Linkage between copepods and bacteria in the North Atlantic Ocean

Daniele De Corte[1],*,, Itziar Lekunberri[1],**, Eva Sintes[1], Juan Antonio L. Garcia[1], Santiago Gonzales[2], Gerhard J. Herndl[1,2]**

[1]Department of Limnology and Oceanography, Center of Ecology, University of Vienna, Althanstrasse 14, 1090 Vienna, Austria
[2]Department of Biological Oceanography, Royal Netherlands Institute for Sea Research (NIOZ), PO Box 59, 1790 AB, Den Burg, The Netherlands

*Corresponding author: daniele.de.corte@univie.ac.at
**Both authors contributed equally to this work

Table S1. Summary of the characteristics from pyrotag reads for the 4 groups of samples (Calanoida and Cyclopoida copepods, and Deep and Surface waters)

	Total
No. of raw reads retrieved	65855
No. of reads after trimming and quality control	25101

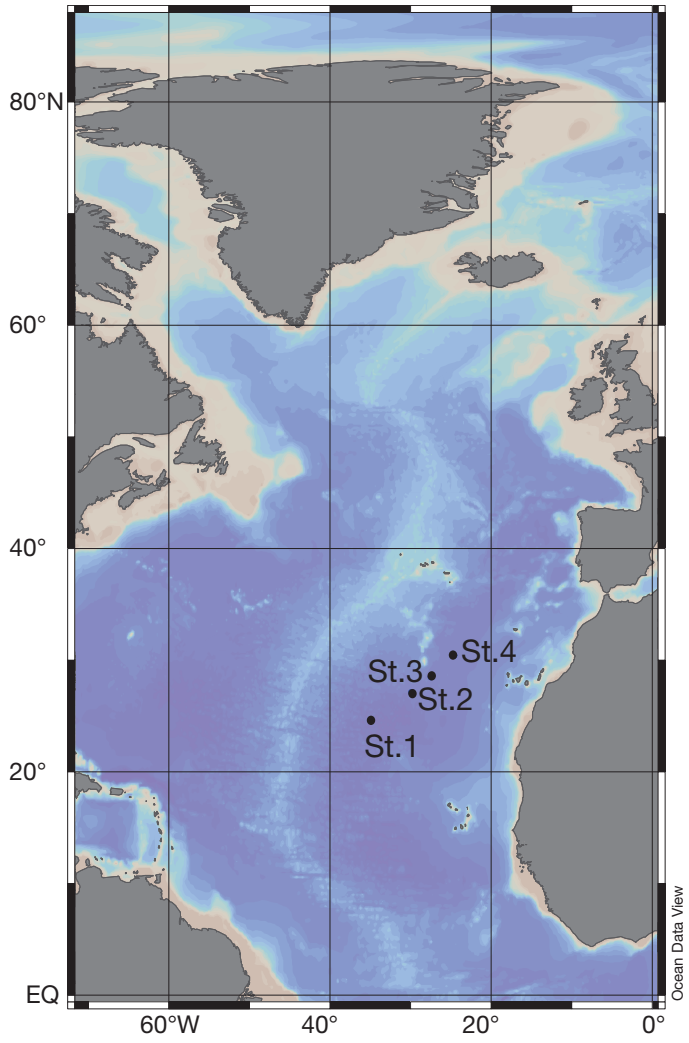|	Calanoida	Cyclopoida	Deep	Surface
No. of total reads	3567	11665	3937	5932
Average read length (bp)	303	305	311	309
GC percentage	53.9	53.5	52.8	51.5

