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Research Article

# A new species of *Calomyscus* Thomas, 1905 (Calomyscidae: Rodentia) from western Iran

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**Abstract:** Eight extant species have been so far recognized for *Calomyscus* Thomas, 1905 which is distributed in the west of Asia. The only species which was reported from the Zagros Mountains in western and southern Iran was *C. bailwardi*. However, based on the integrative methods such as molecular, morphometric and karyological studies a new species is worth to be described other than *C. bailwardi* from the Zagros Mountains. In the present survey a new species which has been distributed in western regions of Iran was described as *Calomyscus behzadi* **sp. nov.** The new species constituted a monophyletic clade in phylogenetic tree which its relationships are unresolved. A new karyotype was reported for the new species as 2N=44 and FNa=48. The results of multivariate statistical analyses also separated the new species from *C. bailwardi* and other recognized species of the genus *Calomyscus*. Based on the size + shape data, *C. behzadi* **sp. nov.** has shorter nasal than *C. bailwardi*, group D and *C. grandis* and narrower than *C. baluchi* but wider than *C. hotsoni* and *C. elburzensis*. Moreover, according to the shape data, the new species has shorter m2 than *C. elburzensis*, *C. bailwardi*, *C. hotsoni*, *C. grandis* and group D and narrower than *C. bailwardi*, *C. grandis* and *C. baluchi*. The new species was described from regions which had been known already as distribution area of *C. bailwardi*.

**Key words**: *Calomyscus behzadi* sp. nov., phylogeny, karyotype, Zagros Mountains, mitochondrial genes

## 1. Introduction

The taxonomic rank of the genus *Calomyscus* Thomas, 1905 or beauty mouse and the number of its species, have been puzzling and underwent many changes from its discovery. It had been recognized as a distinct tribe named Calomyscini, in Cricetidae (Vorontsov and Potapova, 1979). Musser and Carleton once in 1993 elevated this tribe to subfamily Calomyscinae, and again in 2005 to family Calomyscidae (Musser and Carleton, 2005; Norris et al., 2008). Calomyscidae is one of the oldest families of Muroidea that was situated in a new taxon of Eumuroida along with Nesomyidae, Cricetidae, and Muridae by Steppan et al. (2004). Phylogenetic trees reconstructed based on four nuclear genes revealed that Calomyscidae is the basal family of this new taxon (Steppan et al., 2004). Splitting of *Calomyscus* from the rest of the Eumuroid was estimated in the most recent study by Rezazadeh et al. (2020) which is about 21.53 Mya. Two main clades of *Calomyscus* were diverged older than 9.49 Mya, in two stages in the Late Miocene and Pliocene (Rezazadeh et al., 2020).

Nowadays, eight extant species have been recognized for the family which is distributed throughout the west of Asia in Turkmenistan, Iran, Afghanistan, Pakistan, and Syria (Musser and Carleton, 2005; Kilpatrick, 2017). Six *Calomyscus* species were reported from different mountainous regions of Iran. One of the well-known species is *Calomyscus bailwardi* which was the first species recognized in the genus, was described from Khuzistan province in southwestern Iran and its distribution area had been known through Zagros Mountain from western to southern Iran in Kurdistan, Kermanshah, Ilam, Khuzistan, Lorestan, Fars, and Kerman provinces. But different studies showed that this species is distributed only in some localities in central parts of Zagros Mountains and other regions of these mountains are occupied by at least four potential new species which have to be described (Morshed and Patton, 2002; Karami et al., 2008; Akbarirad et al., 2016a; Rezazadeh et al., 2020). *Calomyscus elburzensis* with two subspecies as *C. e. elburzensis* in the north and northwestern Iran and *C. e. isatissus* in the center of Iran (Akbarirad et al., 2016b). *Calomyscus grandis* is known from northern Iran (Karami et al., 2008; Akbarirad et al., 2016b; Rezazadeh et al., 2020). *Calomyscus hotsoni* is distributed in Pakistan and southeastern Iran in Sistan-o-Baluchistan, South Khorasan, Kerman, and Hormozgan provinces (Khajeh et al., 2015; Akbarirad et al., 2016c). *Calomyscus urartensis* in the Azerbaijan Republic and Azerbaijan province in northwestern Iran (Karami et al., 2008; Rezazadeh et al., 2020) and *Calomyscus mystax* from Great Balkhan Mountains in southwestern

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Turkmenistan and northeastern Iran (Akbarirad et al., 2015). However, recent complementary studies on the genus *Calomyscus* in Iran revealed four lineages in the distribution area was recognized as *C. bailwardi*'s area which are distinct from known beauty mouse species and are worth to describe as new species which were named as *Calomyscus* group B, group C, group D and group G (Akbarirad et al., 2016a; Razazadeh et al., 2020). In the present study, we extended *Calomyscus* samplings from the Zagros Mountains in western Iran and applied an integrative approach to evaluate the taxonomic status of the lineage of *Calomyscus* group C which was reported in Akbarirad et al. (2016a) from Kermanshah and described it as new species.

## 2. Methods and materials

### 2.1. Molecular study

To complete our data, some sampling has done in western Iran in the Zagros Mountains. Ten *Calomyscus* samples were collected from Ilam province (2017) near Songhor in Kermanshah province.

