Datasets, methods, and supplementary figures

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Title: Onshore-offshore gradient in metacommunity turnover emerges only over macroevolutionary time scales

Datasets and sequence-stratigraphic framework

The Eocene is represented by the Ypresian siliciclastic deposits of the Pyrenean Foreland (93 samples in total, Dominici and Kowalke 2007) and the Aquitaine Basin (4 samples at Gan, Merle 1985), and by the Lutetian deposits of the Paris Basin (9 samples near Grignon, based on new field data of S.D. and M.Z., see also Huyghe et al. 2012). The Plio-Pleistocene is represented by the Piacenzian siliciclastic deposits of the Lower Arno Basins (35 samples, accessed from four references, including Landini et al. 1990; Benvenuti and Dominici 1992; Dominici 1994; Danise et al. 2010; and new field data of S.D., see also Benvenuti et al. 2007), and the Piedmont-Padan Basins, Apennines (9 samples, supplemented by 4 Gelasian samples, accessed from Benigni and Corselli 1982; Monegatti et al. 1997). The number in samples used in size-standardised analyses of turnover between sequences (n > 50 specimens), within stages, and between stages (n > 100 specimens) is shown in parentheses in Table 1. Four outer shelf samples in the Eocene did not allow the comparison between sequences but allowed to perform within-stage analysis of turnover in outer shelf. Two samples from Eocene were not assigned to sequences, and were thus omitted from analyses of between-sequence dissimilarity. Source data are available at dx.doi.org/10.5061/dryad.943j7

The fossil assemblages are represented by bulk samples collected at bed resolution and sieved with 1-mm mesh size. Both time intervals capture habitats ranging from onshore (intertidal with mangroves, estuaries, tidal flats, and lagoons, and shoreface with seagrass habitats) to offshore habitats (inner and outer shelf).

The Eocene is represented by the total of 47,410 individuals (17,464 bivalves and 29,790 gastropods), 625 species (186 bivalve and 430 gastropod species), 335 genera (109 bivalve and 218 gastropod genera), and 149 families (44 bivalve and 83 gastropod families). The Plio-Pleistocene is represented by the total of 109,771 individuals (80,429 bivalves and 28,697 gastropods), 445 species (166 bivalve and 262 gastropod species), 240 genera (97 bivalve and 136 gastropod genera), and 108 families (41 bivalve and 60 gastropod families).

The sequence-stratigraphic framework is available for the Eocene Pyrenean foreland (Dominici and Kowalke 2007) and the Plio-Pleistocene Valdelsa Basin (Dominici et al. 2008; Benvenuti et al. 2014). The Lower Eocene assemblages from the Pyrenean foreland correspond to two allogroups (Figol and Castigaleu groups) that consist of composite (50-200 m-thick) depositional sequences and stacked, 5-20 m-thick elementary depositional sequences (Dominici and Kowalke 2007). The Figol Group is here represented by three composite sequences (labeled FA, FB, FC). The Castigaleu Group is formed by 11 composite sequences that were pooled into four pairs (here labeled CHCI, CAB, CCD, CFCG. The Lutetian succession in the Paris Basin is subdivided into two sequences separated by a major sequence boundary. The lower sequence corresponds to parasequences A6-A7, the upper sequence to parasequences A8-A10 of Huyghe et al. (2012). The outer shelf deposits of the Aquitaine Basin are represented by four assemblages only and do not allow measuring between-sequence dissimilarity.

The Plio-Pleistocene assemblages from the Valdelsa Basin (Apennines) correspond to four composite depositional sequences, including the Certaldo sequence (S3, lowermost Piacenzian, with base at ~ 3.5 Mya), the Pietrafitta sequence (S4, Lower Piacenzian, starting at ~ 3.0 Mya), the Ponte a Elsa sequence (S5, Upper Piacenzian), and the San Miniato sequence (S6, Gelasian, terminating at ~2.5 Mya) of Benvenuti et al. (2014).

Data will be available at the Dryad database.

Protocol for environmental discrimination of fossil assemblages

Our assignment of assemblages to the four environments rely on sedimentological attributes and on the style and architecture of the vertical stacking-pattern of the studied successions, i.e., on the relative position of each lithofacies in elementary depositional sequences and their relationship with key stratal surfaces such as sequence boundaries, transgressive surfaces, and maximum flooding surfaces. The protocol is analogous to the protocol of Sepkoski (1988).

Peritidal (Foreshore). This environment is represented by light- to dark-grey, stratified muddy sandstones, siltstones, or mudstones. Primary sedimentary structures are usually obliterated by bioturbation, with some lenticular bedding preserved in places. Plant debris is often abundant, either interspersed or in thin, laterally continuous beds. Shells are frequently concentrated in laterally continuous beds, and the biofabric ranges from loosely to tighly packed shells; some monospecific paleopopulations of bivalves in life position, empty or with muddy geopetal filling. Organic-rich, muddy sediments from estuaries close to mangroves are assigned to the peritidal environment (as in Sepkoski 1988). Interpretation: tidal flat or brackish-water lagoon or estuary.

Nearshore. This environment (above fair-weather wave base) is represented by light-brown, light-orange or yellow, rarely light-grey, usually fine- and medium-grained sandstones with high-energy sedimentary structures (ripple lamination, erosional layers), with intercalated fine gravel layers, mud clasts, and higher proportion of abraded or mechanically-fragmented bioclasts (e.g., corallinaceous debris). Trace fossils are locally present (*Ophiomorpha nodosa*, *Thalassinoides*). Shells are concentrated in laterally continuous beds, with some deep-burrowing bivalves that can be preserved in life position (e.g., Eocene: *Gari*; Plio-Pleistocene: *Panopea*, *Pelecyora, Callista*) completely filled with sandy matrix; biofabric from loosely to densely packed, rarely dispersed. Occasional presence of shell pavements and shell lenses with disarticulated, concave-down bivalves, sometimes interspersed with mud clasts. Interpretation: upper shoreface in wave-dominated settings or shelfal sand lobes in settings dominated by gravitational processes.

Inner shelf. This environment is represented by light-grey to grey muddy (clayey or silty) fine-grained sandstones. Bedding ranges from massive to stratified in beds from a few cm to a few dm thick. Primary structures are usually obliterated by bioturbation, but hummocky-cross stratification may be preserved in places. Shell beds are laterally continuous, and bioclastic fabric ranges from dispersed to loosely packed. Interpretation: lower-shoreface or offshore-transition zone, close to storm-weather wave base in wave-dominated settings, prodelta in settings influenced by fluvial dynamics.

