CATEGORICAL VERSUS GEOMETRIC MORPHOMETRIC APPROACHES TO CHARACTERISING THE EVOLUTION OF MORPHOLOGICAL DISPARITY IN OSTEOSTRACI (VERTEBRATA, STEM-GNATHOSTOMATA)

by HUMBERTO G. FERRÓN[1,2]*, JENNY M. GREENWOOD[1], BRADLEY DELINE[3], CARLOS MARTÍNEZ-PÉREZ[1,2],

HÉCTOR BOTELLA[2], ROBERT S. SANSOM[4], MARCELLO RUTA[5] *and* PHILIP C. J. DONOGHUE[1]*

[1]School of Earth Sciences, University of Bristol, Life Sciences Building, Tyndall Avenue, Bristol BS8 1TQ, UK; e-mail: humberto.ferron@bristol.ac.uk, carlos.martinez-perez@bristol.ac.uk, phil.donoghue@bristol.ac.uk

[2]Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Universitat de València, C/ Catedràtic José Beltrán Martínez, 2, 46980 Paterna, Valencia, Spain; e-mails: humberto.ferron@uv.es, carlos.martinez-perez@uv.es, hector.botella@uv.es

[3]Department of Geosciences, University of West Georgia, Carrollton, GA 30118, USA; e-mail: bdeline@westga.edu

[4]School of Earth & Environmental Sciences, University of Manchester, Manchester, M13 9PT, UK; e-mail: robert.sansom@manchester.ac.uk

[5]School of Life Sciences, University of Lincoln, Riseholme Hall, Lincoln LN2 2LG, UK ; e-mail: MRuta@lincoln.ac.uk

*Corresponding authors

ABSTRACT

Morphological variation (disparity) is almost invariably characterised by two non-mutually exclusive approaches: (i) quantitatively, through geometric morphometrics, and (ii) in terms of discrete, 'cladistic', or categorical characters. Uncertainty over the comparability of these approaches diminishes the potential to obtain nomothetic insights into the evolution of morphological disparity and the few benchmarking studies conducted so far show contrasting results. Here, we apply both approaches to characterising morphology in

the stem-gnathostome clade Osteostraci in order to assess congruence between these alternative methods as well as to explore the evolutionary patterns of the group in terms of temporal disparity and the influence of phylogenetic relationships and habitat on morphospace occupation. Our results suggest that both approaches yield similar results in morphospace occupation and clustering, but also some differences indicating that these metrics may capture different aspects of morphology. Phylomorphospaces reveal convergence towards a generalised 'horseshoe'-shaped cranial morphology and two strong trends involving major groups of osteostracans (benneviaspidids and thyestiids), which probably reflect adaptations to different lifestyles. Temporal patterns of disparity obtained from categorical and morphometric approaches appear congruent, however, disparity maxima occur at different times in the evolutionary history of the group. The results of our analyses indicate that categorical and continuous data sets may characterize different patterns of morphological disparity and that discrepancies could reflect preservational limitations of morphometric data and differences in the potential of each data type for characterizing more or less inclusive aspects of overall phenotype.

Key words: disparity, morphospace, categorical data, geometric morphometrics, Osteostraci

QUANTIFICATION of morphology and morphological disparity is integral to assessing general macroevolutionary patterns in the fossil record, such as adaptive radiations, rates of evolution, responses to extinctions, biotic replacements, and the existence of constraints on form (Foote 1997 and references therein). Consequently, there have been many attempts to evaluate the impact of potential biasing factors on morphological disparity estimates, including the possible influence of taphonomy (Webster & Hughes 1999; Bariş 2017), taxonomic or geographic scale (Butler *et al.* 2012; Deline *et al.* 2012), environmental distribution (Hopkins 2014), community structure (Deline 2009), sampling of phenotypic characters (Foth *et al.* 2012; Hopkins 2017), choice of metric (Ciampaglio *et al.* 2001), character selection (Deline & Ausich 2017), and choice of methodology (Villier & Eble 2004; Hetherington *et al.* 2015; Hopkins 2017; Romano *et al.* 2017).

Morphological disparity and morphospace occupation patterns have conventionally been based on two non-mutually exclusive approaches to characterising morphology. Firstly, through geometric morphometrics, morphology is characterised quantitatively in terms of continuous variation in aspects of organismal shape and proportions (e.g., Stayton & Ruta 2006). This approach is most commonly used to assess morphospace occupation at lower taxonomic levels due to the need for homologous features in all specimens within a single study (Wills *et al.* 1994; Bookstein 1997). Therefore, while these methods are very sensitive to morphological variation, their effectiveness in characterising overall phenotype diminishes with increasing taxonomic scale reflecting the concomitant reduction in the number of universally shared homologous features (Hetherington *et al.* 2015). Alternatively, morphology can be characterised in terms of discrete or categorical characters of the sort most commonly employed in the cladistic analysis of morphology. This approach to characterising morphology is usually undertaken in analyses of broad taxonomic scope, where there are large numbers of categorical differences between taxa, but fewer universal homologous structures that might serve as a basis for geometric morphometrics. As such, the categorical characterization of morphology can capture more unique aspects of form (Briggs *et al.* 1992; Wills 1998). However, this approach is also much less sensitive to finer changes in shape and proportion. Despite the differences between these approaches, most of the small number of benchmarking studies that have been conducted have shown that continuous and categorical approaches to characterising morphology yield broadly congruent patterns of disparity (Villier & Eble 2004; Anderson & Friedman 2012; Foth *et al.* 2012; Hetherington *et al.* 2015; Hopkins 2017; Romano *et al.* 2017; Schaeffer et al. 2019). Nevertheless, Mongiardino Koch and colleagues (2017) have shown that these two approaches yield contrasting patterns of disparity in their analysis of the scorpion genus *Brachistosternus*. This difference may reflect the relative power of continuous versus categorical approaches to characterising morphology at different taxonomic scales. However, this study may also reflect the fact that benchmarking studies remain small in number and many more such studies are needed to obtain nomothetic insights into whether different approaches in characterising morphology impact on the perception of the ensuing patterns of morphological disparity and the evolutionary processes that are inferred from them. To that end, we explore the evolution of morphological disparity in osteostracans, the extinct clade of jawless stem-gnathostomes that is generally perceived to be most closely related to jawed

vertebrates (Janvier 1996; Donoghue & Keating 2014). As such, the evolution of morphological disparity within this clade is interesting in its own right, as a parallel to its sister-lineage of jawed vertebrates. However, cranial shape characters contribute extensively to the systematics of the group (Sansom 2009a), making osteostracans an ideal focus for benchmarking the characterization of morphology for disparity analysis using discrete versus categorical characters. We characterise the morphology of this clade based on the distinctive and character-rich headshield, both in terms of geometric morphometric and discrete categorical 'cladistic' data. We compare perceptions of morphological disparity based on these data sets and, further, interpret the results in terms of their implications for understanding this temporal, phylogenetic and ecological context of the evolution of this key clade.