Genomic DNA was extracted from three samples collected from Ilam province from 99% of ethanol preserved tissues according to protocols of DENAzist Asia's Animal DNA isolation kit (S-1033-1). Polymerase chain reaction (PCR) amplification was performed for two mitochondrial genes: *CO1* using primers BatL5310 (5′ CCTACTCRGCCATTTTACCTATG 3′) and R6036R (5′ ACTTCTGGGTGTCCAAAGAATCA 3′) (Herbreteau et al., 2011; Robins et al., 2007) and *CYTB* using L7: 5′-ACT AAT GAC ATG AAA AAT CAT CGT/T3′ and H6: 5′-TCT TCATTT TTG GTT TAC AAG AC-3′ (Montgelard et al., 2002). PCR reactions were performed using Taq PCR master mix kit (Qiagen). *CYTB* amplification protocol was: initial denaturation for 1 min 30 s at 95 °C, followed by 40 cycles of denaturation for 30 s at 95 °C, annealing for 1 min at 48 °C, and elongation for 30 sec at 72 °C, followed by terminal elongation for 2 min at 72 °C. PCR protocol using amplifying *CO1* gene was: initial denaturation step at 94 °C for 4 min, followed by 40 cycles of the 30 s at 94 °C, 30 s at 45–48 °C and 60 s at 72 °C, with a final extension time of 10 min at 72 °C. PCR products were analyzed by agarose gel electrophoresis and visualized with UV light on gel documentation for confirming the lack of any pseudogenes with only one sharp bands of *CYTB* or *CO1* on gel. Moreover, sequences of two mitochondrial genes, *CYTB* and *CO1* belong to *Calomyscus* samples from seven species and two distinct lineages were retrieved from GenBank (Table S1). All the examined stations were indicated in Figure 1. All the sequences were checked, edited and aligned using the CLUSTAL W algorithm in BioEdit (Hall, 1999). Then the sequences were checked for stop codons or gaps in MEGA 6 (Tamura et al., 2013). All the data of *CYTB* and *CO1* were combined in a single dataset and best-fit models of nucleotide substitution were found with the Akaike information criterion using jModelTest2 (Darriba et al. 2012). Bayesian inference (BI) performed using MrBayes 3.2.7a (Ronquist and Huelsenbeck 2003) on the CIPRES Science Gateway3.3 (available online: www.phylo.org). The MCMC was run for 60 million generations and sampled every 1000 generations. The robustness of nodes was tested with the posterior probability which was calculated from remaining trees after discarding the first 25% trees as burn-in. Maximum likelihood phylogenetic analyses were performed in PhyML (Guindon et al., 2010). Kimura 2-parameters distances were estimated using MEGA 6 and ExcaliBAR (Aliabadian et al., 2014) for within and between species genetic divergences. *Nannospalax* from Spalacidae and *Rhyzimys* from Rhizomyidae was chosen as an appropriate outgroup, as it was explained in Akbarirad et al. (2016a).

### 2.2. Morphometric analysis

A total of 107 *Calomyscus* individuals have been analyzed in morphometric methods which all of them were adults with fully erupted molars (Table S1). Four external traits of body length: BL, tail length: TL, hindfoot length to the base of claw: FL, and ear length: EL, along with thirty-one craniodental characters (Figure S1) were measured. A dissecting microscope equipped with an eyepiece graticule for dental measurements and a digital dial caliper (0.1 mm) for other measurements has been used. Statistical analyses were performed on both original data (size + shape) and size-out data (shape) according to Navarro et al. (2004). In this size normalization, overall size defined as the geometric mean between variables for every individual and shape is the log ratios of original variables divide by overall size. All the measurements were checked for normality and homogeneity of variance with the Shapiro-Wilk test (Shapiro and Wilk, 1965) and Levene's tests (Levene, 1960), respectively. Kruskal-Wallis ANOVA and median test used for nonnormal external measurement in univariate analyses. For estimating statistically significant differences between groups ANOVA test were performed. Evaluating the sexual dimorphism and significant differences between species were carried out by two-way multivariate analysis of variance (MANOVA). The significance level for all statistical tests was set at $p < 0.05$. A discriminant analysis (DA) was also performed on craniodental measurements to confirm between-group separation in multivariate space. All morphometric statistical analyses were conducted with the STATISTICA 12 software.

### 2.3. Karyological study

For the preparation of mitotic chromosome preparations bone marrow cells were extracted from the femur of *Calomyscus* samples of Ilam which were treated 45 min with 10% vinblastin solution at a dose of 1 ml/100g of body weight injected under the skin of the abdomen, using the method of Dutrillaux et al. (1982). A total of 10 slides were provided and stained with Giemsa for each individual. The diploid number of chromosomes (2N) and the number of autosomal arms (FNa) were assigned in the photos of 15 well-spread metaphase plates by the Chromosome Image Processing (CIP) software, provided

