

Can mesozooplankton organisms adapt to the changing chemical composition and degradation in food quality caused by ocean acidification?

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Introduction

Very few studies exist dealing with the evolutionary responses of species to ocean acidification, even though the selective forces of OA are potentially strong. Hence, we investigate selection processes in zooplankton, both directly as well as by comparing populations with different selective histories. Potential patterns of adaptation to OA will be uncovered by integrating field observations, laboratory experiments and genetic analyses.

Ecological experiments

Stage distribution of *Acartia tonsa*: Indirect effects of OA seem to be more important

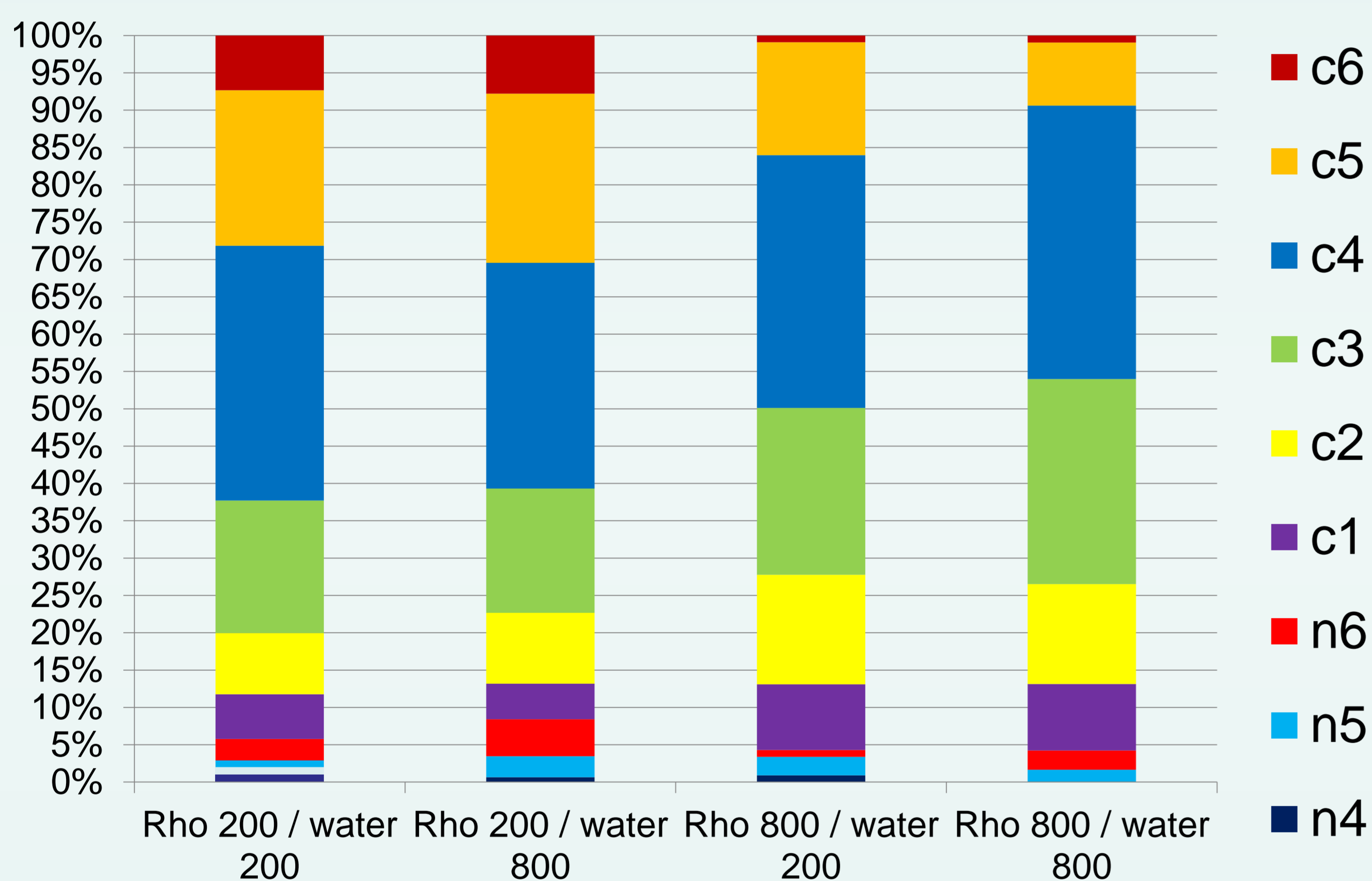
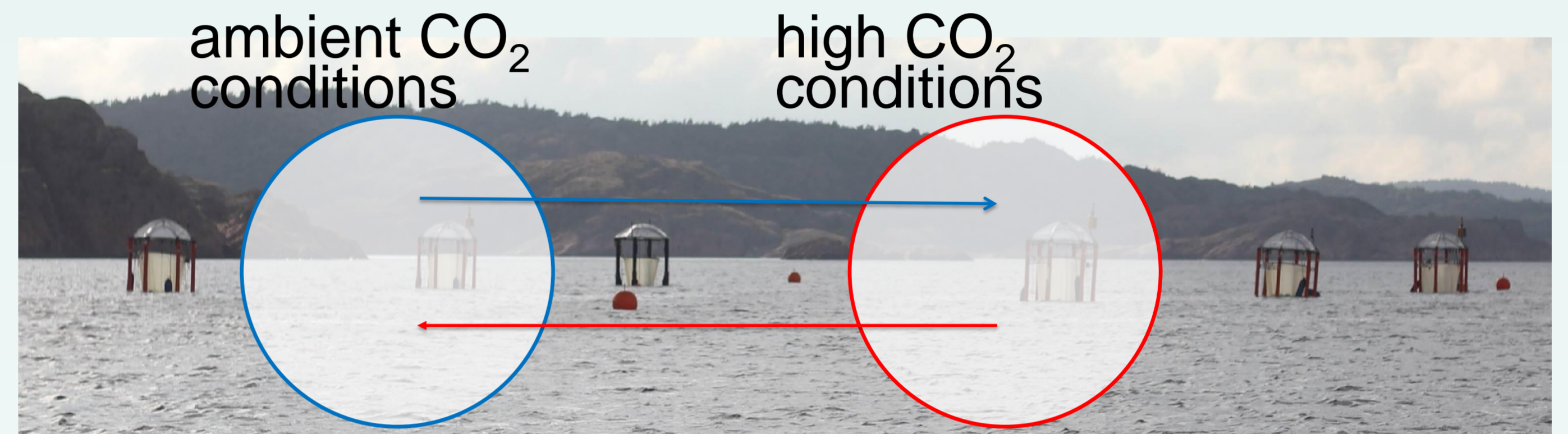