Outer shelf. This environment (below storm wave base) is represented by grey, massively-bedded sandy mudstones, siltstones, and mudstones. Some laterally continuous, loosely or densely packed, sometimes glauconitic shell beds may be present, otherwise shells are frequently dispersed in muddy matrix, with bivalves in life position (e.g., Eocene: *Pholadomya*; Plio-Pleistocene: *Venus*, *Anadara*, *Glossus*).

Methods

Temporal turnover

We measure temporal turnover with dissimilarity indices. These indices depend on sample size of individual samples and on the number of samples per habitat group. Therefore, when comparing turnover *among* depths, we double-standardize assemblages with rarefaction (resampling without replacement) to 50 individuals (between-sequence turnover) and to 100 individuals (within-stage and between-epoch turnover), and to four assemblages per depth ($n = $ 400 individuals), and compute Bray-Curtis dissimilarity and correlation values 1,000 times, generating distributions for mean values and 95% confidence intervals. When comparing local-scale with habitat-scale turnover *within* depths, sample sizes are kept equal at $n = 100$ individuals. We also evaluate turnover in taxon identity with Sorenson dissimilarity to check whether the long-term decline in turnover is also captured by presence-absence data only, and is thus not driven solely by changing abundance patterns. Sorenson dissimilarity is decomposed to (i) a nestedness dissimilarity component and (ii) Simpson dissimilarity. These two indices quantify whether the turnover is related to (1) taxon loss or gain (i.e., changes in richness) and/or to (2) taxon-by-taxon replacement in the absence of richness changes (Baselga 2012). Spearman

rank correlation testing for similarity of species, genus, and family rank abundances between sequences is restricted to assemblages with at least 5 taxa.

Decomposition of turnover at genus and family levels

To disentangle the contributions of turnover in per-genus (or per-family) species abundance and per-genus (or per-family) species richness to total turnover in abundance, we compute turnover where Bray-Curtis dissimilarity for each depth is based (1) on per-genus and per-family median species (proportional) abundance and (2) per-genus and per-per-family species richness. Although these two components are not independent – an increase in per-genus species richness can decrease per-genus median species abundance if the total number of individuals in a genus remains the same – it is possible that one component contributes to turnover in genus abundance much more strongly.

Bathymetric breadth

We measure a bathymetric breadth by measuring the distribution of individuals of a given species within the four depth habitats (i.e., peritidal, nearshore, inner shelf, and outer shelf) with Levins′ and Hurlbert′s measures of niche breadth (Levins 1968; Hurlbert 1978). Levins′ measure for a species *i* is computed as $N_i^2/sum(N_{i1}^2 + N_{i2}^2 + N_{i3}^2 + N_{i4}^2)$, where N_{i1} corresponds to the number of individuals found in habitat 1, and N_i is the total number of individuals, and then rescaled between 0 to 1 (Hurlbert 1978). It attains the maximum when a species has the same abundance in each habitat, and the minimum when all individuals occur solely in one habitat. Hurlbert′s index weights the Levin's index by the availability of individual depths.

Species richness

Species richness and rank-abundance distributions are rarefied to the same sample-size levels. Equivalent results were obtained with shareholder quorum subsampling (Alroy 2010), where the quorum in shareholder subsampling corresponds to a fixed coverage of the empirical rank-abundance distribution, i.e., the sum of the proportions of the species that were sampled. It was set to 0.75 at both scales.

Results

Temporal turnover

Proportional abundances are significantly rank correlated between all sequences at species, genus, and family levels within the Eocene and within the Plio-Pleistocene at regional scales (Table S1). Bray-Curtis dissimilarity does not significantly increase and Spearman rank correlation does not significantly decrease with increasing separation between sequences at regional scales (Mantel test, Table S2). The within-stage turnover in species, genus, and family abundance and identity between sequences does not consistently significantly differ among depths within the Eocene and Plio-Pleistocene (Fig. 1, Fig. S2). The between-epoch turnover in abundance and identity between the Eocene and Plio-Pleistocene is higher in onshore (peritidal and nearshore) than in offshore (inner and outer shelf) habitats (Fig. 1, Fig. S2). To evaluate the congruence between gastropods and bivalves, we analyze them also separately. Gastropods show a stronger family-level turnover than bivalves in all habitats, with many numerically common families being restricted to either the Eocene or Plio-Pleistocene environments. Nonetheless, the family-level composition in deeper habitats is conserved in both bivalve and gastropod families.

The onshore-offshore decline in abundance turnover of families is manifested by both bivalves and gastropods, although gastropod turnover in the outer shelf is relatively large.

Decomposition of turnover in genus and family abundance

Median species abundances in individual genera and families are less variable in deep environments (i.e., they conserve their ecological traits that allow them to achieve comparable abundances), even when the identity of species belonging to the same genera and families in the Eocene and Plio-Pleistocene differs. Genus and family abundance is also less variable in deep environments because per-family species richness varies less through time in deep than in shallow environments. The higher variation in species richness within genera and families in shallow environments thus reveals that the higher long-term turnover in family abundance is also related to changes in species richness in those lineages that declined or increased in abundance.

Families not persisting from the Eocene to Plio-Pleistocene

Ampullinidae and Batillariidae that were dominant in peritidal and nearshore environments during the Eocene are absent in the Plio-Pleistocene of the NE Atlantic and Mediterranean. Ampullinidae are presently represented by a single species occurring in the Philippines (Caze et al. 2011), and Batillariidae disappeared from the NE Atlantic Province at the end of the Miocene (Ozawa et al. 2009).

Changes in abundance of persisting families

Changes in proportional abundances of families that persist from the Eocene to Plio-Pleistocene are summarized in Fig. S3-S4. In peritidal and nearshore environments, Potamididae

were strongly reduced in abundance, whereas Rissoidae, Pyramidellidae, Arcidae, Semelidae, Tellinidae, Cardiidae, and Veneridae increased in abundance. Cerithiidae, Naticidae, Ostreidae, Corbulidae, and Carditidae remain similarly common in the Eocene and Plio-Pleistocene peritidal and nearshore habitats. Species of the family Rissoidae underwent radiation during the Miocene and are presently most diverse in the warm-temperate Mediterranean and Eastern Atlantic (Kowalke and Harzhauser 2004; Azila et al. 2012). Therefore, the high turnover in peritidal and nearshore is not only related to regional-scale family extinctions but also to onshore expansion and species-level radiations of families that were frequent offshore in the Eocene.

