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Morphological diversity in tenrecs (Afrosoricida, Tenrecidae): Comparing tenrec skull diversity to their closest relatives

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Morphological diversity is often studied qualitatively. However, to truly understand the evolution of exceptional diversity, it is important to take a quantitative approach instead of relying on subjective, qualitative assessments. Here, we present a quantitative analysis of morphological diversity in a Family of small mammals, the tenrecs (Afrosoricida, Tenrecidae).

Tenrecs are often cited as an example of an exceptionally morphologically diverse group. However, this assumption has not been tested quantitatively. We use geometric morphometric analyses of skull shape to test whether tenrecs are more morphologically diverse than their closest relatives, the golden moles (Afrosoricida, Chrysochloridae). Tenrecs occupy a wider range of ecological niches than golden moles so we predict that they will be more morphologically diverse.

Contrary to our expectations, We find that tenrec skulls are only more morphologically diverse than golden moles when measured in lateral view. Furthermore, similarities among the species-rich *Microgale* tenrec Genus appear to mask higher morphological diversity in the rest of the Family. These results reveal new insights into the morphological diversity of tenrecs and highlight the importance of using quantitative methods to test qualitative assumptions about patterns of morphological diversity.

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7 Introduction

8 Analysing patterns of morphological diversity has important
9 implications for our understanding of ecological and evolutionary traits.
10 Species morphology can influence niche occupancy and affect speciation
11 and diversification rates through time (Price et al., 2012). High
12 morphological diversity is also a unifying (Losos and Mahler, 2010;
13 Olson and Arroyo-Santos, 2009), although not defining (Glor, 2010;
14 Olson and Arroyo-Santos, 2009), characteristic of adaptive radiations.
15 Furthermore, analysing morphological convergences in groups such as
16 freshwater cichlid fish (Muschick et al., 2012) and anole lizards (Mahler
17 et al., 2013) provides insights into the relative repeatability of evolution
18 (Losos, 2011).

19 Although studies of morphological diversity have clear implications
20 for our understanding of ecological and evolutionary patterns, apart
21 from a few examples (e.g. Ruta et al., 2013; Goswami et al., 2011;
22 Brusatte et al., 2008), it is still common to study morphological diversity
23 from a qualitative rather than quantitative perspective. However, we
24 need to quantify the morphological similarities and differences among
25 species to gain a better understanding of their ecological interactions
26 and evolutionary history. Unfortunately, morphological diversity is
27 difficult to quantify. Studies are inevitably constrained to measure the
28 diversity of specific traits rather than overall morphologies (Roy and
29 Foote, 1997). In addition, our perception of morphological diversity is
30 influenced by the trait being used, and results may depend on the

particular trait being analysed (Foth et al., 2012). Furthermore, linear measurements of morphological traits can restrict our understanding of overall morphological variation; a distance matrix of measurements among specific points is unlikely to give a completely accurate representation of a three dimensional structure (Rohlf and Marcus, 1993). Geometric morphometric approaches can circumvent some of these issues by using a system of Cartesian landmark coordinates to define anatomical points (Adams et al., 2004). This method captures more of the true, overall anatomical shape of particular structures (Mitteroecker and Gunz, 2009). These more detailed approaches are useful tools for studying patterns of morphological diversity.

Here we apply geometric morphometric techniques to quantify morphological diversity in a Family of small mammals, the tenrecs. Tenrecs (Afrosoricida, Tenrecidae) are a morphologically diverse group that is commonly cited as an example of both convergent evolution and an adaptive radiation (Soarimalala and Goodman, 2011; Eisenberg and Gould, 1969). The Family is comprised of 34 species, 31 of which are endemic to Madagascar (Olson, 2013). Body masses of tenrecs span three orders of magnitude (2.5 to > 2,000g); a greater range than all other Families, and most Orders, of living mammals (Olson and Goodman, 2003). Within this vast size range there are tenrecs which convergently resemble shrews (*Microgale* tenrecs), moles (*Oryzorictes* tenrecs) and hedgehogs (*Echinops* and *Setifer* tenrecs, Eisenberg and Gould, 1969). Their similarities include examples of morphological, behavioural and ecological convergence (Soarimalala and Goodman,

2011). Tenrecs are one of only four endemic mammalian clades in Madagascar and the small mammal species they resemble are absent from the island (Garbutt, 1999). Therefore, it appears that tenrecs represent an adaptive radiation of species which filled otherwise vacant ecological niches (Soarimalala and Goodman, 2011).

Although tenrecs are often cited as an example of both an adaptive radiation and exceptional convergent evolution (Soarimalala and Goodman, 2011; Eisenberg and Gould, 1969), these claims have not been investigated quantitatively. There are qualitative similarities among the hind limb morphologies of tenrecs and several other unrelated species with similar locomotory styles (Salton and Sargis, 2009) but the degree of morphological similarity has not been established. Morphological diversity is an important feature of adaptive radiations (Losos and Mahler, 2010) and it also informs our understanding of convergent phenotypes (Muschick et al., 2012). Therefore, it is important to quantify patterns of morphological diversity in tenrecs to gain an insight into their evolution.

We present the first quantitative study of patterns of morphological diversity in tenrecs. We use geometric morphometric techniques (Rohlf and Marcus, 1993) to compare cranial morphological diversity in tenrecs to that of their closest relatives, the golden moles (Afrosoricida, Chrysochloridae). We expect tenrecs to be more morphologically diverse than golden moles because tenrecs occupy a wider variety of ecological niches. The tenrec Family includes terrestrial, semi-fossorial,

80 semi-aquatic and semi-arboreal species (Soarimalala and Goodman,
81 2011). In contrast, all golden moles occupy very similar, fossorial
82 ecological niches (Bronner, 1995). Greater ecological variety is often
83 (though not always) correlated with higher morphological diversity
84 (Losos and Mahler, 2010). However, our results reveal that, in skulls at
85 least, morphological diversity in tenrecs is not as great as it first appears.

