- 1 Running head: ???
- Quantifying cranial morphological
- disparity in tenrecs (Afrosoricida,
- Tenrecidae) with implications for their
- designation as an adaptive radiation
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13 Abstract

₁₄ Introduction

- Phenotypically diverse groups have long attracted the attentions of evolutionary biologists (REFS). Studies which quantify phenotypic variety have important implications for understanding the factors that contribute to high morphological diversity in some groups and not others (REFS). For example...
- These issues are particularly relevant when it comes to the study of
 adaptive radiations: "evolutionary divergence of members of a single
 phylogenetic lineage into a variety of different adaptive forms" (Futuyma
 1998, cited by Losos, 2010). There are many famous examples of
 adaptively radiated groups (Gavrilets & Losos, 2009). However, there has
 also been considerable debate about how adaptive radiations should be
 defined (Glor, 2010; Losos & Mahler, 2010) based on the relative
 importance of speciation rate, species richness and morphological
 diversity. One particular issue is whether it is even meaningful to classify
 a particular group of species as an adaptive radiation or not since any
 classification relies on arbitrary distinctions between what is most likely a
 continua of characteristics which describe the diversity of a particular
 clade (Olson & ArroyoSantos, 2009).
- However, despite the controversies and disagreements, there does
 seem to be a consensus that high morphological diversity is an important
 criteria for identifying a group of species as belonging to the adaptive
 radiation scale (Losos & Mahler, 2010; Olson & ArroyoSantos, 2009). One
 way to test whether a group shows high morphological diversity is
 through sister taxa comparisons. For example, Losos and Miles 2002 used
 this approach to demonstrate exceptional diversity in some but not all

- clades of iguanid lizards. Here we use this approach to test whether
 tenrecs (Afrosoricida, Tenrecidae) exhibit the high levels of phenotypic
 diversity which is the expected characteristic of an adaptively radiated
 clade.
- The tenrec family is comprised of 34 species, 31 of which are endemic to Madagascar (Olson, 2013). From a single common ancestor (Asher & Hofreiter, 2006), Malagasy tenrecs diversified into a wide variety of descendant species which convergently resemble distantly related insectivore mammals such as shrews (*Microgale* tenrecs), moles (*Oryzorictes* tenrecs) and hedgehogs (*Echinops* and *Setifer* tenrecs) (Eisenberg & Gould, 1969). These convergent resemblances are so great that tenrecs used to be considered part of the general "insectivore" clade and only molecular studies revealed their true phylogenetic relationships with the rest of the Afrotheria clade (Stanhope et al., 1998).
- Tenrecs are often cited as an example of an adaptively radiated family
 which exhibits exceptional morphological diversity (Soarimalala &
 Goodman, 2011; Olson & Goodman, 2003; Eisenberg & Gould, 1969).

 However, this apparent exceptional diversity is based on subjective
 comparisons to other groups and it has not been tested. Here we present
 the first quantitative test of patterns of phenotypic diversity in tenrecs and
 examine how morphological diversity in tenrecs compares to their closest
 relatives, the golden moles (Afrosoricida, Chryscholoridae).
- We use disparity, the diversity of organic form (Foote, 1997; Wills et al., 1994; Erwin, 2007), to measure phenotypic variety within the two families.
 There is no single definition of disparity and it can be calculated in many ways including measures of morphospace occupation (e.g. Goswami et al.,

- 2011; Brusatte et al., 2008) and rate-based approaches that assess the
- 67 amount of directed change away from an ancestor (O'Meara et al., 2006;
- ⁶⁸ Price et al., 2013). Here we focus on patterns of phenotypic variety in
- 69 extant species rather than analysing the rate of diversity accumulation
- ₇₀ through time. Using the most complete morphological data set of tenrecs
- ₇₁ and golden moles to date we apply two dimensional geometric
- morphometrics (Rohlf & Marcus, 1993; Adams et al., 2013) to quantify
- variation in cranial and mandible morphologies as proxies for phenotypic
- diversity in the two families.
- Our results indicate an overall trend of higher morphological diversity
- in tenrec compared to golden mole crania. However, most of these
- differences are not statistically significant, indicating that, with regards to
- cranial shape, tenrecs are not as phenotypically diverse as they are often
- 79 though. In contrast, we found significantly greater morphological
- 80 disparity in golden mole mandibles compared to the diversity within
- 81 tenrecs. These findings cast doubt over whether the apparent phenotypic
- 82 diversity within tenrecs should be considered exceptional.