In the inner and outer shelf, some Eocene families with tropical affinities declined in abundance, including Turridae, Conidae, Costellariidae, and Cylichnidae, and some families went regionally extinct, including Marginellidae, which presently extend to the southernmost parts of the Mediterranean and to the Ibero-Moroccan Gulf (Silva et al. 2011), and Olividae with tropical affinities (Davoli 1989). Many families, however, achieved similar proportional abundance in the Eocene and Plio-Pleistocene in the inner and outer shelf and maintained stable species richness, including Cerithiidae, Naticidae, Ringiculidae, Rissoidae, Turritellidae, Pyramidellidae, Carditidae, Cardiidae, Arcidae, Corbulidae, Glycymeridae, Lucinidae, Noetiidae, Ostreidae, Veneridae, and Dentaliidae.

Bathymetric breadth

Even though the turnover does not change with depth, Levin's and Hurlbert's bathymetric breadth at species level increase towards onshore habitats in the Eocene. Both measures of species bathymetric breadth change mildly along an onshore-offshore gradient in the Plio-Pleistocene (Fig. S5). The mean species bathymetric breadth (Hurlbert's index) in the Eocene

(mean=0.12, 95% confidence intervals = 0.11-0.13) is significantly smaller than in the Plio-Pleistocene (mean=0.23, 95% confidence intervals = 0.21-0.24).

Species richness

Species richness increases towards the inner shelf in the Eocene and Plio-Pleistocene The long-term between-epoch turnover is smallest in inner shelf environments, which have the highest species richness, and highest in peritidal environments, which have the lowest species richness both in the Eocene and Plio-Pleistocene (Fig. S6). Long-term family turnover between the Eocene and Plio-Pleistocene is negatively related to the mean species richness (averaged across the Eocene and Plio-Pleistocene).

References

Alroy 2010. Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification. *Palaeontology* 53, 1211-1235

Avila S.P., Goud J., and de Frias Martins A.M. 2012. Patterns of diversity of the Rissoidae (Mollusca: Gastropoda) in the Atlantic and the Mediterranean region. *Scientific World Journal*, Article ID 164890

Benigni C. and Corselli C. 1982. Paleocomunità a molluschi bentonici del Pliocene di Volpedo (AL) [Benthic mollusc paleocommunities from the Volpedo Pliocene (AL)]. *Rivista Italiana di Paleontologia e Stratigrafia* 87, 637-702. Italian.

Benvenuti M. and Dominici S. 1992. Facies analysis, paleoecology and sequence stratigraphy in a Pliocene siliciclastic succession, San Miniato (Pisa, Italy). *Bollettino della Società Paleontologica Italiana* 31, 241-259.

Benvenuti M., Bertini A., Conti C. and Dominici S. 2007. Integrated analyses of litho- and biofacies in a Pliocene cyclothemic, alluvial to shallow marine succession (Tuscany, Italy). *Geobios* 40, 143-158.

Benvenuti M., Del Conte S., Scarselli N. and Dominici S. 2014. Hinterland basin development and infilling through tectonic and eustatic processes: latest Messinian-Gelasian Valdelsa Basin, Northern Apennines, Italy. *Basin Research* 26, 387-402.

Caze, B., Merle, D., Le Meur, M., Pacaud, J.-M., Ledon, D., and Saint Martin, J.-P. 2011. Taxonomic implications of the residual colour patterns of ampullinid gastropods and their contribution to the discrimination from naticids. *Acta Palaeontologica Polonica* 56, 329-347.

Danise S., Dominici S. and Betocchi U. 2010. Mollusk species at a Pliocene shelf whale fall (Orciano Pisano, Tuscany). *Palaios* 25, 449-456.

Davoli F. 1989. Olividae (Gastropoda) miocenici: Ultima testimonianza nell'area mediterranea di un clima intertropicale. *Bollettino della Società Paleontologica Italiana* 28, 101-132. [Italian.]

Dominici S. 1994. Regressive–transgressive cycles from the Pliocene of the San Miniato area (Tuscany, Italy): paleoecology and sequence stratigraphy *Bollettino della Società Paleontologica Italiana* Supplemento 2, 117-126.

Dominici S, Conti C, Benvenuti M 2008. Foraminifer communities and environmental change in marginal marine sequences (Pliocene, Tuscany, Italy). *Lethaia* 41, 447-460.

Foote M. 2012. Evolutionary dynamics of taxonomic structure. *Biology Letters* 8, 135-138.

Huyghe D., Merle, D., Lartaud F., Cheype F., and Emmanuel L. 2012. Middle Lutetian climate in the Paris Basin: implications for a marine hotspot of paleobiodiversity. *Facies* 58, 587-604.

Kowalke T. and M. Harzhauser. 2004. Early ontogeny and palaeoecology of the Mid-Miocene rissoid gastropods of the Central Paratethys. *Acta Palaeontologica Polonica* 49, 111-134.

Landini W., Menesini E. and Ragaini L. 1990. Paleocomunità a molluschi ed otoliti nel Pliocene di Castelfiorentino (Firenze, Italia) [Mollusc and otholit paleocommunities from the Pliocene of Castelfiorentino (Florence, Italy)]. *Atti della Società Toscana di Scienze Naturali* 97. [Italian.]

Merle D. 1985. Les communautés fossiles en tant qu'indicateurs paléobiologiques de milieux: exemples pris sur le Cuisien de Gan (Pyrénées-Atlantiques) et l'Égérien de Hongrie [Fossil communities as paleobiological environmental proxies: examples from the Cuisian of Gan (Atlantic Pyrenees) and the Egerian of Hungary]. *Bulletin du Muséum national d'Histoire naturelle de Paris* 7, 257-262. [French.]

Monegatti P., Raffi S., and Raineri G. 1997. The Monte Falcone–Rio Riorzo composite section: biostratigraphic and ecobiostratigraphic remarks. *Bollettino Società Paleontologica Italiana* 36, 245-260.

Monegatti P. and Raffi S. 2001. Taxonomic diversity and stratigraphic distribution of Mediterranean Pliocene bivalves. *Palaeogeography Palaeoclimatology Palaeoecology* 165: 175-193.

