

# A Geometric Morphometric Analysis of Two fossil Macaques

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Summary

## Introduction

Macaques (Genus *Macaca*) are Old World monkeys (Family Cercopithecoidea), and are the most geographically widespread primate other than *Homo sapiens*. They are currently found in Northern Africa and across Asia, and are known to have previously lived in Europe. Despite being so common, little is known about their evolutionary history.

Macaque fossils are rare and spread over a wide geographic range, but are found in a narrow geological time period. Macaques seem to have spread out and assumed their current phenetic characteristics and geographic niches during the Plio-Pleistocene, between roughly 5 mya and 10,000 years ago.

**Relative similarity of fossils to extant forms could suggest that little phenotypic divergence has occurred in the last 5 million years, while greater difference might imply that we are missing a significant “transitional” portion of the macaque fossil record.**

In this study we analyze two fossil macaque crania, one from Europe and one from Asia, with geometric morphometrics. Our aim was to determine whether or not the fossil specimens have any physical similarities with extant groups.

## Materials and Methods

| Genus         | Species                         | # of       | Location      |
|---------------|---------------------------------|------------|---------------|
| <i>Macaca</i> | <i>mulatta</i>                  | n=9        | S. Asia       |
| <i>Macaca</i> | <i>fuscularis</i>               | n=7        | SE. Asia      |
| <i>Macaca</i> | <i>nemestrina</i>               | n=3        | S. Asia       |
| <i>Macaca</i> | <i>maura</i>                    | n=3        | SE. Asia      |
| <i>Macaca</i> | <i>sylvanus</i>                 | n=2        | Africa        |
| <i>Macaca</i> | <i>arctoides</i>                | n=2        | SE. Asia      |
| <i>Macaca</i> | <i>cyclopis</i>                 | n=2        | Asia & Japan  |
| <i>Macaca</i> | <i>fuscata</i>                  | n=2        | Japan         |
| <i>Macaca</i> | <i>thibetana</i>                | n=2        | S. Asia       |
| <i>Macaca</i> | <i>tonkeana</i>                 | n=2        | SE. Asia      |
| <i>Macaca</i> | <i>nigra</i>                    | n=1        | SE. Asia      |
| <i>Macaca</i> | <i>ochreata</i>                 | n=1        | SE. Asia      |
| <i>Macaca</i> | <i>assamensis</i>               | n=1        | S. Asia       |
| <i>Macaca</i> | <i>brunnescens</i>              | n=1        | SE. Asia      |
| <i>Macaca</i> | <b><i>robusta</i> (fossil)</b>  | <b>n=1</b> | <b>Asia</b>   |
| <i>Macaca</i> | <b><i>majori</i> (fossil)</b>   | <b>n=1</b> | <b>Europe</b> |
| <i>Papio</i>  | <i>hamadryas (ursinus)</i>      | n=1        | S. Africa     |
| <i>Papio</i>  | <i>hamadryas (papio)</i>        | n=1        | W. Africa     |
| <i>Papio</i>  | <i>hamadryas (cynocephalus)</i> | n=1        | S. Africa     |

Table 1: species used in analyses

We digitally modeled 45 crania (see Table 1) scanned with the NextEngine 3D, which generates accurate computerized models of specimens with the Geomagic editing software. Individual frames were cleaned and aligned manually and with the software's built-in protocols.

Digital landmarks were laid down in Landmark Editor, where 50 homologous points were applied to crania based on the landmark set of Frost *et al.*, 2003 (See Fig. 1).

Due to differing degrees of fossil preservation, the full landmark set was inapplicable to either fossil cranium, and those points held in common would have been inadequate for a meaningful analysis. This necessitated the use of two different landmark subsets, 34 for *M. robusta* and 35 for *M. majori*, and the generation of two different statistical assessments of variation.

Statistical analyses were performed after data collection in *morphologika v 2.5* and *PAST v 2.04*. 3D coordinate data were aligned in *morphologika* using a Generalized Procrustes Analyses (GPA) which reduces the differentiation caused by translation, rotation, and scale. A Principal Components Analysis (PCA) was performed and a Neighbor Joining Tree was built in *PAST*.