83 Materials and Methods

84 Data collection

85 Morphological data collection

- 86 One of us (SF) photographed cranial specimens of tenrecs and golden
- 87 moles at the Natural History Museum London (NHML), the Smithsonian
- 88 Institute Natural History Museum (SI), the American Museum of Natural

- History (AMNH), Harvard's Museum of Comparative Zoology (MCZ) and the Field Museum of Natural History, Chicago (FMNH). We photographed the specimens with a Canon EOS 650D camera fitted with an EF 100mm f/2.8 Macro USM lens using a standardised procedure to minimise potential error (see supplementary material for details).
- We collected pictures of the skulls in dorsal, ventral and lateral views
 (right side of the skull) and of the outer (buccal) side of the right
 mandibles. A full list of museum accession numbers and details for how
 to access the images can be found in the supplementary material.
- In total we collected pictures from 182 skulls in dorsal view (148 tenrecs and 34 golden moles) and 181 mandibles in lateral view (147 tenrecs and 34 golden moles), representing 31 species of tenrec (out of the total 34 in the family) and 12 species of golden moles (out of a total of 21 in the family (Asher et al., 2010)). We used the taxonomy of Wilson and Reeder (2005) supplemented with more recent sources (IUCN, 2012; Olson, 2013) to identify our specimens.
- We used a combination of both landmarks (type 2 and type 3,

 (Zelditch et al., 2012)) and semilandmarks to characterise the shapes of

 our specimens. Our landmarks (points) and semilandmarks (outline

 curves) used to represent shape variation in the dorsal and ventral skull

 view are depicted in figures 1 and the landmarks for skulls and mandibles

 in lateral view are shown in figure 2. Corresponding definitions of each of

 the landmarks can be found in the supplementary material.
- We digitised all landmarks and semilandmarks in tpsDIG, version 2.17 (Rohlf, 2013). We re-sampled the outlines to the minimum number of evenly spaced semilandmark points required to represent each outline

accurately (MacLeod, 2013, details in supplementary material). We used TPSUtil (Rohlf, 2012) to create sliders files (Zelditch et al., 2012) to define 116 which points were semilandmarks. We conducted all subsequent analyses in R version 3.0.2 (R Development Core Team, 2013) within the geomorph 118 package (Adams et al., 2013). We used the gpagen function to run a general Procrustes alignment (Rohlf & Marcus, 1993) of the landmark 120 coordinates while sliding the semilandmarks by minimising procrustes 121 distance (Bookstein, 1997). We used these Procrustes-aligned coordinates 122 of all species (n=43) to calculate average shape values for each species 123 which we then used for a principal components (PC) analysis with the plotTangentSpace function (Adams et al., 2013).

126 Phylogeny

Instead of basing our analyses on individual trees and assuming that their topologies were known without error (e.g. Ruta et al., 2013; Foth et al., 2012; Brusatte et al., 2008; Harmon et al., 2003) we used a distribution of 101 pruned phylogenies derived from the randomly resolved mammalian supertrees in (Kuhn et al., 2011).

Eight species (six *Microgale* tenrecs and two golden moles) in our morphological data were not in the phylogenies. Phylogenetic relationships among the *Microgale* have not been resolved more recently than the (Kuhn et al., 2011) analysis, therefore we added the additional *Microgale* species at random to the *Microgale* genus within each phylogeny (Revell, 2012). We could not use the same approach to add the two missing golden mole species because they were the only representatives of their respective genera within our data. Therefore we randomly added

these species to the common ancestral node (using the findMRCA function in phytools (Revell, 2012)) of all golden moles within each phylogeny.

Adding these extra species to the phylogenies created polytomies which we resolved arbitrarily using zero-length branches (Paradis et al., 2004).

We calculated pairwise phylogenetic distances among species using the cophenetic function (R Development Core Team, 2013).

146 Analyses

147 Disparity calculations

We calculated morphological disparity separately for golden moles and tenrecs in each of the morphological datasets. We used the PC axes which accounted for 95% of the cumulative variation to calculate four disparity metrics; the sum and product of the range and variance of morphospace occupied by each family (Brusatte et al., 2008; Foth et al., 2012; Ruta et al., 2013). We also calculated morphological disparity directly from the Procrustes-superimposed shape data based on the sum of the squared inter-landmark distances among species pairs (ZelditchMD, Zelditch et al., 2012).