Ozawa T., Kohler F., Reid D. G. and Glaubrecht M. 2009. Tethyan relicts on continental coastlines of the northwestern Pacific Ocean and Australasia: molecular phylogeny and fossil record of batillariid gastropods (Caenogastropoda, Cerithioidea). *Zoologica Scripta* 38, 503-525

Sepkoski, J. J. 1988. Alpha, beta, or gamma: where does all the diversity go? *Paleobiology* 14, 221-234.

Silva C. M. Da, Landau B., and La Perna R. 2011. Biogeography of Iberian Atlantic Neogene marginelliform gastropods (Marginellidae, Cystiscidae): global change and transatlantic colonization. *Journal of Paleontology* 85, 1052-1066.

Table S1 - Between-sequence Spearman rank correlations in abundances of species, genera, and families are moderately high and consistently significantly positive within onshore and offshore habitats at regional scales.

Eocene between-sequence comparisons	Species-Mean rho	Combined p-value	Genera-Mean rho	Combined p-value	Families-Mean rho	Combined p-value
Peritidal Figol A vs. Peritidal Figol B	0.425	<0.001	0.479	<0.001	0.601	<0.001
Peritidal Figol A vs. Peritidal Figol C	0.363	<0.001	0.4	<0.001	0.634	<0.001
Peritidal Figol A vs. Peritidal Castigaleu FG	0.372	<0.001	0.405	<0.001	0.658	<0.001
Peritidal Figol A vs. Peritidal Castigaleu HI	0.43	<0.001	0.52	<0.001	0.773	<0.001
Peritidal Figol A vs. Nearshore Castigaleu AB	0.18	0.01	0.193	0.036	0.368	0.006
Peritidal Figol A vs. Nearshore Castigaleu CD	0.252	0.003	0.324	0.004	0.495	<0.001
Peritidal Figol A vs. Nearshore Castigaleu FG	0.273	<0.001	0.286	<0.001	0.457	0.001
Peritidal Figol B vs. Peritidal Figol C	0.479	<0.001	0.509	<0.001	0.606	<0.001
Peritidal Figol B vs. Peritidal Castigaleu FG	0.426	<0.001	0.459	<0.001	0.553	<0.001
Peritidal Figol B vs. Peritidal Castigaleu HI	0.322	<0.001	0.423	<0.001	0.601	<0.001
Peritidal Figol B vs. Nearshore Castigaleu AB	0.321	<0.001	0.321	0.004	0.464	0.001
Peritidal Figol B vs. Nearshore Castigaleu CD	0.371	0.001	0.413	0.003	0.545	0.001
Peritidal Figol B vs. Nearshore Castigaleu FG	0.394	<0.001	0.402	<0.001	0.515	<0.001
Peritidal Figol C vs. Peritidal Castigaleu FG	0.438	<0.001	0.479	<0.001	0.607	<0.001
Peritidal Figol C vs. Peritidal Castigaleu HI	0.362	<0.001	0.428	<0.001	0.662	<0.001
Peritidal Figol C vs. Nearshore Castigaleu AB	0.314	0.001	0.341	<0.001	0.417	0.004
Peritidal Figol C vs. Nearshore Castigaleu CD	0.338	0.001	0.388	<0.001	0.487	0.001
Peritidal Figol C vs. Nearshore Castigaleu FG	0.386	<0.001	0.412	<0.001	0.47	<0.001
Peritidal Castigaleu FG vs. Peritidal Castigaleu HI	0.371	<0.001	0.401	0.001	0.744	<0.001
Peritidal Castigaleu FG vs. Nearshore Castigaleu AB	0.393	0.007	0.395	0.006	0.462	0.005
Peritidal Castigaleu FG vs. Nearshore Castigaleu CD	0.455	<0.001	0.487	<0.001	0.515	0.002
Peritidal Castigaleu FG vs. Nearshore Castigaleu FG	0.549	<0.001	0.551	<0.001	0.579	<0.001
Peritidal Castigaleu HI vs. Nearshore Castigaleu AB	0.195	0.008	0.203	0.04	0.381	0.017
Peritidal Castigaleu HI vs. Nearshore Castigaleu CD	0.259	0.004	0.297	0.01	0.492	0.006
Peritidal Castigaleu HI vs. Nearshore Castigaleu FG	0.274	0.001	0.272	0.01	0.497	0.002
Nearshore Castigaleu AB vs Nearshore Castigaleu CD	0.517	<0.001	0.526	<0.001	0.603	<0.001
Nearshore Castigaleu AB vs Nearshore Castigaleu FG	0.551	<0.001	0.549	<0.001	0.633	<0.001
Nearshore Castigaleu CD vs Nearshore Castigaleu FG	0.557	<0.001	0.58	<0.001	0.615	<0.001
Inner shelf A8-A10 vs Inner shelf A6-A7	0.123	0.06	0.217	0.012	0.424	<0.001

Plio-Pleistocene between-sequence comparisons	Species-Mean rho	Combined p-value	Genera-Mean rho	Combined p-value	Families-Mean rho	Combined p-value
Peritidal S4 vs. Peritidal S6	0.161	0.033	0.208	0.047	0.301	0.029
Peritidal S4 vs. Nearshore S4	0.026	0.392	0.102	0.235	0.137	0.263
Peritidal S4 vs. Nearshore S5	-0.014	0.483	0.036	0.447	0.081	0.409
Peritidal S6 vs. Nearshore S4	0.048	0.36	0.065	0.422	0.176	0.144
Peritidal S6 vs. Nearshore S5	0.039	0.439	0.082	0.313	0.135	0.276
Nearshore S4 vs. Nearshore S5	0.288	0.002	0.418	<0.001	0.49	0.001
Inner shelf S4 vs. Inner shelf S5	0.222	0.008	0.297	0.002	0.453	<0.001
Inner shelf S4 vs. Inner shelf S6	0.206	0.005	0.238	0.011	0.352	0.007
Inner shelf S5 vs. Inner shelf S6	0.19	0.016	0.262	0.014	0.37	0.005
Inner shelf S4 vs. Outer shelf S3	0.207	0.004	0.31	0.002	0.487	<0.001
Inner shelf S4 vs. Outer shelf S4	0.196	0.012	0.276	0.006	0.451	<0.001
Inner shelf S5 vs. Outer shelf S3	0.274	0.002	0.321	0.002	0.37	0.011
Inner shelf S5 vs. Outer shelf S4	0.239	0.004	0.283	0.011	0.347	0.01
Inner shelf S6 vs. Outer shelf S3	0.145	0.163	0.197	0.104	0.32	0.03
Inner shelf S6 vs. Outer shelf S4	0.107	0.169	0.148	0.133	0.293	0.036
Outer shelf S3 vs. Outer shelf S4	0.391	<0.001	0.452	<0.001	0.527	<0.001

