

Supplementary Material for

Niche Evolution and Phylogenetic Community Paleoecology of Late Ordovician Crinoids

by

Selina R. Cole

National Museum of Natural History, Smithsonian Institution and American Museum of Natural History

David F. Wright

National Museum of Natural History, Smithsonian Institution and American Museum of Natural History

Part of

Elements of Paleontology

edited by

Colin D. Sumrall

University of Tennessee

ISBNs: 9781108810012 (PB) 9781108893459 (OC)

Information on this title: www.cambridge.org/9781108810012

DOI: 10.1017/9781108893459

Elements of Paleontology

Supplemental Information for

Niche Evolution and Phylogenetic Community Paleoecology of Late Ordovician Crinoids

Selina R. Cole* and David F. Wright

*Corresponding author. Email: colesr@si.edu

1 Supplemental Methods

1.1 Measurement of ecomorphologic traits

For all specimens examined, ten quantitative traits were collected (where preserved) using the following measurement guidelines:

1. *Calyx width*: the maximum width of the calyx, which may either be at the top of the calyx where the arms become free or at some point below the top of the calyx.
2. *Calyx height (h)*: the distance between the base of the calyx to the point where the arms become free.
3. *Arm length (L)*: the distance between where the arms become free from the calyx to their distal tips.
4. *Number of arm openings*: the number of arms present at the upper margin of the calyx where the arms become free.
5. *Arm branching*: the maximum number of in line bifurcations occurring within a single arm.
6. *Terminal feeding appendages (Ω)*: The total number of feeding appendages on an individual, including arms and/or pinnules/ramules. Since it may not be practical or possible to count all feeding appendages because of the number of structures (hundreds to thousands in some species) and/or their exposure, this number is estimated from

empirical data. Total number of terminal feeding appendages is calculated differently for apinnulate versus pinnulate or ramulate taxa. For apinnulate taxa, the total number of feeding structures is equal to the total number of arm tips. For pinnulate or ramulate taxa, total number of terminal feeding structures is found by measuring the spacing of pinnules or ramules and then estimating the number of feeding structures given cumulative arm length (the summed length of all pinnule- or ramule-bearing portions of the arms). As a result, terminal number of feeding appendages for a crinoid with pinnulate or ramulate arms, is calculated by the following equation, using a 5 mm portion of the arm:

$$\Omega = \frac{\text{cumulative arm length} \times \text{arm number} \times \text{pinnules per 5 mm}}{5}$$

7. Brachial width: The width of a brachial at the midpoint of the arms.
8. Brachial height: The height of a brachial at the midpoint of the arms.
9. Pinnule/ramule density: The number of pinnules or ramules present in a 5 mm arm section at the midpoint of the arms.
10. Pinnule/ramule width: The width of a pinnule or ramule.

Measured traits were used to calculate three additional variables that relate to ecology using the methods described by Cole et al. (2019):

1. Calyx volume (V), calculated using the standard equation for a cone based on measurements of calyx radius (r , $\frac{1}{2}$ measured trait 1) and height (h , measured trait 2):

$$V = \frac{1}{3}\pi r^2 h$$

2. Filtration fan area (f_A), calculated using the Ausich (1980) equation with modifications by Cole (2017b), where L is arm length (measured trait 3):

$$f_A = \pi(L + r)^2 - \pi r^2$$

3. Filtration fan density (F_D), calculated by dividing the total number of terminal feeding appendages (Ω , measured trait 6) by the total area of the filtration fan (f_A):

$$f_D = \frac{\Omega}{f_A}$$

1.2 Sensitivity tests for missing data

Because ecological information is primarily extracted from skeletal features of the arms, species that are only represented by specimens with incomplete or absent arms may have extensive missing data. This can generate spurious results in a number of analyses, such as ecomorphospace occupation and disparity. Several of the species from the Bromide fauna have

missing or incomplete arms due to poor preservation, and thus were candidates for exclusion from the study. To determine the effect of missing data on results of this study, four different thresholds for vetting missing data were applied and compared. These thresholds were (1) all species included regardless of the amount of missing data, (2) only species with at least partial arms included, (3) only species with complete arms included, and (4) only complete species with no missing data included.

