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Interactive comment on "Spatially explicit analyses of gastropod biodiversity in ancient Lake Ohrid" *by* T. Hauffe et al.

T. Hauffe et al.

torsten.hauffe@bio.uni-giessen.de

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Reply to interactive comment of S. Giokos

We highly appreciate the fruitful comments of the referee Sinos Giokas. We incorporated suggested changes as follows:

General comments

"Apparently the authors having available and using only presence/absence data of the molluscan species they found tried to overanalyze that information. I think that their study would be much more comprehensive and informative if they had estimated in each sapling site species abundances and environmental correlates that possibly affect species distribution and richness. I suppose that this would be the next step in the analysis of the molluscan fauna of Lake Ohrid."

The referee is absolutely right, a detailed analysis of environmental correlates will be subject of future analyses. This is simply due to the fact that our current sampling design (hand picking of snails, dredging etc.) does not allow for a statistically sound comparison of abundances of species. We state these problems more clearly in the revised ms. However, based on the comment of Sinos Giokas as well as on the suggestion of another referee, Peter Solymos, we address in the revised ms the correlation between community and environment, and test the explanatory power of three different classes. The classes are: (i) Purely spatial explanatory factors (i.e. PCNMs), (ii) collecting depth and slope of the shore, and (iii) abiotic factors like substrate, geology of substrate and chlorophyll-a as proxy of algal biomass.

Specific comments

"I think that it would be useful using their presence/absence data to detect possible non-random associations of pairs of species enforcing a null-model approach. I understand that this would add more length and weight to the manuscript but it could help to understand if certain species or guild (e.g. endemics vs. non-endemics) associations are random or not."

According to the suggestion of the referee, we now test for non-random co-occurrence of species pairs (Gotelli and Ulrich, 2010). We show (i) so far no community disassembling due to recently invading widespread species (see authors reply to Peter Solymos) and (ii) that species pair aggregations occur within one depth layer and species segregation between separated depth layers.

Technical comments

"Concerning the form of the manuscript I think that it is quite lengthy. I suggest that authors could cut off it by 20

We followed the suggestion of all three referees and the editor and shortened the previous Material and Method section considerably (though we had to include new analyses of non-random species co-occurrence and the correlation between gastropod communities and environment).

Reply to interactive comment of M. Harzhauser

We would like to thank Mathias Harzhauser for valuable and constructive comments on our manuscript.

“The paper is strongly statistics-oriented and chapter 2.3 could be slightly condensed.”

We followed the suggestion of all three referees and the editor and shortened the Material and Method section considerably (though some new analyses had be newly included).

“Fig. 4CD is a bit artificial due to the threefold zonation. If possible and feasible it might be better to print the data (in addition) on a map without fixed zonation to get a single color strip with fading colours.”

We have thought about this suggestion ourselves. Unfortunately, we do not have strict transects, thus, incorporation into one strip is not feasible. Moreover, since some areas are densely covered by collecting points, point specific values are not visible on a single map. Original data are available by the corresponding author on request.

“In addition, a map showing bottom-types and environments (partly as given in fig 1) would help to evaluate the results in fig 4.”

Unfortunately, for most areas of Lake Ohrid, no high resultion information for bottom type is available. However, recently the first lake sediment characteristics were provided (Vogel et al., 2010). Therefore, we included in the revised ms biological meaningful parameters like chlorophyll-a as proxy of algal biomass in a correlation analysis of gastropod communities and environmental factors (see authors comment to the referee P. Solymos).

"Chapter 4.3: couldn't it be the other way round, that surrounding habitats benefit from species-rich hot-spots from where taxa get dispersed? (same problem as in marine biogeography)"

The referee might be right. Therefore we deleted this statement from the manuscript.

Reply to interactive comment of P. Solymos

We are grateful to the referee Peter Solymos and his useful suggestions that improved our manuscript. In the following pages we address the individual comments.

Main comments

"... is known that invasive molluscs often are altering biogeochemical systems through their massive abundances (Potamopyrgus, Dreissena), consequently might indirectly threaten other species. So the false illusion of "endemics are fine" as a conclusion should be avoided by augmenting the argument."

We agree with the referee and therefore down-toned our conclusion on p. 4968, line 14. Moreover, according to the suggestion of the referee S. Giokas, we utilized a test for non-random co-occurrence of species pairs (Gotelli and Ulrich, 2010), in order to test for aggregation of recently invading non-endemic gastropods or segregation between widespread/endemic species. This paragraph reads now as follows: "Probably because of a comparatively recent eutrophication (Matzinger et al., 2006b) and still local invasion of Lake Ohrid by widespread species (Fig 2), no community disassembling due to aggregation or segregation of either widespread-/widespread- nor widespread-/endemic species was observed (Table 1). In contrast to Lake Ohrid, an increase in abundances of widespread gastropods at the expense of endemic species has been shown in ancient Lake Malawi (Genner et al. 2004), the Caspian Sea (Grigorovich et al., 2002) and potential ancient lakes in the Balkans (Albrecht et al., 2009)."