Table S2 - Mantel test (using Pearson correlation) shows that Bray-Curtis dissimilarity (using square-root transformed proportional abundances at regional scales) between sequences does not increase with increasing temporal separation between sequences, and Spearman rank correlation in proportional abundances between sequences does not decrease with increasing temporal separation between sequences within the Eocene and Plio-Pleistocene.

|	Mean r	2.5th percentile	97.5th percentile	Combined p-value
Eocene correlation between between-sequence BC dissimilarity and temporal separation between sequences				
Onshore species	0.312	0.137	0.473	0.092
Onshore genera	0.233	0.080	0.421	0.148
Onshore families	-0.030	-0.177	0.128	0.520
Eocene correlation between between-sequence rank correlation and temporal separation between sequences				
Onshore species	-0.268	-0.506	-0.030	0.861
Onshore genera	-0.161	-0.403	0.097	0.757
Onshore families	0.073	-0.182	0.325	0.407
Plio-Pleistocene correlation between between-sequence BC dissimilarity and temporal separation between sequences				
Onshore species	-0.320	-0.579	-0.082	0.662
Onshore genera	-0.200	-0.475	0.073	0.591
Onshore families	-0.322	-0.604	-0.018	0.710
Offshore species	0.333	-0.211	0.693	0.228
Offshore genera	0.375	-0.218	0.737	0.204
Offshore families	0.435	-0.159	0.814	0.171
Plio-Pleistocene correlation between between-sequence rank correlation and temporal separation between sequences				
Onshore species	0.284	-0.054	0.599	0.454
Onshore genera	0.121	-0.354	0.492	0.561
Onshore families	0.268	-0.178	0.614	0.436
Offshore species	-0.305	-0.650	0.213	0.772
Offshore genera	-0.352	-0.742	0.208	0.797
Offshore families	-0.449	-0.774	0.142	0.852
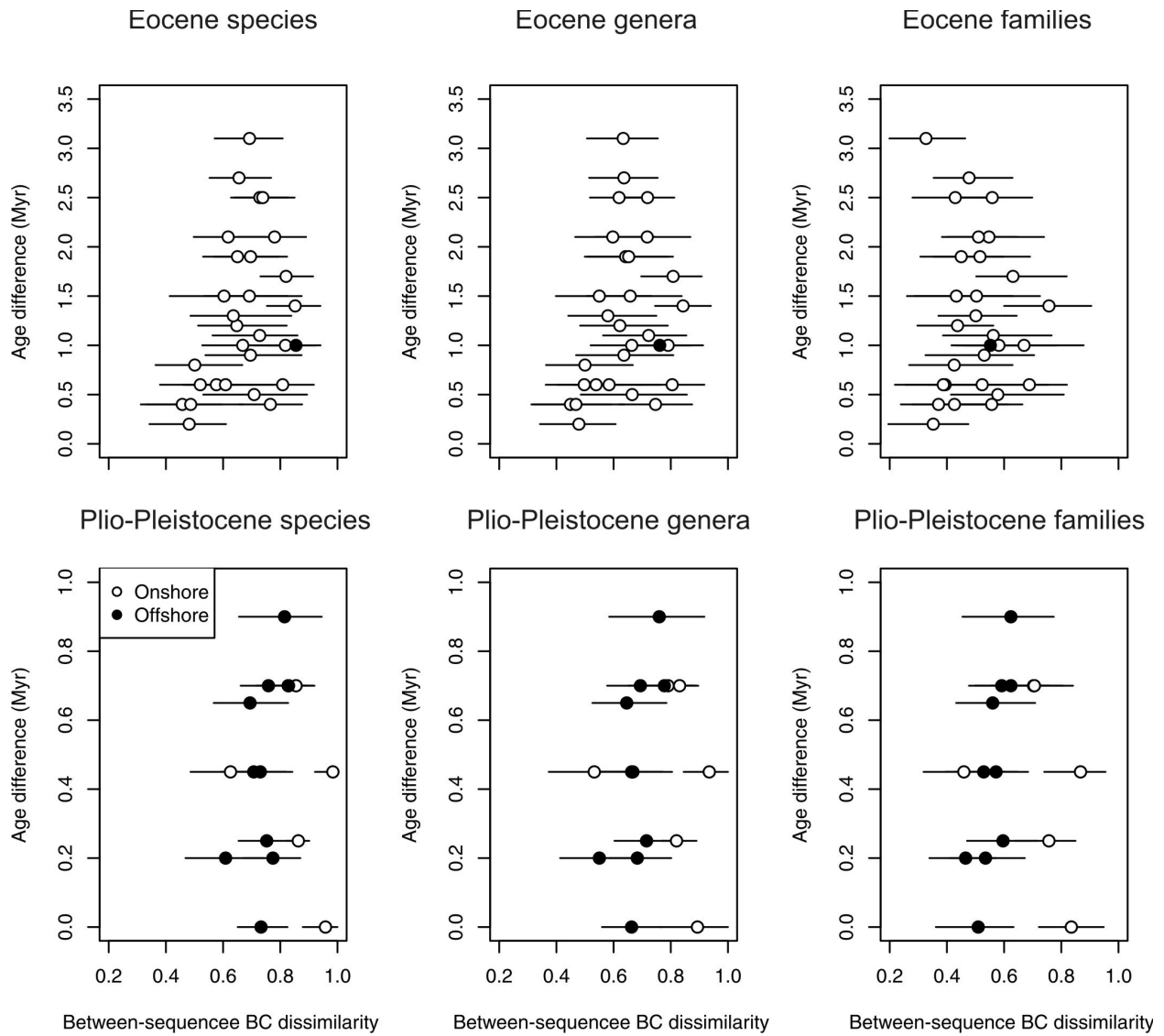
Figure S1 – Spearman rank correlations in species and family proportional abundance at regional scales do not decline with increasing temporal separation between sequences, implying some degree of short-term recurrence (< 5 Myr) in composition of molluscan metacommunities. Error bars represent 2.5th and 97.5th percentiles derived from 1,000 standardizations.
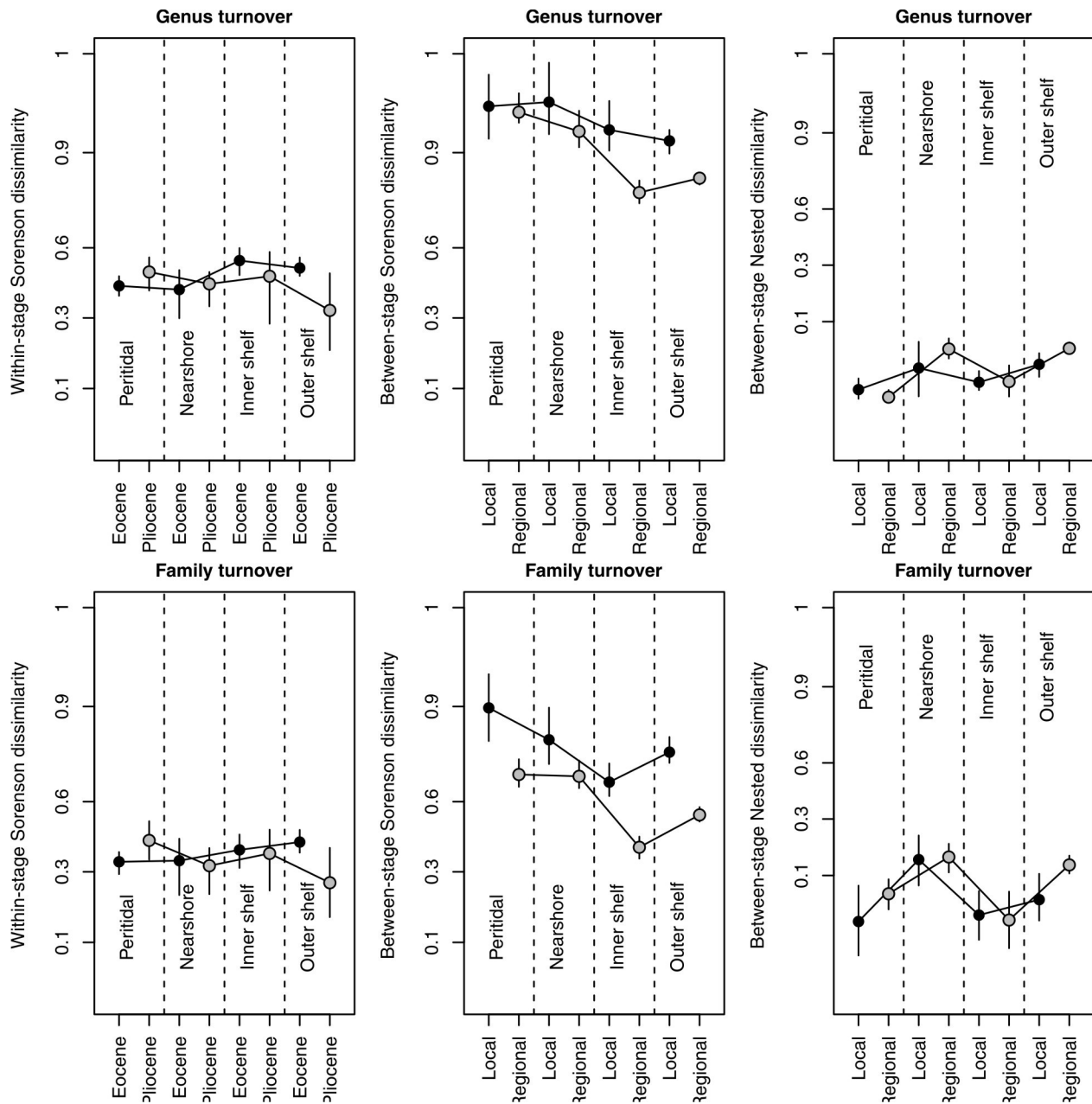
Figure S2 – Turnover in genus and family identity (Sorenson dissimilarity) within the Eocene
and Plio-Pleistocene does not consistently change along onshore-offshore gradients (left
column). However, the Eocene-Plio-Pleistocene turnover in genus and family identity declines
towards the inner shelf, at both local and regional scales (middle column). The higher turnover in
family identity (expressed by Sorenson dissimilarity) in the peritidal and nearshore is not