Osteostraci as case study

Osteostracans constitute a clade of extinct jawless vertebrates that ranges from the Llandovery (lower Silurian) to the Frasnian (Upper Devonian) (Sansom 2009a). Osteostracans are a taxonomically and morphologically diverse group, characterized by a semicircular dermal headshield encompassing the cranial and pectoral regions, a number of cephalic fields, pineal foramen, nasohypophysial opening, and a postcranial body covered in thick scales (Janvier 1996). Cornual and/or rostral processes extending from the headshield are well developed in a number of independent lineages and paired fins are present in many taxa but lost in others (Janvier 1985; Sansom 2008) - or they evolved convergently between jawed vertebrates and derived Osteostraci (Denison 1951). Most osteostracans have headshields that are strongly oblate dorso-ventrally although some have a more approximately circular or prolate in cross-sectional profile (Janvier 1996) (Fig. 1A and B). Remarkably, such morphological disparity, despite being a potential source of valuable biological and ecological information (e.g., Janvier & Lawson 1985; Belles-Isles 1987; Bunker & Machin 1991; Afanassieva 1992; Mark-Kurik 1992; Janvier 1996; Morrissey *et al.* 2004; Davies 2009), has not been analysed quantitatively. The headshield is the aspect of osteostracan anatomy that varies most through osteostracan phylogeny, as well as being the anatomical division most common preserved. Hence, it is the source of almost all characters that have been exploited in osteostracan phylogenetics (e.g. Janvier 1985; Sansom 2009a). Geometric morphometric characterization of the osteostracan headshield will, therefore, provide for a fair

and effective comparison to existing categorical characterizations of osteostracan morphological variation, facilitating insights into the evolution of osteostracan morphological disparity and the equivalence of competing approaches to characterizing morphological disparity.

MATERIALS AND METHODS

Geometric morphometric analysis

Our study was confined principally to species of established genera, although a small number of taxa with resolved phylogenetic affinity have also been included, enabling comparison with the most complete osteostracan phylogeny (Sansom 2009a) (Fig. 2). The study was conducted at genus level, with each genus represented by a single specimen. The type species and holotype specimen for the genus was used except where this specimen was poorly preserved or unavailable for characterization; in such circumstances another better-represented species was used. A total of 29 specimens were included in the geometric morphometric analysis (Fig. 2). Some specimens exhibit minor deformation, principally due to dorso-ventral compression. No attempt was made to correct for deformation as this would lead to the inclusion of human error and preliminary studies have suggested that biological signal is still well preserved when deformation is minor (Angielczyk & Sheets 2007). Images of specimens for digitization were obtained from photographs of original specimens (see Ferrón *et al*. 2020, Appendix S1 and File S1). When complete specimens could be pieced together from counterparts, images of these counterparts were superimposed (see Ferrón *et al*. 2020, Appendix S1 for a list of sources and information on the nature of deformation of these specimens). A total of 123 landmarks of type I, II and III were digitized using TpsDig v.2.26 (Rohlf 2016*a*) (Fig. 1B). The choice of landmarks was (by definition) constrained by homology (Bookstein 1997), but also by preservation. Therefore, only frequently preserved characters were included as landmarks in the study. Landmarks of type III were equally interpolated along the specimen outlines in six separate open curves. The number of landmarks chosen to represent each curve reflects the relative length and complexity of each portion of the headshield and was determined visually. TpsRelw v.1.65 (Rohlf 2016*b*) was used to fit landmark coordinates of all specimens by generalised Procrustes superimposition to remove variation in rotational, scale and translational differences between specimens so that only geometric information was left.

Categorical characters

Our categorical characterization of osteostracan morphology is based on the cladistic data set of Sansom (2009a) which comprises 112 characters and 65 taxa (see Ferrón *et al*. 2020, Appendix S1). We analysed these data in two ways: (i) the complete data set including cranial and postcranial characters and (ii) a subset of characters that relate to the cephalothoracic 'headshield', including external shape characters, but also neurocranial and histological features. Analyses of this subset of cranial characters facilitates a direct comparison to the analyses of the geometric morphometric data which are similarly limited to the headshield.

Disparity quantification from categorical and morphometric data

The disparity of osteostracans was explored from temporal, phylogenetic and ecological perspectives considering stratigraphic ranges, phylogenetic relationships, major taxa and habitat interpretations established in Sansom (2009a) and Sansom *et al*. (2015). Disparity was quantified from both categorical and continuous character data sets in two different ways: (1) the preordination distance, which is the average squared distance between taxa based on the original data and (2) the ratio of generalized variance, which is the ratio between the taxa within a time bin to the entire data set (in this case the generalized variance is the determinant of the covariance matrix from the first three axes of the principal coordinate analysis).

Distance matrices were obtained from both categorical and geometric morphometric data sets (considering Gower and Euclidean distances, respectively) using the package 'cluster' (Maechler *et al.* 2019) implemented in R (R Development Core Team 2017). Distance matrices were then subjected to principal coordinate analysis in the R package 'ape' (Paradis & Schliep 2018). The same procedure was repeated with a categorical data subset considering only the 29 genera included in the continuous data analysis. This allowed us to determine how much of the total morphological disparity was represented by the subset of genera used in the morphometric analysis and also to assess whether discrete and continuous characterisation of form yielded similar results. In parallel, Mantel tests were implemented using the R package 'vegan' (Oksanen *et al.* 2013)

to establish the strength and significance of linear correlations among the distance matrices derived from each of the data sets.

Morphospaces and phylomorphospaces were constructed using the R packages 'Phytools' (Revell 2012) and 'ggplot2' (Wickham 2016). We followed two alternative approaches to creating phylomorphospaces based on post- and pre-Ordination Ancestral State Estimation (OASE) (see Lloyd (2018) for a review). In the case of the pre-ordination procedure, ancestral state reconstruction was achieved through stochastic character state mapping (Huelsenbeck *et al.* 2003) using the R packages 'Phytools' (Revell 2012) and 'geomorph' for categorical and geometric morphometric data respectively. We used the phylogenetic tree from Sansom (2009a) after time-calibration, using the minimum branch length method (Laurin 2004), in the R package 'paleotree' (Bapst 2012). Tip ages were established from stratigraphic ranges published in Sansom *et al*. (2015).

Often comparisons of disparity between groups are more valuable than characterizations of the distribution of taxa within morphospace. To assess whether the different data types (categorical observations versus continuous measurements) yield similar conclusions about the relative disparity of groups we randomly selected 9 taxa and 12 taxa (with no overlap) and calculated the ratio of disparity considering both the categorical and geometric morphometric data. We selected groups of this size to mirror the largest clades within the data set (Benneviaspida and Thyestida). This subsampling routine was repeated 10,000 times. If both data sets capture similar morphological signals, the relative disparity between the two samples should be the same or similar for both metrics and there should be agreement on the more disparate subsample. Our null model was based on a simulation approach, involving morphological data evolving under Brownian motion on a phylogeny, following Schaeffer *et al.* (2019). We first generated 1000 phylogenetic trees using the topology from Sansom (2009a), time-calibrated 500 times using both the equal (Brusatte *et al.* 2008) and minimum branch length (Laurin 2004) dating approaches in the R package 'paleotree' (Bapst 2012). For each of these trees, tip ages were established by randomly sampling ages between each taxon's first and last stratigraphic occurrences. We then simulated both categorical and continuous morphology-like data on all

of the 1000 dated phylogenies. We simulated discrete character data sets in the R package 'dispRity' (Guillerme 2018) using the equal-rates (ER=Mk) model (Paradis & Schliep 2018). For the model parameters, we randomly sampled gamma distributions with shapes of 0.5, 1 or 2 and rates of 5, 10 or 20 (higher rates increased phylogenetic signal) following Schaeffer *et al.* (2019). We simulated geometric shape data, generating 29 'headshield-like' structures defined by 123 landmark coordinates for each tree in the R package 'Evomorph' (Cabrera and Giri 2016). As inputs, we considered the consensus shape of the original analysis as the ancestral morphology and the Procrustes residuals from our original landmark configurations as co-variance data. The resulting categorical and continuous data sets were then subjected to similar subsampling routines to those described above and the results were compared with our empirical data. In this case, the disparity ratios were calculated on randomly selected groups as well as on the benneviaspidids and the thyestids of each simulated data set, which include 9 and 12 taxa, respectively.

