

## Microbiomes of live feed products have an important contribution to the rearing water microbiomes in *Litopenaeus vannamei* larviculture

Heyse Jasmine<sup>1</sup>, Props Ruben<sup>1</sup>, Kongnuan Pantipa<sup>2</sup>, De Schryver Peter<sup>2</sup>, Rombaut Geert<sup>2</sup>, Defoirdt Tom<sup>1</sup> and Boon Nico<sup>1</sup>

<sup>1</sup> Center for Microbial Ecology and Technology (CMET), Department of Biochemical and Microbial Technology, Ghent University, Coupure Links 653, 9000 Gent, Belgium

E-mail: [jasmine.heyse@ugent.be](mailto:jasmine.heyse@ugent.be)

<sup>2</sup> INVE Technologies NV, Hoogveld 93, 9200 Dendermonde, Belgium

Outbreaks of microbial diseases have posed one of the main impediments to the sustainable growth of the aquaculture industry. To allow for effective microbial management, a thorough understanding of the composition, drivers and dynamics of the microbiomes present in these systems is needed. An aquaculture farm consists of several microbial compartments, including the water column, the cultivated organisms, the feed products, etc. Most studies up till now have focussed on the rearing water and host-associated microbiomes, but did not investigate the community composition and dynamics of the peripheral microbiomes such as those of dry and live feeds.

In our study, we performed a sampling campaign on *Litopenaeus vannamei* larviculture and investigated the extent to which bacterial taxa present in the rearing water originate from the peripheral microbiomes (i.e. live and dry feeds or the exchange water). For each of the peripheral microbiomes a high batch-to-batch variability in community composition was observed. These batch-differences were mainly attributed to large differences in the relative abundances of members within a set of 'core' taxa. Also in terms of bacterial abundances we observed a high variability both within and between batches. Since each source had a different bacterial abundance and was added in a different quantity and with a different frequency, it introduced different microbial loads to the rearing water. Through a source tracking analysis, we found that 37% of all bacteria in the rearing water were introduced via one of the peripheral microbiomes. The contribution of the algae was the largest, followed by the Artemia, the exchange water and the dry feeds.

Together, our results illustrate that these peripheral microbiomes have an important contribution to the rearing water microbiome. Given this contribution, careful preparation and storage of these inputs will be paramount to maintain stable, healthy systems.

Keywords: Aquaculture; Source tracking; *Litopenaeus vannamei*; Artemia; Algae; Community composition; Microbial management