Vetting datasets based on the amount and type of missing data resulted in broadly similar plots of ecomorphospace occupation (Fig. S1). Although the relative distribution and position of species within ecomorphospace shifted, strong differentiation between subclasses was consistently recovered in both faunas across all four vetting thresholds. Within the Brechin fauna, there are only two species for which complete arms are not known. As a result, the different preservational thresholds applied for vetting had very little effect on ecomorphospace plots. Within the Bromide, however, a number of taxa are known only from incomplete material, including some that are represented by isolated calyces without arms attached. Between the first threshold (all taxa included regardless of missing data) and second threshold (only taxa with at least partial arms included), ecomorphospace occupation of species in the Bromide constricted and differentiation between subclasses became more defined. Subsequent vetting that removed taxa without complete arms (threshold 3) and those with any missing data (threshold 4) resulted in minimal changes to ecomorphospace occupation.

Based on these results of these sensitivity tests (Fig. S1), we determined the second threshold, inclusion of species with at least partial arms, was most appropriate for this study because it minimized the amount of missing data while also maximizing the number of species that can be reliably included. After excluding taxa that did not preserve at least partial arms, a total of 30 species remained in Bromide dataset. Of the seven taxa excluded from the Bromide, five were from Diplobathrida, one was from Euclidida, and one was from Porocrinoidea. Because all species in the Brechin had representatives with at least partial arms, no species were excluded from this fauna. Results presented in the main text use vetting threshold 2, which only includes species with at least partial arms.