Finally, correlation between disparity and taxonomic diversity over time was evaluated in PASW, considering the different data sets and disparity metrics; taxonomic diversity data were obtained from Sansom *et al.* (2015). Correlation on first-difference transformed data were also checked in order to eliminate the role of autocorrelation.

RESULTS

Morphospace occupation and phylomorphospaces

Plots of taxa in the multivariate space generated from the categorical and geometric morphometric data sets as well as the percentage of total variance summarized by each axis are shown in Figure 3 and Table 1 respectively. Analysis of both the complete and subsampled categorical data sets recovered similar patterns of taxon clustering within ordination space (note that the mirroring of taxa on PCo1 and PCo2 is an artefact of the arbitrary direction of ordination). Ordinations of categorical data sets tend to disperse variance explained across a large number of axes (Lloyd 2016) and, thus, considering just the first three axes may give an incomplete view of morphological disparity. However, K-means clustering recovered identical grouping of

taxa using the first three (52.7% variance explained) and the first 15 axes (84.6% variance explained) of the ordination of categorical data. Therefore, even though considering just a subset of the axes can be problematic, it is unlikely to play a large role in the major structure and clustering of the current data set. Benneviaspidids and thyestiids, which cover most of the morphospace, occupy different regions showing only a small overlapping area. A number of zenaspidids are also relatively well separated in both ordinations based on the complete and subsampled categorical data sets. Non-cornuates (e.g., *Hemicyclaspis*), basal cornuates (e.g., *Cephalaspis*) and some generalised cornuate forms with uncertain phylogenetic affinities (e.g., *Pattenaspis*, *Hildenaspis*, *Mimetaspis*, *Zychaspis*) occupy smaller areas that exhibit significant overlap with those of other groups in the ordination based on the complete categorical data set, but separate better in the ordination based on the subsampled data set (mostly on PCo3). Freshwater and marine genera are restricted to different areas of the morphospace with brackish representatives in intermediate positions. This is likely due to the existence of a strong association between taxonomic affinity, morphology, and habitat in benneviaspidids and thyestiids, which are represented mostly by freshwater and marine forms respectively. Phylomorphospaces obtained following the pre- and post-ordination methods show similar patterns. In both cases, two strong branching trends are recognised, one within Benneviaspidida (along PCo2) which is characterised by an antero-lateral extension of the cornua and increasing length of the rostrum (e.g., *Boreaspis*, *Spatulaspis*, *Hoelaspis*), and another within Thyestiida (along PCo3), characterised by a reduction and eventual loss of the cornuae (e.g., *Oeselaspis*, *Witaaspis*). The latter is better represented in the subsampled data set. Reversals are much more common among non-cornuates, basal and generalised cornuates, and Zenaspidida. The ordination based on the continuous character data set exhibits a similar pattern of taxon clustering to ordinations based on categorical data sets, but there appears to be a greater overlap when genera are grouped by both major taxa and habitats. The phylomorphospaces obtained from the continuous data set following pre- and post-ordination methods are again extremely similar, revealing in both cases that there is a high degree of morphological convergence towards forms with well-developed caudally positioned cornual processes, most corresponding to freshwater genera of Benneviaspidida (e.g., Ectinaspis), Thyestiidae (e.g., Waengsjoeaspis), Zenaspidida (e.g., Stensiopelta) and basal and generalised cornuates (e.g., *Cephalaspis*, *Mimetaspis*) (towards negative values of PCo1). On the other hand, two similar

branching trends to those recorded by categorical data are here recognizable; a first one within Thyestiidae which is characterized by the reduction and loss of cornuae within Thyestiidae, as captured along the PCo1 and 2, and a second one reflecting a notable development of cornual and rostral processes in Benneviaspidida, both captured along the PCo1 and PCo2.

A comparison of the pre-ordination distances (Cat-Gower, GM- Euclidean) for the continuous and categorical data sets suggests the existence of strong correlation (Mantel State r=0.3098, p=0.001). These results contrast with K-means clustering on the two data sets, existing only around 58% agreement on cluster placement in the three-cluster solution. The three clusters found in the categorical data are composed of two groups that are environmentally and largely taxonomically consistent along with a more heterogeneous group. The morphometric data has one small group that is taxonomically and environmentally consistent and two larger mixed groups.

Temporal patterns of morphospace occupation and morphological disparity

Silurian and Devonian osteostracans occupy disparate regions within the morphospace in all three analyses showing important differences in taxonomic composition and habitats (Fig. 4). Wenlock and Ludlow age genera are mainly represented by marine thyestiids and non-cornuates. Pridolian genera comprise brackish thyestiids and non-cornuates that occupy intermediate positions between Wenlock-Ludlow and Devonian taxa. Devonian genera are mostly represented by freshwater representatives of all major osteostracan groups. The two measures of disparity we employ, preordination distance and generalized variance, characterise different temporal patterns within each data set (Fig. 5). In the complete cladistic data set, maximum disparity occurs at the beginning of the clade's history, although a second peak is revealed by the preordination distance metric in the Emsian (Fig. 5A and B). In the geometric morphometric and categorical subsets, the recorded temporal patterns of disparity appear congruent for each of the metrics, but differ strongly with those characterised by the complete categorical data set (compare Fig. 5A and B with Fig. 5C and D). Thus, the preordination distance metric reveals a peak in disparity in the early Devonian (Lochkovian-Pragian) whereas generalized variance metric suggests comparatively stable values of disparity through the

evolutionary history of the group. A positive correlation exists between taxonomic diversity and disparity, measured as generalized variance and preordination distance in the categorical subset. These results remain the same after detrending data for autocorrelation by applying first-difference transformation (Table 2).

Categorical versus continuous measurements of morphology in disparity analyses

Results derived from the subsampling routines, although displaying an important spread of the data, show positive trends (Fig. 6A). In fact, significant correlation is detected when considering results derived from both preordination distance (R = 0.186) and generalized variance disparity metrics (R = 0.065). In almost half of the sampled cases, the categorical and the geometric morphometric data sets disagree on which sample is most disparate (i.e., in 45.0% and 44.8% of the cases when considering preordination distance and generalized variance disparity metrics respectively), which is also the case for the empirical data from Benneviaspida and Thyestida (see red dot in Fig. 6A). Positive trends, consistent with those obtained for the empirical data, are also detected in the simulated data when considering both the disparity ratios between randomly selected groups (Preordination distance R = 0.233, 46.8% disagreement; Generalized variance R = 0.025, 21.3% disagreement; Fig. 6B) and between Benneviaspida and Thyestida (Preordination distance R = 0.299, 33.0% disagreement; Generalized variance R = 0.037, 43.9% disagreement; Fig. 6B).