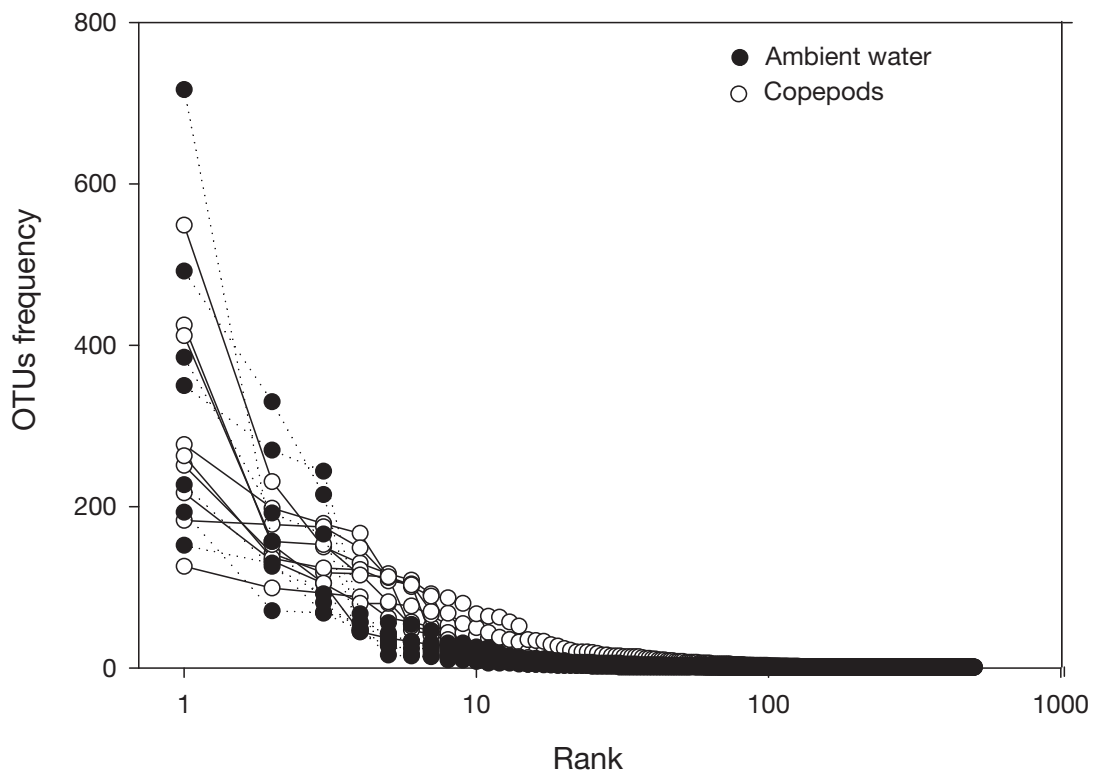Fig. S1. Location of the sampling stations in the North Atlantic

Fig. S2. Rank-frequency distribution of operational taxonomic units (OTUs) sharing 97% sequence similarity obtained from copepod-associated and ambient-water bacteria

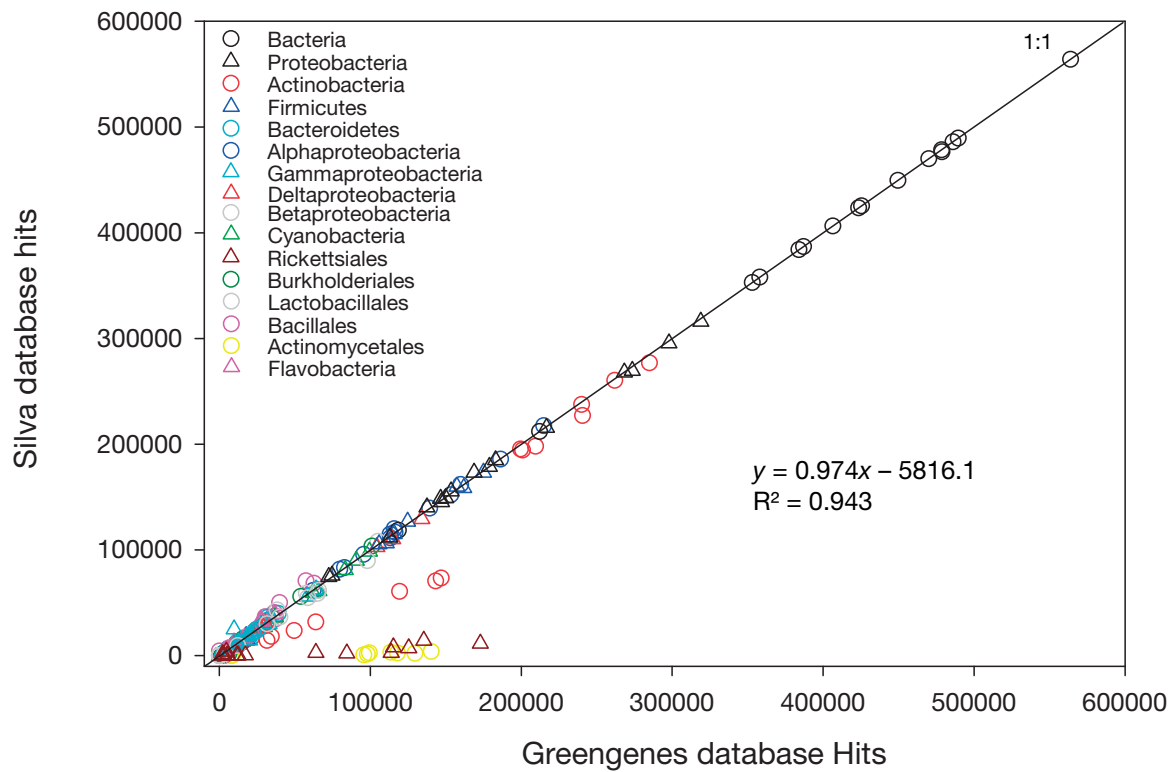$y = 0.974x - 5816.1$
$R^2 = 0.943$

Fig. S3. Comparison between the phylogenetic assignments obtained by the BLAST hit-scores using 2 different databases (SILVA and Greengenes)