



Methanogenic Archaea Versus Methane Oxidising Bacteria as Food Source for Chironomid Larvae Markedly Depleted in their Biomass ^{13}C Content

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Stable carbon isotope analysis of *Chironomus plumosus* larvae revealed, that these larvae feed on a carbon source in the sediment strongly depleted in ^{13}C , i. e. on microorganisms involved in the methane cycle. We investigated, if the larvae feed on methanogenic *Archaea* or methane oxidising bacteria (MOB), and whether the carbon transfer is based on digestion of the microbial biomass or on a symbiotic relation. FISH with larval tissue thin sections showed that the larvae are not inhabited by methanogenic archaea or MOB as symbionts or part of their gut microflora. Furthermore, clone libraries for the 16S rRNA gene from larval tissue and DGGE of sediment and larval DNA samples revealed, that the eubacterial community present in the larval gut is dominated by anaerobic and facultatively anaerobic bacteria, whereas MOB were only found in low numbers. Additionally, comparative quantitative PCR for *Eubacteria* and *Archaea* in sediment, larval tissue and gut content revealed a strong enrichment of *Eubacteria* in the larvae, while numbers of *Archaea* were very low compared to the bulk sediment. Calculations based on the ^{13}C -signatures of substrates, and the fractionation factors between substrates and microbial biomass of MOB and methanogens, showed that unrealistically high amounts of methanogens, but only 10-20 % of MOB, in the chironomids diet would explain their ^{13}C -values. In conclusion, methanogenic *Archaea* seem not to cause the ^{13}C -depletion detected in larval biomass. Instead, the larvae feed on MOB present in the sediment, thus incorporating high amounts of methane derived carbon, which is subsequently exported from the microbial loop into higher trophic levels of the lake food web.