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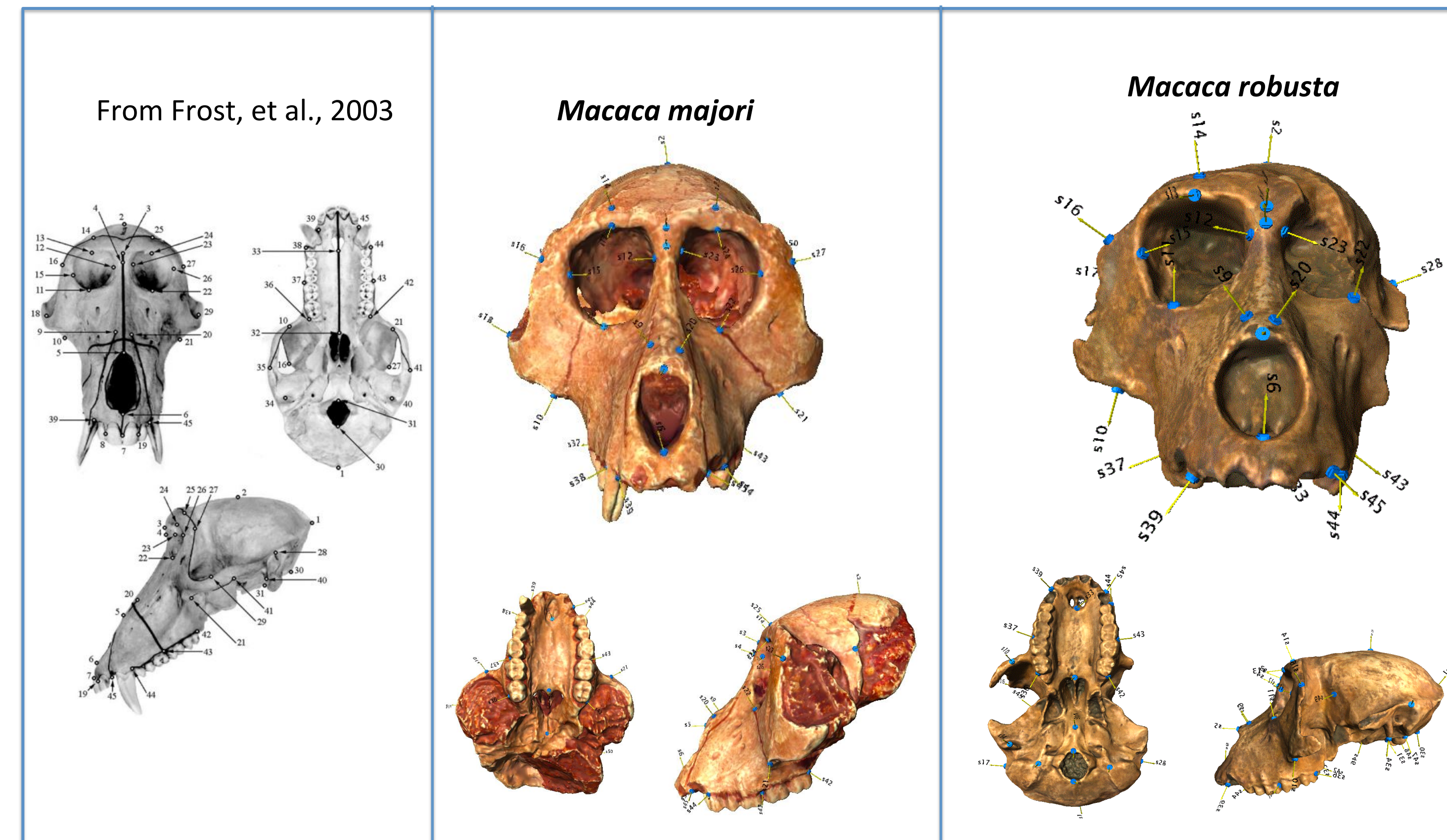


Fig. 1: Landmark arrangements

## Results

### General Results

Overall, macaques and the baboon out-group clearly cluster at the opposite ends of PC1, which in both data sets is primarily associated with facial length.

### *M. majori*

This PCA plot depicts the fossil *M. majori* as bearing the most resemblance with *M. cyclopis*, these two each possess similar snout length and crania width. However, the *M. majori*'s appearance is not consistent with the baboons and the extant macaca, which was originally presumed (See Fig. 2). Neighbor joining tree affirms this.

### *M. robusta*

PCA plot shows that *M. robusta* most resembles *M. fuscata*, based mostly on shared features such as a short facial length and the proportionality and orientation of the facial structure to the neurocranium (See Fig. 3).