86 **Materials and Methods**

87 Our methods involved i) data collection, ii) geometric morphometric
88 analyses and iii) estimating morphological diversity. For clarity, Figure 1
89 summarises all of these steps and we describe them in detail below.

90 **Data collection**

91 One of us (SF) collected data from five museums: Natural History
92 Museum, London (BMNH), Smithsonian Institute Natural History
93 Museum, Washington D.C. (SI), American Museum of Natural History,
94 New York (AMNH), Museum of Comparative Zoology, Cambridge M.A.
95 (MCZ) and Field Museum of Natural History, Chicago (FMNH). We
96 used the taxonomy in Wilson & Reeder's Mammal Species of the World
97 (2005), except for the recently discovered tenrec species *Microgale jobihely*
98 (Goodman et al., 2006). We photographed all of the tenrec and golden
99 mole skulls available in the collections. This included 31 of the 34
100 species in the tenrec Family (Olson, 2013) and 12 of the 21 species of

101 golden moles (Wilson and Reeder, 2005).

102 We took pictures of the skulls using photographic copy stands. To
 103 take possible light variability into account, we took a photograph of a
 104 white sheet of paper each day and used the custom white balance
 105 function on the camera to set the image as the baseline "white"
 106 measurement for those particular light conditions. We photographed the
 107 specimens with a Canon EOS 650D camera fitted with a EF 100 mm
 108 f/2.8 Macro USM lens and using a remote control (Hähnel Combi TF) to
 109 avoid camera shake. We photographed the specimens on a black
 110 material background with a light source in the top left-hand corner of
 111 the photograph. We used small bean bags to hold the specimens in
 112 position to ensure that they lay in a flat plane relative to the camera, and
 113 used the grid-line function on the live-view display screen of the camera
 114 to position the specimens in the centre of each image.

115 All skulls were photographed in three views: dorsal, ventral and
 116 lateral (right side) (Figure 1). When the right sides of the skulls were
 117 damaged or incomplete, we photographed the left sides and later
 118 reflected the images (e.g. Barrow and Macleod, 2008). After taking the
 119 photographs we converted the raw files to binary (grey scale) images
 120 and re-saved them as TIFF files (uncompressed files preserve greater
 121 detail, RHOI, 2013). Photographs of the specimens from the American
 122 Museum of Natural History and the Smithsonian Institute Natural
 123 History Museum are available on figshare (dorsal; Finlay and Cooper
 124 (2013a), ventral; Finlay and Cooper (2013c) and lateral; Finlay and

125 Cooper (2013b)). Copyright restrictions from the other museums prevent
126 public sharing of their images but they are available on request.

127 **Geometric morphometric analyses**

128 We used a combination of landmark and semilandmark approaches to
129 assess the shape variability in the skulls. We used the TPS software suite
130 (Rohlf, 2013) to digitise landmarks and curves on the photos. We set the
131 scale on each image individually to standardise for the different camera
132 heights used when photographing the specimens. We created separate
133 data files for each of the three morphometric analyses (dorsal, ventral
134 and lateral views). One of us (SF) digitised landmarks and
135 semilandmark points on every image individually. Some specimens
136 were too damaged to use in particular views so there were a different
137 total number of images for each analysis. Our final data sets included
138 photographs of 182 skulls in dorsal view (148 tenrecs and 34 golden
139 moles), 173 skulls in ventral view (141 tenrecs and 32 golden moles) and
140 171 skulls in lateral view (140 tenrecs and 31 golden moles).

141 Figure 2 depicts that landmarks and curves which we used for each
142 skull view. For landmarks defined by dental structures, we used
143 published dental sources (Repenning, 1967; Eisenberg and Gould, 1969;
144 Nowak, 1983; MacPhee, 1987; Knox Jones and Manning, 1992; Davis and
145 Schmidly, 1997; Quéroutil et al., 2001; Nagorsen, 2002; Wilson and
146 Reeder, 2005; Goodman et al., 2006; Karataş et al., 2007; Hoffmann and
147 Lunde, 2008; Asher and Lehmann, 2008; Muldoon et al., 2009; Lin and

148 Motokawa, 2010) where available to identify the number and type of
149 teeth in each species. Detailed descriptions of the landmarks can be
150 found in the supplementary material.

151 When using semilandmark approaches there is a potential problem
152 of over-sampling: simpler structures will require fewer semilandmarks
153 to accurately represent their shape (MacLeod, 2012). To ensure that we
154 applied a uniform standard of shape representation to each outline
155 segment (i.e. that simple structures would not be over-represented and
156 more complex features would not be under-represented), we followed
157 the method outlined by MacLeod (2012) to determine the minimum
158 number of semilandmark points which would give accurate
159 representations of morphological shape.

160 After creating the files with the landmarks and semilandmarks
161 placed on each photograph, we used TPSUtil (Rohlf, 2012) to create
162 "sliders" files that defined which points in the TPS files should be
163 treated as semilandmarks (Zelditch et al., 2012). We combined the
164 landmarks and taxonomic identification files into a single
165 morphometrics data object and carried out all further analyses in R
166 version 3.1.1 (R Core Team, 2014).

