**DATA AND METHODS**

**a. TAXA**

The taxa chosen for our analysis represent a significant component of the diversity of bivalve and gastropod taxa in the Neogene of the Western Atlantic. Taxonomic and geographic information on these species, as well as images and distributional maps, are available in the Neogene section of the *Digital Atlas of Ancient Life* [1]. Species were included in our dataset if they can be readily and consistently identified in the fossil record, if accurate measurements of body size could be obtained, if specimens within the species could be accurately assigned geospatial coordinates at a resolution at least equivalent to the resolution of our palaeoclimatic data (see below), and if their stratigraphic position corresponded to the study interval. Ultimately, 299 species form our dataset (Supplementary Table 1), comprising 156 species of bivalves (73 extant, 83 extinct) from 19 families and 143 species of gastropods (48 extant, 95 extinct) from 26 families. Among these 299 species, 86 are species that have been previously identified as broadly distributed and consistently abundant (see [2] and references therein) such that they might represent generalists (listed as distribution: broad in Supplementary Table 1). Given it has been previously demonstrated that geographic range size is a determinant of species survival [33], we also assessed whether these putative generalists show a different relationship between metabolic rate and extinction likelihood, as compared to the remaining more narrowly distributed species.

 **(b) BODY SIZE**

A total of 493 measurements of body size were obtained using all available pertinent images of specimens housed in the general collections at both the Florida Museum of Natural History (FLMNH), the most significant repository of material from this time interval and region [3], and the Yale University Peabody Museum of Natural History (YPM). We use the assumption that exemplar specimens from bulk samples adequately characterize body size (and ultimately BMR) of taxa [4], a method employed in all previous studies of metabolic rates in the fossil record [5-7] and appropriate given known levels of inter and intra-specific variation in molluscs [8]. Body sizes for each specimen were calculated by taking maximum linear dimension measurements using *ImageJ* [9]. Previous studies have shown that maximum linear dimension is directly correlated with important components of body size such as shell volume [10] and soft tissue mass [11]. For bivalves, maximum length was converted to biomass using the scaling coefficient and exponent presented by Payne et al. [7]. For gastropods, ordinary least-squares regression was applied to the length-biomass data provided in Eklöf et al. [12] to develop a suitable scaling coefficient and exponent for conversion of gastropod shell length to ash-free dry mass ($6.95×10^{-5}×L^{1.905}$; Supplementary Table 2). Body size measurements and biomass values for all specimens are provided in Supplementary Table 3.

**(c) PALAEOCLIMATE**

Temperature (T) data for BMR calculations (described more fully below) were derived from the coupled atmosphere–ocean HadCM3 general circulation model (GCM) [13], using the alternative PRISM3D PlioMIP dataset [14] for the Mid-Pliocene Warm Period (mPWP) and the boundary conditions for the Last Glacial Maximum (LGM) from Singarayer et al. [15]. Four time slices were used corresponding to all available GCMs: mPWP (~ 3.264–3.025 Ma); Last Interglacial (LIG, ~ 130–123 ka); LGM (∼21 Ka) and the pre-industrial interval (PI, ~1850 to 1890). These time slices correspond to when distinctive climate conditions were attained during the study interval. GCM experiments were run to equilibrium and then for a further 500 model years and environmental parameters were averaged from the final 30 years of each experiment at 1.25º x 1.25º resolution [2, 3]. Modelled temperature outputs were converted to maximum, minimum and average yearly coverages using ArcGIS 10.1. Finally, the geographic position of each measured specimen was then mapped onto a temperature map for the appropriate time slice using *raster* for R [16] to determine the ambient temperature for that individual when it was alive. For specimens from the mPWP, to account for shifts in geographic position associated with continental drift that has occurred since the Pliocene, palaeo-coordinates were used to calculate relevant temperature values. Palaeo-latitude and longitude were reconstructed based on a UTIG plate model from PaleoWeb for ArcMap 10.1. For all other specimens, modern geographic coordinates were applied. The temperature values assigned to each specimen are provided in Supplementary Table 3.

**(d) ESTIMATING METABOLIC RATES FOR SPECIES**

Following Gillooly et al. [17], BMR of an individual was calculated as:

Bind = b0 e -E/kT M3/4 (1)

where Bind is the BMR of the individual, b0 is a clade specific scaling constant, E is the typical activation energy of rate-limiting metabolic reactions (approximately 0.65 eV), k is Boltzmann’s constant, T is the absolute temperature (ºK) at which metabolic activity occurs (equivalent to ambient water temperature for marine ectotherms) and M is the biomass of the individual (ash-free dry mass in this study). We follow Kleiber’s Law [18] and use three quarter power scaling for our calculations, as opposed to the sometimes used 2/3 scaling. The debate about which exponent is more appropriate to use is one that extends well beyond the scope of this study (e.g. [19]). However, since we are primarily focusing on the relative difference amongst species within the same clade, a change in the exponent used would not affect our results. For b0 values, we follow both Brey [20] and Payne et al. [7] and use 1.4 x 1011 W kg-3/4 for heterodont bivalves and 1.3 x 1011 W kg-3/4 for all other bivalves. For gastropod b0 values, we follow the method of Finnegan et al. [6] and use the average b0 for multicellular ectotherms (9.91 x 107 W g3/4) multiplied by the ordinal-level coefficients of Vladimirova [21]. For the twelve species that could not be assigned to the familial and ordinal taxonomic categories used in Vladimirova [21], specimens were given the average coefficient for all gastropods (0.71). Combining our biomass and temperature results with b0 values we then calculated a Bind value for all specimens in our dataset. A species level BMR value (Bspecies; Supplementary Table 1) was then determined by calculating the mean of all Bind values for the relevant individual specimens of a species.