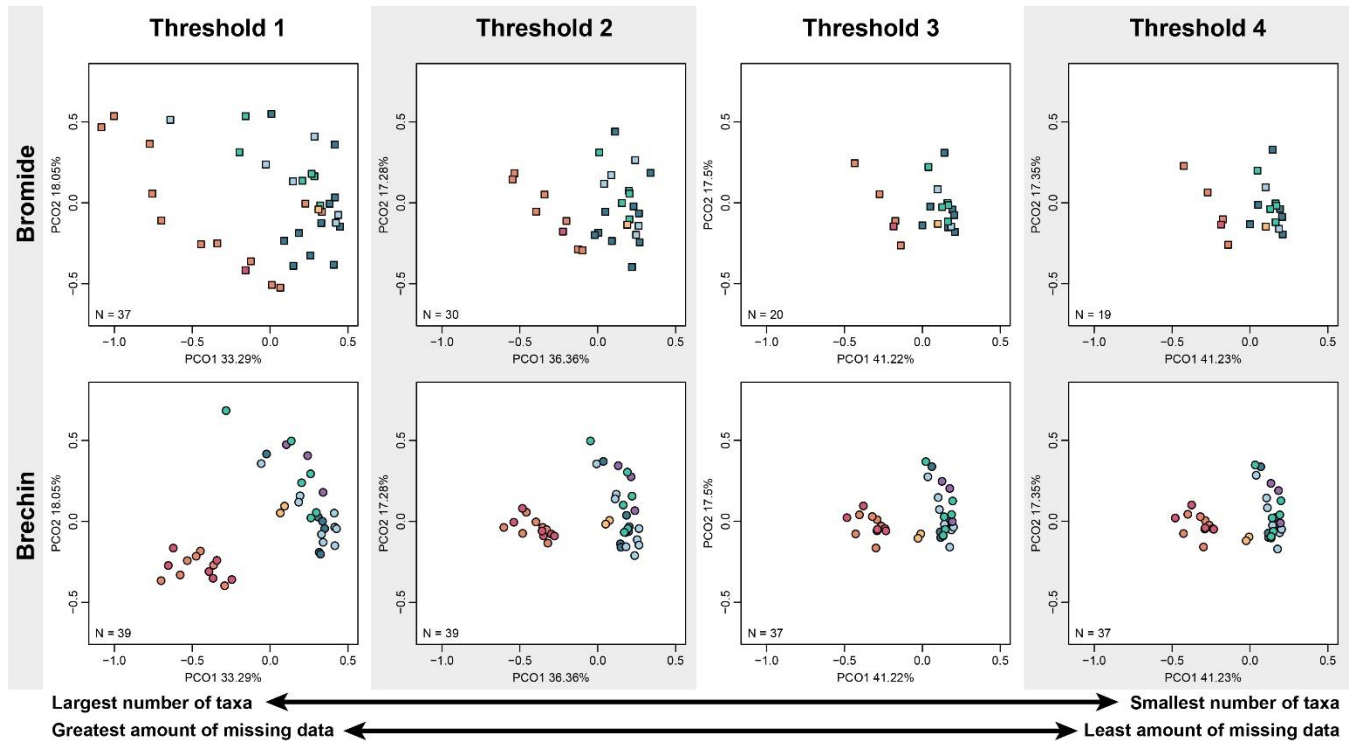


Figure S1. Ecomorphospace occupation plots of the Bromide fauna (upper panels) and the Brechin fauna (lower panels) with different thresholds for vetting based on the completeness of taxa (columns). For threshold 1, all species are included regardless of the level of completeness (i.e., some species have extensive missing data). For threshold 2, only taxa with at least partial arms are included; this threshold was used for the analyses presented in the main text of the paper. For threshold 3, only taxa with complete arms are included. For threshold 4, only taxa with no missing data are included. Sample size after vetting under each threshold is given in the bottom left of each panel.

