

Corrigendum

Retention efficiency of 0.2 to 6 μm particles by the appendicularians *Oikopleura dioica* and *Fritillaria borealis*

Diego Fernández, Ángel López-Urrutia, Antonio Fernández, José Luis Acuña*, Roger Harris

Mar Ecol Prog Ser 266: 89–101, 2004

*Email: acuna@uniovi.es

• On page 98, conversion factors used to calculate prey and predator body carbon for Fig. 6 were incorrect, as well as the resulting predator:prey body carbon ratios. This ratio is now $2.21 \times 10^6:1$ for the appendicularians, and not $1.45 \times 10^4:1$ as originally reported. It is still within the range for the mesozooplankton (now $6.2 \times 10^{-1}:1$ to $2.6 \times 10^8:1$). However, it is now significantly higher than the copepod:prey body carbon ratio ($8.66 \times 10^3:1$; regressions of log prey-carbon on log predator-carbon for appendicularians and copepods had similar slopes but significantly different intercepts; ANCOVA, $p = 0.48$ and $p < 0.001$ respectively). The authors thank Fabien Lombard for pointing out this error.

A revised figure is shown below.

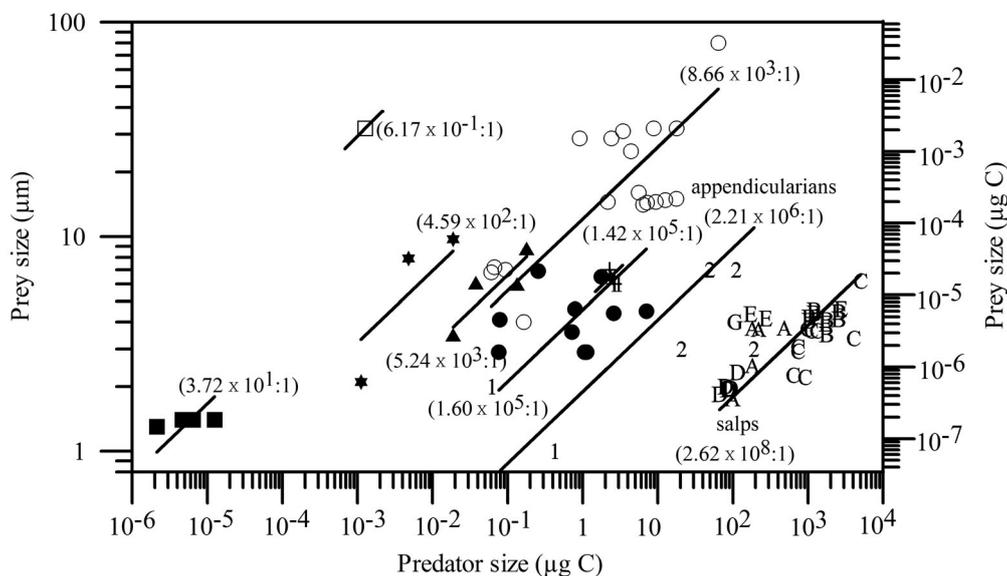


Fig. 6. Prey size in carbon units (right vertical axis), and in equivalent spherical diameter (left vertical axis) versus predator size, in carbon units. Symbols correspond to data compiled by Hansen (1994), while numbers and letters represent our compilation of data from the literature on appendicularians and salps, respectively: (■) nanoflagellates; (□) dinoflagellates; (★) ciliates; (▲) rotifers; (+) cladocerans; (●) meroplankton larvae; (O) copepods. 1, *Oikopleura dioica*, present study; 2, *Oikopleura vanhoffeni*, Deibel & Lee (1992); A, *Cyclosalpa floridana* solitary; B, *C. affinis* solitary; C, *C. polae* solitary; D, *C. floridana* aggregate; E, *C. affinis* aggregate. Data for A to E from Harbison & McAlister (1979). F, *Pegea bicaudata* aggregate; G, *P. confederata* aggregate. Data for F and G from Kremer & Madin (1992). Solid lines have slopes = 1, therefore they join points with the same predator:prey body carbon ratio (between brackets). Their intercepts were calculated by fitting data for each taxonomic category to linear functions with fixed slope = 1 (using SPSS non-linear regression routine)