Conversely, our neighbor joining tree aligns *M. robusta* most closely with *M. assamensis*, though the low bootstrap values suggest this alignment is not well supported.

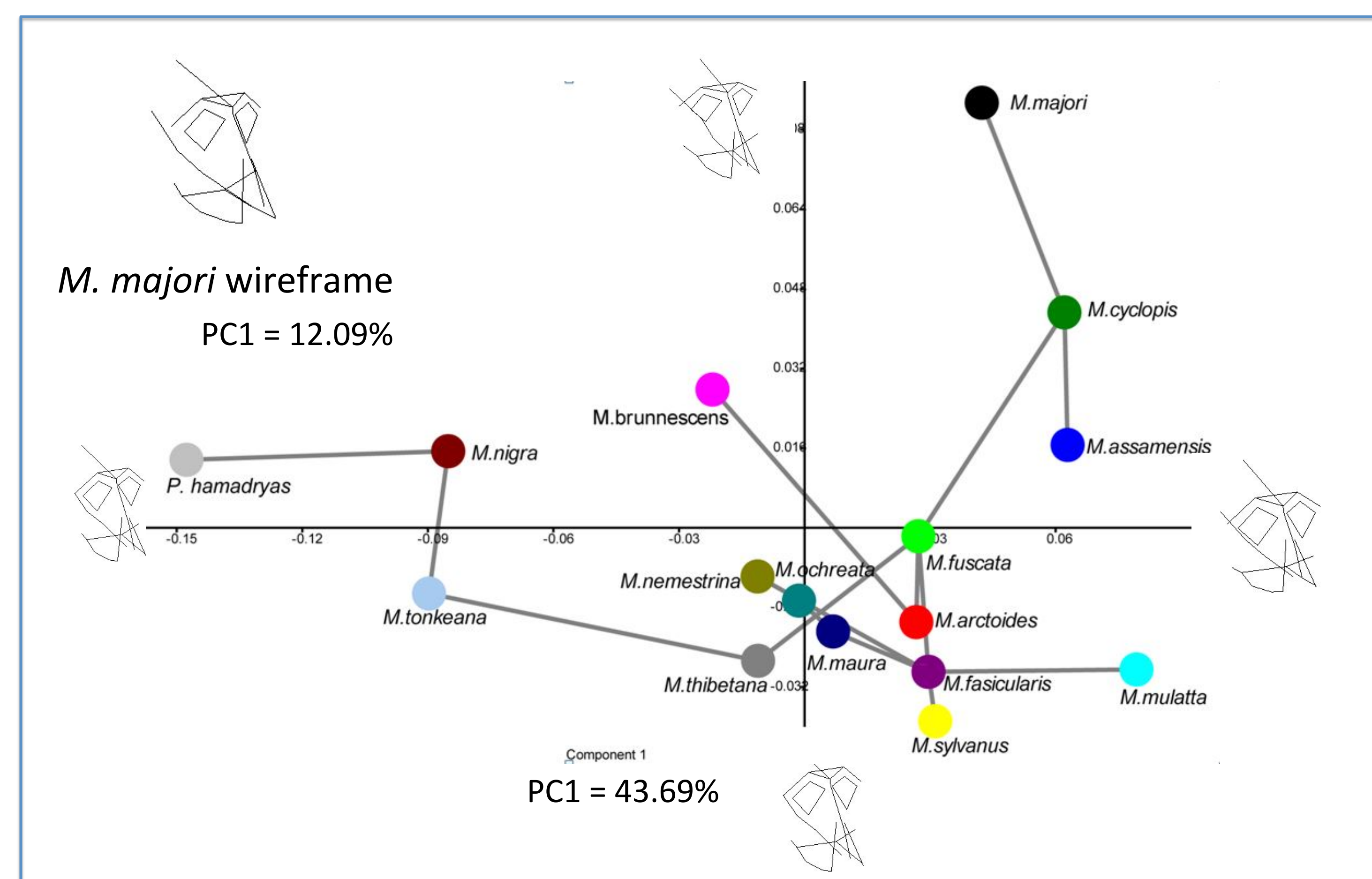


Fig. 2: PC Analysis of extant species means and *M. majori*

### General Summary

The two fossils do not align closely with each other, suggesting different evolutionary relationships to extant taxa.

