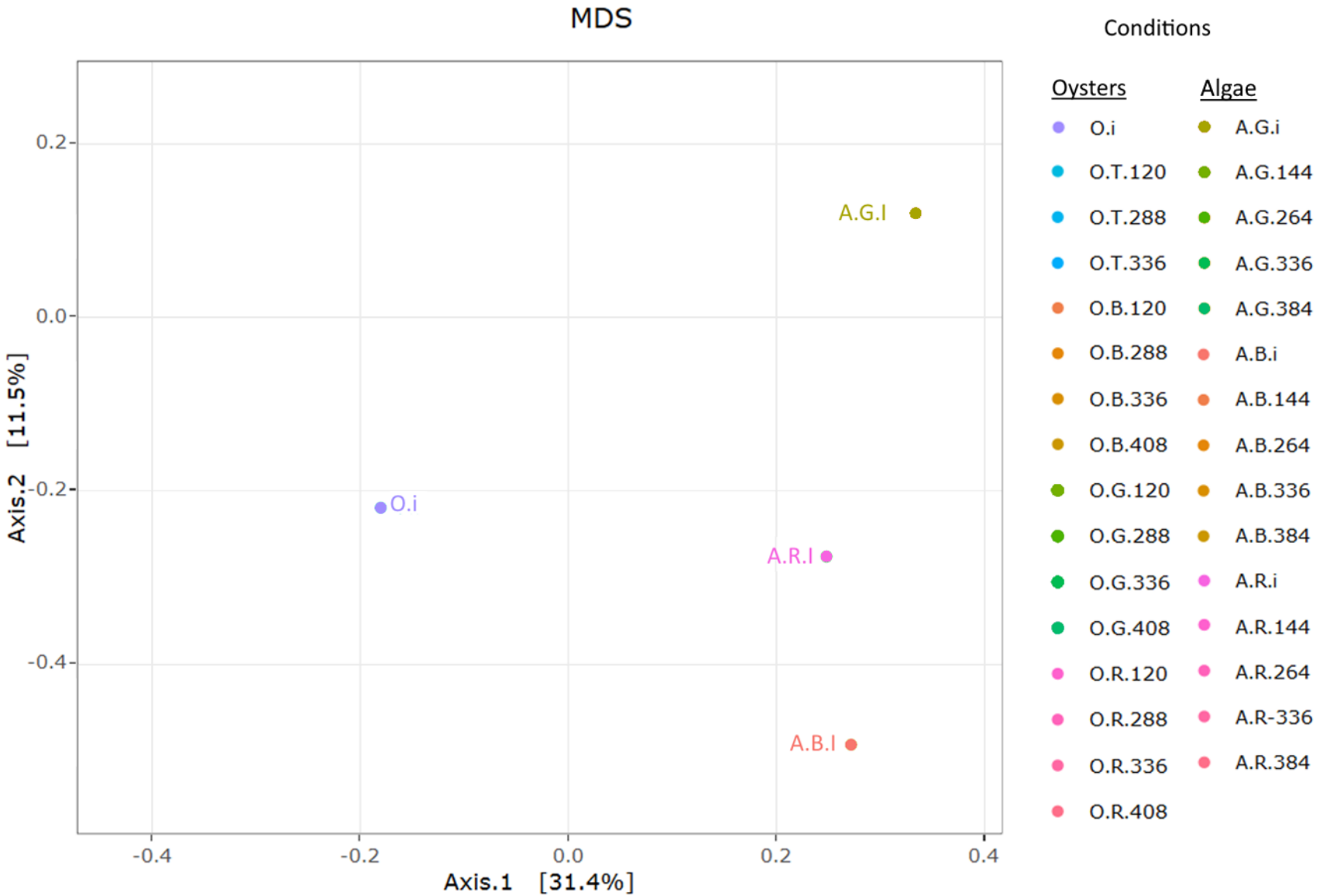
  - Do algae induce changes in oysters microbiotia composition ?
  - Is bacterial community changing in the time ?



