Molecular gut content analysis of *Calanus* sp. copepods suggests decoupling of prey selection and abundance

Jessica Louise Ray¹, Katrine Sandnes Skaar¹, Paolo Simonelli², Aud Larsen¹

¹ Uni Research Environment, Uni Research AS, Postboks 7810, N-5020 Bergen, Norway ² Department of Biology, University of Bergen, Postboks 7803, N-5020 Bergen, Norway

Predators such as copepods shape the community within an ecosystem by regulating prey abundance and distribution. Investigating predator grazing activity within an ecosystem is therefore of great importance to understand its structure and function. To test the influence of phytoplankton growth phase on mesozooplankton feeding, we conducted a seawater mesocosm experiment and incubated Calanus sp. copepods inside mesocosms that were nutrient-manipulated to promote Phaeocystis pouchetii (Haptophyta) or Skeletonema marinoi (Diatomea) blooms. We further developed prey specific TagMan gPCR assays to quantify relative grazing by Calanus on these dominant phytoplankton taxa. In addition, we conducted a metabarcoding analysis of microbial eukaryote diversity in seawater and Calanus guts, to investigate Calanus prey selection across the mesocosm manipulations. Our TaqMan qPCR results indicated that grazing on both P. pouchetii and S. marinoi was low regardless of phytoplankton growth phase, suggesting a decoupling from relative prey abundances. This low relative grazing by Calanus on P. pouchetii and S. marinoi was confirmed in a more complete assessment of the gut content using the metabarcoding approach, which identified ciliates and large diatoms as the preferred prey. Our data suggest an inverse relationship between S. marinoi abundance and copepod grazing, possibly due to a change in S. marinoi bioavailability with growth phase. Elucidation of copepod grazing selection is clearly a complex issue, however the use of molecular techniques to measure relative grazing rates can shed light on the feeding choices in mixed prey communities.