We used two approaches to test whether tenrecs have significantly
different morphologies compared to golden moles. We compared
morphospace occupation between the two groups with non parametric
MANOVAs (Anderson, 2001) to test whether tenrecs and golden moles
occupy significantly different areas of morphospace (e.g Serb et al., 2011;
Ruta et al., 2013). We used pairwise permutation tests to test our null
hypothesis that tenrecs and golden moles have equal disparity. If this

hypothesis were true then the designation of each species as belonging to either tenrecs or golden moles should be arbitrary because each group 165 would have the same disparity. Therefore we permutated the data by assigning family identities at random to each specimen and calculated the 167 differences in disparity for each of the new family groupings. We repeated these permutations 1000 times to generate a null distribution of the 160 expected differences in family disparity. We compared our observed (true) 170 measures of the differences in disparity between tenrecs and golden moles 171 to these permutated distributions to test whether the families had 172 significantly different levels of disparity.

The majority of tenrecs (19 out of 31 in our data) are members of the

Microgale (shrew-like) genus which is notable for its relatively low

phenotypic diversity (Soarimalala & Goodman, 2011; Jenkins, 2003). The

strong similarities among these species may mask signals of higher

disparity among other tenrecs. Therefore we repeated our family-level

comparisons of disparity with a reduced data set that excluded the

Microgale so that we could compare disparity within the remaining 12

tenrec species to disparity within the 12 species of golden moles.

Results

183 Morphological disparity in tenrecs and golden moles

Figures 3 depict the morphospace plots derived from our principal components analyses of average Procrustes-superimposed shape coordinates for each species in our skull and mandible data respectively.

We used the principal components axes which accounted for 95% of the

cumulative variation (n = 7, 8, 8 axes for the dorsal, ventral and lateral skull analyses respectively and n = 12 axes for the mandibles) to calculate the disparity of each family.

Tenrecs and golden moles clearly have very different cranial and mandible morphologies: in each analysis, the families occupy significantly different areas of morphospace (npMANOVA, table 3). Our comparisons of disparity levels within each family yielded different trends for the skulls compared to the mandible analyses.

In our analyses of the three different views of the skulls, when
disparity is calculated from principal component - based metrics there is
there is an overall trend for tenrecs to have higher disparity than golden
moles. However, none of these differences are statistically significant
(table 1). In contrast, when we calculated disparity based on the sum of
squared interlandmark differences between species pairs (Zelditch et al.,
2012) then golden moles had significantly higher levels of disparity than
tenrecs (table 1).

There is a less clear pattern from our analysis of disparity in the
mandibles. Three of our five metrics indicate that golden moles have
significantly higher disparity in the shape of their mandibles than tenrecs
(table 1) although one metric (sum of ranges) indicated the opposite result.

The three curves that we placed at the back of the mandibles (figure 2)
place a particular emphasis on shape variation in the posterior of the
bone; the ramus, coronoid, condylar and angular processes. Therefore,
higher disparity in golden mole mandibles compared to tenrecs could be
driven by greater morphological variation in these structures. To test this
idea, we repeated our morphometric analyses of the mandibles with a

reduced data set of points; just the seven landmark points and one single curve at the base of the jaw between landmarks 1 and 7 (figure 2). When we compared familial disparity levels with this reduced data set we found that golden moles no longer had significantly higher disparity than tenrecs but rather there were some indications that the opposite was true (table 1).

Morphological disparity in non-Microgale tenrecs and golden moles

We repeated our disparity comparisons with a subset of the tenrec specimens to remove the large and phenotypically similar *Microgale* tenrec genus. In this case we found that tenrecs have significantly higher disparity than golden moles when the skulls are analysed in lateral view (table 2). However, none of the other comparisons in any of the analyses were significant. Similarly, the trend in the main analysis for golden moles to have significantly higher disparity measured as the sum of squared inter-landmark distances (table 1) was not repeated in this comparison of disparity in non-*Microgale* tenrecs and golden moles (table 2).

Discussion Discussion

Our findings provide new insights into phenotypic diversity within the
tenrec family. When we compared tenrecs' cranial morphologies to their
closest relatives we found a trend towards higher disparity in tenrecs than
in golden moles. However, these apparent differences were only
significant for some disparity metrics. In contrast, the analyses of the
mandibles indicated that golden moles have more diverse mandible

shapes than tenrecs.

It is evident that tenrecs are a diverse group, both phenotypically and ecologically. Body sizes of extant tenrecs span three orders of magnitude (2.5 to > 2,000g) which is a greater range than all other Families, and most Orders, of living mammals (Olson & Goodman, 2003). Within this vast size range there is striking morphological diversity, from the spiny *Echinops, Setifer* and striking *Hemicentetes* to the shrew-like *Microgale*. Furthermore, tenrecs inhabit a variety of ecological niches and habitats including terrestrial, arboreal, semi-aquatic and semi-fossorial forms (Soarimalala & Goodman, 2011).