DISCUSSION

Osteostracan morphological disparity in space and time

Overall, both categorical and morphometric approaches to characterising morphology yield similar patterns of morphospace occupation and clustering (Fig. 3). Several forms that exhibit a generalised semi-circular headshield outline, such as non-cornuate genera (e.g., *Hemicyclaspis*) or some basal cornuates, appear very close to the mean form in all analyses, which may be considered as the ancestral state for the group given their early branching topology in osteostracan phylogeny (Sansom 2009a). This morphology has been related to a benthic mode of life, where the headshield is oriented flat on the substrate and is able to withstand strong currents, while remaining an agile organism (Bunker and Machin 1991). Phylomorphospaces reveal convergence on this headshield morphology within early-branching zenaspidids, the earliest-branching

benneviaspidids and thyestiids, as well as other cornuate taxa, presumably reflecting the optimality or, rather, the general effectiveness of one successful form. This is also reflected in the fact that this area of the morphospace is more densely occupied than most others. Two evolutionary trends separated in time are clearly recognizable in the phylomorphospaces, involving different major groups of osteostracans occupying disparate habitats (Figs. 2 and 3). The first such trend is characterised by the reduction and loss of the cornual processes in thyestiids inhabiting marine environments during the Silurian. This has previously been interpreted as an adaptation to burrowing life habits in the more derived groups including tremataspidids and kiaeraspidids (Janvier & Lawson 1985). The second trend is characterized by the development of long cornual and/or rostral processes in freshwater benneviaspidids, during the Devonian. These structures have been the focus of competing functional interpretations in other early vertebrate groups where they have been interpreted as either locomotory adaptations to enhance lift generation or reduce drag (e.g., Mark-Kurik 1992; Botella & Fariña 2008; Novitskaya 2000; Moloshnikov 2001; Fletcher *et al.* 2014), or for predator deterrence (e.g., Janvier 1977), as housing for sensory organs (e.g., Voichyshyn 2006), a substrate anchor (e.g., Dineley 1976; Janvier 1985; Wells & Dorr 1985), or an adaptation to specific feeding habits (e.g., Tarlo 1961; Dineley 1994).

We employed both pre- and post-ordination approaches to phylomorphospace construction, the relative merits of which were considered by Lloyd (2018). Post-ordination approaches are readily and therefore commonly applied, but ancestral values are forced to be within the range of sampled tip values and may lead to an underestimation of convergence. In contrast, post-ordination approaches are more complex, requiring prior estimation of the characteristics of the hypothetical ancestors predicted by phylogenetic hypotheses, but have some advantages including allowing increased sample size, reconstruction of missing data, and avoiding the assumption that estimated ancestors must fall within the range of tip values. However, the prior inclusion of inferred ancestors in pairwise distances and the ensuing ordination can have the effect of inflating clade disparity, perhaps artefactually. Nevertheless, in this instance, our results indicate that both pre- and post-ordination based approaches to estimating phylomorphospace recovered similar overall patterns (Fig. 3). Conspicuously, large areas of morphospace characterised by both the categorical and

continuous character data sets remain unoccupied which presumably reflects morphological character combinations and shapes that are hydrodynamically or functionally inefficient, unexplored as a consequence of phylogenetic, developmental or structural constraints, unpreserved or perhaps unrealised because of insufficient evolutionary time.

Categorical and continuous character data sets convey different patterns of variation in the range of morphospace occupation, as do the different measures of disparity. Characterization of disparity with categorical data suggests that the maximum was established early in osteostracan evolution (Fig. 5A and B), consistent with the derived nature of some Silurian thyestiids (Figs. 1 and 3). This pattern is more significant when measuring disparity from preordination distances. However, capturing disparity with geometric morphometric data suggests that maximal variation was achieved later in osteostracan phylogeny, in the Pridolian or early Devonian (depending on the metric used). Overall, both data types appear to evidence a post-Pragian decline in the morphological disparity of the Osteostraci before their Late Devonian extinction. This pattern could be interpreted literally, congruent with Janvier & Newman's (2005) hypothesis on the decline of ostracoderm groups, reflecting an increase of ecological restriction during the Middle and Late Devonian imposed by changes on marginal marine and freshwater environments and/or food resources, combined with limited dispersal capability (Sansom 2009b). However, flux in the diversity of osteostracans through this interval has been interpreted to reflect facies shifts in the rock record (Sansom *et al.* 2015). Indeed, a Pearson Correlation test finds evidence for a significant correlation between diversity (raw standing diversity or corrected for ghost lineages) and some metrics of morphological disparity based on the categorical data (Table 2). Parallel changes in diversity and disparity most likely reflect the environmentally non-uniform fossil record (Sansom *et al.* 2015) and the adaptation of osteostracans to the environments in which they lived.

Categorical versus continuous measurements of morphology in disparity analyses

Categorical observations and continuous measurements are non-mutually exclusive approaches to the characterization of morphology in analyses of the evolution of morphological disparity. In attempting to

derive nomothetic insights in this sense, to address hypotheses such as the universality of maximal initial disparity (Hughes *et al.* 2012), or the relationship between disparity and diversification (Foote 1993), it is important that the aspects of morphological variation summarised in disparity analyses are in some sense equivalent (Hetherington *et al.* 2015). Given the nature and scope of the phenotypic features that these approaches can characterise, it could be expected that categorical characters, which usually sample from across the breadth of phenotype, capture different aspects of morphological disparity to geometric morphometrics, which is usually focussed on a subsample of overall phenotype as a proxy for the whole. Furthermore, categorical data sets which, as here, are mostly repurposed cladistic data sets, have a tendency to eschew invariant, convergent, and autapomorphic characteristics. Continuous character data sets should not suffer these same ascertainment biases but capturing morphological variation through continuous characters has its own limitations. Principally, this is the need to limit landmarks to homologous structures present in all taxa and, therefore, the challenge of capturing neomorphic structures and losses.

Despite this, the majority of benchmarking studies have found that categorical and continuous characters capture similar patterns of morphological disparity (Villier & Eble 2004; Anderson & Friedman 2012; Foth *et al.* 2012; Hetherington *et al.* 2015; Hopkins 2017; Romano *et al.* 2017; Schaeffer et al. 2019). However, few of these studies (Romano *et al.* 2017; Schaeffer et al. 2019) compare categorical and continuous characters based on the same anatomical structures; most characterize disparity based on different body regions. For example, Villier & Eble (2004) incorporated data sets for echinoids where eighty percent of categorical characters have no equivalence in their morphometric characters; Hetherington *et al.* (2015) compared geometric morphometric data on the skull surface and categorical data on internal cranial structures in caecilian amphibians; Foth *et al.* (2012) compared pterosaur disparity based on cranial morphometrics versus categorical characters from the entire skeleton (Prentice *et al.* 2011; Butler *et al.* 2012), and limb measurements and ratios (Dyke *et al.* 2009). Different anatomical divisions may well co-evolve, exhibiting equivalent patterns of morphological disparity through time, supporting the practise of using proxy data sets as representative of the whole (Hopkins 2017). However, this should not be a null expectation not least since anatomical partitions of categorical data commonly generate different phylogenetic hypotheses (Brinkworth

et al. 2019; Mounce *et al.* 2016; Yi *et al*. 2019) and, therefore, they should be expected to generate equally different characterization of disparity.

Our results suggest that the patterns of osteostracan morphological disparity captured by categorical and continuous characters are correlated when cladistic geometric morphometric data sets are based on equivalent taxa and anatomical components (Fig. 6). This result is not surprising since it is possible to express continuous measurements as categorical states (e.g. Thiele 1993) and, therefore, it is possible to compile categorical data sets that are equivalent to continuous character data sets, though they have less information content since they objectively and explicitly summarise continuous variation. The correlation between the empirical and simulated data implies a strong phylogenetic signal within the morphological data. However, the empirical data exhibit greater disagreement on the relative disparity within the groups. Despite this apparent equivalence in the results derived from categorical and geometric morphometric subsets, the complete categorical data set (which samples trunk as well as cranial characters) provides a very different perspective on the evolution of morphological diversity within osteostracans both in terms of the timing of peak disparity within the clade and the relative disparity between subclades. Therefore, while both data types appear to capture similar patterns of disparity, the nature of morphometric data (highly dependent on preservation and limited to areas with recognizable homologous structures) could lead in practice to very partial results in some cases and, ultimately, to conclusions more strongly biased by the vagaries of preservation.