generated by the nestedness dissimilarity component, which does not decline towards the inner

shelf (right column).
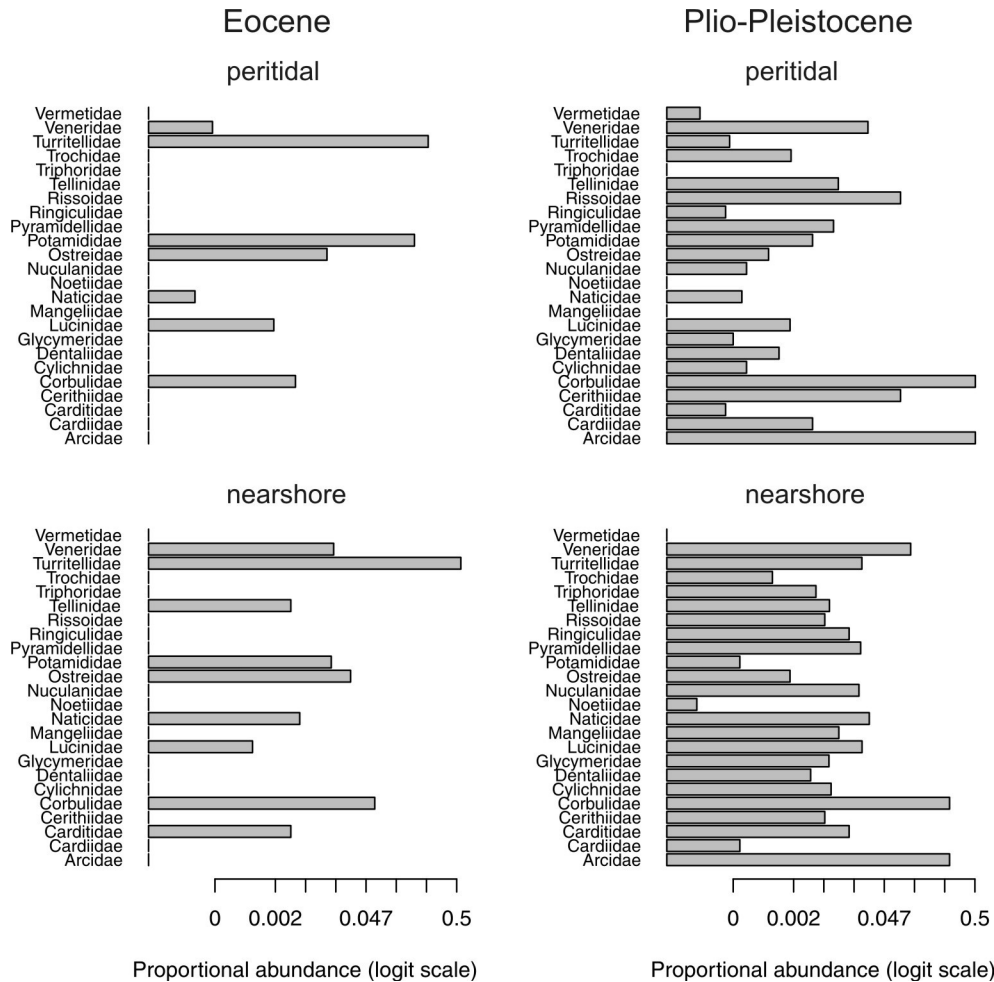
Figure S3 – Changes in proportional abundances of families persisting from the Eocene to Plio-