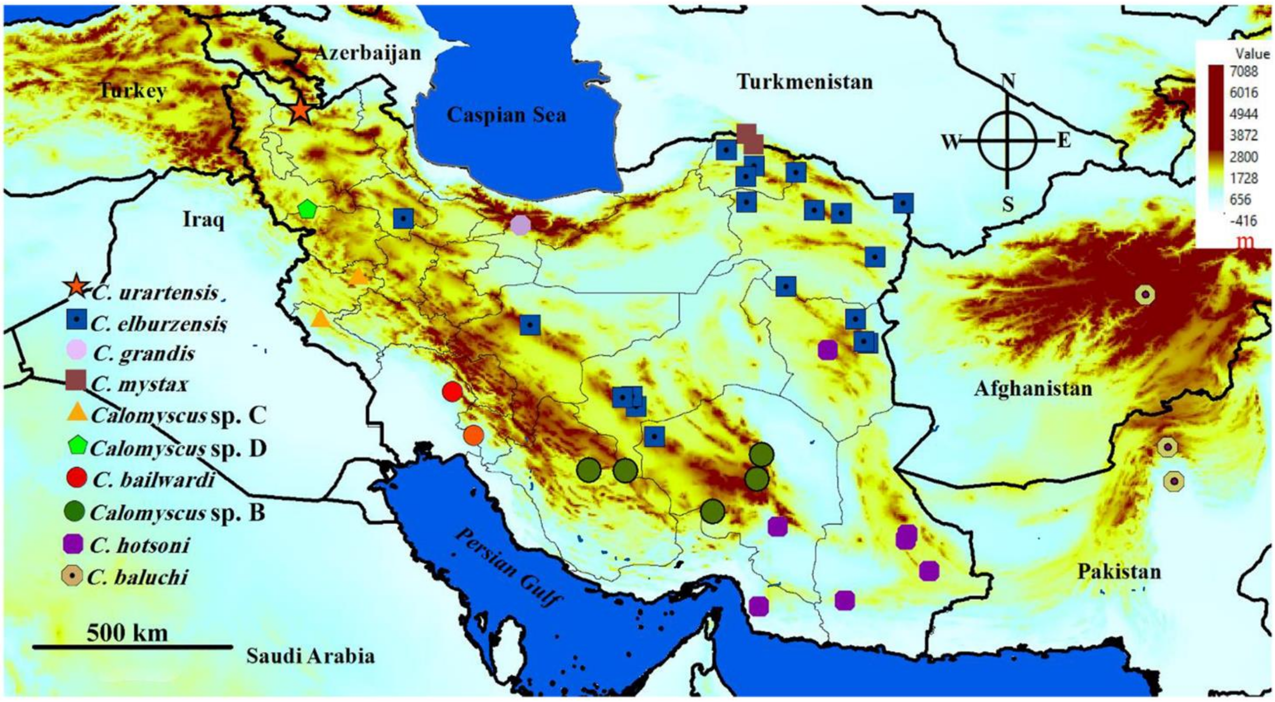


**Figure 1**. Sampling localities of examined *Calomyscus* specimens in this study.

**Table.** K2P genetic distances between groups and species of *Calomyscus* samples for *CYTB* gene.

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|---|---|---|---|---|---|---|---|---|---|
| *1.C. bailwardi* | | | | | | | | | |
| *2. Calomyscus* group B | 10.5 | | | | | | | | |
| *3. C. hotsoni* | 10.2 | 9.4 | | | | | | | |
| *4. Calomyscus* sp. group C | 16.0 | 15.8 | 14.8 | | | | | | |
| *5. C. elburzensis* | 15.5 | 14.3 | 14.6 | 10.5 | | | | | |
| *6. C. baluchi* | 10.5 | 9.0 | 8.5 | 15.8 | 14.4 | | | | |
| *7. C. grandis* | 14.9 | 15.4 | 14.4 | 9.2 | 8.6 | 15.5 | | | |
| *8. C. urartensis* | 17.2 | 14.8 | 15.4 | 9.6 | 9.1 | 14.2 | 9.6 | | |
| *9. Calomyscus* group D | 15.8 | 13.9 | 14.0 | 10.6 | 9.5 | 13.5 | 9.2 | 6.9 | |
| *10. C. mystax* | 15.6 | 14.8 | 13.3 | 10.4 | 9.8 | 13.7 | 9.8 | 8.6 | 8.6 |

by the Rodentology Research Department of Ferdowsi University of Mashhad.

## 3. Results

### 3.1. Molecular results

Totally, 1616 bp sequences (988 bps of *CYTB* and 628 bps of *CO1*) were obtained for two combined mitochondrial genes, with 397 variable sites (25 %) and 465 mutations of which 350 positions (23%) were parsimony informative. The best-fit models of sequence evolution for maximum likelihood reconstruction was GTR+I+G and for Bayesian reconstruction was GTR+I+G for combination of two genes. Two phylogenetic trees of Bayesian inference and ML analyses resulted from combined data of *CYTB* and *CO1* sequences showed the same results so only Bayesian tree is presented in Figure 2 with bootstrap values of ML analyses on each node. The distinct group which was explained by Akbarirad et al. (2016a) from Kermanshah (*Calomyscus* sp. group C) was resolved in the tree along with more specimens from Ilam province. This group is highly supported in both phylogenetic analyses. *Calomyscus* sp. group C was separated from the other *Calomyscus* groups by high genetic *p*-distances value (with C. *elburzensis* (10.5%), C. *mystax* (10.4%), C. *urartensis* (9.6%), C. *grandis* (9.2%), *Calomyscus* sp. group B (15.8.%), *Calomyscus* sp. group D (10.6%), C. *bailwardi* (16%), C. *hotsoni* (14.8%) and C. *baluchi* (15.8%) (Table).

### 3.2. Morphometric results

MANOVA analysis ($p > 0.05$) determined significant differences between *Calomyscus* sp. group C and other specimens of examined *Calomyscus* species in this study in both original and shape data. However, there were not any significant differences between sex in all the species.

Discriminant analyses classified 98.76% and 97.49% of *Calomyscus* specimens correctly based on size + shape and shape data, respectively. The canonical variates analysis (CVA) for craniodental measurements was performed and the between-group mahalanobis distances were calculated. The first two functions included 63% and 60%

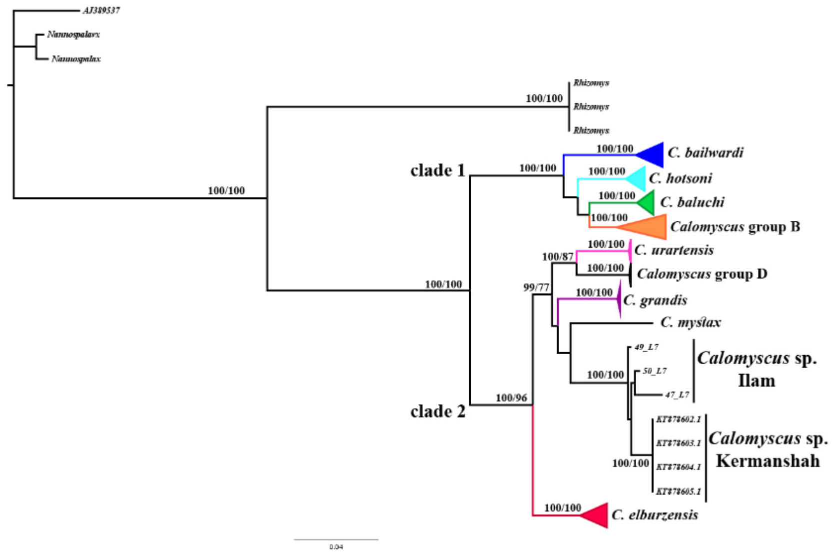


**Figure 2.** The combined tree resulted from Bayesian analysis on *CYTB* and *CO1* genes. Posterior probability are the numbers on the left which were presented as percentages values and bootstraps of maximum likelihood analyses are the ones on the right sides on each node.