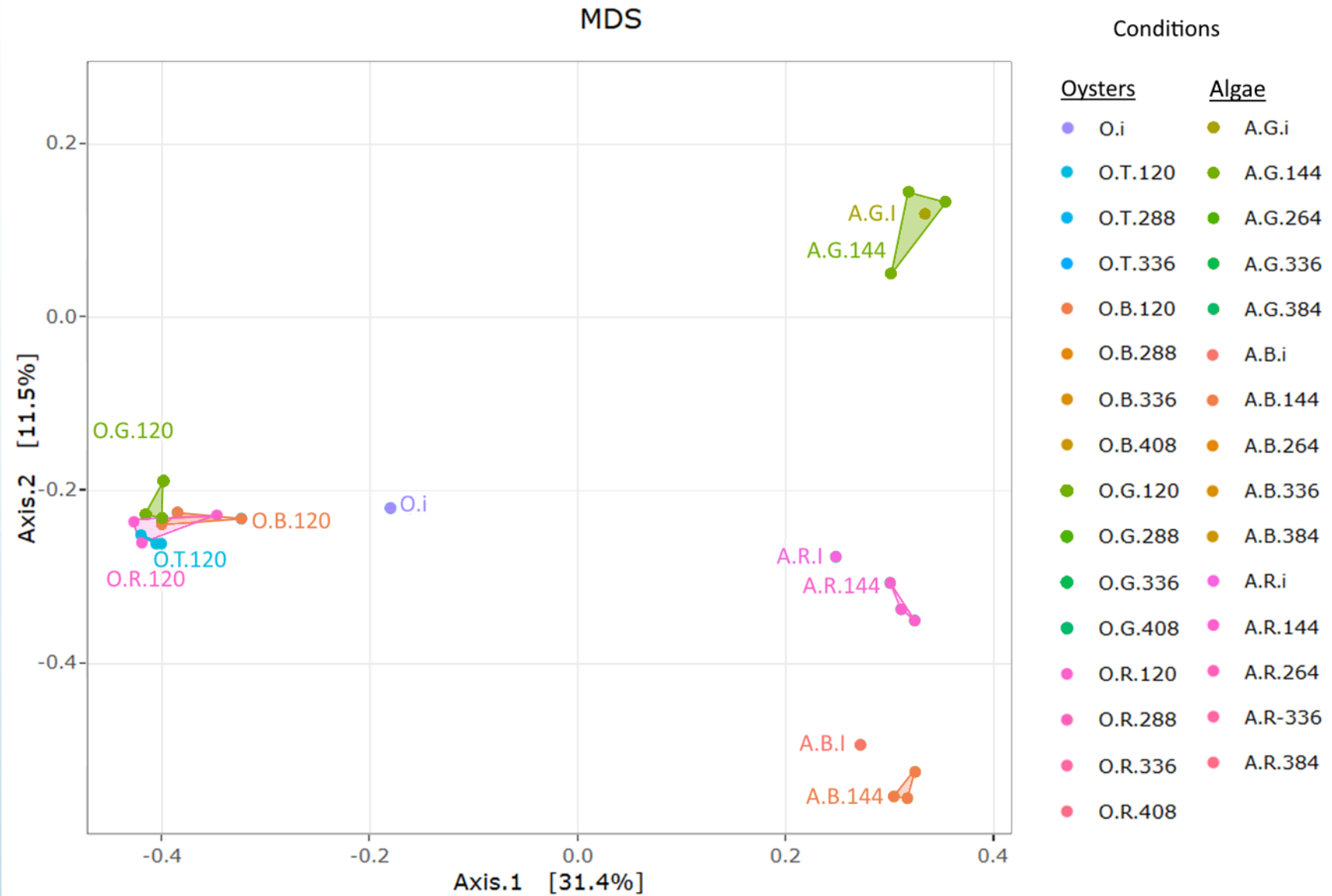
Bacterial composition visualisation