167 Next we used the `gpagen` function in the `geomorph` package (Adams
168 et al., 2013) to run a general Procrustes alignment (Rohlf and Marcus,
169 1993) of the landmark coordinates while sliding the semilandmarks by
170 minimising Procrustes distance (Bookstein, 1997). We used these
171 Procrustes-aligned coordinates of all specimens to calculate average

172 shape values for each species which we then used for a principal
173 components (PC) analysis with the `plotTangentSpace` function (Adams
174 et al., 2013). We selected the number of principal component (PC) axes
175 that accounted for 95% of the variation in the data (Figure 1) and used
176 these axes to estimate morphological diversity in each Family.

177 The majority of tenrec species (19 out of 31 in our data) belong to the
178 *Microgale* (shrew-like) Genus that has relatively low morphological
179 diversity (Soarimalala and Goodman, 2011; Jenkins, 2003). This may
180 mask signals of higher morphological diversity among other tenrecs. To
181 test this, we created a subset of the tenrec data that included just five of
182 the *Microgale* species, each representing one of the five sub-divisions of
183 *Microgale* outlined by Soarimalala & Goodman (2011), i.e. small,
184 small-medium, medium, large and long-tailed species. We repeated the
185 general Procrustes alignment described above using this reduced data
186 set. We then compared the morphological diversity of the full data set
187 (31 species of tenrec) or a reduced data set with just 17 species of tenrec
188 (five *Microgale* and 12 non-*Microgale* species; Figure 1) to that of the 12
189 species of golden moles.

190 **Estimating morphological diversity**

191 We grouped the PC scores for tenrecs and golden moles separately so
192 that we could estimate the diversity of each Family and then compare
193 the two groups (Figure 1). We compared morphological diversity in two
194 ways. First, we used non parametric multivariate analysis of variance

(npMANOVA; Anderson, 2001) to test whether tenrecs and golden moles occupied significantly different positions within the morphospaces defined by the PC axes that accounted for 95% of the overall variation in the data (e.g. Serb et al., 2011; Ruta et al., 2013). A significant difference between the two Families would indicate that they have unique morphologies which do not overlap. Second, we compared morphological diversity within tenrecs to the diversity within golden moles. We define morphological diversity as the mean Euclidean distance (sum of squared differences) between each species and its Family centroid (Figure 3). This is summarised in the equation below where n is the number of species in the Family, i is the number of PC axes and c is the average PC score for each axis (the centroid).

$$Diversity = \frac{\sqrt{\sum (PCn_i - PCc_i)^2}}{n} \quad (1)$$

If tenrecs are more morphologically diverse than golden moles, then they should be more dispersed within the morphospaces and have, on average, higher values of mean Euclidean distance.

One possible issue with these analyses is that the two Families have unequal sample sizes: 31 (or a subset of 17) tenrec species compared to just 12 golden mole species. Morphological diversity is usually decoupled from taxonomic diversity (e.g. Ruta et al., 2013; Hopkins, 2013) so larger groups are not necessarily more morphologically diverse. However, comparing morphological diversity in tenrecs to the diversity of a smaller Family could still bias the results. We used pairwise

217 permutation tests to account for this potential issue.

218 We tested the null hypothesis that tenrecs and golden moles have the
219 same morphological diversity (the same mean Euclidean distance to the
220 Family centroid). If this is true, when we randomly assign the group
221 identity of each species (i.e. shuffle the "tenrec" and "golden mole"
222 labels) and then re-compare the morphological diversity of the two
223 groups, there should be no significant difference between these results
224 and those obtained when the species are assigned to the correct
225 groupings.

226 We performed this shuffling procedure (random assignation of group
227 identity) 1000 times and calculated the difference in morphological
228 diversity between the two groups for each permutation. This generated
229 a distribution of 1000 values which are calculations of the differences in
230 morphological diversity under the assumption that the null hypothesis
231 (equal morphological diversity in the two Families) is true. This method
232 automatically accounts for differences in sample size because shuffling
233 of the group labels preserves the sample size of each group: there will
234 always be 12 species labelled as "golden mole" and then, depending on
235 the analysis, either 31 or 17 species labelled as "tenrec". Therefore, the
236 1000 permuted values of differences in morphological diversity create a
237 distribution of the expected difference in diversity between a group of
238 sample size 31 (or 17 in the case of the tenrec data subset) compared to a
239 group of sample size 12 under the null hypothesis that the two groups
240 have the same morphological diversity. We compared the observed

measures of the differences in morphological diversity between the two Families to these null distributions to determine whether there were significant differences after taking sample size into account (two-tailed t test). Data and code for all of our analyses are available on GitHub (Finlay and Cooper, 2015).

Results

Figure 4 depicts the morphospaces defined by the first two principal component (PC) axes from our principal components analyses (PCAs) of skull and mandible morphologies. The PCAs are based on the average Procrustes-superimposed shape coordinates for skulls in three views (dorsal, ventral and lateral).

To compare morphological diversity in the two Families, we used the PC axes which accounted for 95% of the cumulative variation in each of the skull analyses: dorsal (n=6 axes), ventral (n=7 axes) and lateral (n=7 axes). First, we compared the position of each Family within the morphospace plots. Tenrecs and golden moles occupy significantly different positions in the dorsal (npMANOVA: $F_{1,42}=68.13$, $R^2=0.62$, $p=0.001$), ventral (npMANOVA: $F_{1,42}=103.33$, $R^2=0.72$, $p=0.001$) and lateral (npMANOVA: $F_{1,42}=76.7$, $R^2=0.65$, $p=0.001$) skull morphospaces, indicating that the Families have very different, non-overlapping cranial and mandible morphologies (Figure 4). Second, we compared the morphological diversity within each Family. Based on our measures of

mean Euclidean distance to the Family centroids, tenrec skulls are more morphologically diverse than golden mole skulls when they are measured in lateral view but not in dorsal or ventral view (Table 1). In contrast, when we analysed morphological diversity of skulls within the sub-sample of 17 tenrecs (including just five *Microgale* species) compared to the 12 golden mole species, we found that tenrec skulls were significantly more morphologically diverse than golden moles in all analyses (Table 1). The pairwise permutation tests for each analysis confirmed that differences in morphological diversity were not artefacts of differences in sample size (Table 2)

Discussion

Tenrecs are often cited as an example of a mammalian group with high morphological diversity (Olson, 2013; Soarimalala and Goodman, 2011; Eisenberg and Gould, 1969). They are also more ecologically diverse than their closest relatives (Soarimalala and Goodman, 2011; Bronner, 1995) so we predicted that they would be more morphologically diverse than golden moles. However, our results do not support our original prediction, highlighting the importance of quantitative tests of perceived morphological patterns.