Here we have presented the first quantitative investigation of
morphological disparity in tenrecs and our results suggest that perhaps
phenotypic variation in tenrecs is not as uniformly exceptional as it first
appears.

We found an overall pattern of higher disparity in tenrec skull shape
than golden moles but only the range and Procrustes distance-based
metrics are significant. This is probably because variance and range-based
measures describe different aspects of morphospace occupation.

Another apparent anomaly in our results is that we found opposite 255 patterns of group dissimilarities in the analyses of skulls and mandibles. 256 Our landmarks and curves for the mandibles (figure 2) include aspects of 257 variation in the dentition but they focus particular attention on the 258 ascending ramus (condyloid, condylar and angular processes). Therefore 259 higher disparity in golden moles could reflect greater morphological 260 variability in these posterior mandible structures. To test this idea we 261 deleted the semi-landmark curves around these structures (curves A, B, 262

and C, table x in supplementary material) and repeated our disparity
analyses on all of the specimens. In this case we retrieved the opposite
pattern: tenrecs had higher morphological disparity than golden moles
(see supplementary material). Therefore, our results indicate that golden
moles have greater morphological variation in the posterior structures of
their mandibles compared to tenrecs.

It proved impossible to position reliable landmarks on the
corresponding mandibular articulation areas of the skull in lateral view
(see supplementary). Therefore we could not test whether higher
morphological disparity in the rami were correlated with associated
morphological variety in the articulation areas of the skull.

There are certain caveats to consider which could modify the 274 interpretation of our results. Phenoypic variation can evolve for reasons 275 other than adaptive radiation. Therefore, to describe phenotypic 276 divergence as the product of an adaptive radiations requires exceptional morphological diversity in traits which have specific and proven adaptive 278 significance (Losos & Mahler, 2010). The evolution of cranial shape (both 279 upper skull and mandible), particularly dental morphology, has obvious correlations with dietary specialisations (REFS) and occupation of specific 281 ecological niches (REFS). 282

Considering the wide ecological diversity of our study species; the fossorial golden moles and semi-fossorial, arboreal, terrestrial and semi-aquatic tenrecs (REFS) it is reasonable to expect that this variety should be reflected in skull morphology. We assume that variation in cranial shape is an adaptive characterstic which allows the animals to survive in their divergent niches but we have not tested this assumption

289 explicitly.

Cranial shape similarities are commonly used to delineate species
boundaries (REFS) or for cross-taxonomic comparative studies of
phenotypic (dis)similarities (REFS). However, disparity studies are
inevitably constrained to be measures of diversity within specific traits
rather than overall morphology (Roy & Foote, 1997). Therefore it is
possible that other morphological proxies of phenotype; analyses of linear
measurements and/or discrete characters of either cranial or post-cranial
morphologies could yield different results.

However, the results of (Foth et al., 2012) are encouraging. In an analysis of morphological disparity in pterosaurs, they found that disparity calculations based on geometric morphometric characterisation of skull shape yielded broadly similar results compared to analyses of whole-skeleton discrete characters and limb proportion data sets.

Therefore the disparity patterns we find here based on geometric morphometric analyses of cranial shape most likely represent approximations of disparity which are accurate for morphological diversity in the clades.

These results highlight the importance of applying quantitative methods to testing our assumptions about adaptively radiated groups.

These analyses represent the first attempt to find evidence to support the common claim that tenrecs are an adaptive radiation. Future work will develop our results by expanding the analyses to non-cranial morphology and also measures of ecological diversity. However, our current results provide a clear indication that phenotypic variety within tenrecs is perhaps not as exceptional as it first seems and therefore their

designation as an adaptive radiation may need to be re-considered.

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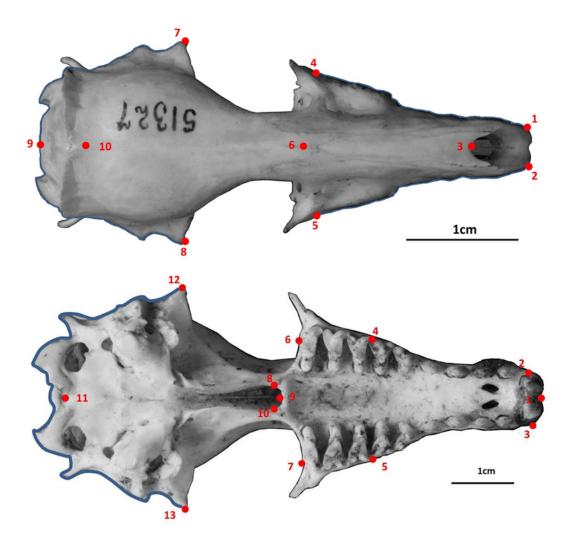