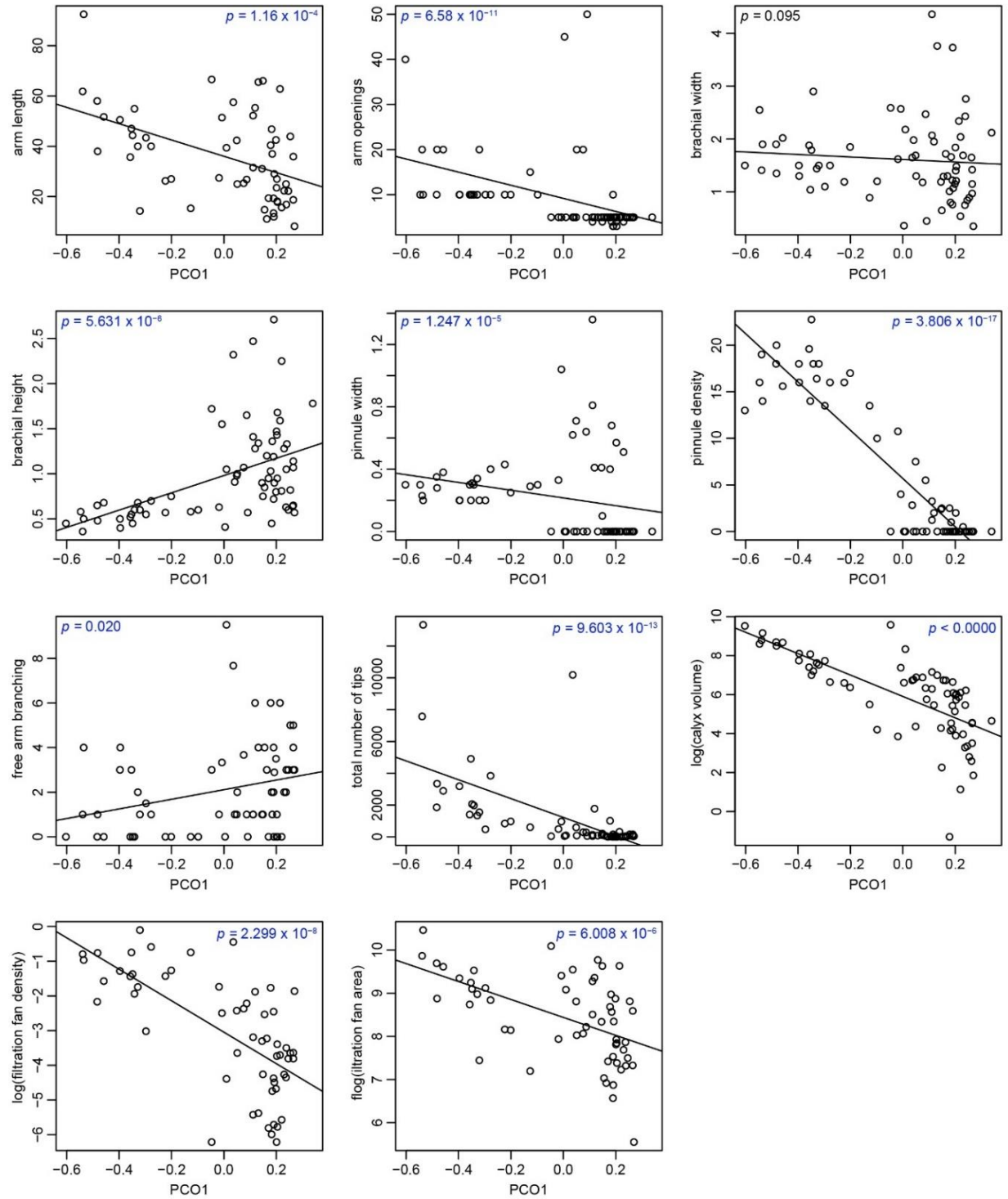


Figure S2. Correlations between measured traits and the first principal component recovered from analysis of the Bromide and Brechin faunas. *P*-values for Spearman's rank correlation tests are given in each panel; values in blue text are statistically significant at $p < 0.05$.