In our full analysis, tenrecs only had higher morphological diversity than golden moles when the skulls were measured in lateral view (Table 1). There was no difference in morphological diversity when we

285 analysed the skulls in dorsal or ventral views. This is most likely due to
 286 our choice of landmarks. The two outline curves in lateral view (Figure
 287 2) emphasise morphological variation in the back and top of the skulls.
 288 These curves summarise overall shape variation but they do not identify
 289 clear anatomical differences because they are defined by relative features
 290 rather than homologous structures (Zelditch et al., 2012). Therefore, high
 291 morphological diversity in tenrecs when analysed in this view may not
 292 indicate biologically or ecologically relevant variation. These lateral
 293 aspects of the skull morphology were not visible in the dorsal and
 294 ventral photographs so they could not be included in those analyses. In
 295 contrast, our landmarks in the dorsal, and particularly ventral, views
 296 focus on morphological variation in the overall outline shape of the sides
 297 of the skull and palate (Figure 2). The result that tenrecs are no more
 298 diverse than golden moles in these areas makes intuitive sense: most
 299 tenrecs have broad, non-specialised diets (Olson, 2013) so there is no
 300 obvious functional reason why they should have particularly diverse
 301 palate morphologies. The different results for our analysis of lateral
 302 skull morphologies compared to dorsal and ventral views highlight the
 303 importance of using multiple approaches when studying 3D
 304 morphological shape using 2D geometric morphometrics techniques
 305 (Arnqvist and Mårtensson, 1998).

306 Landmark choice and placement will inevitably influence the results
 307 of a geometric morphometrics study. Our interest in broad-scale,
 308 cross-taxonomic comparisons of cranial morphology constrained our
 309 choice of landmarks to those that could be accurately identified in many

different species (e.g. Ruta et al., 2013; Goswami et al., 2011; Wroe and Milne, 2007). In contrast, studies that use skulls to characterise morphological variation within species (e.g. Blagojević and Milošević-Zlatanović, 2011; Bornholdt et al., 2008) or to delineate species boundaries within a clade (e.g. Panchetti et al., 2008) tend to focus on more detailed, biologically homologous landmarks (Zelditch et al., 2012). Repeating our analyses with a narrower taxonomic focus may give greater insight into the specific morphological differences among subgroups of tenrecs and golden moles.

In addition to the differences among the three skull views, our results indicate that, in skulls at least, the overall morphological diversity within tenrecs is not as large as is often assumed (e.g. Eisenberg and Gould, 1969; Olson, 2013). Studies of morphological variation are sensitive to the sampling used. If a particular morphotype is over-represented then the similarities among those species will reduce the overall morphological variation within the group (Foote, 1991). This appears to be the case for our data; it was only when we included a sub-sample of *Microgale* tenrecs that we found higher morphological diversity in tenrecs compared to golden moles across all three skull analyses (Table 1). While there are clear physical differences among Family members (Olson, 2013; Eisenberg and Gould, 1969), the majority of tenrecs are very morphologically similar (Jenkins, 2003) so morphological diversity in the Family as a whole is not as large as it first appears.

The goal of our study was to quantify morphological variation in

tenrecs instead of relying on subjective assessments of their high morphological diversity (Olson, 2013; Soarimalala and Goodman, 2011; Eisenberg and Gould, 1969). However, it is difficult to quantify overall morphological diversity because any study is inevitably constrained by its choice of specific traits (Roy and Foote, 1997). Variation in skull shape is only one aspect of overall morphology. Quantifying variation in other morphological traits could yield different patterns. Therefore future work should extend our approach beyond skulls to gain a more complete understanding of the overall morphological diversity of tenrecs and golden moles. While recognising these limitations, our results provide valuable insights into the differences between subjective and quantitative assessments of morphological diversity.

Conclusions

We have presented the first quantitative investigation of morphological diversity in tenrecs. Our results indicate that, overall, tenrec skulls are not more morphologically diverse than golden moles and that similarities among the species rich *Microgale* tenrecs mask signals of higher morphological diversity among the rest of the Family. Of course the results presented here are restricted to just one axis of morphological variation and further analysis of other traits is required. However, our findings provide a foundation for future investigations and represent a significant step towards a more quantitative understanding of patterns of morphological and evolutionary diversity in tenrecs.

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Figure 1: Flowchart diagram of data collection and analysis

Summary of the main steps in our data collection, processing and analysis protocol. Note that the analyses were repeated separately for each set of photographs: skulls in dorsal, ventral and lateral views. The dashed arrows refer to the stage at which we selected a subsample of the tenrecs (including just five species of the *Microgale* Genus) so that we could compare the morphological diversity of this reduced subsample of tenrec species to the diversity of golden moles.

