



COMMENT

## Does plankton diversity peak at intermediate salinities? Comment on Telesh et al. (2011)

Robert Ptacnik<sup>1,\*</sup>, Kalle Olli<sup>2</sup>, Sirpa Lehtinen<sup>3</sup>, Timo Tamminen<sup>3</sup>, Tom Andersen<sup>4</sup>

<sup>1</sup>Institute of the Marine Environment, University of Oldenburg, Schleusenstrasse 1, 26384 Wilhelmshaven, Germany

<sup>2</sup>Institute of Ecology and Earth Sciences, University of Tartu, Lai 40, 51005 Tartu, Estonia

<sup>3</sup>Marine Research Centre, Finnish Environment Institute, PO Box 140, 00251 Helsinki, Finland

<sup>4</sup>Department of Biology, University of Oslo, PO Box 1066, Blindern, 0316 Oslo, Norway

**ABSTRACT:** Based on an analysis of published data, Telesh et al. (2011; Mar Ecol Prog Ser 421:1–11) claim that plankton diversity peaks at intermediate salinities in the Baltic Sea. They thereby challenge Remane's curve, which was originally derived from observations of macrozoobenthos (Remane 1934; Zool Anz 7(Suppl):34–74), and conclude that high speciation rates allowed for development of high diversity in microscopic species in the Baltic, as opposed to larger organisms. However, instead of performing appropriate statistical analyses, Telesh et al. merely pool species lists within salinity bands, thereby obtaining patterns that reflect sampling effort rather than species richness. Moreover, Telesh et al. derive patterns of richness to a considerable extent from coastal sites, including bays and lagoons, which are not representative of the corresponding salinities in the open Baltic Sea. We propose that spatially representative data are required for elucidating patterns of plankton richness along the freshwater–marine continuum. Moreover, the analysis should address both species richness and community composition by appropriate statistical tools.

**KEY WORDS:** Plankton diversity · Salinity · Baltic Sea · Remane's curve

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Understanding patterns of diversity in space is a pivotal issue in ecology, since species loss and the relationship between biodiversity and ecosystem functioning have become central aspects of conservation biology and ecology (e.g. Hooper et al. 2005). Using a number of published datasets on phyto- and zooplankton in the Baltic Sea, Telesh et al. (2011) try to approximate patterns of total taxon richness along the salinity gradient by binning taxa within arbitrary salinity bands. Their analysis results in a hump-shaped diversity pattern for protist plankton along the freshwater–marine continuum, implying maximum diversity at intermediate salinities.

Telesh et al. (2011) thereby challenge the concept of an 'Artenminimum' (minimum diversity at intermediate salinities) first described for macrozoobenthos in the Baltic Sea by Remane (1934; 'Remane's curve'). The analysis by Telesh et al. (2011), however, is biased

because the authors (1) pool species lists within salinity bands, thereby creating patterns which may be due to methodology, and (2) derive patterns of richness to a large extent from coastal sites which are not representative of the open Baltic Sea. Moreover, in several cases Telesh et al. (2011) do not present actual data, but only smooth lines without confidence intervals, leaving the reader without any information as to how representative these lines might be (their Figs. 2 & 3).

Richness patterns of protist plankton along the salinity continuum in Telesh et al. (their Fig. 2) are mostly derived from monitoring data collected at the German Bodden coast (Sagert et al. 2008). These low-salinity sites are actually 'semi-enclosed inner coastal waters' (Sagert et al. 2008, their Fig. 1), while the remaining sites are situated close to the coast. Semi-enclosed bays of the Bodden coast are not representative of areas having the same salinities in the open Baltic Sea (e.g.

\*Email: ptacnik@icbm.de

in the Gulf of Bothnia), neither in terms of hydrography nor in terms of system size and depth. The same applies to other datasets used to produce Fig. 2 (Telesh et al. 2008 and Olenina & Olenin 2002, including data from the Neva Estuary and the Curonian Lagoon).

Furthermore, richness of protist plankton was estimated by pooling all taxa within arbitrary salinity bands (Telesh et al. 2011, their Figs. 2B,C & 4). This leads to an obvious correlation between sampling effort and species richness, especially evident in Fig. 2C (compare lines and bars). The peak seen in diversity thus seems to stem largely from the peak in sampling effort at intermediate salinities. Conversely, it should be obvious that no estimates can be given for salinities outside the range of observation. However, Telesh et al. (2011) extrapolate beyond the salinity range covered by Sagert et al. (2008), and indeed predict zero diversity at salinities >28 (Fig. 2C).

While it may be true that the frequency of salinities in Sagert et al. (2008) has some similarity with the percentage of area with corresponding salinity in the open Baltic (Telesh et al. 2011), pooling a given number of samples does not give reliable estimates for the total species richness (Gotelli & Colwell 2001). The number of species found increases with number of samples pooled and depends both on the richness of each sample as well as on the turnover (i.e. dissimilarity) among samples. Rarefaction curves (or species accumulation curves) should therefore be applied when comparing diversity among different regions (Gotelli & Colwell 2001).

Telesh et al. (2011) draw further support for high protist plankton diversity at intermediate salinities from published species lists, especially the HELCOM Checklist of Baltic Sea Phytoplankton Species (Hällfors 2004, continued in Olenina et al. 2006), which seems to be the dataset underlying Fig. 4A (though this is not specified in their text). The same problems as outlined above, i.e. an inherent correlation between (unknown) sampling effort and the number of species detected, applies to Hällfors' (2004) checklist. While such checklists provide invaluable assistance for proper species identification in practical microscopy, they are mis-treated if taken as quantitative spatial data. Moreover, Telesh et al. (2011) apparently summed up all taxonomic units found in Hällfors (2004), no matter whether genus or species level was given, thereby inflating the number of 'species'; for example, in the case of cryptophytes, Hällfors (2004) mentions 23 species plus 6 genus-level identifications (e.g. *Teleaulax* sp.), and Telesh et al. (2011) mention 29 species (their Table 1).

Essentially, Telesh et al (2011) suggest that plankton diversity along the Baltic salinity gradient correlates with the size of the area having a given salinity; correspondingly, there is maximum diversity at intermediate salinity, which is the salinity of its largest basin, the

Baltic Proper. This would confirm the existence of a positive species–area relationship: the total number of phytoplankton species increases with the surface area of the system (Smith et al. 2005). Furthermore, such a pattern fits well with the null hypothesis that salinity itself has no effect on plankton diversity.

A proper analysis of plankton diversity across the Baltic Sea has to be based on a spatially representative dataset. This should encompass 2 steps: (1) Analysis of changes in community composition along the salinity gradient (e.g. Olli et al. 2011)—this may lead to the identification of 'biogeographic provinces' with regard to plankton diversity; (2) rarefaction analysis of the regions thus identified (Gotelli & Colwell 2001), and calculation of the cumulative species richness in a given area or basin, based on species–area curves.

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