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SUPPLEMENTARY MATERIAL

Metabarcoding to monitor the crustacean zooplankton of a lake improves when using a reference DNA library from local samples

Giuseppe Garlaschè,[1,2] Giulia Borgomaneiro,[1] Roberta Piscia,[1] Marina Manca,[1]
Ester M. Eckert,[1,3] Diego Fontaneto[1,3*]

[1]Water Research Institute (IRSA), National Research Council of Italy (CNR), Largo Tonolli 50, 28922 Verbania Pallanza, Italy
[2]Département de Biologie Chimie et Géographie, Université du Québec à Rimouski, 300 Allée des Ursulines, Rimouski, QC G5L 3A1, Canada
[3]National Biodiversity Future Center (NBFC), 90133 Palermo, Italy

***Corresponding author:** diego.fontaneto@cnr.it

Supplementary Data. Dataset used for the comparisons between numbers of reads and abundances for each species in the 21 samples with data from morphology and Illumina with custom COI primers (https://www.jlimnol.it/index.php/jlimnol/article/view/2087).

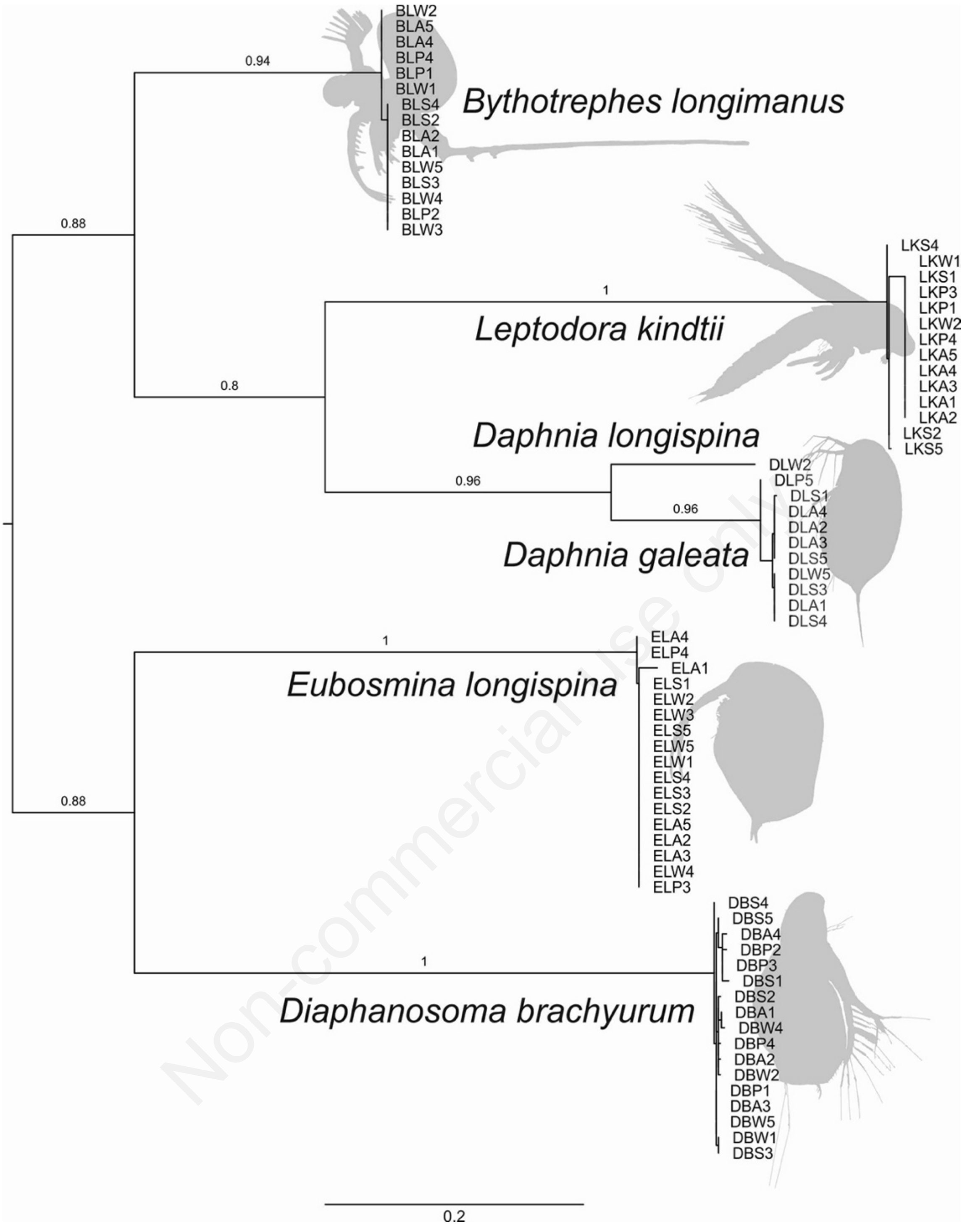

Fig. S1. Maximum Likelihood (ML) phylogenetic reconstruction for the COI sequencies belonging to Cladocera to construct the internal reference library. Branch length is proportional to substitutions/sites in the scale bar, from a GTR + invgamma evolutionary model. Numbers on branches refer to aLRT support values, not reported for short terminal branches and for values below 0.8. Acronyms for terminals are: first two letters initial of species name, then a letter indicating the season (P: Spring, S: Summer, A: Autumn, W: Winter 2019), and a number to indicate different individuals within each season. GenBank Accession numbers for the 74 sequences are MH321324-MH321397.