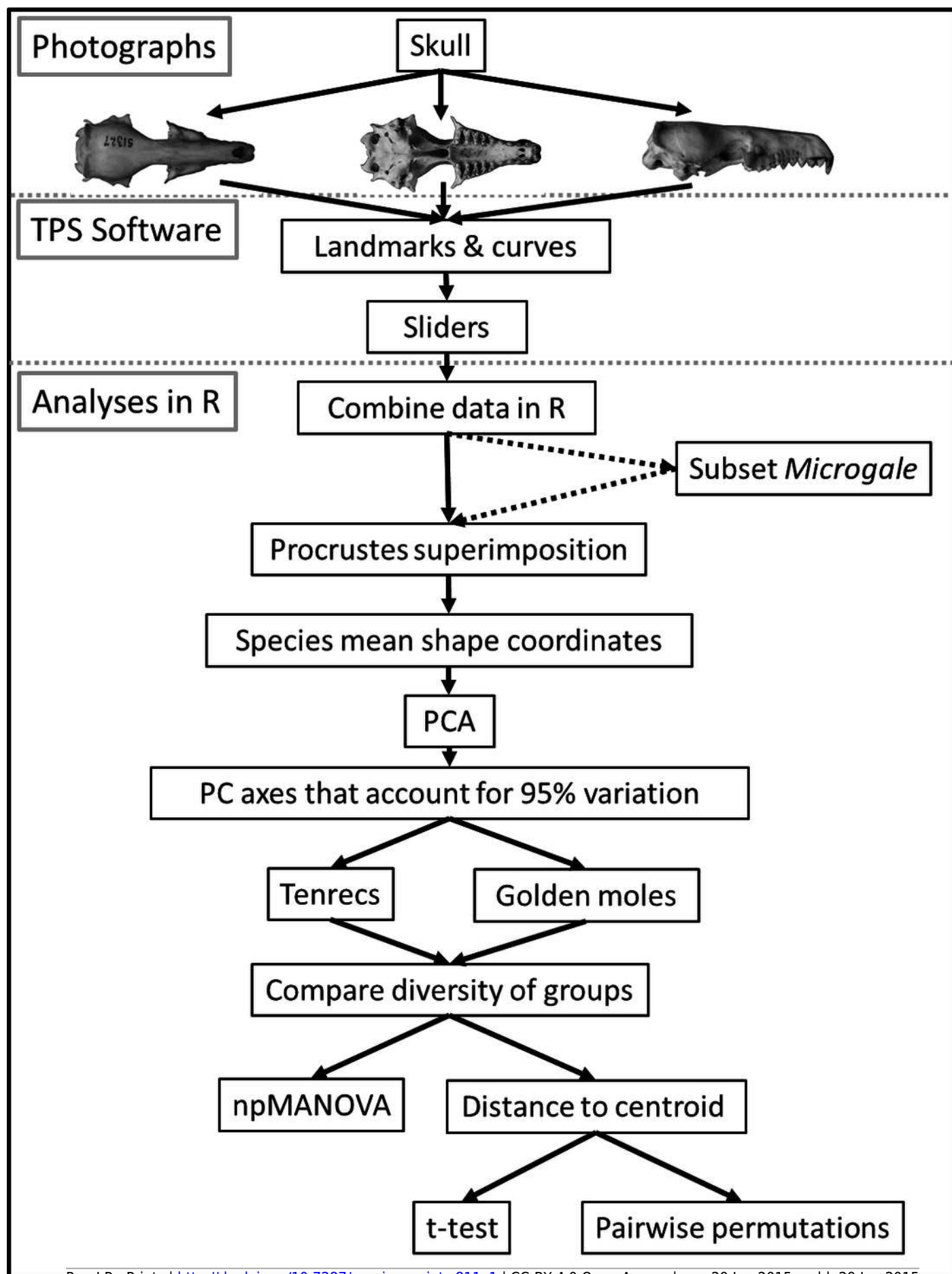


Figure 2: Skulls: dorsal, ventral and lateral landmarks

Landmarks (numbered points) and curves (outlines) for the skulls in dorsal, ventral and lateral view. See Supplemental Information for detailed landmark descriptions. The skulls are two different specimens of *Potamogale velox* (otter shrew tenrec), museum accession numbers AMNH 51327 (dorsal picture) and BMNH 1934.6.16.2 (ventral and lateral pictures).