In a very real sense, it does not matter that these two approaches to summarising morphology results in different perceptions of morphological variation. They provide different perspectives on the same phenomenon and that, based on the nature of the data, enriches understanding of the evolution of morphology within species and clades. Further, these alternative approaches may be better suited to different questions. For example, characterization of disparity in terms of shape variation may be of greater importance when exploring the constraining role of the aquatic environment in which osteotracans lived. Meanwhile, categorical characters may be better suited to capturing the overall disparity of osteostracan

phenotype. In this sense, neither approach is necessarily superior. Nevertheless, if the objective is to capture the evolution of phenotypic disparity in general, both within and between lineages, it appears clear that the while a dense sampling of phenotype is advantageous, diverse sampling of phenotype is paramount. In attempting to integrate over the vagaries of variable fossil preservation, this may be achieved most effectively by summarising phenotype using categorical characters.

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DATA ARCHIVING STATEMENT

Data for this study are available in the Dryad Digital Repository:

https://datadryad.org/stash/share/EA8P7rwCoxZimQPB2p47xsoFl-QMdQpMu2p9-gkGfxE
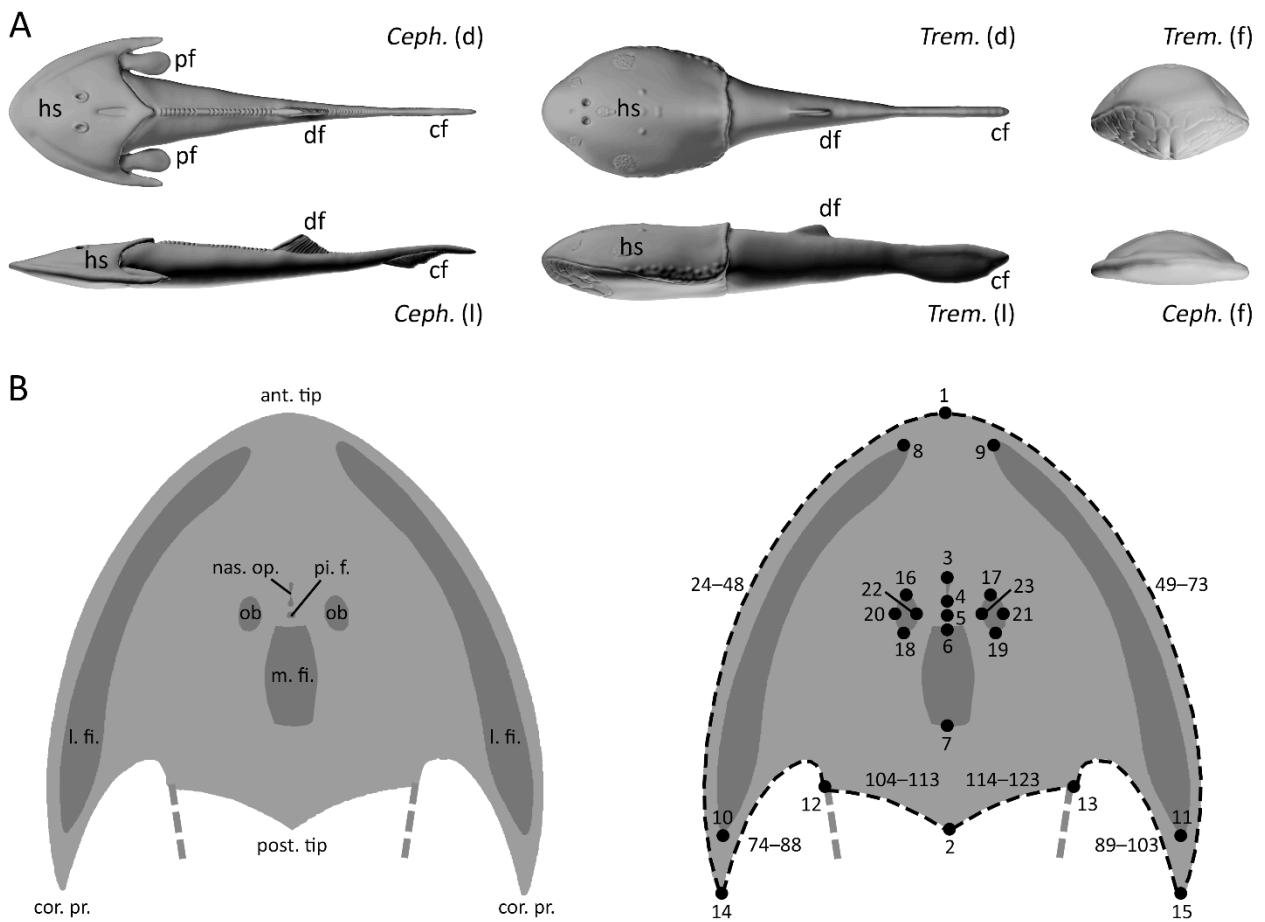
Figure 1. (A) Drawings illustrating the general morphology of two distinct well-known osteostracans (*Cephalaspis* and *Tremataspis*) in dorsal (d), lateral (l) and frontal views (f). Position of the pectoral fins (pf), dorsal fin (df), caudal fin (cf) and the headshield (hs) is indicated. (B) Descriptive diagrams showing the terminology of commonly referred anatomical characters of osteostracan headshield (upper diagram) and the landmark configuration used in the geometric morphometric analysis (lower diagram). Landmark 1, anterior tip of the headshield or the rostral process (ant. tip.); Landmark 2, posterior tip of the headshield (post. tip.); Landmarks 3 and 4, most anterior and most posterior medial points of the nasohypophysial opening (nas. op.) respectively; Landmark 5, pineal foramen (pi. f.); Landmarks 6 and 7, most anterior and most posterior medial points of the median field (m. fi.) respectively; Landmarks 8 and 9, most anterior points of the lateral fields (l. fi.); Landmarks 10 and 11, most posterior points of the lateral fields (l. fi.); Landmarks 12 and 13, points of connection between the headshield and the body; Landmarks 14 and 15, most distal points of the corneal processes (cor. pr.) ; Landmarks 16-23, most anterior, posterior, lateral and medial points of the eye orbits (ob.); Landmarks 24-73, landmarks situated between Landmarks 1 and 14 and