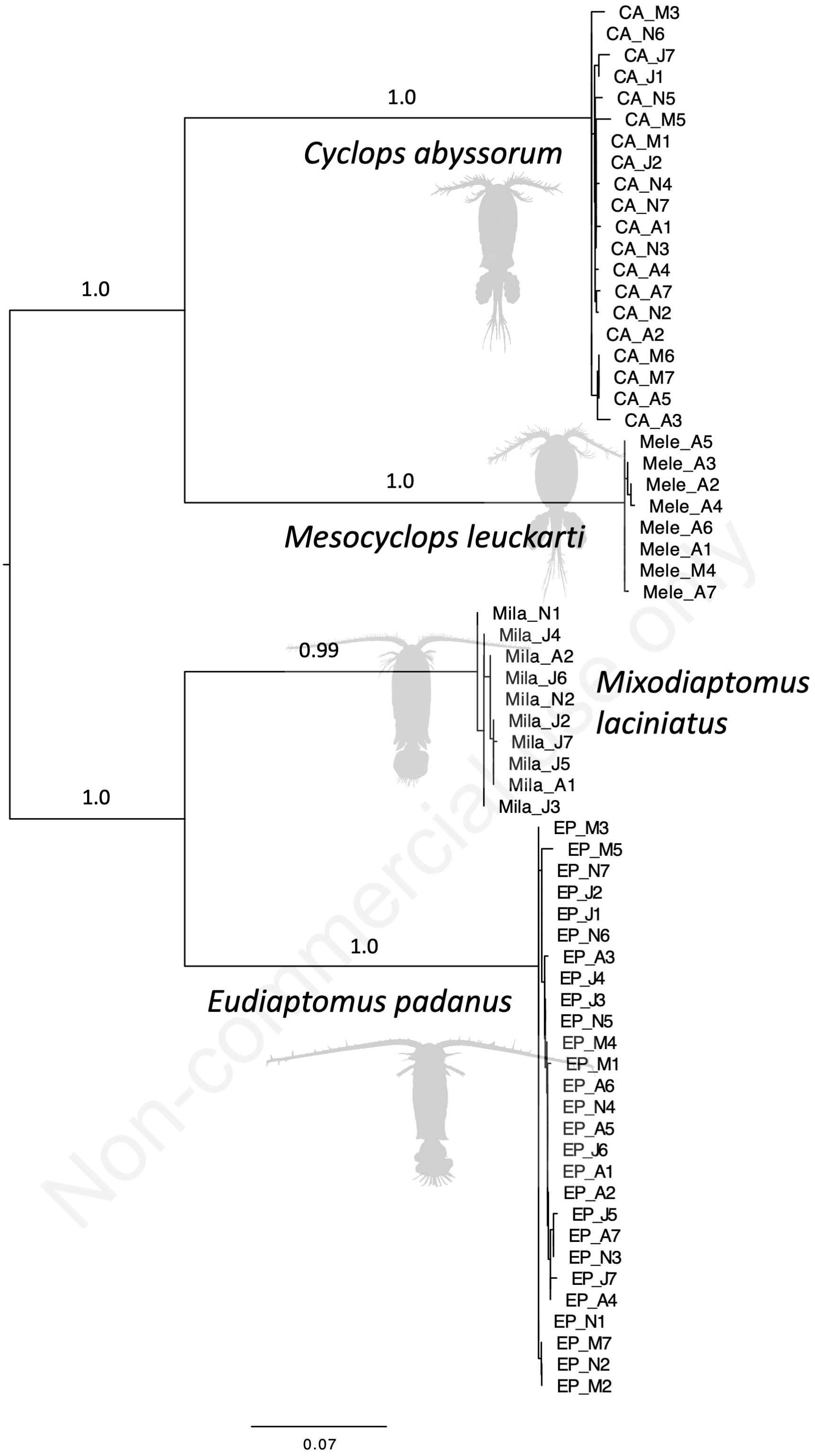

Fig. S2. Maximum Likelihood (ML) phylogenetic reconstruction for the COI sequencies belonging to Copepoda to construct the internal reference library. Branch length is proportional to substitutions/sites in the scale bar, from a GTR + invgamma evolutionary model. Numbers on branches refer to aLRT support values, not reported for short terminal branches and for values below 0.8. Acronyms for terminals are: first two letters initial of species name, except for two species with the same initials, ML, separated as Mila and Mele, then a letter indicating the month of sampling (A: August, J: January, M: March, N: November) 2019), and a number to indicate different individuals within each season. GenBank Accession numbers for the 65 sequences are MN635799-MN635853 and MN635855-MN635864.

