

Response to comment on “Dispersal limitations matter for microbial morphospecies”

Richard J. Telford^{*1,2}, Vigdis Vandvik¹ and H.J.B. Birks^{1,2,3}

1 EECRG, Department of Biology, University of Bergen, Allégaten 41, N-5007 Bergen, Norway.

2 Bjerknes Centre for Climate Research, Allégaten 55, N-5007 Bergen, Norway.

3 Environmental Change Research Centre, University College London, London, WC1E 6BT, U.K.

* Corresponding author

Email: Richard.Telford@bjerknes.uib.no

Abstract

Pither argues that the relationship we found between regional species-richness maxima and modal lake-pH is expected because both values are constrained by the regional pH range and therefore cannot be interpreted as a signal of regional metacommunity dynamics. However, the null model he uses sets inappropriate parameters, generating unrealistic simulated data. We confirm our previous conclusions using a more appropriate null model.

Text

The ubiquitous dispersal hypothesis (1) of microbial biogeography has been difficult to test because of under-sampling and taxonomic uncertainties. We developed a novel test of this hypothesis (2), arguing that if dispersal is ubiquitous, microbial metacommunities should be global in scale, but that if dispersal is limited, metacommunity processes will operate at regional scales. We predicted that regional species richness-environment relationships would reflect sampling from the global diatom species pool if there was ubiquitous dispersal (see figure 1A in (2)), but would be modified by the regional environmental-commonness if dispersal is limited. Figure 1B in (2) showed that for three regions with different modal lake-pH, the statistically-significant richness maxima (referred to as 'optima' in (2)) are very different and reflect the regional environmental commonness. The majority of the 16 regions presented in figure S1 in (2) had statistically significant richness maxima that reflected the regional pH-commonness rather than a global species pool: this was our primary evidence against the ubiquitous dispersal hypothesis.

Figure 1C in (2) summarised the data shown in figures 1B and S1 and showed a strong positive relationship between the regional pH-modes and richness maxima. This is expected if diatom metacommunities are regional in scale; if they are global, no trend is expected. Pither (3) demonstrates that, because the regional pH-mode and the richness maximum are both constrained to lie within the pH range of each dataset, a positive correlation between these two variables is also expected if the maxima are randomly located. Exploring the consequences of this constraint with a null model, Pither (3) draws two values from a uniform distribution $U(0,1)$ to represent the range of pH values, and then draws two values from

within this range to represent the pH-mode and the richness maximum, for each of 16 simulated datasets. The correlation coefficient between the modes and maxima was then calculated.

We were initially surprised by the strength of the relationship reported by Pither's null model: the mean correlation coefficient between the modes and maxima (0.76) is almost as high as the observed value (0.85), suggesting that the relationship we showed can be expected by chance. However, Pither's simulation generates datasets that do not reflect reality. Most of the observed datasets span more than half the entire pH gradient found across all the datasets, all span more than a third (table S1 in (2)). In contrast, half the simulated ranges generated by Pither's (3) null model span less than a third of the gradient, and a sixth span less than 10%. This imposes a much stronger constraint on the relationship between pH-modes and richness maxima in the simulation than in the data.

A more appropriate null model is to maintain the observed pH range and mode for each dataset and randomise only the position of the richness maxima within the pH range. The mean Pearson correlation coefficient between the modes and maxima in 1000 simulations of this null model is 0.44, and the observed correlation is significant ($p=0.01$). Therefore, although Pither (3) identifies a potential confounding factor, it does not affect our conclusions.

In rejecting the "everything is everywhere" hypothesis, we took the position that "not everything is everywhere" (2), rather than the proposition that "nothing is everywhere", which Pither appears to ascribe to us (3), but which cannot be tested with our data. Pither's conclusion that common generalist diatom taxa are likely to experience less dispersal limitation is entirely consistent with our position that specialists in rare habitats will be most affected (2).

References

1. B. J. Finlay, *Science* **296**, 1061 (2002).
2. R. J. Telford, V. Vandvik, H. J. B. Birks, *Science* **312**, 1015 (2006).
3. J. Pither, *Science* **316**, 1124 (2007); www.sciencemag.org/cgi/content/full/316/5828/1124b.