

Impact of cyanobacteria on the mesozooplankton trophic structure and amino acid metabolism in the Central Baltic Sea

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Future oceans may suffer from increasing cyanobacteria blooms with unknown consequences for higher trophic levels. We collected seston and mesozooplankton size fractions (100-300 μm , >300 μm) from the mixed layer, the ‘‘winter water’’ between the thermo- and halocline, and from below the halocline at day and night during *Nodularia* blooms in the Gotland Basin in July 2014 and 2015. Concentrations and stable nitrogen ($\delta^{15}\text{N}$) isotope distributions of bulk-N and 13 amino acids (AA) were analysed by EA-IRMS, GC-MS, and GC-C-IRMS. The trophic positions (TP) were estimated using the Glutamic acid/Phenylalanine $\delta^{15}\text{N}$ stable isotope approach. Transfer of N from N_2 -fixation (diazotroph N) into the different TPs was quantified using N-isotope-mixing models.

The TPs in seston suggested heterotrophic contributions to the Chl. a maximum at night. Rotifers and *Temora longicornis* dominated the zooplankton in the mixed layer and the ‘‘winter water’’, respectively. Both communities had omnivore TPs. Below the halocline, zooplankton was co-dominated by *Pseudocalanus* spp. and *Paracalanus* spp. and had carnivore TPs. Diazotroph N contributed $39\pm 7\%$ and $29\pm 8\%$ to zooplankton in the mixed layer and ‘‘winter water’’, respectively. Both communities showed large diurnal changes in non-essential AA molar ratios. In contrast, zooplankton from below the halocline received little or no diazotroph N and kept conservative AA molar ratios. These results point to fundamentally different N metabolism in communities below and above the halocline. The efficient incorporation of diazotroph N by *T. longicornis* may add to the success of *T. longicornis* and its predators in the Central Baltic Sea.

Keywords: Stable Isotopes, Compounds-specific isotope analysis, Amino acids, Trophic structure, Diazotrophic nitrogen, Food webs, Central Baltic Sea

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