Pleistocene in intertidal and nearshore environments (showing families with at least 100

specimens in both time intervals). Note that the persistence applies to regional persistence rather
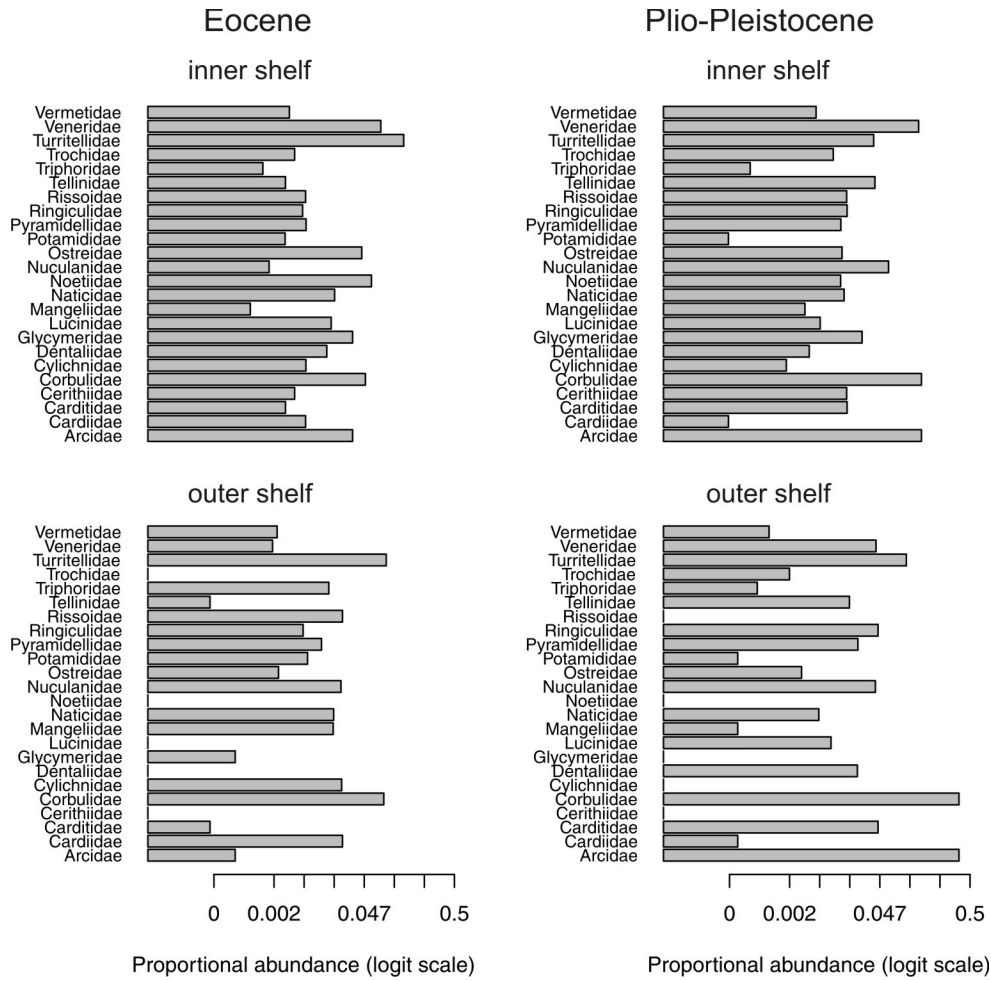
than to habitat-specific persistence.