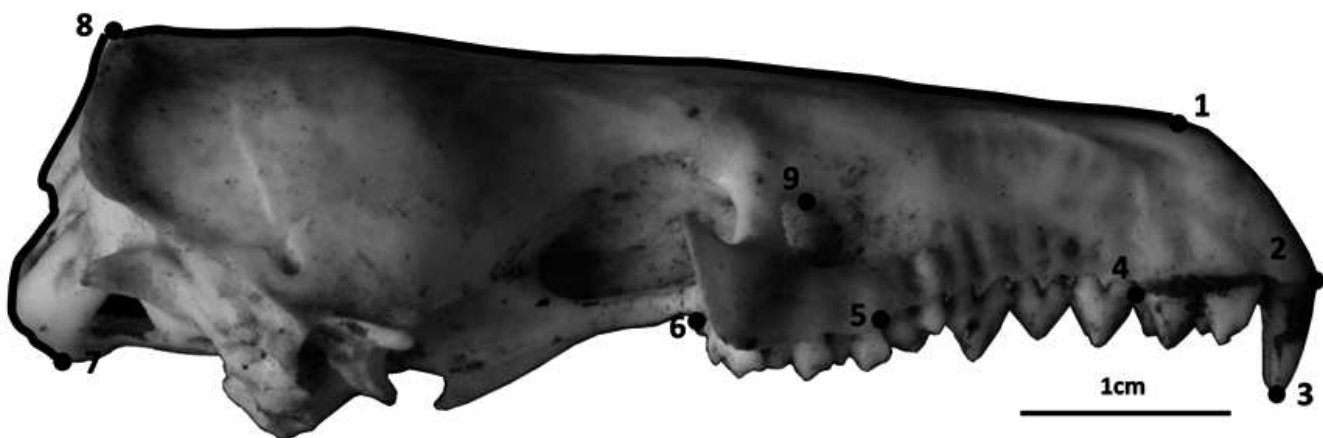
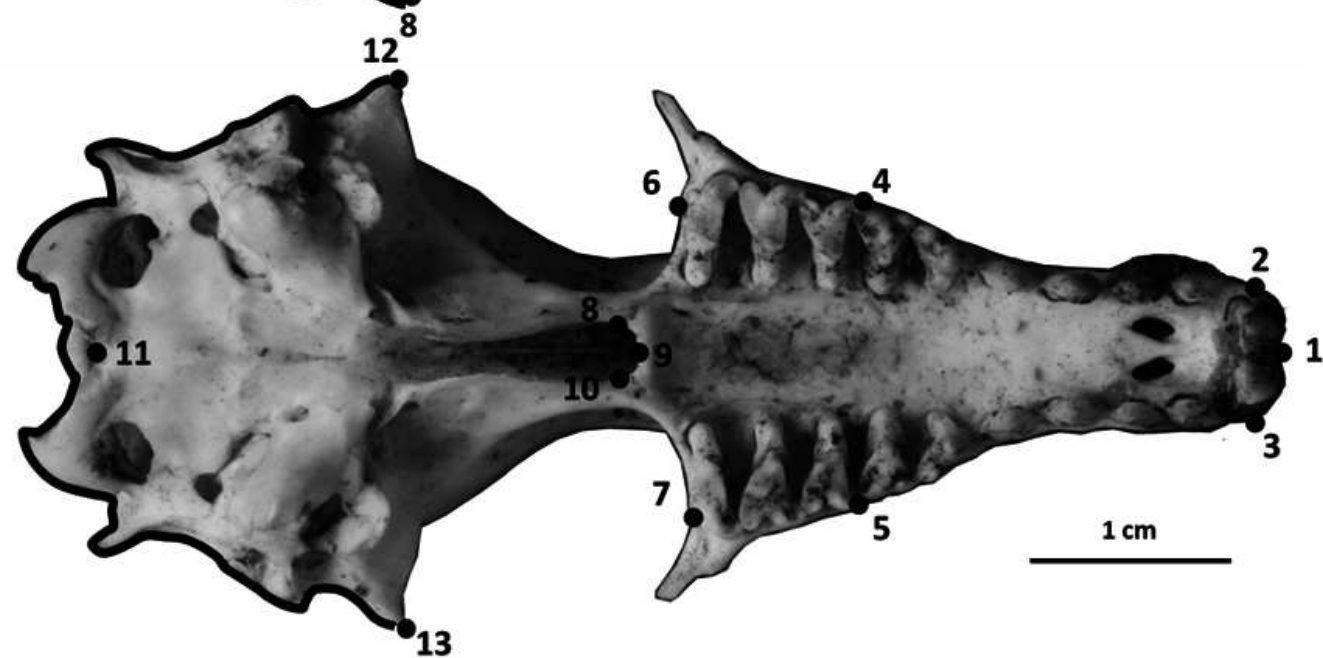
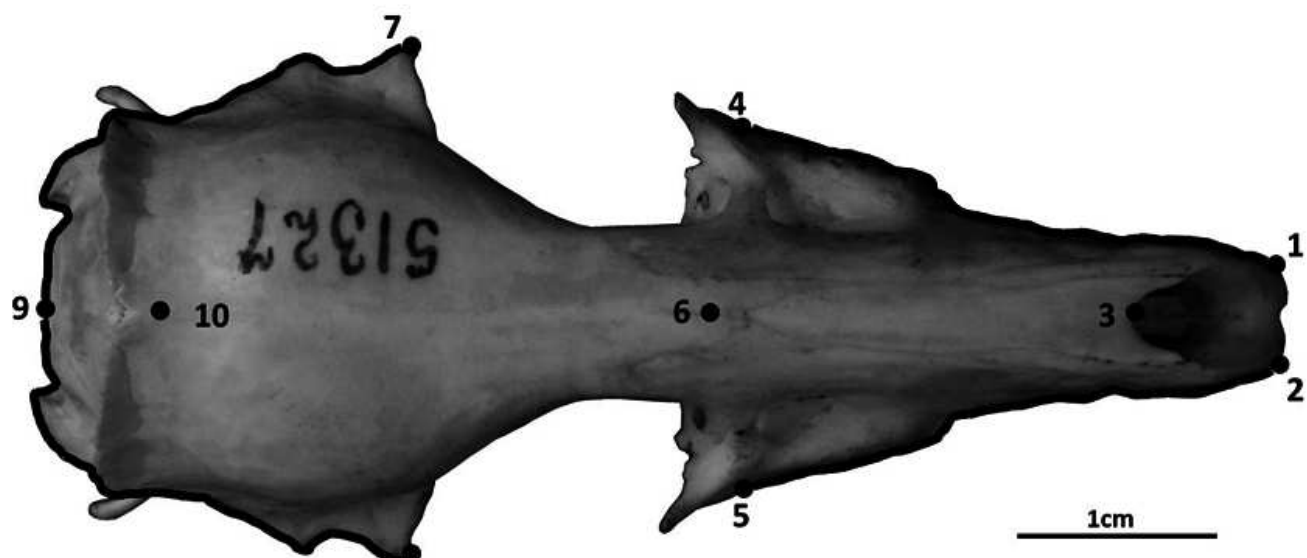


Figure 3: Calculating diversity as mean Euclidean distance to Family centroid.