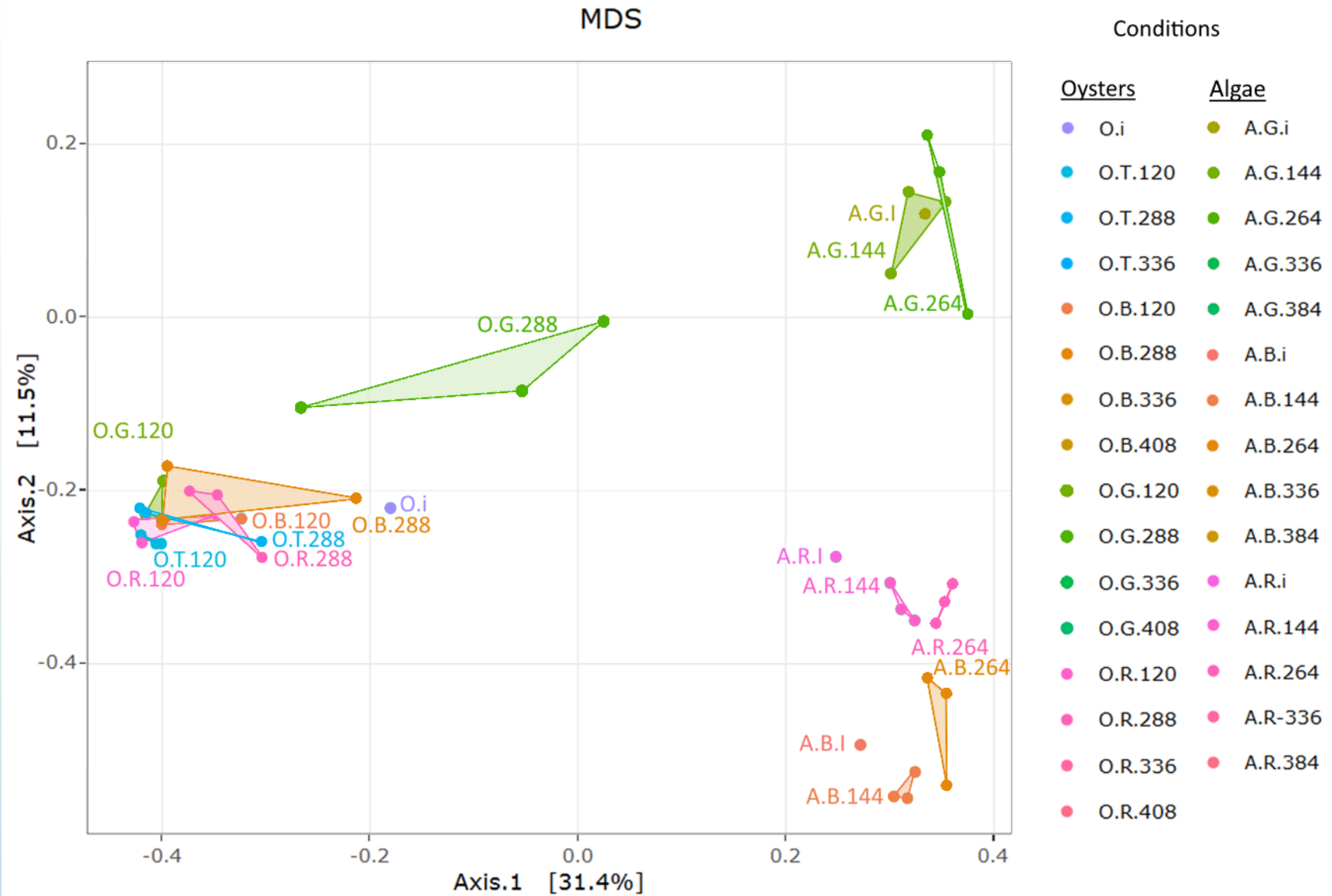
Bacterial composition visualisation



Bacterial composition visualisation



