American deer: Morphometrics and taxonomy of the *Mazama americana* species complex (Mammalia: Cervidae)

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Introduction

Neotropical deer (Cervidae: Capreolinae) are among the least-studied large mammals in the world despite being heavily hunted in many countries that lack proper management plans. Together with the genus *Odocoileus*, *Mazama*, which is widely distributed from Mexico to Brazil[1], is one of the most taxonomically complex genera of the tribe Rangiferini. Molecular studies have shown that the genus *Mazama* is not monophyletic and has extreme molecular and chromosomal variability[1–3], indicating the need for taxonomic work at both the genus and species levels. **In this study we investigated the morphological variability of species in the *Mazama americana* complex and discuss its taxonomic implications.**

Methods

We assessed the morphological variability of the genus *Mazama* using linear morphometrics. We took sixteen cranial measurements from 185 specimens (Fig. 1). Measurements followed or were adapted from previous studies[4–7]. The analyses (see below) were based only on data from adult specimens (i.e. those having complete dentition)[8]. Missing data (e.g. resulting from partially broken bones) were estimated using the average for the corresponding measurement of specimens of the same sex, taxon, and locality. The raw data was transformed utilizing the natural logarithm before analyses.

Based on the resulting dataset, we conducted a cluster analysis (CA) and a principal component analysis (PCA). Because previous studies did not find significant differences between males and females[5,9], we combined data from both sexes for these analyses. The CA was conducted based on Euclidian distances; the PCA was performed employing the covariance matrix.

Figure 1—Measurements used for the cluster analysis and PCA. **(a) dorsal:** frontal length (FL), interorbital breadth (IB), **(b) ventral:** zygomatic breadth (ZB), intercondylar width (IW), condylobasal length (CBL), foramen magnum to premaxillary length (MPL), palatine to premaxillary length (PPL); **(c) lateral:** condylo-premolar length (CPL), upper tooth row length (UTRL), maxillary diastema length (DLM).

Results

For the *Mazama americana* species complex, our analyses identified two large groups of specimens that differed mainly in size. Examination of the loadings derived from the PCA showed that the first component (PC 1) largely captured differences in size and explained 84.22% of the variation among analyzed specimens (Table 1). A bivariate plot of specimens' scores for PC 1 and PC 2 showed separation of taxa (Fig. 2). *Mazama americana* specimens were the largest in our dataset, and *M. temama* and *M. pandora* the smallest.

The CA produced similar separation, identifying two major clusters. The first includes *Mazama. cf. zetta* and *M. americana*, and the second includes *M. temama* and *M. pandora* (Fig. 3).