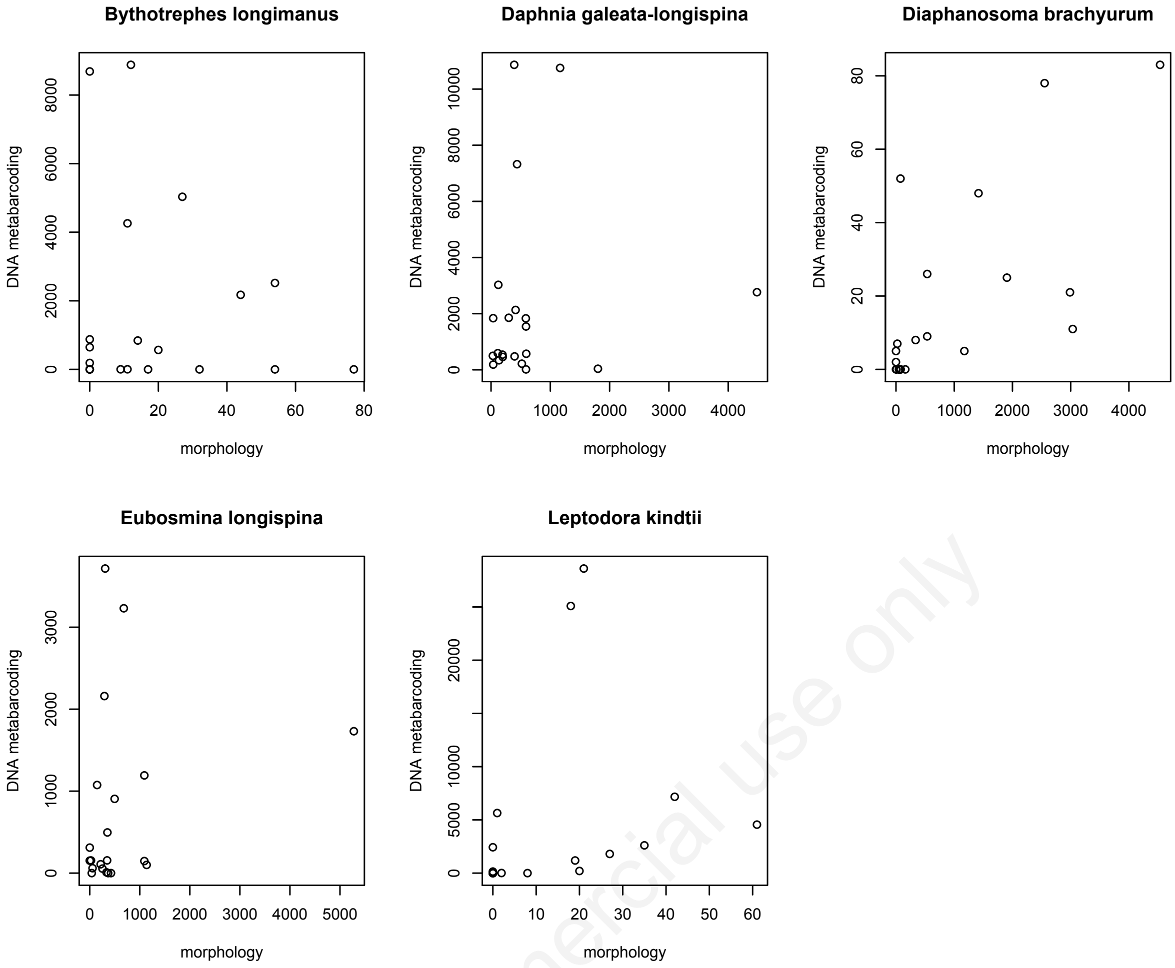

Fig. S3. Scatterplots of the influence of abundance of individuals identified from morphology on the number of reads from DNA metabarcoding for each of the taxa of Cladocera.

