
Cross-feeding of algal and anaerobic microbiota in the digestive system of a marine herbivore

Angélique Gobet^{*†1}, Laëtitia Mest¹, Morgan Perennou², Simon Dittami¹, Claire Caralp³, Céline Coulombet⁴, Sylvain Huchette⁴, Sabine Roussel³, Gurvan Michel¹, and Catherine Leblanc¹

¹Station biologique de Roscoff [Roscoff] (SBR) – Université Pierre et Marie Curie (UPMC) - Paris VI, CNRS : UMR8227 – Place Georges Teissier - BP 74 29682 ROSCOFF CEDEX, France

²Station biologique de Roscoff [Roscoff] (SBR) – Université Pierre et Marie Curie (UPMC) - Paris VI, CNRS : FR2424 – Place Georges Teissier - BP 74 29682 ROSCOFF CEDEX, France

³Laboratoire des Sciences de l'Environnement Marin (LEMAR) – CNRS : UMR6539, Université de Bretagne Occidentale (UBO), Institut Universitaire Européen de la Mer (IUEM) – Technopôle Brest-Iroise, Place Nicolas Copernic, 29280 Plouzané, France

⁴France Haliotis – France Haliotis – Kerazan, Lilia, 29880 Plouguerneau, France

Abstract

The gut microbiota is of major importance for terrestrial herbivores; grinding and host enzymes are not sufficient for a complete digestion of plant material. Indeed, specific bacterial groups help degrade complex plant polysaccharides such as cellulose or starch (*Bacteroidetes* and *Firmicutes* in cow's rumen). In the marine world, herbivore digestion is still poorly understood. Red, green, and brown algae present a large array of complex polysaccharides for herbivores to digest. The abalone is a good study-case as it can digest these three algal groups but the role and fluctuations of the associated microbiota are poorly known. We thus investigated the effect of 4 algal diets (*Palmaria palmata*, *Ulva lactuca*, *Saccharina latissima* and *Laminaria digitata*) on abalone digestive microbiota on the Northwest coast of France over a year. Bacterial community composition from abalone digestive glands sampled every 2 months was explored using Illumina sequencing. Three bacterial genera dominated the community (86%-92%) for the whole year; the strictly anaerobic *Psychrilyobacter*, and facultatively anaerobic *Mycoplasma* and *Vibrio*. Their respective genomes showed their ability to ferment pyruvate but only *Vibrio* contained necessary enzymes for algal polysaccharide degradation, implying its role as a preliminary degrader. Diversity analyses showed specific seasonal patterns of the bacterial community according to algal diet. Communities associated to *L. digitata* and *P. palmata* diets seemed more stable over the year than those associated to *S. latissima* or *U. lactuca*. Altogether, in comparison to terrestrial herbivores, abalone presents a specific digestive microbiota, where diet-specific bacteria may assist in algal polysaccharide degradation.

Keywords: cross, feeding, gut microbiota, algae, algal polysaccharides

*Speaker

†Corresponding author: agobet@sb-roscoff.fr