Bacterial composition visualisation



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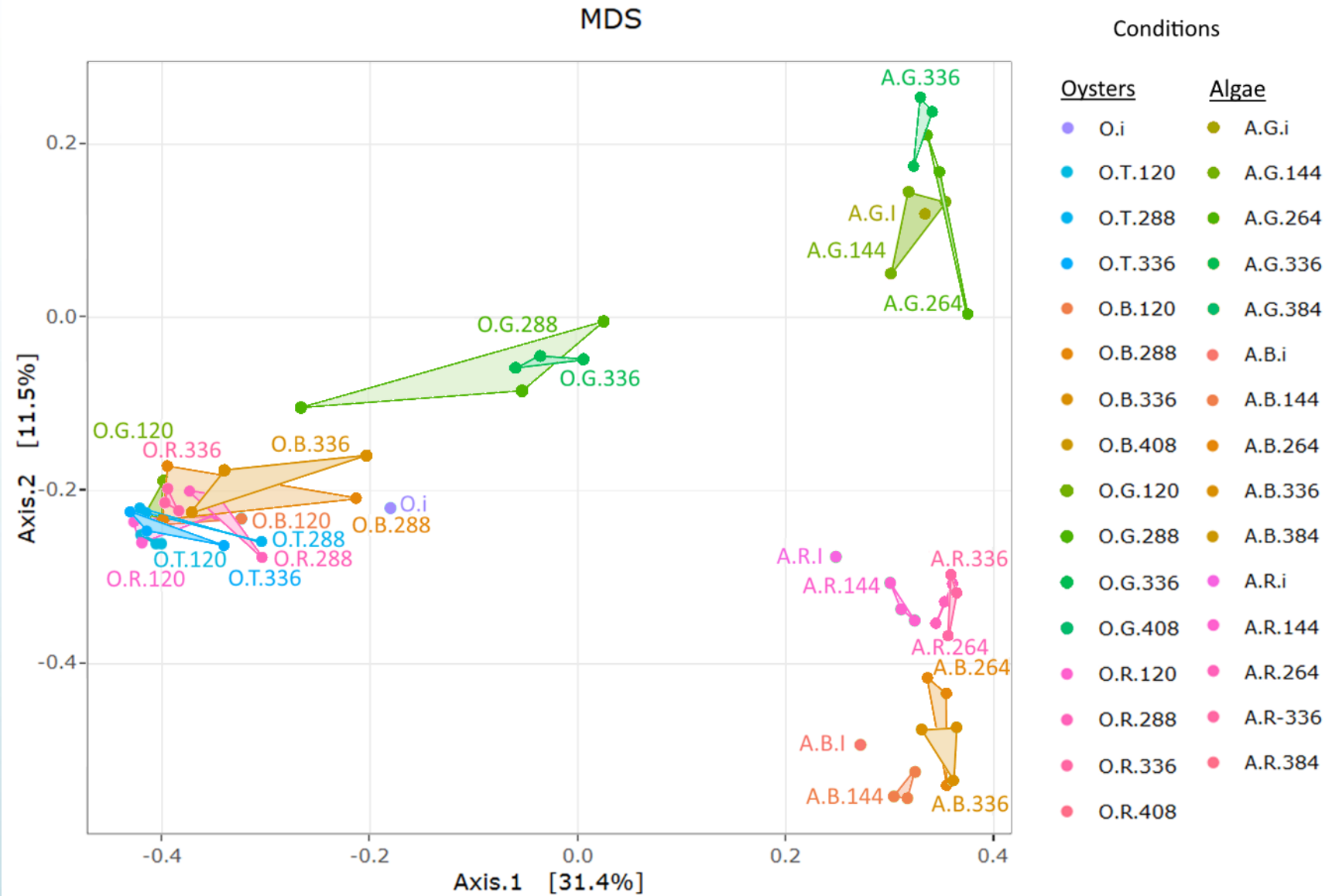
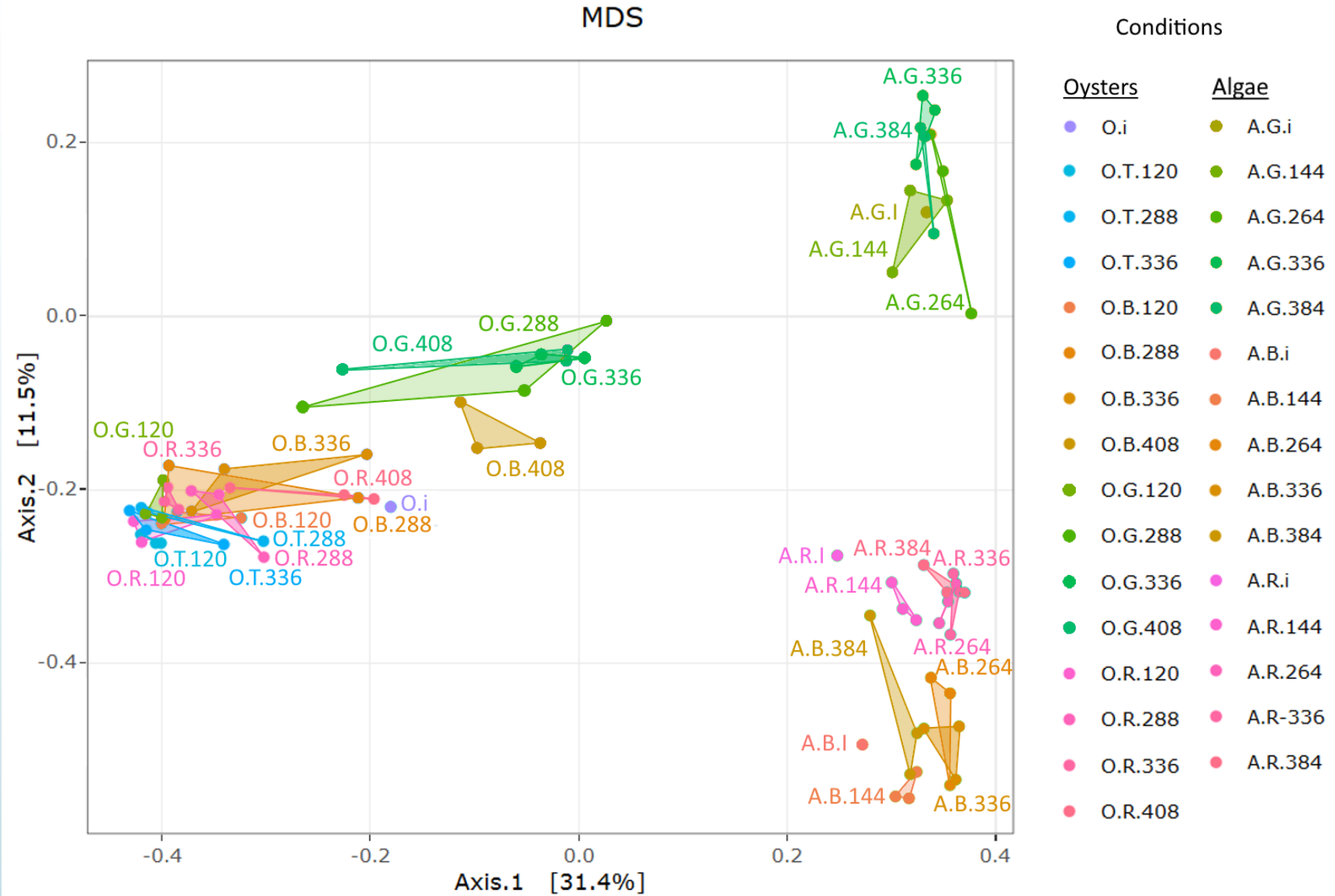