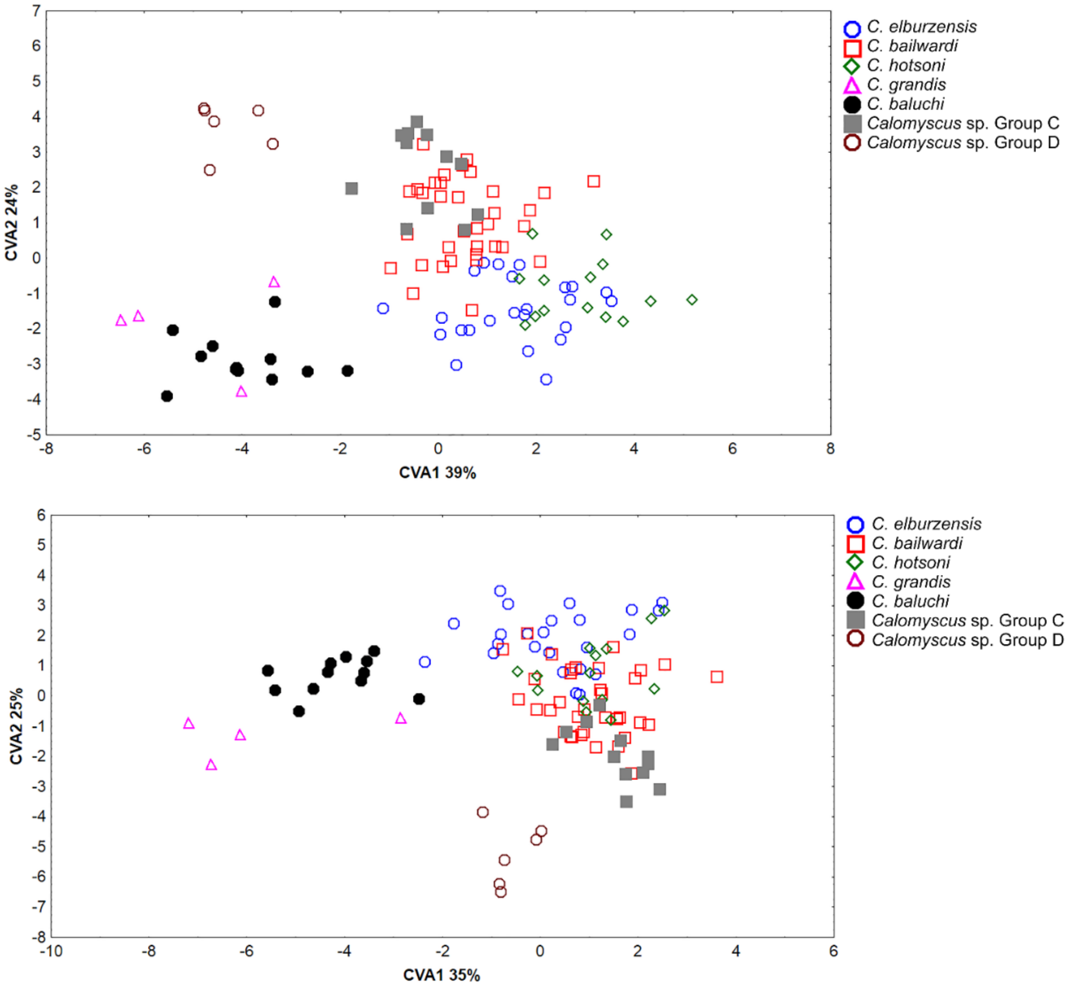


**Figure 3**. Canonical variate analyses (CVA) based on the size + shape data (A) and shape data (B) in *Calomyscus* species.

of the total pool of variance based on the size + shape and shape data, respectively. Both CVA analyses on size + shape (Figure 3A) and shape (Figure 3B) data showed that the first two canonical axes were separated *Calomyscus* sp. individuals (Kermanshah and Ilam) are overlapped with *C. bailwardi*, but discriminated from all other *Calomyscus* group. Univariate analysis on skull size (geometric mean between variables) of examined species showed that *Calomyscus* sp. group C had a significantly greater value in comparison with *C. elburzensis* and C. *hotsoni*. This group had significantly different overall dental size compared to *C. elburzensis* and C. *grandis* (Table S2**)**. The results of Welch's t-test and Student's t-test are presented in the description section and Table S2.

### 3.3. Karyology results

One male and one female specimen of *Calomyscus* sp. group C, from Ilam province, were used in the karyological studies. They have 21 pairs of autosomal chromosomes with three pairs of subtelocentric and 18 pairs of acrocentric chromosomes. The X chromosomes were subtelocentric and Y chromosome was acrocentric (Figure 4).

According to the present analyses and due to the study of Akbarirad et al. (2016a) we suggested defining a new species from Kermanshah and Ilam provinces in Zagros folded belt.

### 3.4. Taxonomy

***Calomycus behzadi*** Akbarirad, Dezhman, Aliabadian, Siahsarvie, Shafaeipour, Mirshamsi **sp. nov.**

#### 3.4.1. Holotype

1♂ (ZMFUM-5383), IRAN: Ghalarang Mountains, 11 km to the north of Ilam, Ilam province (33.63°N, 46.53° E), 2473 m, 15 August 2017, skin, skull and tissues preserved in 99% ethanol (all parts in good condition), leg. M. Dezhman (Figures 5 and 6).

**Holotype measurements** (in mm): BL: 85; TL: 92; FL: 22; EL: 19.

#### 3.4.2. Paratypes

♂ (ZMFUM-5379), 1♂ (ZMFUM-5380), 1♀ (ZMFUM-5381), (ZMFUM-5382), 1♂ (ZMFUM-5384), 1♂ (ZMFUM-5385), ZMFUM-5386, ZMFUM-5387 and 1♂ (ZMFUM-5388) from Ghalarang Mountains, 11 km to the north of Ilam, Ilam province, Iran (33.63°N, 46.53° E), other data same as holotype.

#### 3.4.3. Etymology

The epithet '*behzadi*' is named in honoring Professor Mahmoud Behzad (1913–2007), known as the father of modern biology in Iran.

#### 3.4.4. Description

*Calomyscus behzadi* **sp. nov.** (or group C, in Akbarirad et al., 2016a) is a medium size brush-tailed mouse with head and body length = 83.25 ± 0.89, tail length = 92.25 ± 0.45, ear length = 18.08 ± 0.23 and hind foot length = 21 ± 0.28. The upper parts are light brown and under parts are white, there is a distinct border line between upper and under parts colors. *C. behzadi* **sp. nov.** has long hind foot, long ear, long mandible, palatine and upper diastema and broad rostrum, narrow cranium, narrow and short parietal region, large depth of braincase and long maxillary tooth row, broad interorbital region; connecting line between articluar and angular process is less curved.