### *M. majori*

Despite initial expectations for *M. majori*, it has apparently diverged from the evolutionary path of other macaques, including *M. sylvanus*, which is another European macaque. Relative to one another these two macaques are morphologically distant and have little to no similarities. Also it is important to note that this species developed in isolation on the island of Sardinia, likely this is the source for *M. majori*'s PCA position. This species likely does not represent an ancestral morphotype for macaque.

### *M. robusta*

Although the PCA plot and neighbor joining trees show *M. robusta* being most similar to different extant species, its relative similarity to the extant taxa is clear. This suggests that it could represent an ancestral morphotype for *Macaca* in east Asia, and that little divergence from this morphology has occurred over the last 5 million years.

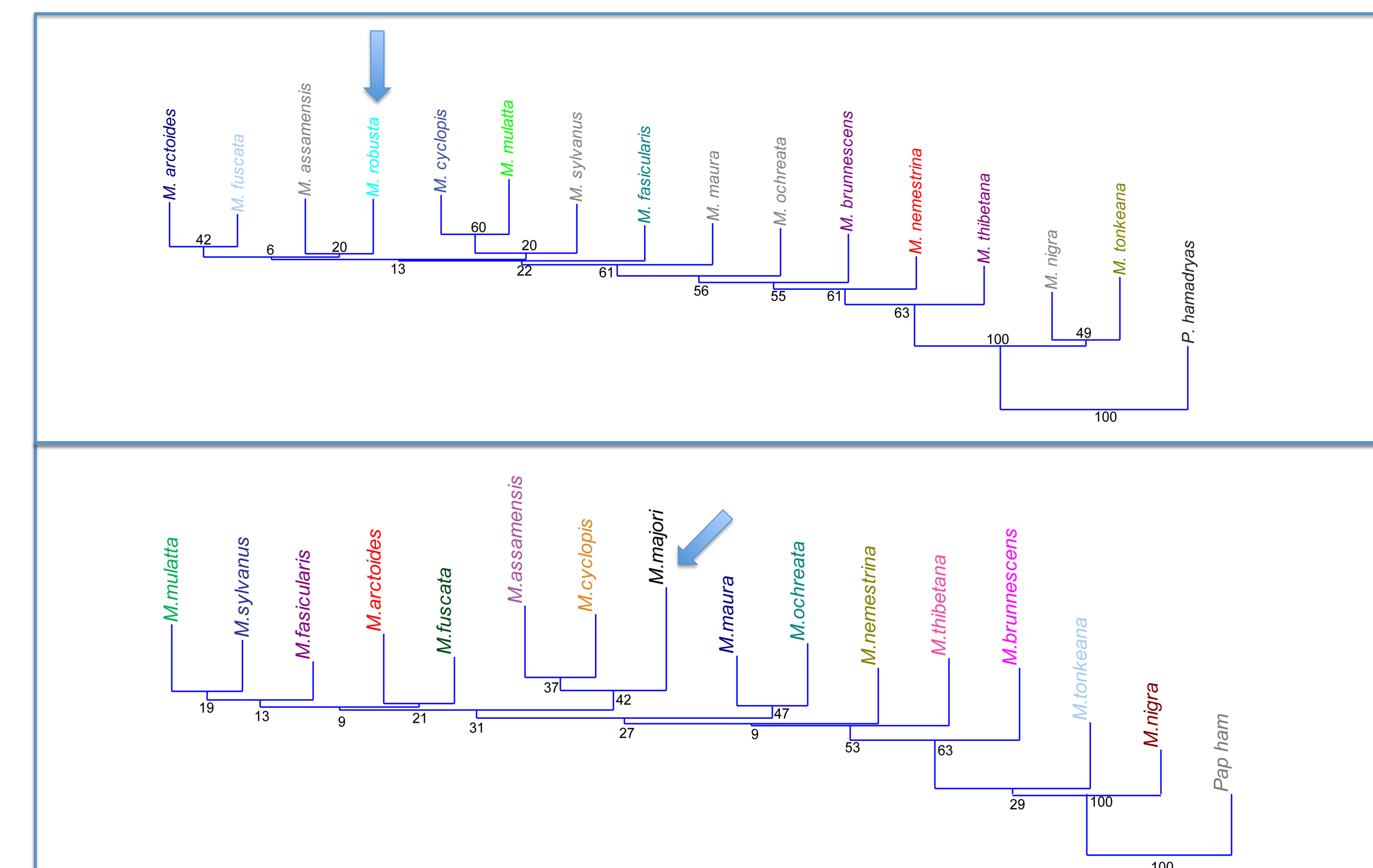


Fig. 4: Neighbor joining trees showing extant species means and fossils.

