

Reproducibility of species recognition in modern planktonic foraminifera

Nadia Al-Sabouni^{1,2,3} & Michal Kucera¹

¹Tübingen University, Tübingen, Germany

²Royal Holloway University, London, U.K.

³Natural History Museum, London, U.K. - *n.alsabouni@gmail.com*

Planktonic foraminifera are extensively used in paleoceanographic and biostratigraphic studies. Many of these applications require a high degree of taxonomic certainty and recognition. Any discrepancy between researchers has the potential to affect temperature or diversity reconstructions. Despite this potential source of uncertainty, the reproducibility of species recognition has never been tested. In order to ascertain the degree of species recognition reproducibility, a modern subtropical sample was selected for its high species richness and sieved through the >125 μm and >150 μm size fractions respectively. These fractions were then split using a microsplitter into aliquots of approximately 300 individuals, and a representative 300 individuals were then selected and fixed. Participants of varying expertise from different institutions were asked to identify each individual and note down their classification. This procedure allowed for a direct comparison of each participant's identification for each of the individuals. It was then possible to determine the absolute levels of consistency between participants and the overall effects of inconsistency on diversity and temperature estimates. The absolute levels of consistency between all participants were surprisingly low: 50% in the >150 μm size fraction and 35% in the >125 μm size fraction. When all of the participants identifications were compared individually with one another, the maximum pairwise conformity was found to be 80% in the >150 μm size fraction and 65% in the >125 μm size fraction. The minimum pairwise concurrence was found to be 65% in the >150 μm and 55% in the >125 μm size fraction. This implies that there are a substantial number of specimens among modern planktonic foraminifera which are difficult to identify unambiguously. However, it was astonishingly found that the overall effect of this inconsistency was negligible in the >150 μm size fraction on SST estimates using the Transfer function technique as well as on diversity estimates. Conversely, in the >125 μm size fraction the effect on diversity estimates was found to be significant. The causes and effects of these findings will be outlined later. The fact that the consistency of species identification between two researchers can