"I feel that the manuscript is overly technical relative to its important and interesting topic. A whole arsenal of techniques is used, but the real story is somewhat hidden behind technical jargon. This might subtract readers from fully comprehending the message. A suggest to the Editor that a minor revision of the manuscript should address some issues with respect to specific technical details of the analysis, and the text should be revised to make the topic more accessible to readers not familiar with spatial methods. Most technical details (what function was used in which R package) can be placed in an Appendix. [footnote: it is rather exceptional to give full credit to all R packages used.]"

We followed the suggestions of all three referees and reduce the Material and Methods section by deleting, for example, detailed names of software functions. In the revision of the manuscript, only the main R packages used are given in the references. Two referees recommended useful, but additional analyses, which, however, expanded this paragraph.

Specific comments:

"The word 'analyses' in title should be 'analysis"'

We have modified the title accordingly.

"It is not clear if relative abundances were used for calculating Bray-Curtis dissimilarities. It is important to give some hints about the relative magnitude of abundances in each rank categories, because it does matter if ranking was applied (1) to reflect differences in magnitudes (1, 10, 100 inds.) or (2) because of inaccuracy of the abundance measure. This should be clarified. Strictly speaking, ordered ordinal scaled variables are not really suitable for calculating Bray-Curtis dissimilarities unless an underlying ratio scale measurement exists."

No abundances were used for calculating the Bray-Curtis dissimilarities. As explained in line 23, page 4961 only presence/absence data were used. However, in concordance with the referee comment of Sinos Giokas, we address this fact in more detail in chapter 2.2 (p 4960, line 24), which reads now as follows: "... 284 samples were obtained during field work. Due to unequal sampling techniques by e.g. qualitative hand picking or comparatively random collecting using a triangular dredge, no comprehensive abundance data are available. Thus we had to rely on strict presence/absence information of gastropod occurrence. . .”

“I might have missed it, but I can’t see area corrected endemic richness appearing in the results.”

In order to condense the manuscript we decided to delete this section of the Material and Method paragraph.

“I can’t always see the clear distinction between elements of the paper dealing with species composition and species richness.“

In the revised manuscript we tried to separate these two elements more strictly and name them precisely in the discussion section. Both are, however, necessary since biodiversity is a multifactorial concept, integrating genetic variation, species richness, species turnover and community variability.

“From a methodological point of view, these approaches require different methodologies. While using NMDS along with Bray-Curtis dissimilarities and PCNM is totally legitimate for multivariate data sets, i.e. for multiple response variables, these are not optimal choices for univariate modeling situations. The choice of permutational multivariate ANOVA for the univariate analysis of species richness is opaque.”

According to the manual of Primer, page 15, a PERMANOVA is suitable for univariate data. We therefore preferto leave the analysis as is.

“Similarly, the use of multivariate spatial filtering technique for uni-variate non-independence case is unjustified. Spatial autocorrelation of the univariate residuals after regressing for environmental covariates can tell if autocorrelation is still significant. If it is the case, some autoregressive model (SAR, CAR) could be employed. If I misunderstood the text, it needs clarification.”

According to the developer of the spatial analysis method using PCNMs, this filtering technique is also adequate for univariate data. (Borcard et al., 2004, pages 1826 1828; Legendre et al., 2009, species richness)

“The use of the null modeling approach to validate the NMDS stress value is not indicative to the goodness of mapping of the original dissimilarities onto the 2-3 dimensional space. This piece can be dropped from the manuscript, because irrelevant. A null distribution of stress values tells nothing about the goodness of the observed statistic, because the observed statistic is a final result of an iterative procedure minimizing an objective function. Thus there is no need for other justification. Parameter free methods do not require parameters.”

We agree and have deleted this part of the manuscript as well as figure 3.

“Spatial autocorrelation in the spatial distribution of species richness is not an indication of biotic interactions. To study biotic interactions, the proper modeling of species identities required as opposed to lumping them together in a richness measure. (Inhibition and mutual stimulation might refer something different than competition and facilitation, but if this is true, the authors must define what do they mean by these terms).”

We agree with the referee′s comment and deleted this section and figure 6.

“The true potential of the data lies in differentiating between environmental (depth layers, horizontal habitat classes) and purely spatial drivers of biodiversity (variation partitioning of partial Mantel tests could have been used to measure the relative significance of these factors). This should be reflected more intensively in the text.”

We followed the suggestion and included variance partitioning of three different classes: (i) Purely spatial explanatory factors (i.e. PCNMs), (ii) collecting depth and slope of the shore, and (iii) abiotic factors like substrate, geology of substrate and chlorophyll-a as proxy of algal biomass (Vogel et al. 2010). We decided to use the distance-based redundancy analysis (Legendre and Anderson, 1999), because it has been shown that partial Mantel tests often perform poorly (e.g. Harmon and Glor, 2010; Legendre, 2000; Oden and Sokal, 1992).

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