Bacterial composition visualisation



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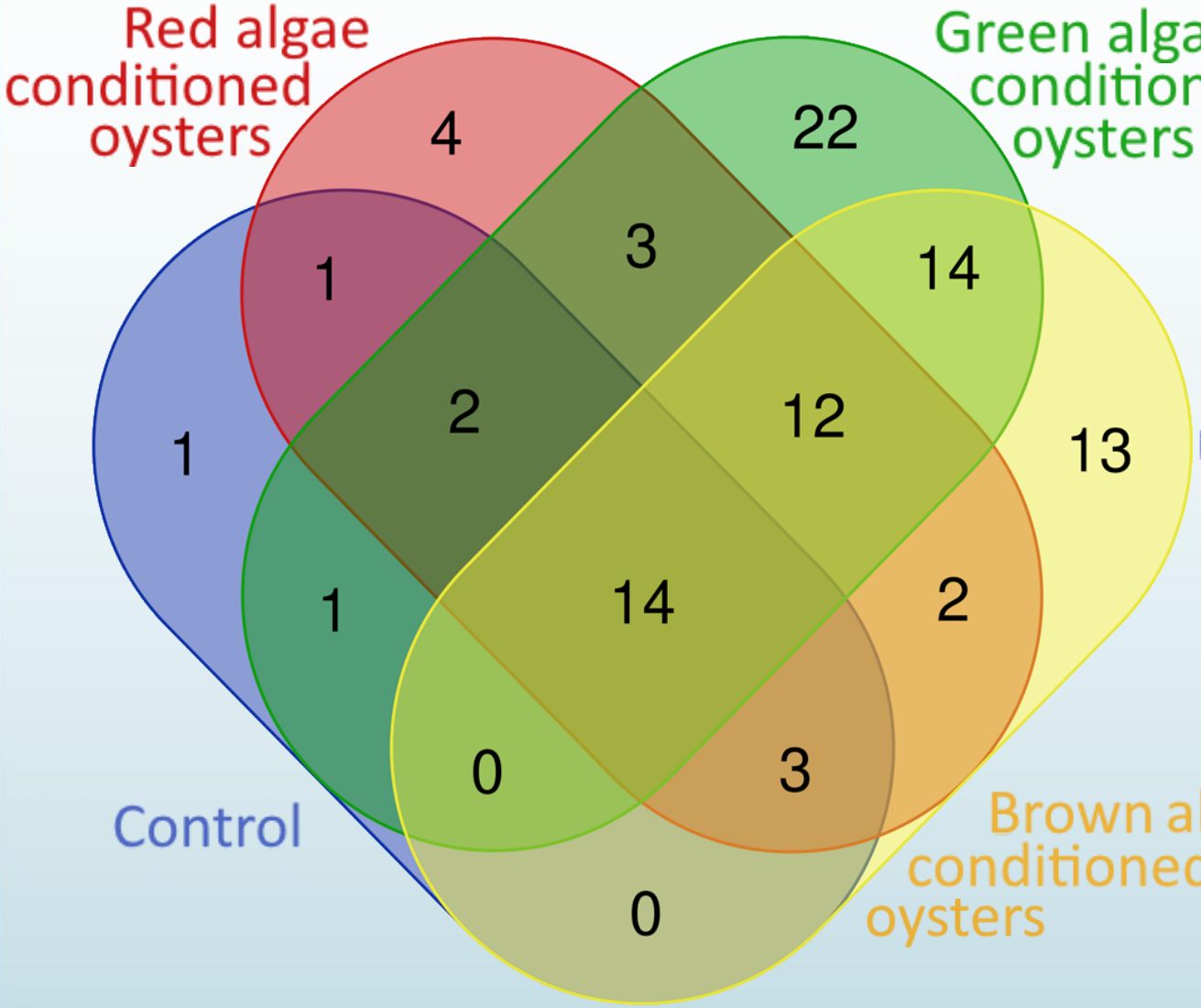
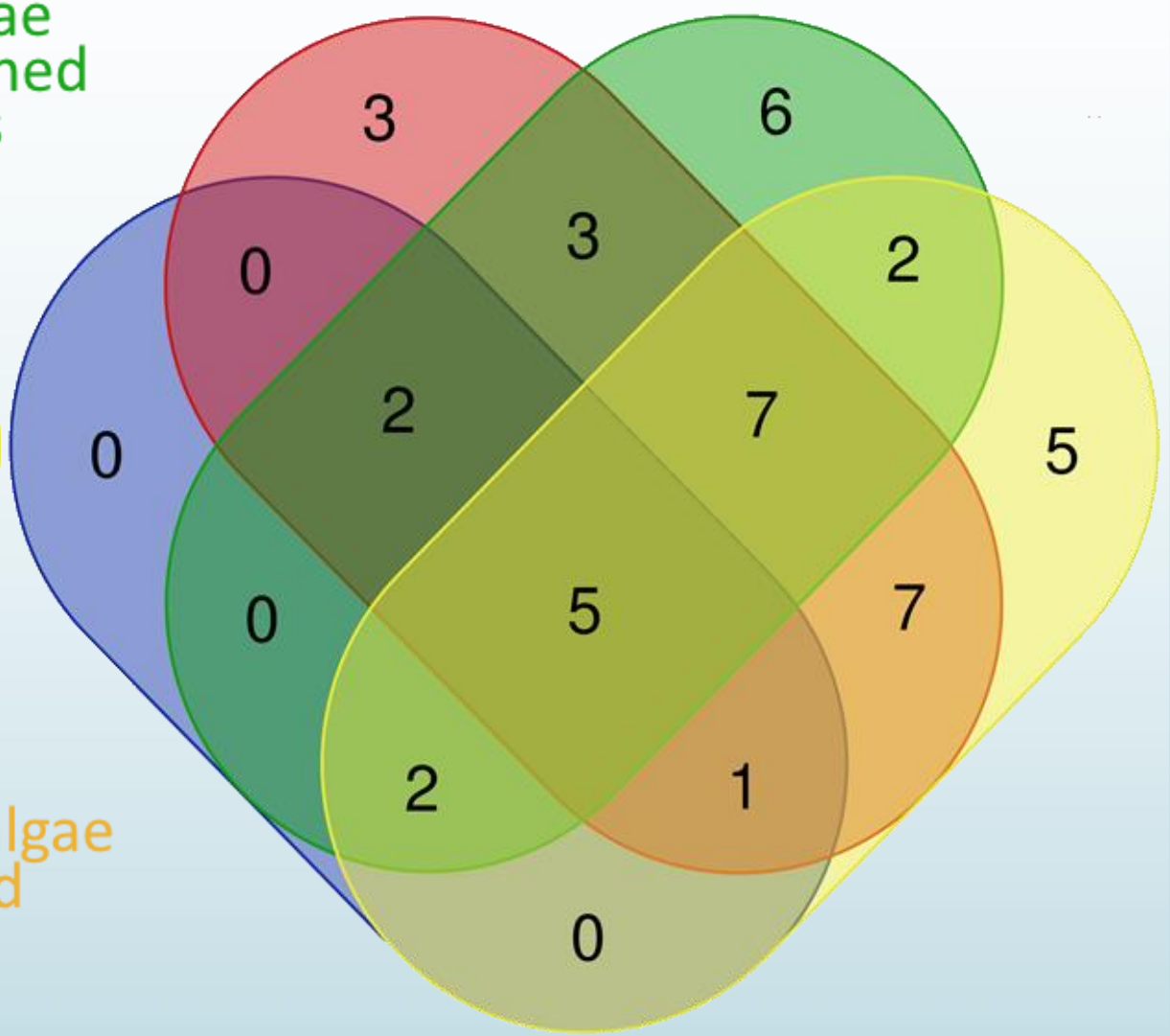
DeSeq analysis for Bacteria

① Acclimatation phase

Up-expressed bacterial strains



Down-expressed bacterial strains



Further work and perspectives

Log 2 Foldchange distance

New bacteria species occuring after two weeks of acclimatation

Removed bacteria species after two weeks of acclimatation

- Identified bacteria species behind the sorted OTUs
  - Plot Heatmaps of the OTU significantly varying
  - Determine the role of those characterized bacteria

Thank you for your attention

A warm thanks to all the contributors who brought their help during the experiments

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Preventing and mitigating farmed bivalve diseases

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