Figure 1: Landmarks (red points) and curves (blue lines) used to capture the morphological shape of skulls in dorsal and ventral views respectively. Curves were re-sampled to the same number of evenly-spaced points. Descriptions of the curves and landmarks are in the supplementary material. The specimens belong to two different *Potamogale velox* (Tenrecidae) skulls: accession number AMNH 51327 for the dorsal picture and NHML 1934.6.16.2 for the ventral picture

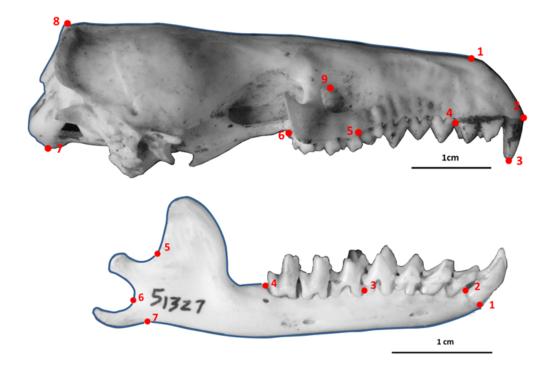


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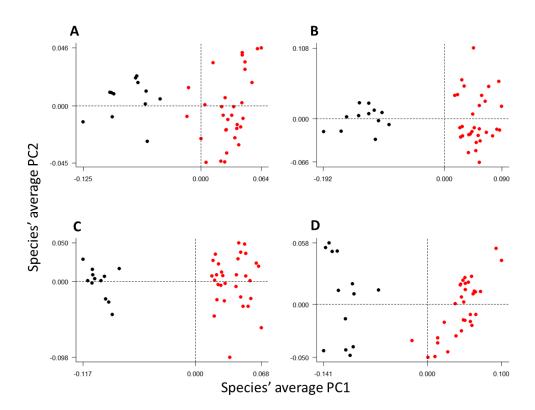


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462		brackets. Disparity metrics are; sum of variance, product	
463		of variance, sum of ranges, product of ranges and sum of	
464		squared distances among species	26
465	3	Summary of the npMANOVA comparisons of morphospace	
466	-	occupation for tenrecs and golden moles in each of the four	
467		analyses (three views of skulls and mandibles). In each case	
468		the two families occupy significantly different areas of mor-	
469		1	27

Table 1: Summary of disparity comparisons between tenrecs (T) and golden moles (G) for each of our data sets(rows) and five disparity metrics (columns). "Mandibles:one curve" refers to our shape analysis of mandibles excluding the three curves around the posterior structures of jaw (figure 2). Significant differences are highlighted in bold with the corresponding p value in brackets. Disparity metrics are; sum of variance, product of variance, sum of ranges, product of ranges and sum of squared distances among species.

Disparity metric	SumVar	ProdVar	SumRange	ProdRange	SSqDist
Skulls dorsal	T>G	T>G	T>G	T>G	$G>T^*$ (o)
Skulls lateral	T>G	T>G	T>G	T>G	$G>T^*$ (o)
Skulls ventral	T>G	G>T	T>G	T>G	$G>T^*$ (o)
Mandibles	G>T	G > T* (0.008)	$T>G^*$ (0.025)	T>G* (0.009)	$T>G^*$ (o)
Mandibles: one curve	G>T	G>T	T>G	T>G	$T>G^*$ (o)

Table 2: Summary of disparity comparisons between non-*Microgale* tenrecs (T) and golden moles (G) for each of our data sets(rows) and five disparity metrics (columns). Significant differences are highlighted in bold with the corresponding p value in brackets. Disparity metrics are; sum of variance, product of variance, sum of ranges, product of ranges and sum of squared distances among species.

Disparity metric	SumVar	ProdVar	SumRange	ProdRange	SSqDist
Skulls dorsal	T>G	T>G	T>G	T>G	T>G
Skulls lateral	$T > G^* \text{ (o.014)}$	T>G	$T>G^*$ (0.001)	T>G*(0.003)	G>T* (0.014)
Skulls ventral	T>G	T>G	T>G	T>G	T>G
Mandibles	T>G	G>T	T>G	G>T	G>T

Table 3: Summary of the npMANOVA comparisons of morphospace occupation for tenrecs and golden moles in each of the four analyses (three views of skulls and mandibles). In each case the two families occupy significantly different areas of morphospace.

Analysis	F	R ²	p value
Skulls dorsal	66.02	0.62	0.001
Skulls ventral	100.74	0.71	0.001
Skulls lateral	75.07	0.65	0.001
Mandibles	59.34	0.59	0.001