In both analyses we found a few specimens provisionally assigned to *Mazama americana* that were atypically small for that species. *Mazama zetta*, *M. whitelyi*, and *M. americana carrikeri* were found embedded in clusters with *M. a. sheila*, *M. a. americana*, and *M. temama*, respectively.
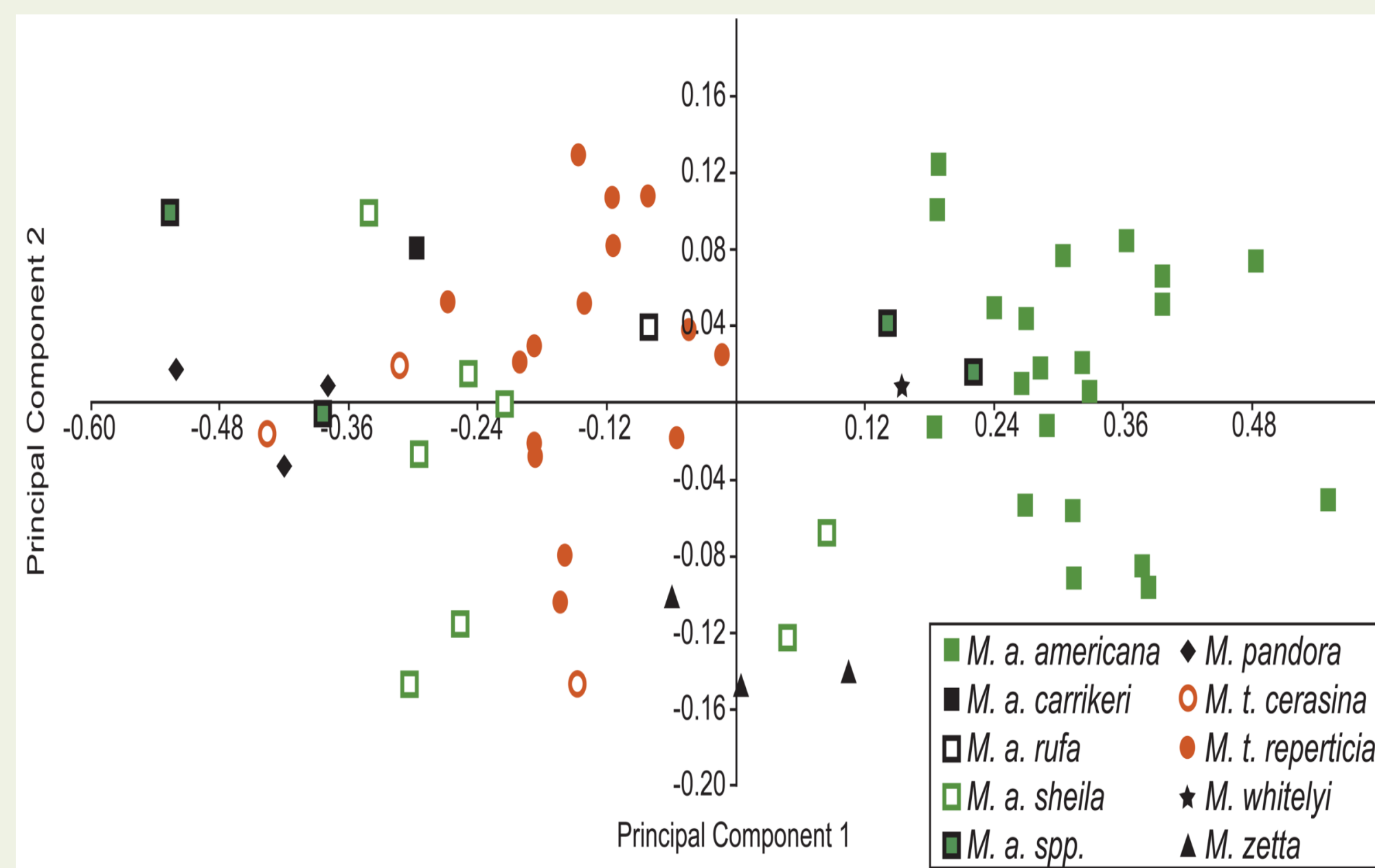

Figure 2—Bivariate plot of specimens' scores on PC 1 and PC 2 from the PCA of the *Mazama americana* complex.

Table 1—Loadings derived from the PCA of the *Mazama americana* complex. PC 1 primarily accounts for variation in size, whereas PC 2 accounts for variation in proportion.