FIG.1 Diagram of the developmental stage distribution. The x-axis shows the experimental treatments; (Rho) Rhodomonas, (water) artificial sea water, (200) bubbled with 200ppm CO₂, (800) bubbled with 800ppm CO₂. The left y-axis shows the percentage of the respective stages. The legend shows the developmental stages; (n4-n6) nauplii stages 4-6, (c1-c6) copepodite stages 1-6. The ANOVA showed only a significant food effect (p=0,047), but none for pCO₂ nor for an interaction.

Transplant experiments: exchange of organisms between high CO₂ and ambient CO₂ mesocosms



Higher hatching success after exposition to a high CO₂ environment

mesocosm pairs	zp: high MC food: ambient MC	zp: ambient MC food: high MC	control: high MC	control: ambient MC
2_3	83	85	65	69
4_1	84	74	64	74
6_5	54	79	78	57
8_9	69	68	71	77
7_10	62	78	78	73
mean after 9 days	67 (σ=25)	75 (σ=23)	72 (σ=21)	66 (σ=26)

TAB.1 Documentation of the mean hatching success (%) of the nauplii after exposing to different environments. (zp) zooplankton, (MC) mesocosm. No significant pattern was detected because of high variation among replicates and mesocosms.

Genetics

Barcoding

Setup of a genetic database of the most abundant copepod species inside the Gullmar fjord.

Metabarcoding

Investigation of differences in species composition and genotype frequency between populations suffering under ocean acidification and those that were exposed to present-day CO₂ conditions.

Preliminary results

We analyzed (barcoding approach according to Folmar et al. 1994) the DNA of 15 individuals per mesocosm and the fjord of the copepod *Pseudocalanus acuspes*, from three time points (26.03 05.05 14.06) to investigate the intraspecific genotype frequency.

With this approach we were able to detect enough intra specific variation (seven haplotypes) within *P. acuspes* populations for further genetic investigations.