Figure S4 – Changes in proportional abundances of families persisting from the Eocene to Plio-Pleistocene in the inner and outer shelf (showing families with at least 100 specimens in both time intervals). Note that the persistence applies to regional persistence rather than to habitat-specific persistence.
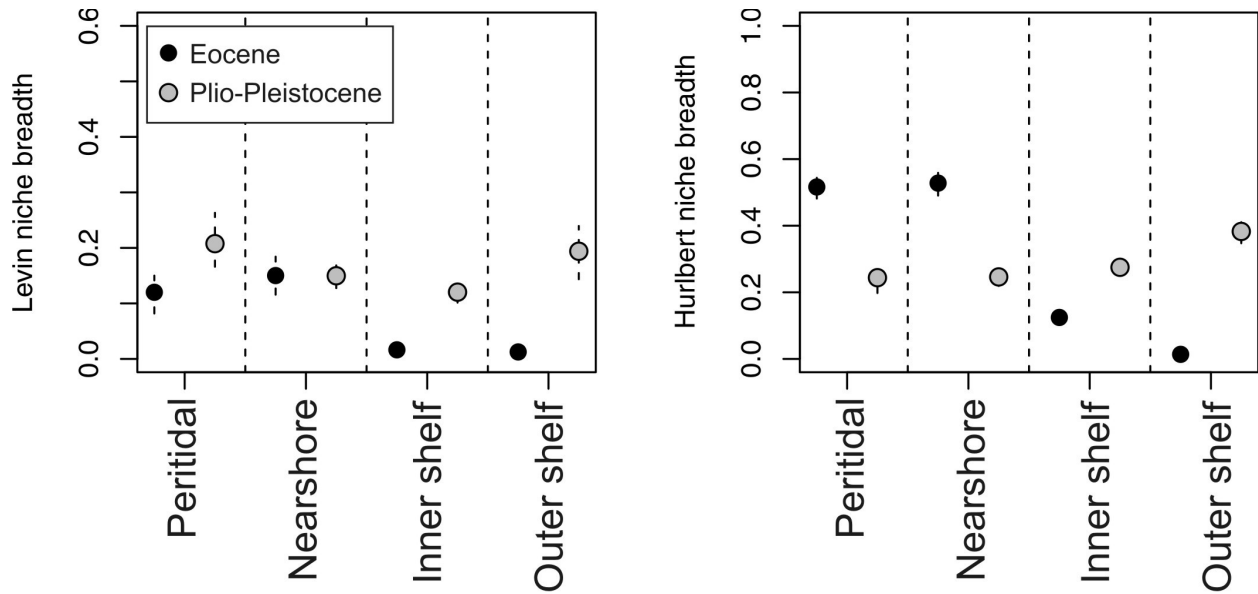
Figure S5 – Bathymetric decrease in Levin and Hurlbert niche breadth of Eocene (black dots) and Plio-Pleistocene mollusk species (grey dots) implies that, in the Eocene, species inhabiting onshore environments have broader bathymetric breadth than species inhabiting offshore environments, but otherwise no strong gradient is obvious. Bathymetric breadth of species inhabiting offshore environments becomes significantly higher in the Plio-Pleistocene and attains similar values as the breadth of species inhabiting onshore environments. The mean bathymetric breadth (Hurlbert's index) of all species in the Eocene (mean=0.12, 95% confidence intervals = 0.11-0.13) is significantly smaller than in the Plio-Pleistocene (mean=0.23, 95% confidence intervals = 0.21-0.24).
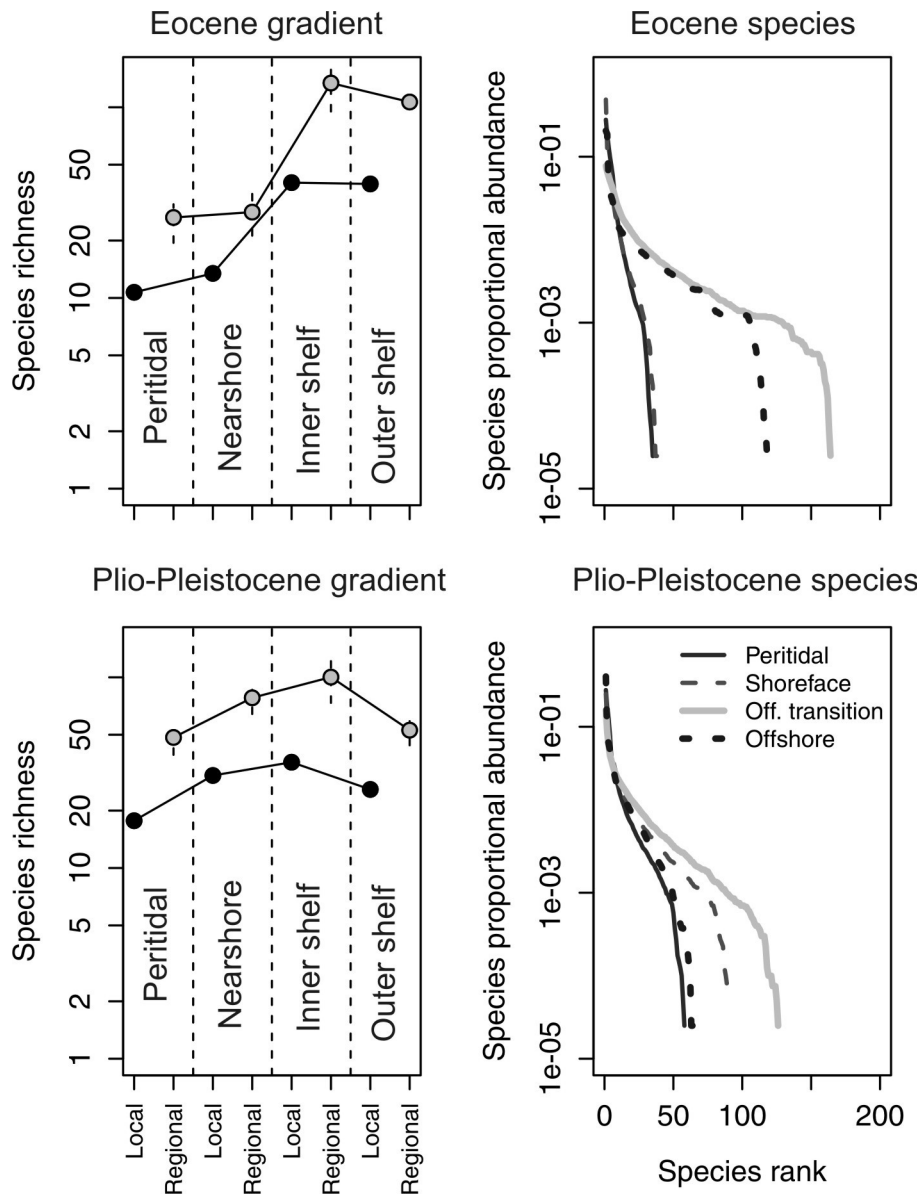
Figure S6 – *Left column:* Onshore-offshore gradients in species richness at local and regional scales peak in inner shelf in the Eocene and Plio-Pleistocene. *Middle column:* Species rank-abundance distributions at regional scales change markedly in shape along onshore-offshore gradients from high species dominance to more even, sigmoidal distributions with many rare species.

Figure S7 – Modern latitudinal transects in annual temperature minima and maxima at four depth intervals show that deeper habitats (blue lines) experience on average a smaller variation in temperature than shallow habitats (red lines) in the Eastern Atlantic and Eastern Pacific. Annual temperature monthly minima and maxima measured at the scale of 1º cells are extracted from the World Ocean Atlas 2009.