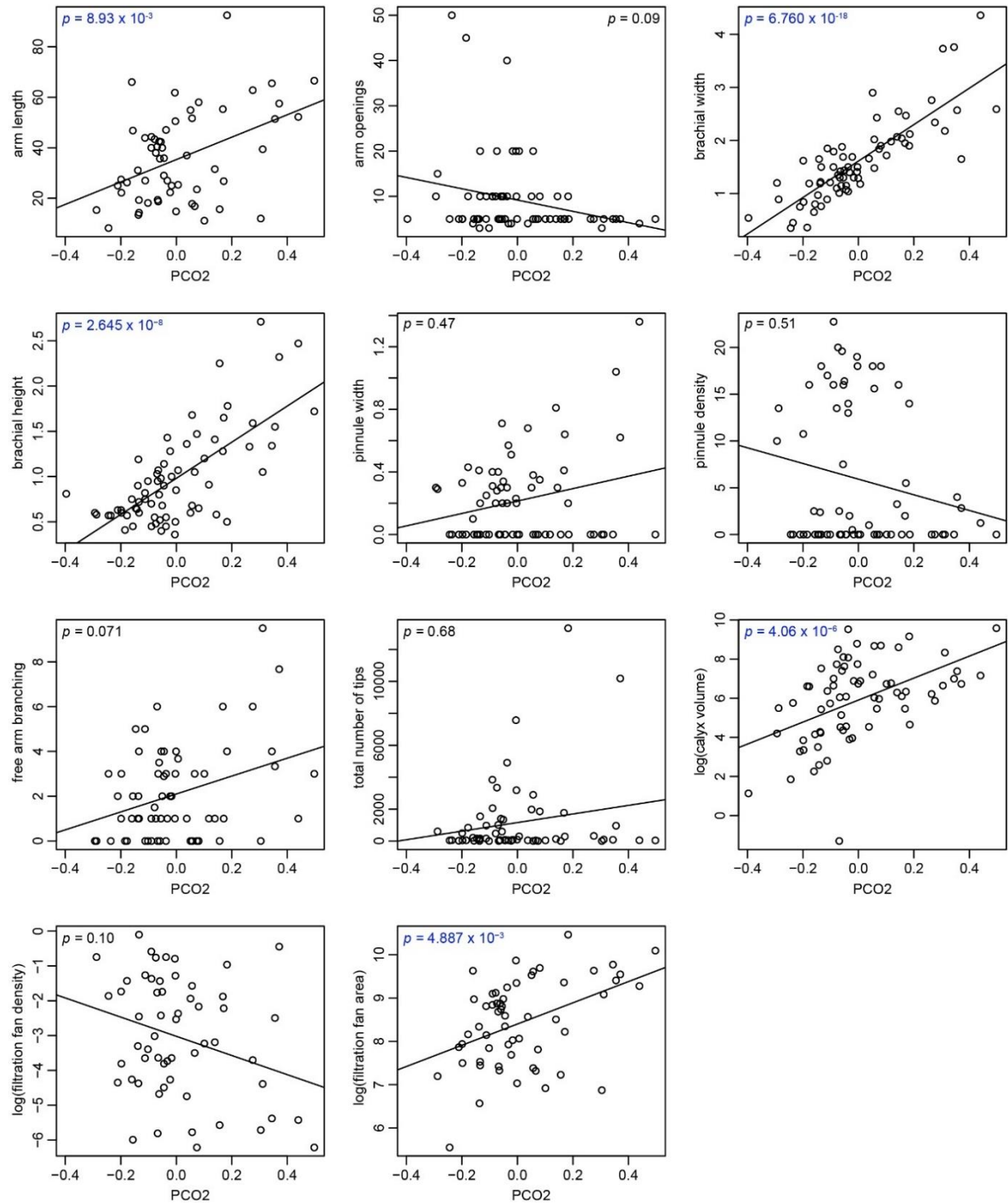


Figure S3. Correlations between measured traits and the second principal component recovered from analysis of the Bromide and Brechin faunas. *P*-values for Spearman's rank correlation tests are given in each panel; values in blue text are statistically significant at $p < 0.05$.