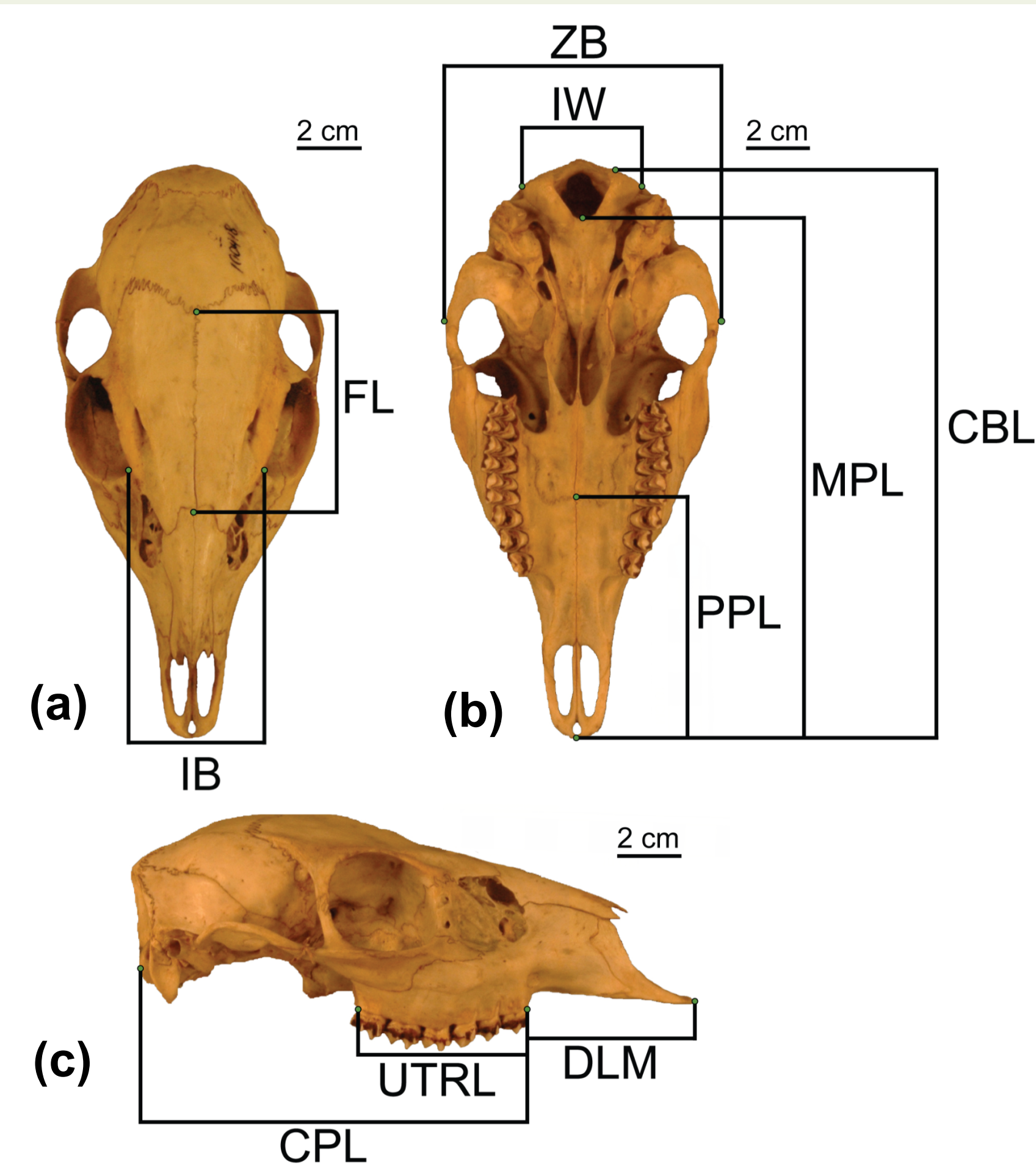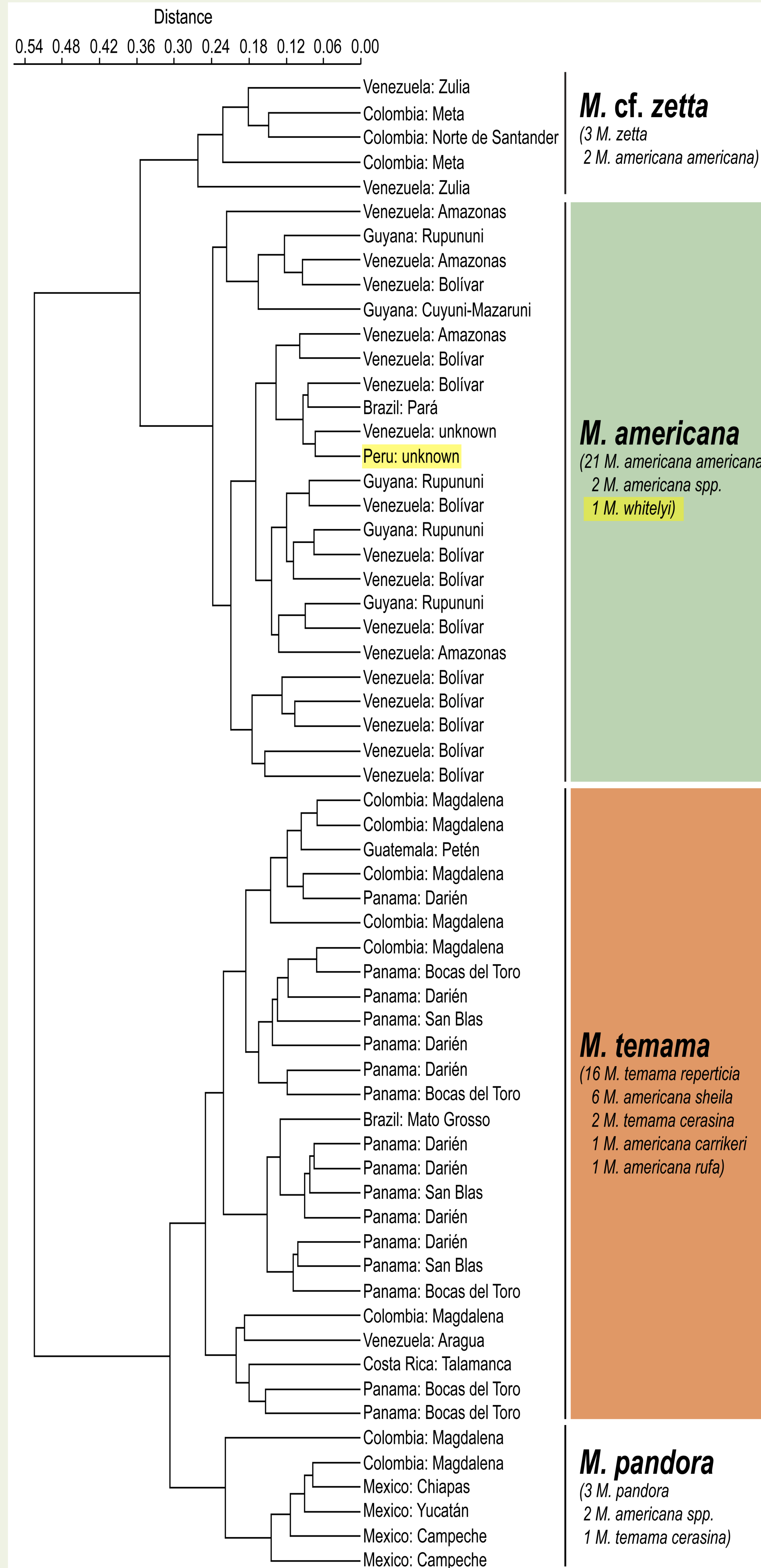|	PC 1	PC 2	PC 3	PC 4
FL	0.295	-0.874	0.164	0.221
MPL	0.313	0.059	-0.208	0.095
PPL	0.372	0.067	-0.398	-0.221
UTRL	0.284	0.207	-0.024	0.704
IW	0.327	-0.091	0.455	-0.392
ZB	0.321	0.075	0.134	-0.331
CPL	0.282	0.037	-0.015	0.237
DLM	0.372	0.051	-0.325	-0.248
IB	0.266	0.400	0.632	0.112
CBL	0.311	0.084	-0.205	0.058
Eigenvalue	0.079	0.005	0.003	0.002
% variance	84.218	5.797	3.525	2.466