Estimating morphological diversity as the mean Euclidean distance between each species and the Family centroid. Every species had scores on the principal components (PC) axes that accounted for 95\% of the variation in the principal components analysis. The number of axes (PCn) varied for each analysis but they were the same within a single analysis. PC scores were used to calculate the Euclidean distance from each species to the Family centroid (average PC scores for the entire Family). Morphological diversity of the Family is the average value of these Euclidean distances.

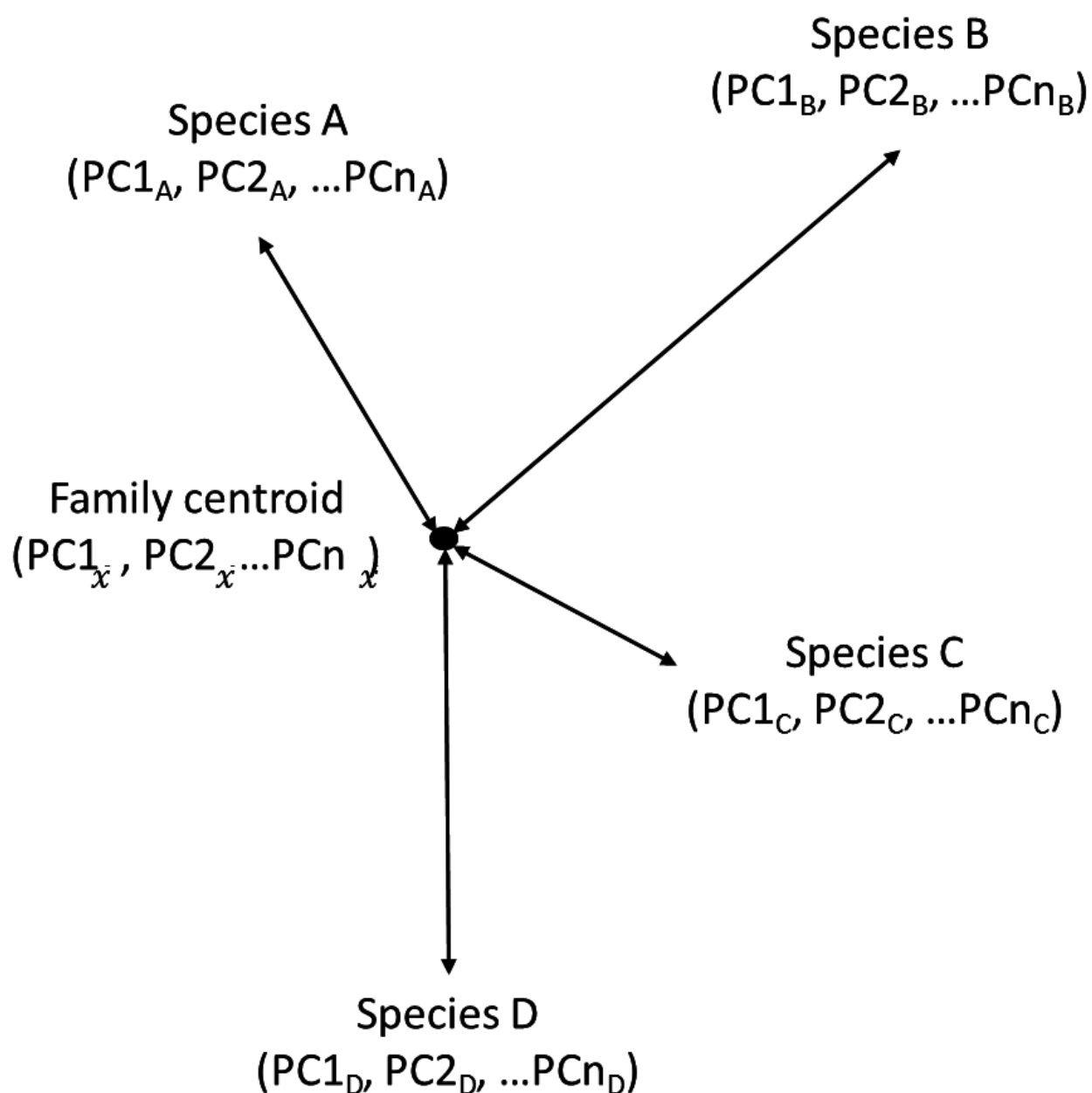


Figure 4: Morphospace (principal components) plot of morphological diversity in tenrec and golden mole skulls.

Principal components plots of the morphospaces occupied by tenrecs (triangles, n=31 species) and golden moles (circles, n=12 species) for skulls in dorsal (top left), ventral (top right) and lateral (bottom left) views. Each point represents the average skull shape of an individual species. Axes are principal component 1 (PC1) and principal component 2 (PC2) of the average scores from principal components analyses of mean Procrustes shape coordinates for each species.