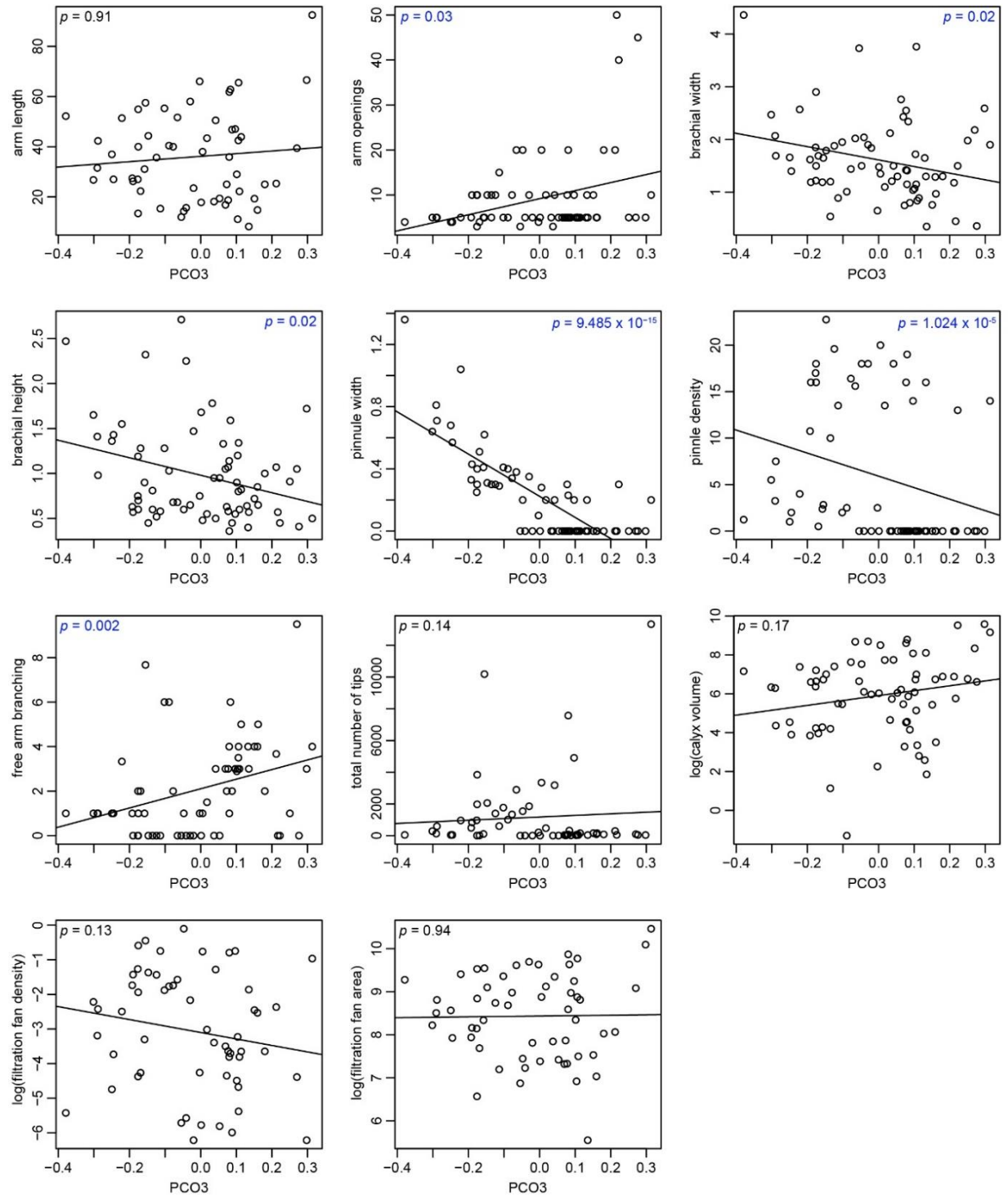


Figure S4. Correlations between measured traits and the third principal component recovered from analysis of the Bromide and Brechin faunas. P -values for Spearman's rank correlation tests are given in each panel; values in blue text are statistically significant at $p < 0.05$.

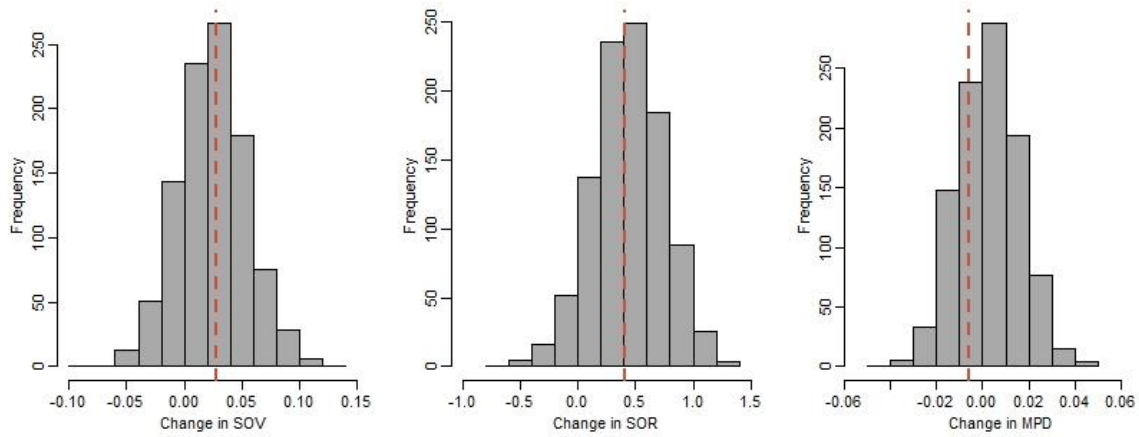


Figure S5. Changes in disparity between the Bromide and Brechin faunas. Histograms show distribution of bootstrapped values for changes in disparity, and red dashed lines give observed changes in disparity calculated between the Bromide and Brechin. No statistically significant change in disparity is observed across any of the disparity indices ($p=0.54$, 0.48 , and 0.2 , respectively).