between Landmarks 1 and 15; Landmarks 74-103, landmarks situated between Landmarks 14 and 12 and between Landmarks 15 and 13; Landmarks 104-123, landmarks situated between Landmarks 12 and 2 and between Landmarks 13 and 2.
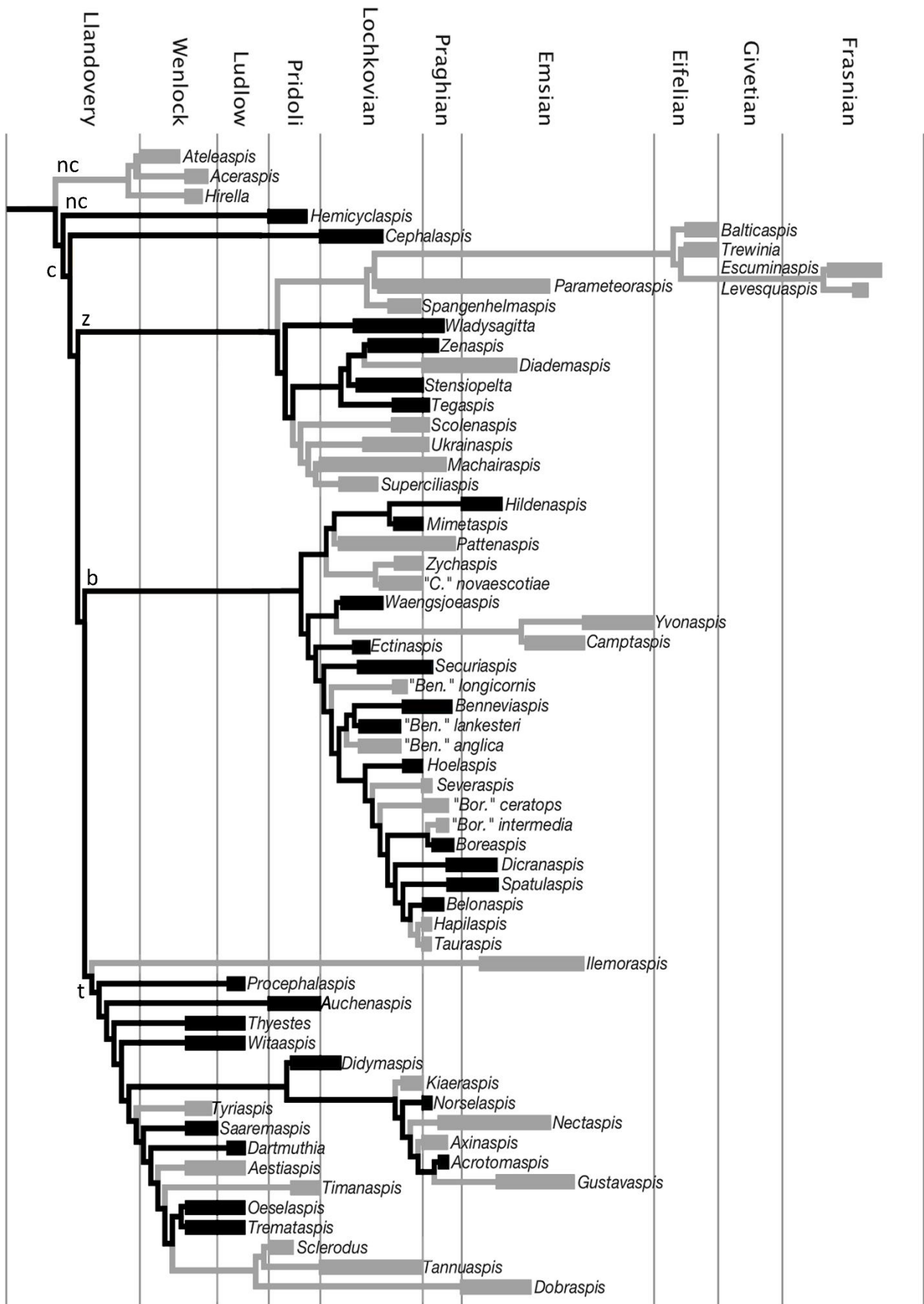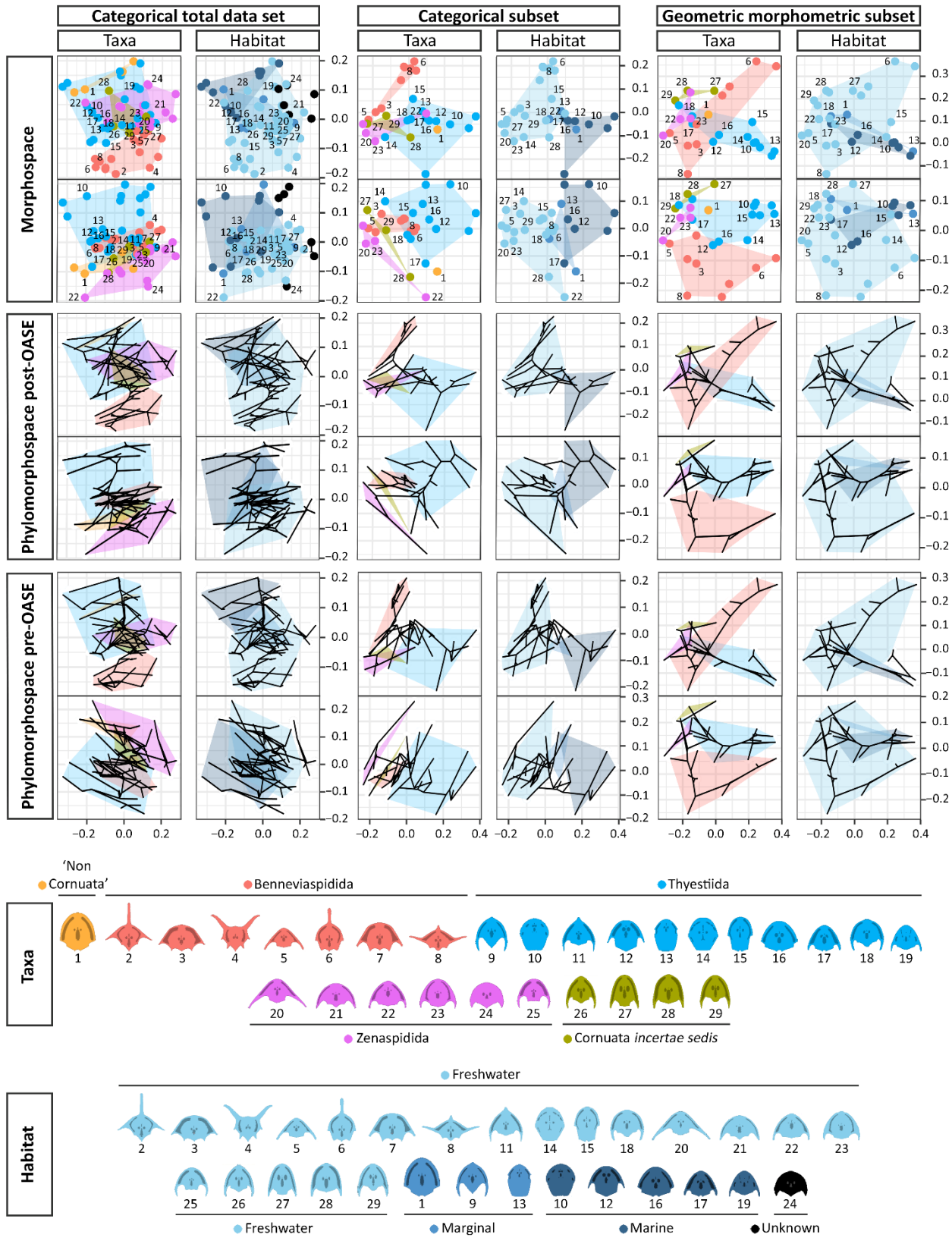
Figure 2. Phylogenetic hypothesis of the Osteostraci (modified from Samson *et al.* 2015), highlighting in black

the species represented in the geometric morphometric analysis. *Major groups:* b, Benneviaspidida; c, Cornuata; nc, 'Non Cornuata'; t, Thyestiida; z, Zenaspida.