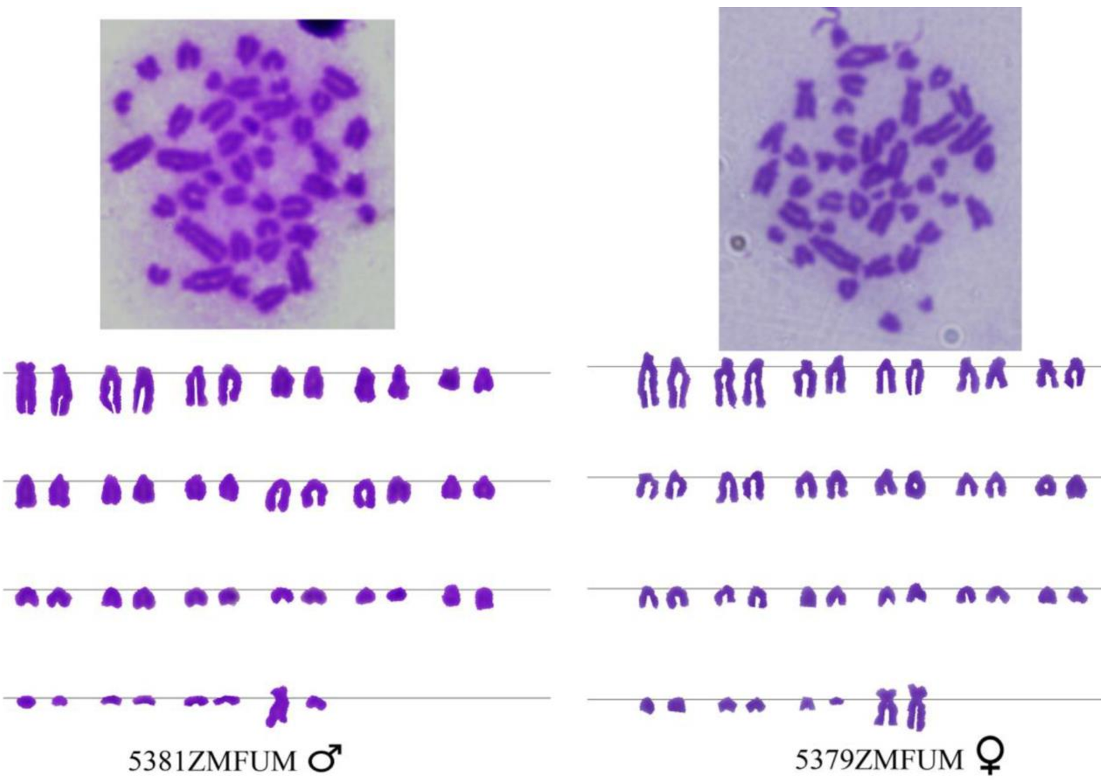


**Figure 4.** Two karyotypes of Ilam specimens belong to *Calomyscus* sp. group C. (2N=44, FNa=48).

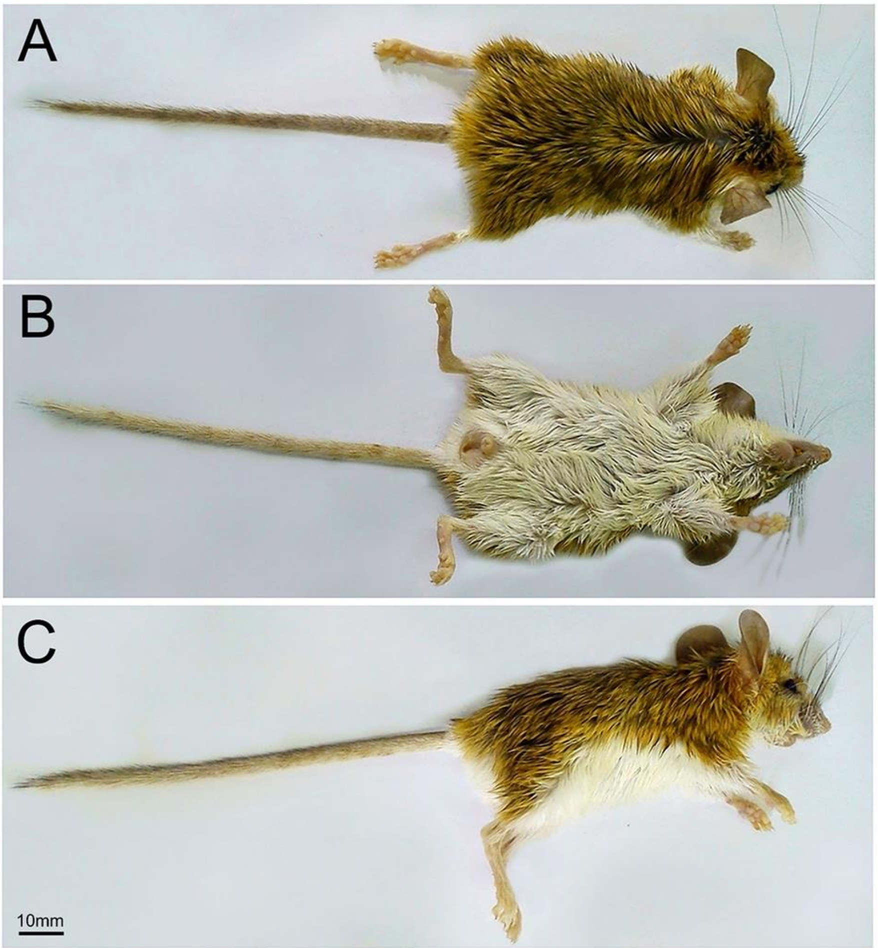


**Figure 5.** Dorsal, ventral and lateral views of holotype sample of *Calomyscus behzadi* sp.

Tail is narrow and haired along the terminal one-third of its length with a terminal brush. M2 is long, M3 is wide and m2 is short and narrow. Mitochondrial gene sequences situated them in a distinct cluster with high genetic diversity with other species of *Calomyscus*.