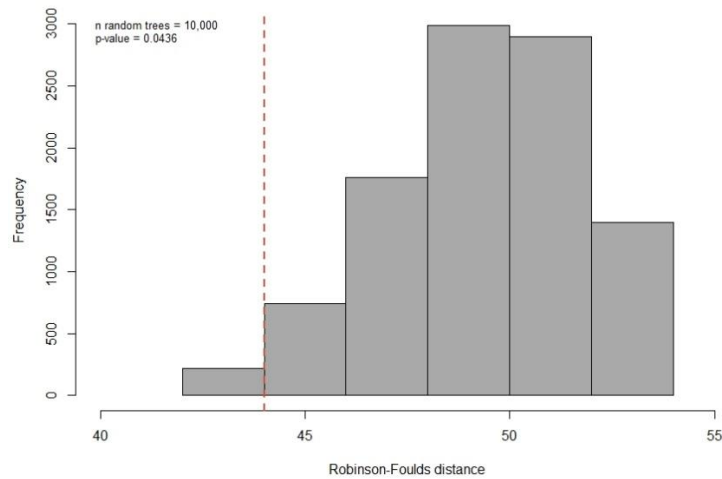


Figure S6. Histogram of Robinson-Foulds distances between the dendrogram produced from the cluster analysis and 10,000 random phylogenies. Dashed red line indicates the observed RF distance between the cluster analysis and inferred phylogeny (empirical distance), which is statistically significant ($p=0.043$).

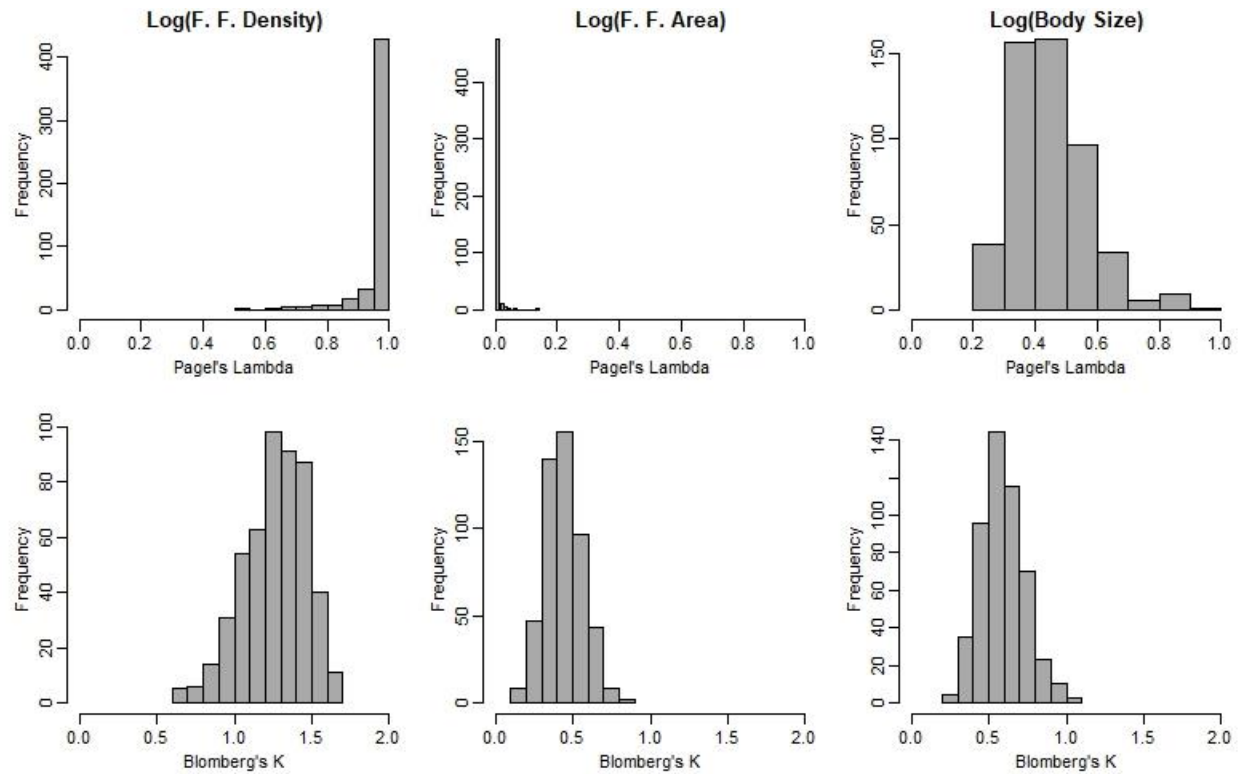


Figure S7. Phylogenetic signal of major ecological traits. Histograms give results for two metrics of phylogenetic signal, Pagel's λ (upper panels) and Blomberg's K (lower panels), calculated over a distribution of 100 time-scaled trees. Values for phylogenetic signal are for filtration fan density (left panels), filtration fan area (middle panels), and body size (right panels).