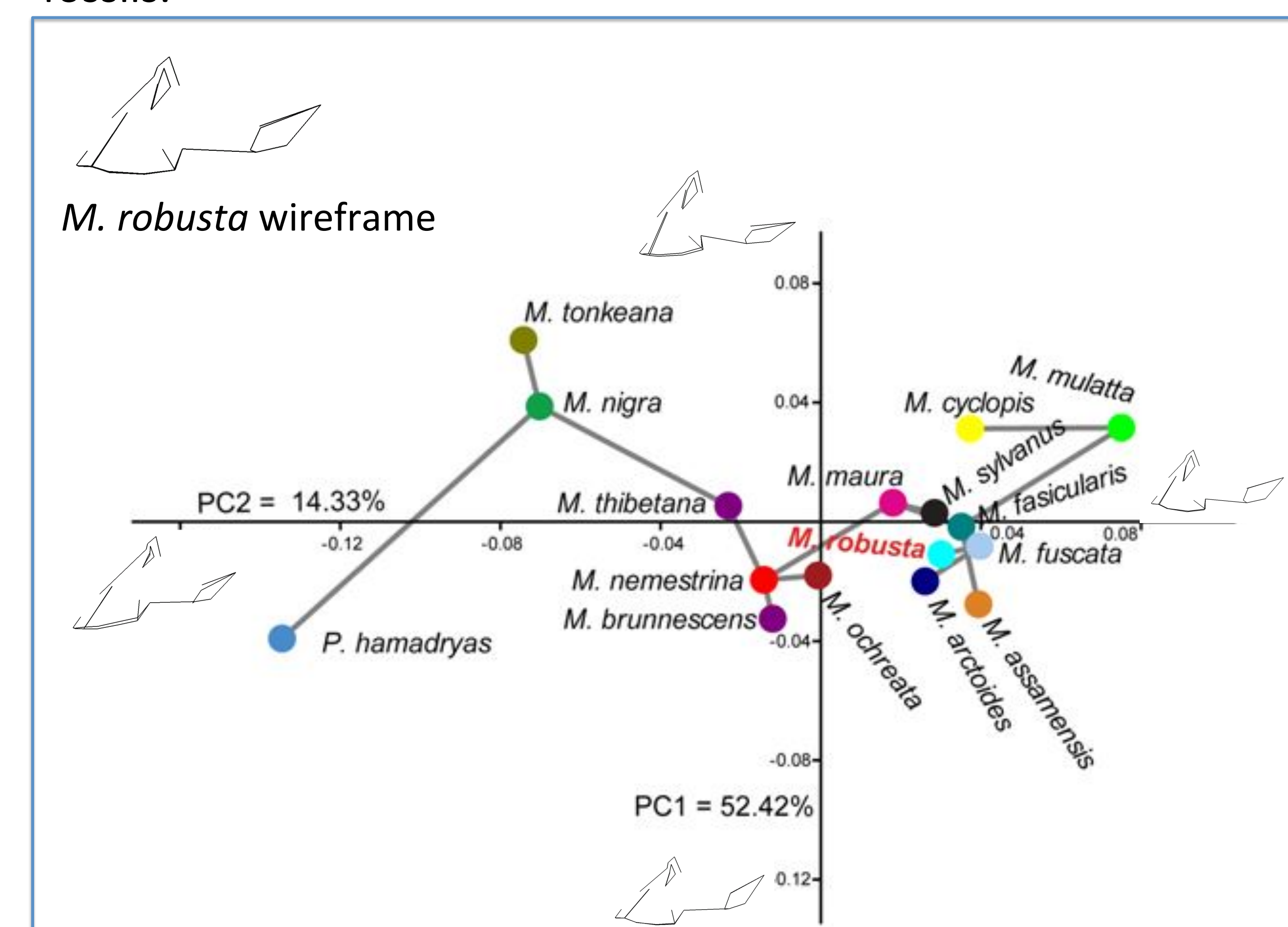


Fig. 3: PC Analysis of extant species means and *M. robusta*