### 3.4.5. Diagnosis

Although *Calomyscus* species are similar in external morphology but craniodental measurements can discriminate *C. behzadi* **sp. nov.** from other *Calomyscus* species. Univariate analyses based on size + shape data showed that in this group, cranium is narrower than *C. bailwardi*, group D and *C. baluchi* but wider than *C. hotsoni*, higher than *C. hotsoni* and longer than *C. hotsoni* and *C. elburzensis* and interorbital region is wider than *C. grandis*, *C. elburzensis* and *C. hotsoni* but narrower than group D. In this group, condylobasal is longer than *C. hotsoni* and *C. elburzensis* but shorter than group D and *C. baluchi*. *C. behzadi* **sp. nov.** show shorter nasal than *C. bailwardi*, group D and *C. grandis* and narrower than *C. baluchi* but wider than *C. hotsoni* and *C. elburzensis*. In the new species, the mandible is longer than *C. hotsoni* and *C. elburzensis* but shorter than group D and higher than *C. elburzensis* but lower than group D. *C. behzadi* **sp. nov.** has lower height of lower diastema than *C. bailwardi*, group D and *C. baluchi*. Specimens from Kermanshah and Ilam have longer mandibular tooth row than *C. bailwardi*, *C. grandis*, *C. hotsoni* and *C. elburzensis*.

Also, in shape data, *C. behzadi* **sp. nov.** show longer cranium than *C. elburzensis*, *C. grandis* and *C. baluchi*, narrower than *C. elburzensis* and *C. baluchi* and higher than *C. baluchi* and group D; shorter nasal than *C. elburzensis*, *C. bailwardi* and *C. grandis* and narrower than *C. grandis* and *C. baluchi* but wider than group D; lower height of lower diastema than *C. elburzensis*, *C. bailwardi*, *C. hotsoni*, *C. baluchi* and group D; longer mandible than *C. elburzensis*, *C. bailwardi*, *C. hotsoni* and *C. baluchi* and lower mandible than *C. hotsoni* and group D; longer M1 than group D but shorter than *C. baluchi*, narrower than *C. elburzensis*, *C. bailwardi*, *C. baluchi* and *C. grandis* but wider than *C. hotsoni*; shorter m2 than *C. elburzensis*, *C. bailwardi*, *C. hotsoni*, *C. grandis* and group D, narrower than *C. bailwardi*, *C. grandis* and *C. baluchi*; longer m3 than *C. grandis*, *C. baluchi* but shorter m3 than *C. hotsoni* and group D.

In karyology, this new species has the different chromosome formula; it has 44 chromosomes and 48 autosomal arms.

### 3.4.6. Comparisons

Based on size + shape data, *C. behzadi* **sp. nov.** is distinct from *C. bailwardi* by shorter ear, longer mandible, lower height of lower diastema, shorter nasal, narrower cranium, shorter and narrower m2, narrower M1, narrower m1, longer M2, wider M3 and in shape data lower height of lower diastema, shorter nasal, longer mandible, narrower M1, wider M3, narrower m1, shorter and narrower m2.

The new species is distinguished from *C. grandis* with longer maxillary tooth row, shorter distance between two meatus, shorter tympanic bulla, shorter anterior palatine foramen, narrower and shorter nasal, shorter m2, shorter M1, shorter M2, longer M3, longer cranium, longer mandible, longer m3, wider inter orbital region and in shape data shorter nasal, shorter anterior palatine foramen, narrower nasal, higher cranium, longer occipitonasal, wider inter orbital region, shorter distance between two meatus, narrower M1, narrower M2, shorter and narrower m2 and longer m3.

*C. behzadi* **sp. nov.** distinct from *Calomyscus* group D by lower mandibular height, shorter condylobasal, lower height of lower diastema, shorter nasal, shorter cranium, shorter mandibular tooth row, longer M1, longer m3, wider nasal, higher cranium, narrower cranium and interorbital region, shorter tympanic bulla; and longer M1, shorter m2 and in shape data, lower height of lower diastema, lower mandibular height, narrower nasal, higher cranium, shorter mandibular tooth row, longer M1, shorter m2 and shorter m3.

Individuals of the new species have longer maxillary tooth row, longer palatal length, higher mandibular height, higher upper diastema, longer occipitonasal, longer condylobasal, longer and narrower cranium, shorter and wider nasal, longer maxillary and mandibular tooth row, longer mandible, longer and wider M3 and wider m1 than *C. elburzensis* and in shape data, lower height of lower diastema, shorter nasal, shorter Length of anterior palatine foramen, longer occipitonasal, narrower cranium, wider inter orbital region, longer condylobasal, longer mandible, narrower M1, shorter m2 and wider M3.

*C. behzadi* **sp. nov.** have longer body, tail and hind foot; wider zygomatic, longer condylobasal, longer palatal length, longer occipitonasal, wider nasal, higher upper diastema, longer lower diastema, higher, longer and wider cranium, longer mandible and mandibular tooth row, wider interorbital width, shorter M2, wider M3 than *C. hotsoni* and in shape data, lower height of lower diastema, lower mandibular height, higher upper diastema, shorter tympanic bulla, longer condylobasal, shorter distance between two meatus, longer mandibular tooth row, longer mandible, narrower M1, narrower m1, shorter and narrower m2 and wider M3.

*C. behzadi* **sp. nov.** show shorter distance between two meatus, shorter anterior palatine foramen, lower height of lower diastema, shorter condylobasal, narrower nasal, narrower, shorter and higher cranium; narrower and shorter M1, shorter m2, longer m3 than *C. baluchi* and in shape data lower height of lower diastema, shorter anterior palatine foramen, narrower nasal, longer occipitonasal, higher and narrower cranium, shorter distance between two meatus, longer mandible, shorter and narrower M1, narrower M2, narrower m2 and longer m3.

*C. behzadi* **sp. nov.** has the same chromosome number as *C. elburzensis* and *C. grandis*; but the number of autosomal arms is different from these two species. In *C. elburzensis* autosomal arms were ranged from 60 to 72, and in *C. grandis* is 46, while *C. behzadi* **sp. nov.** has 48 autosomal arms. Chromosome number of the new species is different from other *Calomyscus* species in Zagros Muntains as *C. bailwardi*, *Calomyscus* group B.