Figure 3. Morphospace occupation and phylomorphospaces of osteostracans grouped by major taxa and habitats obtained from categorical and geometric morphometric approaches. Morphospaces and phylomorphospaces are represented by PCo1 (horizontal), PCo2 (upper vertical) and PCo3 (lower vertical)

axes. Osteostracan phylogenetic relationships and headshield drawings modified from Sansom (2009a). *Taxa:*

1, *Hemicyclaspis*; 2, *Boreaspis*; 3, "*Benneviaspis*" *lankesteri*; 4, *Tauraspis*; 5, *Ectinaspis*; 6, *Spatulaspis*; 7, "*Benneviaspis*" *longicornis*; 8, *Hoelaspis*; 9, *Camptaspis*; 10, *Oeselaspis*; 11, *Yvonaspis*; 12, *Thyestes*; 13, *Didymaspis*; 14, *Acrotomaspis*; 15, *Norselaspis*; 16, *Witaaspis*; 17, *Procephalaspis*; 18, *Waengsjoeaspis*; 19, *Ilemoraspis*; 20, *Stensiopelta*; 21, *Trewinia*; 22, *Zenaspis*; 23, *Tegaspis*; 24, *Escuminaspis*; 25, *Spangenhelmaspis*; 26, *Pattenaspis*; 27, *Hildenaspis*; 28, *Cephalaspis*; 29, *Mimetaspis*.
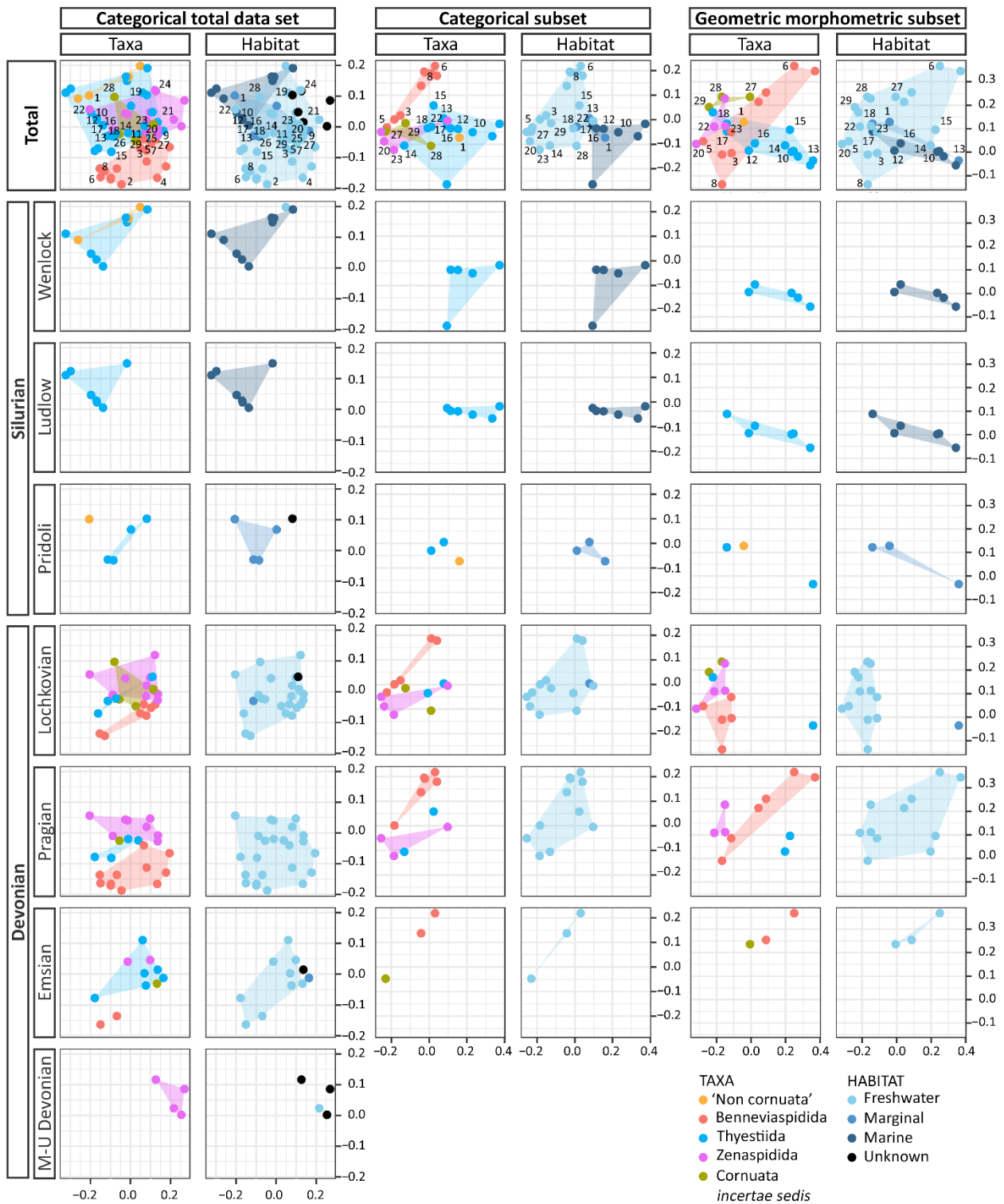
Figure 4. Temporal patterns of morphospace occupation of osteostracans grouped by major taxa and habitats obtained from categorical and geometric morphometric approaches. Morphospaces are only represented by PCo1 (horizontal) and PCo2 (vertical) axes. Numbers in the morphospaces refer to taxa in Figure 3.
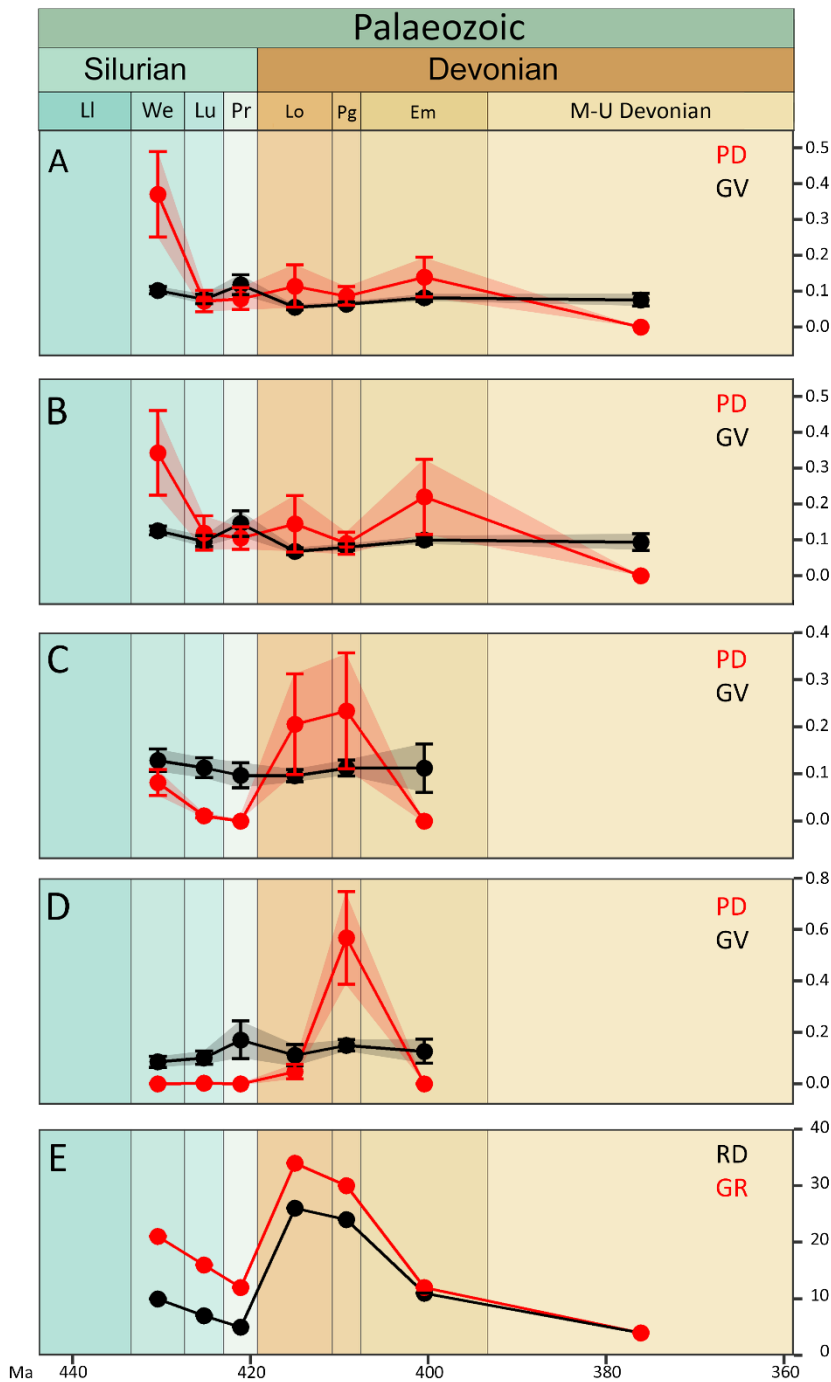
Figure 5. A–B, categorical total data set including (A) both corporal and headshield characters and (B) only headshield characters. C, categorical subset. D, geometric morphometric subset. Disparity is calculated as the preordination distance (PD) and as the ratio of generalized variance (GV). E, taxonomic diversity of osteostracans through time based on raw data (RD) and including ghost ranges (GR) (data taken from Sansom et al. 2015). *Timescale*: Ll, Llandovery; We, Wenlock; Lu, Ludlow; Pr, Pridoli; Lo, Lochkovian; Pg, Pragian; Em, Emsian; M-U Devonian, Middle-Upper Devonian.
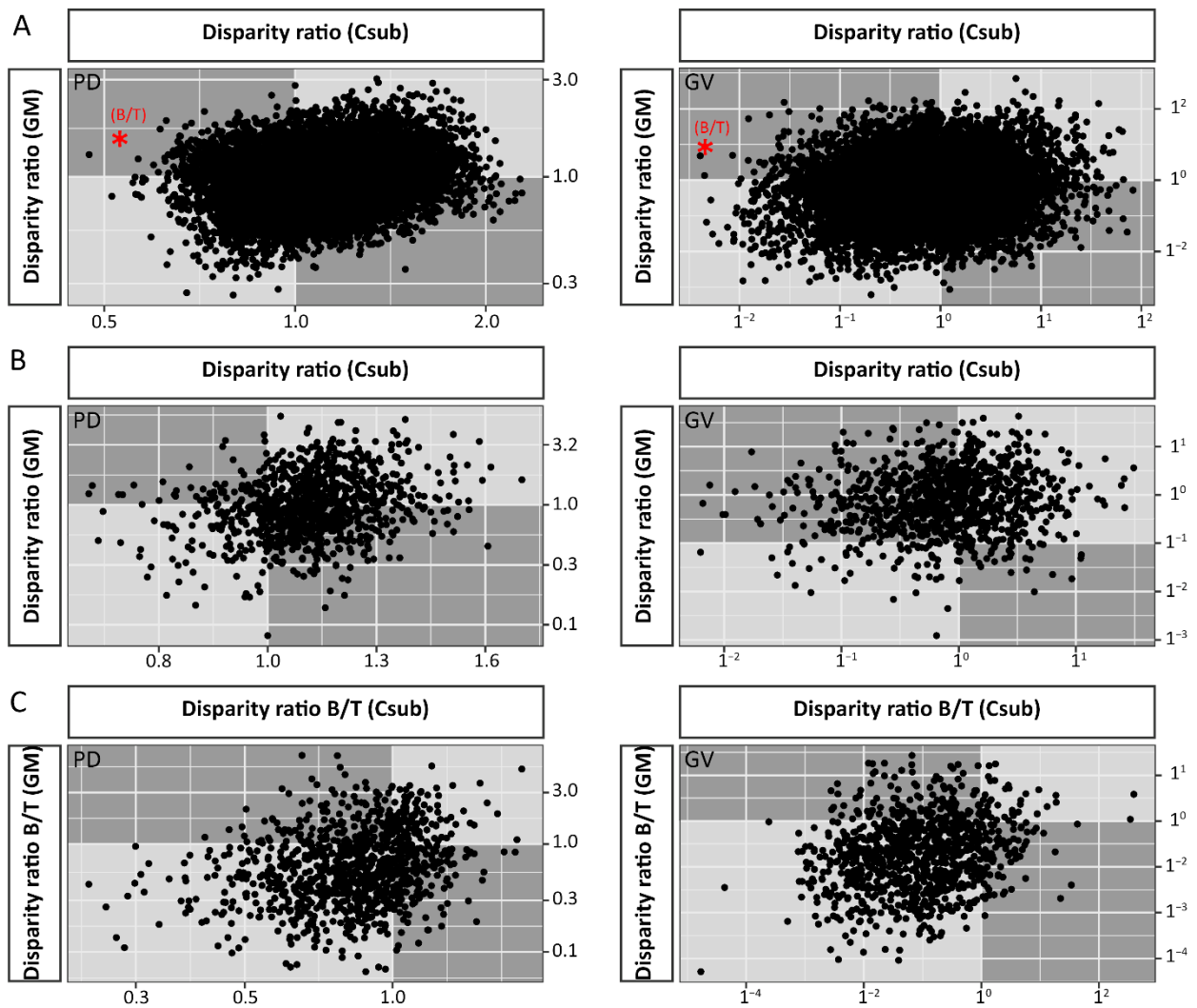
Figure 6. Plots showing the disparity ratios derived from the categorical (Csub) and the geometric morphometric (GM) data sets in both (A) the empirical and (B-C) the modelled approaches. Disparity is calculated as both the preordination distance (PD) and as the ratio of generalized variance (GV). The disparity ratios are calculated on two randomly selected groups of 9 and 12 taxa in (A) the empirical and (B) the modelled data as well as on Benneviaspida and Thyestida in (C) the modelled data. Actual ratio of Benneviaspida and Thyestida (B/T) is denoted by an asterisk in the empirical data plots. Points on dark grey areas correspond to sampled cases where the categorical (Csub) and the geometric morphometric (GM) data sets disagree on which group is more disparate.