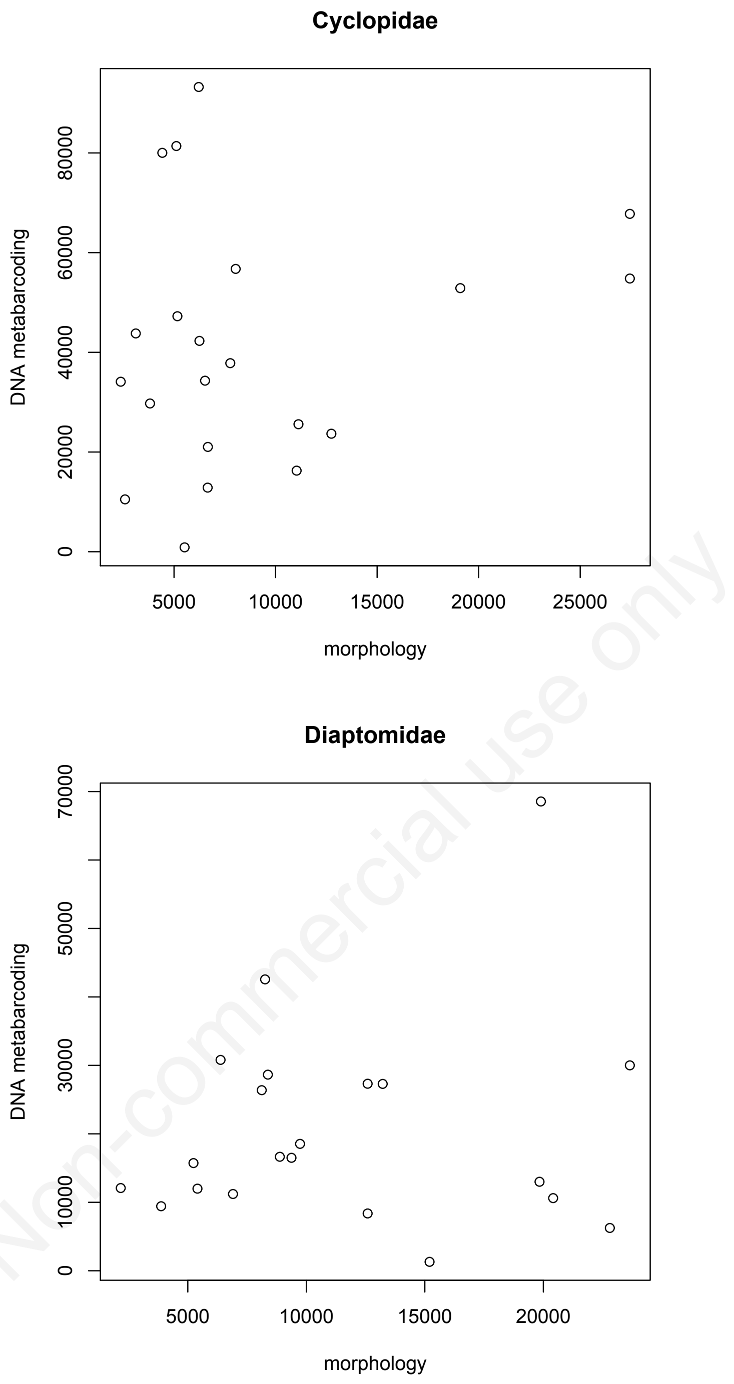

Fig. S4. Scatterplots of the influence of abundance of individuals identified from morphology on the number of reads from DNA metabarcoding for each of the taxa of Copepoda.