### 3.4.7. Distribution

*Calomyscus behzadi* **sp. nov.** is known from two locations in western Iran: one from type locality situated in Songhor of Kermanshah province and Ghalarang in Ilam province (see Figure 1).

## 4. Discussion

Phylogenetic analyses of *CYTB* and *CO1* genes showed a distinct clade in specimens of the Zagros Mountains which were separated from all other beauty mice species with high genetic divergences. This separation was first represented for the Kermanshah population in Akbarirad et al. (2016a) and also in Rezazadeh et al. (2020). However, the phylogenetic position of this new species was unresolved. In Akbarirad et al. (2016a) monophyletic group C (Kermanshah population) was placed as a sister group with *C. grandis* without any support. And in Rezazadeh et al. (2020) with adding a group of *Calomyscus* samples named as group G was placed as a supported sister group to *C. grandis*, the specimens of Kermanshah constituted a distinct clade in a sister position with *C. urartensis*/*Calomyscus* sp. group D with no support. In the present study Kermanshah and Ilam specimens as *C. behzadi* **sp. nov.** formed a monophyletic group with high support and situated as the sister group to *C. mystax* but again with no support. So, this unclear position of *C. behzadi* **sp. nov.** showed that it has a sister group or near relationship with another group or unknown species of *Calomyscus* which is not described until now. The patchy distribution of *Calomyscus* species and several mountain chains which are their habitats, in Iran, Afghanistan, Pakistan, Turkmenistan, and Turkey resulted in the existing of several possible species that were not identified in the available published studies. Describing of this possible species will resolve the phylogenetic relationships of *Calomyscus* species.

Morphometric characters of cranial, dental, and mandibular measurements also separated Zagros Mountains populations from Kermanshah and Ilam from *C. bailwardi*. Besides, these analyses showed some characters which could describe the *C. kemranshahi* **sp. nov.** as a new species.

Karyotype analysis also presented a different diploid number of chromosomes and autosomal arms in the Ilam population of *C. behzadi* **sp. nov.** (2N=44, FNa=48) with *C. bailwardi* (2N=46, FNa=44) (Akbarirad et al., 2016a).

*Calomyscus behzadi* **sp. nov.** in Songhor of Kermanshah province and Ghalarang in Ilam province in western Iran and north of *C. bailwardi*'s distribution range is a new species recorded from regions which were recognized as distribution area of *C. bailwardi* by all other authors (Graphodatsky et al., 2000; Morshed and Patton, 2002; Musser and Carleton, 2005; Karami et al., 2008).

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**Conflict of interest**
The authors declare that they have no conflict of interest, financial or other, exist.

