

INVERTEBRATE-BACTERIAL ASSOCIATIONS AS HOTSPOTS OF BENTHIC NITROGEN CYCLING IN ESTUARINE ECOSYSTEMS (INBALANCE)

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Background

While bacteria have been considered driving much of the Earth's nitrogen (N) cycle, recent research shows that ecological interactions between meio-, macrofauna and bacteria are important in regulating N cycling in soft sediments (Bonaglia et al. 2014). The collection of microbes in benthic invertebrates in both N rich and depleted environments reveals a diverse N cycling community (Heisterkamp et al. 2012; Kessel et al. 2016; Petersen et al. 2016; Stief et al. 2017), but:

- the N cycling microbial assemblages associated with invertebrate hosts in coastal and estuarine ecosystems are poorly characterized worldwide;
- role of invertebrate-bacterial association in ecosystem functioning remains essentially unknown in shallow estuarine systems.

Task: quantify target microbial N transformation processes in benthic invertebrate hosts and identify specificity of animal-bacterial associations along spatial and physical-chemical gradients (*geography and eutrophication*).

Key hypothesis

Hypothesis 1. Invertebrate-bacterial associations are hotspots for N cycling processes in the coastal benthic compartment.

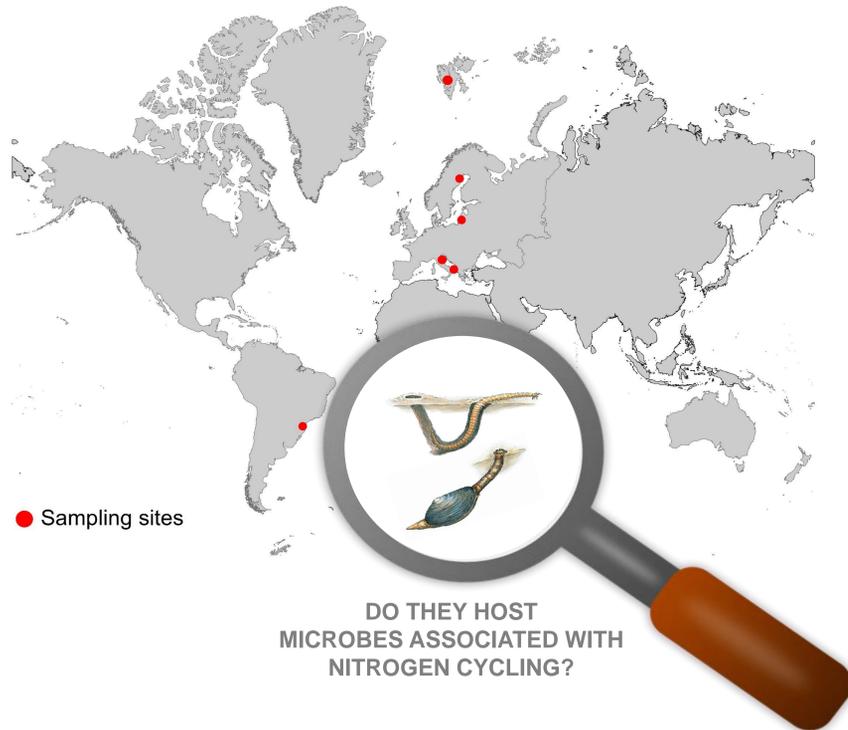
Hypothesis 2. Along geographical gradient, invertebrate-bacterial associations shift from casual associations to intimate symbioses.

Hypothesis 3. N removal processes dominate in invertebrate-bacterial associations from estuarine environments and these are tightly related to the degree of eutrophication.

Hypothesis 4. Filter and deposit feeders also host N₂-fixers and thus act as direct conduits of bioavailable N to estuarine ecosystems, but process relevance shifts along the eutrophication gradient.

Hypothesis 5. A nutrient loading threshold exist, beyond which intimate symbioses disappear and only facultative interactions persist.

Where we look for microbe host?

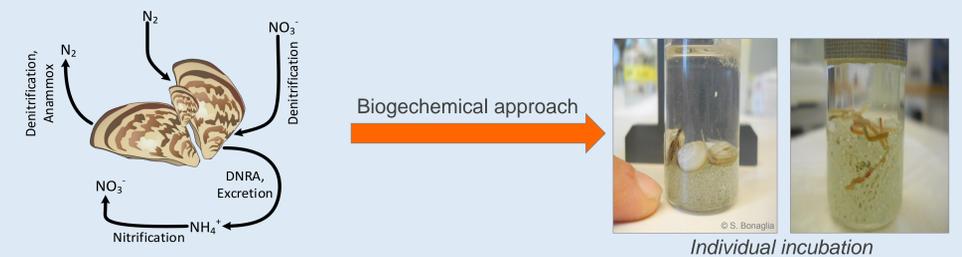


Expected results

- Comparison of incubation results between intact community and single individuals will highlight importance of microbe host, particularly in oligotrophic lagoons.
- The concentration of N is important in shaping a microbiome in the invertebrate host.
- Biogeochemical processes within invertebrates (*filter feeders or burrowers*) may largely differ those measured within surrounding sediments.

Experimental activities

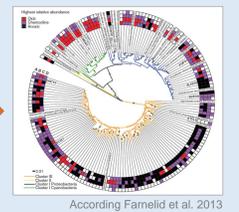
Activity: Quantify target microbial N transformations in selected benthic invertebrate hosts;



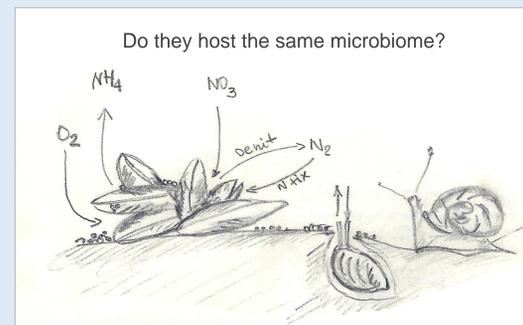
Activity: Identify the genetic and functional diversity of the microbiome;

- nifH* gene for N-fixation
- hzsA* gene for anammox
- narG* and *napA* genes for nitrate reduction
- nirS* and *nrfA* genes for nitrite reduction

Functional genomic approach



Activity: Determine the specificity and plasticity of the animal-bacterial associations;



Activity: Evaluate the role of animal-bacterial associations in N cycling pathways in the benthic estuarine habitats using ecological network and systematic N balance analysis;