Data set	Percentage variance summarized			
	Axis 1	Axis 2	Axis 3	Sum
Cladistic	19.11%	10.29%	7.58%	36.98%
Cladistic subset	27.45%	15.41%	9.85%	52.71%
Geometric morphometric	57.67%	18.99%	13.33%	89.99%

Table 1. Percentage variance summarized on the first three PCo axes for each of the three data sets.

		Cladistic (GV)	Cladistic (PD)	Cladistic Sub. (GV)	Cladistic Sub. (PD)	Geom. Morph. (GV)	Geom. Morph. (PD)
Diversity	**Pearson Correlation**	0.075	-0.694	0.946	-0.235	0.621	-0.011
(Raw data)	**Sig.**	0.872	0.084	0.004	0.654	0.189	0.983
Diversity	**Pearson Correlation**	0.260	-0.502	0.968	-0.181	0.545	-0.181
(Ghost ranges includ.)	**Sig.**	0.574	0.251	0.002	0.808	0.264	0.731
Diversity*	**Pearson Correlation**	0.141	-0.745	0.946	0.064	0.419	-0.483
(Raw data)	**Sig.**	0.789	0.089	0.015	0.918	0.408	0.410
Diversity*	**Pearson Correlation**	0.077	-0.750	0.955	0.054	0.436	-0.452
(Ghost ranges includ.)	**Sig.**	0.884	0.086	0.011	0.931	0.387	0.445

Table 2. Correlation results between disparity and taxonomic diversity over time in osteostracans.