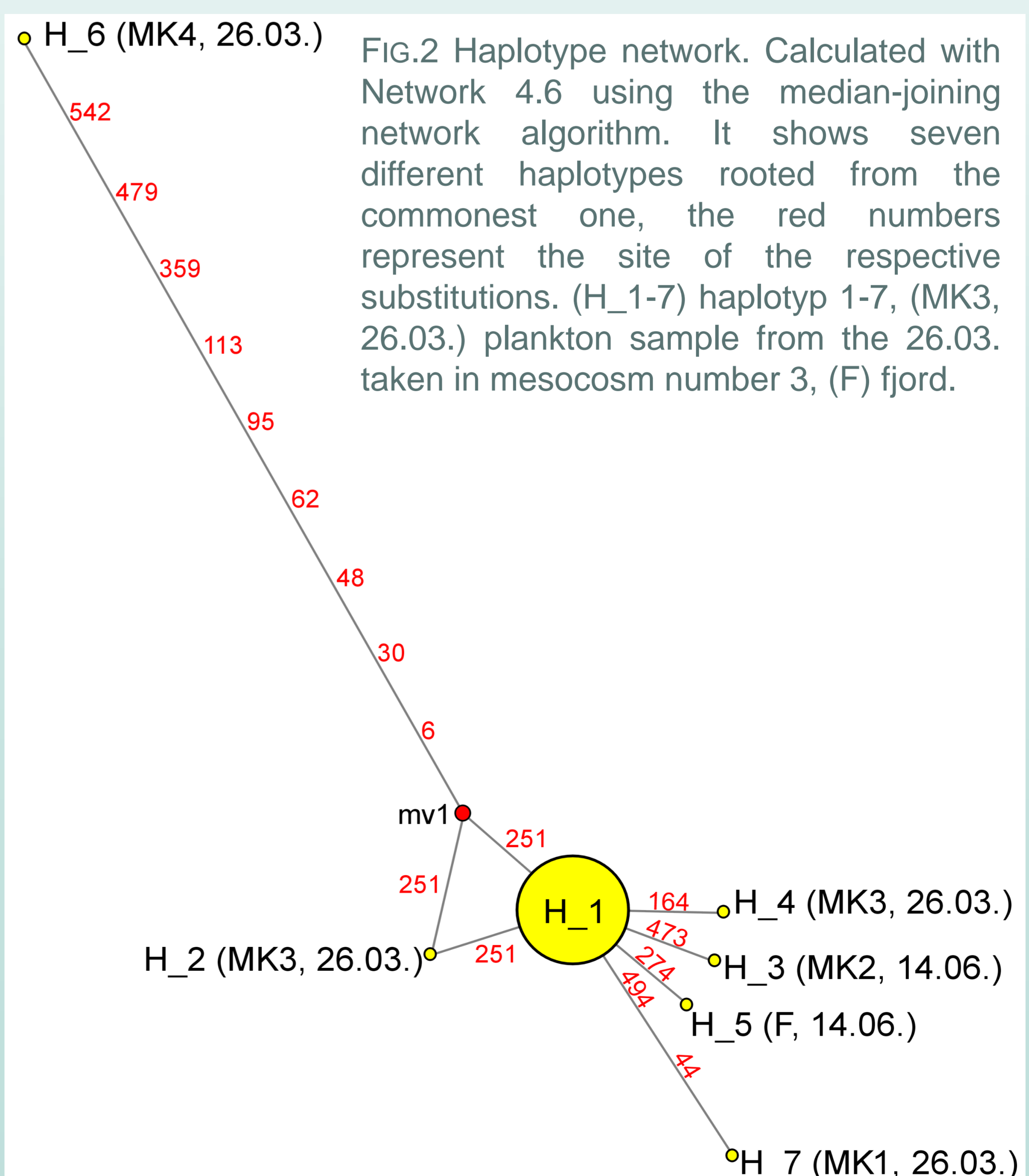


FIG.2 Haplotype network. Calculated with Network 4.6 using the median-joining network algorithm. It shows seven different haplotypes rooted from the commonest one, the red numbers represent the site of the respective substitutions. (H_1-7) haplotyp 1-7, (MK3, 26.03.) plankton sample from the 26.03. taken in mesocosm number 3, (F) fjord.