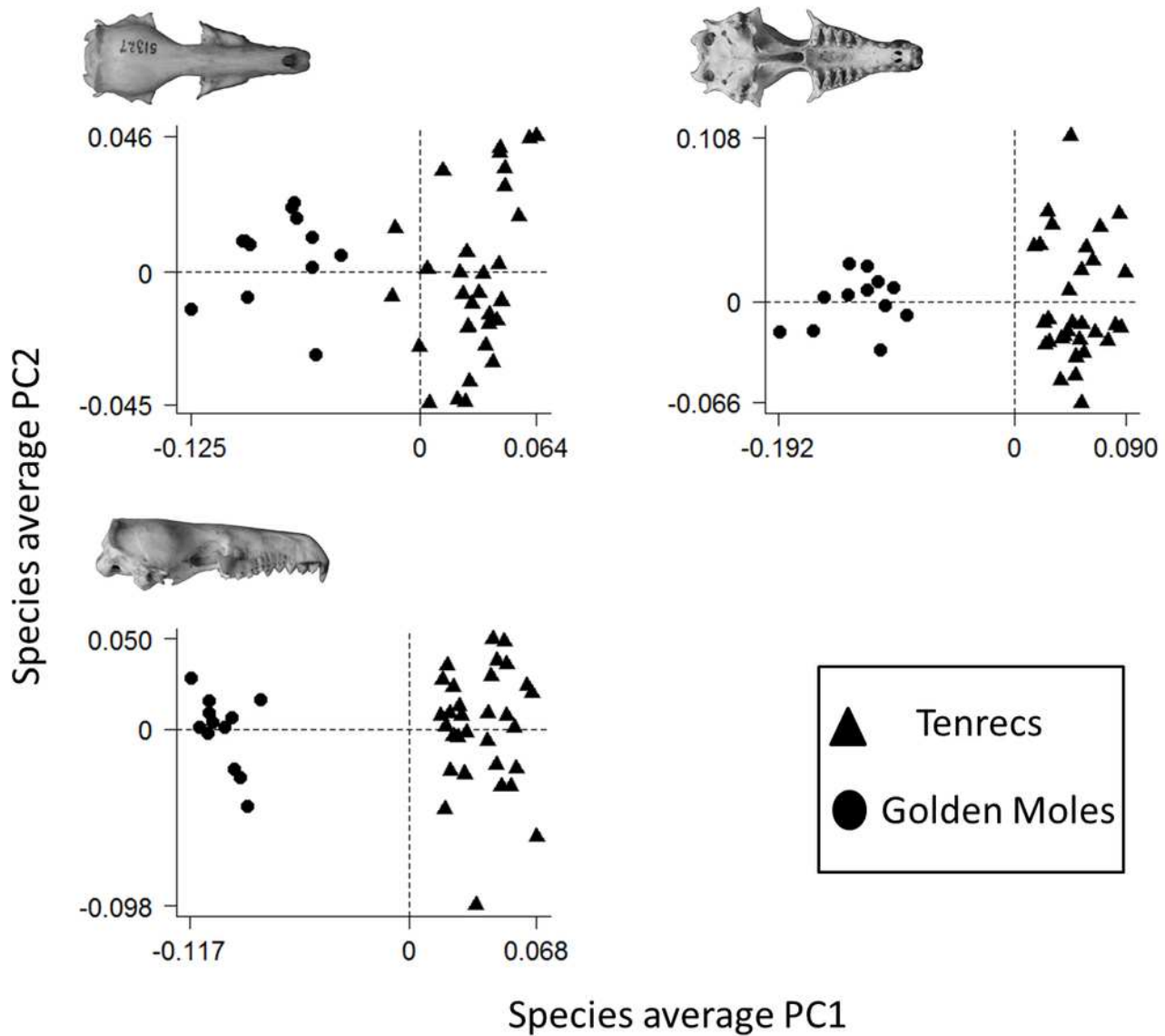


Table 1 (on next page)

Table 1: Comparing morphological diversity in tenrecs and golden moles.

Morphological diversity in tenrecs compared to golden moles (12 species). N is the number of tenrec species: 31 species or 17 species including just five representatives of the *Microgale* Genus. Morphological diversity of the Family is the mean Euclidean distance from each species to the Family centroid. Significant differences between the two Families ($p < 0.05$) from two-tailed t-tests are highlighted in bold.

N	Analysis	Morphological diversity		t_{df}	p value
		Tenrecs	Golden moles		
		mean \pm se	mean \pm se		
31	dorsal	0.036 \pm 0.0029	0.029 \pm 0.0032	-1.63 _{29.88}	0.11
	ventral	0.048 \pm 0.0034	0.044 \pm 0.0041	-0.68 _{26.99}	0.51
	lateral	0.044 \pm 0.0041	0.032 \pm 0.0037	-2.16 _{35.03}	0.04
17	dorsal	0.044 \pm 0.0025	0.029 \pm 0.0032	-3.62 _{22.75}	<0.01
	ventral	0.054 \pm 0.0039	0.042 \pm 0.0041	-2.23 _{25.46}	0.04
	lateral	0.054 \pm 0.0053	0.031 \pm 0.0037	-3.47 _{26.31}	<0.01

Table 2 (on next page)

Table 2: Results of the permutation tests.

Results of the permutation analyses comparing the observed differences in morphological diversity to a null distribution of expected results. Morphological diversity of the Family is the mean Euclidean distance from each species to the Family centroid. Results are shown for both the full (N=31 species of tenrec compared to 12 species of golden mole) and reduced (N=17 species of tenrec compared to 12 golden moles) data sets. Significant values ($p < 0.05$) indicate that the observed morphological diversity is different to the expected differences under a null hypothesis of equivalent diversities in the two Families.

N	Analysis	Morphological diversity					p value
		Measured values			Permuted values		
		Tenrecs	Golden moles	Difference	Min	Max	
31	dorsal	0.036	0.029	0.007	-0.011	0.009	0.013
	ventral	0.048	0.044	0.004	-0.014	0.013	0.023
	lateral	0.044	0.032	0.012	-0.012	0.011	<0.001
17	dorsal	0.044	0.029	0.015	-0.011	0.014	<0.001
	ventral	0.054	0.042	0.013	-0.017	0.019	0.023
	lateral	0.054	0.031	0.022	-0.018	0.019	<0.001