Figure 3—Phenogram resulting from cluster analysis of logarithmically transformed cranial measurements of specimens of the *Mazama americana* complex. The taxa analyzed included *Mazama americana*, *M. temama*, *M. pandora*, *M.whitelyi*, *M. zetta* and some of their currently recognized subspecies.

Discussion

The results of our morphometric analyses have taxonomic implications. The specimens provisionally assigned to *Mazama americana* embedded in several clusters across the phenogram demonstrates the urgent need for a comprehensive taxonomic revision in this group.

Despite this, our results yielded some broad patterns of variability relevant to taxonomic issues. *Mazama zetta*—a taxon traditionally treated as a synonym of *M. americana*[10]—was found to be morphometrically distinctive. Similarly, our results support the recognition of *Mazama temama* at the species level. This species was previously considered a synonym of *Mazama americana* and raised to the species level based mainly on karyotypic data[11]. In contrast, our results provide modest evidence against the recognition of *Mazama whitelyi*—recently elevated to the species level by Groves and Grubb (2011)—as the single specimen analyzed was embedded within a large cluster of *M. americana*.

Future Directions

Our results showed similar morphologies between *Mazama temama* and two forms traditionally assigned to *M. americana* (*sheila* and *rufa*). Future studies should reevaluate the taxonomic status of these taxa. Our results and additional side-by-side comparisons of qualitative cranial traits did not reveal differences between two specimens identified in the USNM collection as *Mazama americana sheila* from Venezuela and three specimens of *M. zetta* from Colombia. Consequently, we consider that all of these specimens are conspecific and likely correspond to *M. zetta,* which occurs in the inter-Andean valleys of Colombia. This remains to be confirmed via comparisons with typical material of *M. zetta,* in which case these specimens would represent the first records of *M. zetta* for Venezuela.

We plan to further investigate the taxonomy of deer traditionally included in the genus *Mazama* by gathering additional morphological data (including comparisons with typical material) and obtaining genetic data.

Acknowledgements

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