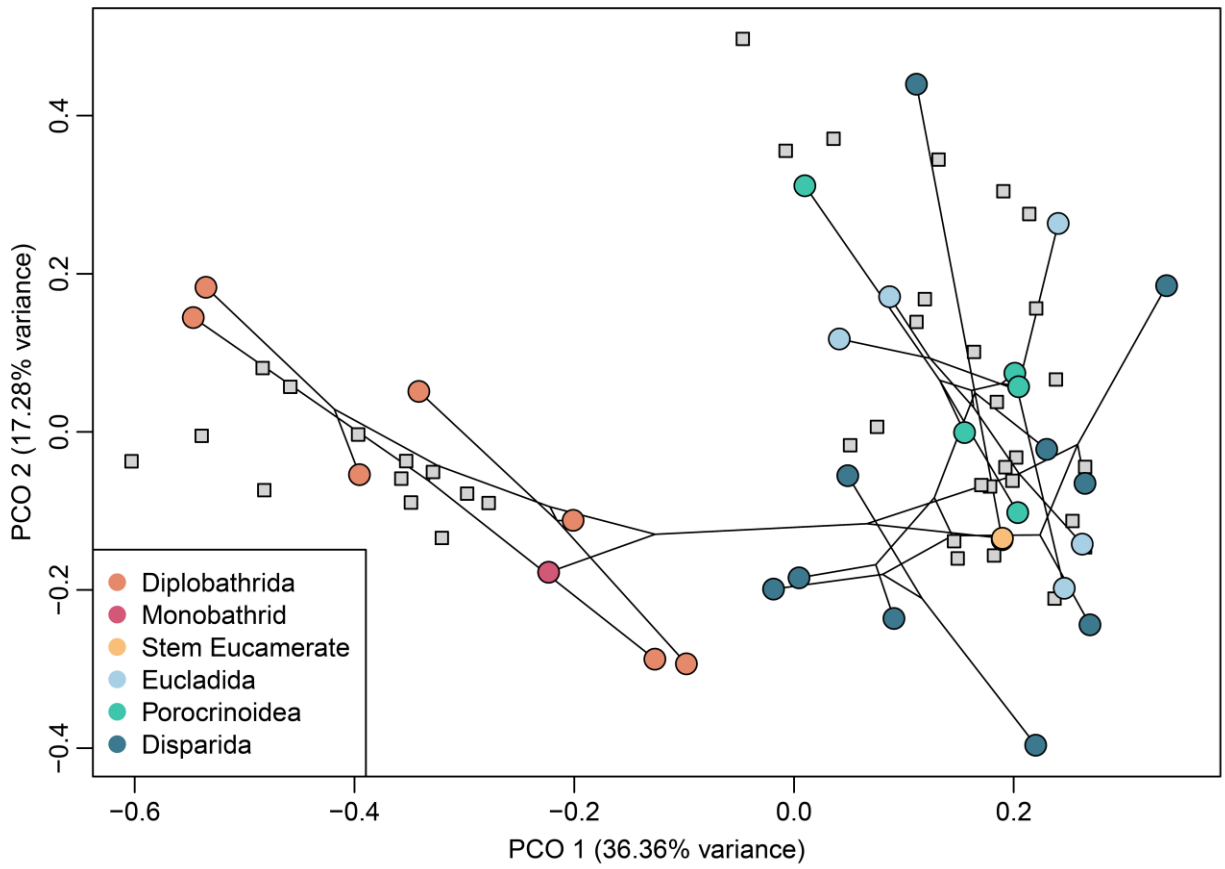


Figure S8. Phylomorphospace of the Bromide fauna. Colored points represent species from the Bromide fauna, and grey points represent species from the Brechin fauna.