**(e) ESTIMATING METABOLIC RATES FOR ASSEMBLAGES USING FOSSIL ABUNDANCE DATA**

To assess changes through time in mean BMR in a macroecological context, fossil occurrence data for early Pliocene to late Pleistocene bivalve and gastropod taxa from our study area were obtained from *iDigBio*. These specimen records primarily come from the FLMNH, with additional records from the Academy of Natural Sciences of Drexel University (ANSP), the Delaware Museum of Natural History (DMNH), the Paleontological Research Institution (PRI), the Virginia Museum of Natural History (VMNH), and the YPM. Only specimens that could be definitely assigned to a specific stratigraphic formation were included. A total of 43,499 individual occurrences from 29 formations of early Pliocene to late Pleistocene age form our fossil abundance dataset (Supplementary Table 4).

To determine the minimum number of individuals of each species present in each formation, we follow the method of Finnegan and Droser [5]. In particular, in the case of gastropods each shell represents an individual. For bivalves, in life each individual is represented by two shells, but the number of individual left or right values represented in paleontological collections cannot always be ascertained, so we assume each shell represents a single individual. This potentially overestimates the number of bivalves, but as we follow the same method for all formations, it should not affect comparisons between formations. The number of individuals for each species in each formation was then used to calculate values of relative abundance for each species.

Combining these relative abundances with the previously calculated Bspecies values for each species we then calculate a mean BMR for each formation (Bassemblage) based upon the following:

$B\_{assemblage}= \frac{\sum\_{ i=1}^{ n}(B\_{i}A\_{i})}{N}$ (2)

where Bassemblage equals the mean per capita BMR of an assemblage of N individuals composed of n species, Bi is the BMR value for the ith species in the assemblage and Ai is the abundance of that ith species (provided in Supplementary Table 4). Whilst calculating a metabolic rate for each species for each time interval would be a preferred method to determine Bi values, the necessary data to do so are not currently available in sufficient quantity, and we instead rely on our exemplar BMR values (Bspecies). Bassemblage values were then grouped into five separate time bins (early Pliocene, late Pliocene, early Pleistocene, middle Pleistocene, late Pleistocene) to determine if any significant changes in assemblage level BMR occurred across the studied time interval.

To understand how changes in diversity across the five time bins may influence or explain the assemblage level results, diversity accumulation curves were generated with associated rarefaction/extrapolation, calculated based upon Hill Numbers [22] using the iNEXT package [23]. Herein we utilise the first three Hill Numbers: species richness (q = 0); the exponential of Shannon’s Entropy Index (q = 1); and the inverse of Simpson’s Concentration Index (q = 2).

**(f) STATISTICAL ANALYSES AND SENSITIVITY TESTS**

All analyses were performed using R [24]. Bspecies data were not normally distributed (identified using a Shapiro-Wilk test and Q-Q plot) so the non-parametric Mann-Whitney U test was used to assess differences in BMR between extinct and extant taxa. Effect sizes were calculated as Cliff’s Delta [25] using the ‘effsize’ package. Bassemblage data were also not normally distributed so for the comparison of Bassemblage across the five time bins a Kruskal-Wallis test was employed.

To assess if our results are dependent upon assumptions such as the accuracy of climate models, the use of valid metabolic scaling constants (b0), or the extent to which the fossil assemblages considered in our study reasonably reflect the living assemblages that existed at the time they were deposited, a variety of sensitivity analyses were conducted. First, we repeated our analysis using the maximum and minimum yearly surface water temperatures from our climate models. We also treated all taxa as experiencing the same ambient temperature by removing T from our calculation of Bind entirely. Similarly, we assumed that b0 was constant by repeating our analyses with it removed from our calculations. Moreover, to investigate potential sampling biases associated with using the fossil record, we repeated our analyses excluding the smallest and largest taxa in our dataset. In particular, taxa below 10mm can be poorly sampled in fossil datasets [26, 27] and mean values can be skewed by large outliers, so we omitted all specimens whose body size fell below the 10mm threshold and taxa in the top 10% of body size, following Payne et al. [7].

As the number of extinct versus extant species is unequal for both bivalves and gastropods, albeit within the same order of magnitude for both, we generated a series of datasets (10,000 replicates) where extinct and extant taxa are present in equal proportion by randomly assigning all species a status category. Primary analyses were then repeated on these datasets.

With no phylogeny currently available for either of our bivalve or gastropod datasets, we cannot directly assess how phylogenetic signals may impinge on our analyses. However, to indirectly address this issue to some degree, we repeated our analyses assuming metabolic scaling constants are equal for all taxa. We also performed pairwise comparisons of mean Bspecies for all families using Dunn’s test [28] to assess whether there are family-level differences in BMR. Adjusted P-values for pairwise comparisons were generated using the Bonferroni correction [29].

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