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**Appendix**

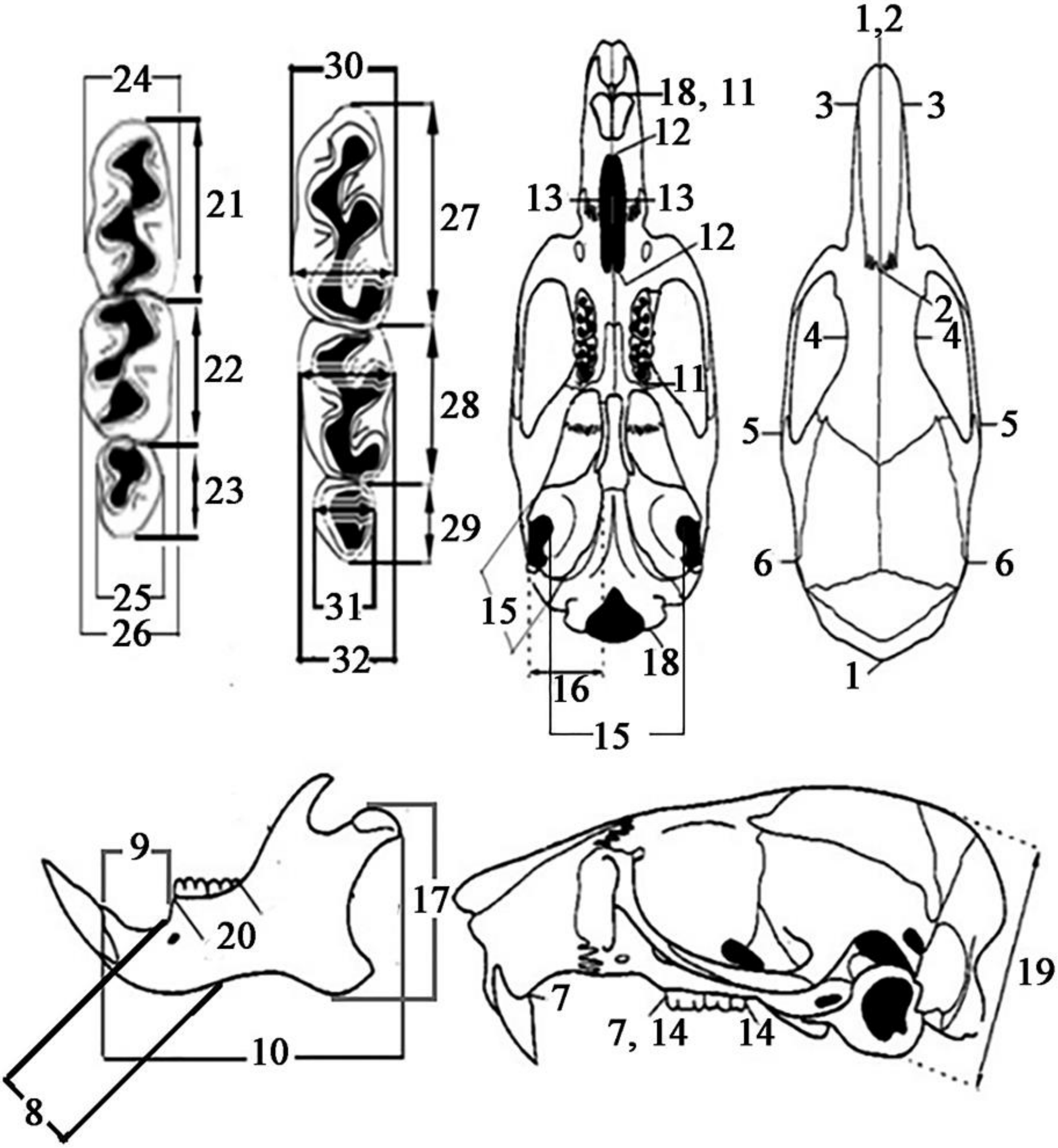


**Figure S1.** Thirty two craniodental characters were measured in examined samples of *Calomyscus* based on Peshev (1991) and Shahabi et al. (2011): 1- occipitonasal length (Occl); 2- nasal length (NL); 3- nasal width (NW); 4- interorbital width (Intw); 5- zygomatic width (ZW); 6- cranium width (CW); 7- upper diastema length (UDL); 8- height of lower diastema ( HLD); 9- length of lower diastema (LLD); 10- mandible length (Mndl); 11- palatal length (Patl); 12- length of anterior palatine foramen (Forl); 13- width of anterior palatine foramen (Forw); 14- maxillary tooth row length (Mxl); 15- distance between two meatus (DB2M); 16- length of tympanic bulla (BULL); 17- maximum mandibular height (MH); 18- condylobasal length (CBL); 19 - maximum cranial height (SH); 20- mandibular tooth row length (Mnl); 21- length of m1 (m1L); 22- length of m2 (m2L); 23- length of m3 (m3L); 24- width of m1 (m1W); 25- width of m2 (m2W); 26- width of m3 (m3W); 27- length of M1 (M1L); 28- length of M2 (M2L); 29- length of M3 (M3L); 30- width of M1 (M1W); 31- width of M2 (M2W); 32- width of M3 (M3W).

**Table S1.** Details of sampled localities, tissue and voucher numbers and accession numbers of specimens examined in this study (for each sample the first accession number is for *CYTB* and the second is for *CO1* genes).

| Species | Locality (city, province) | Voucher no. | Accession no. | |
|---|---|---|---|---|
| | | | ***CYTB*** | ***CO1*** |
| ***Calomyscus* sp. Group D** | Saghez, Kurdistan | ZMFUM3869 | KT878596 | KT878556 |
| ***Calomyscus* sp. Group D** | Saghez, Kurdistan | ZMFUM3870 | KT878597 | KT878557 |
| ***Calomyscus* sp. Group D** | Saghez, Kurdistan | ZMFUM3878 | KT878600 | KT878560 |
| ***Calomyscus* sp. Group D** | Saghez, Kurdistan | ZMFUM3881 | KT878598 | KT878558 |
| ***Calomyscus* sp. Group D** | Saghez, Kurdistan | ZMFUM3882 | KT878599 | KT878559 |
| ***Calomyscus* sp. Group D** | Saghez, Kurdistan | ZMFUM3897 | KT878601 | KT878561 |
| ***C. behzadi* sp. nov. (C)** | Songhor, Kermanshah | ZMFUM3871 | KT878603 | KT878563 |
| ***C. behzadi* sp. nov. (C)** | Songhor, Kermanshah | ZMFUM3880 | KT878605 | KT878565 |
| ***C. behzadi* sp. nov. (C)** | Songhor, Kermanshah | ZMFUM3891 | KT878604 | KT878564 |
| ***C. behzadi* sp. nov. (C)** | Songhor, Kermanshah | ZMFUM3896 | KT878602 | KT878562 |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5380 | | |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5382 | MW888462 | MW892625 |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5383 | | |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5384 | MW888460 | MW892623 |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5385 | MW888459 | MW892624 |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5386 | | |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5387 | | |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5388 | | |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5379 | | |
| ***C. behzadi* sp. nov. (C)** | Ilam, Ilam | ZMFUM 5381 | | |
| ***C. grandis*** | Fasham, Tehran | ZMFUM 3992 | KT884559 | KT884587 |
| ***C. grandis*** | Fasham, Tehran | ZMFUM1985 | KT878591 | KT878551 |
| ***C. grandis*** | Fasham, Tehran | ZMFUM3992 | KT878592 | KT878552 |
| ***C. grandis*** | Fasham, Tehran | ZMFUM1948 | KT878593 | KT878553 |
| ***C. grandis*** | Fasham, Tehran | ZMFUM1943 | | |
| ***C. mystax*** | Taklah Quz, North Khorasan | ZMFUM 2984 | KU129019 | KU129021 |
| ***C. elburzensis*** | Mashhad, Khorasan-e-Razavi | ZMFUM1542 | KT878581 | KT878542 |
| ***C. elburzensis*** | Mashhad, Khorasan-e-Razavi | ZMFUM2023 | | |
| ***C. elburzensis*** | Sarakhs, Khorasan-e-Razavi | ZMFUM1874 | KT878585 | KT878546 |
| ***C. elburzensis*** | Sarakhs, Khorasan-e-Razavi | ZMFUM1922 | KT878586 | KT878547 |
| ***C. elburzensis*** | Torbat, Khorasan-e-Razavi | ZMFUM2088 | KT878587 | KT878548 |
| ***C. elburzensis*** | Saluk, North- Khorasan | ZMFUM2978 | KT878588 | KU043034 |
| ***C. elburzensis*** | Shirvan, North- Khorasan | ZMFUM3533 | KT878590 | KT878550 |
| ***C. elburzensis*** | Chenaran, North- Khorasan | ZMFUM3100 | | |
| ***C. elburzensis*** | Bijand, Gazik, South Khorasan | ZMFUM 4529 | KT884557 | KT884586 |
| ***C. elburzensis*** | KhajeMor, Khorasan-e-Razavi | ZMFUM 1546 | KT884547 | KT884576 |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2148 | KT884550 | KT884580 |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2152 | KT884551 | KT884581 |
| ***C. elburzensis*** | Ghaen, South Khorasan | ZMFUM 3304 | KT884553 | KT884583 |
| ***C. elburzensis*** | Kurkhud, North Khorasan | ZMFUM 3629 | KT884555 | KT884584 |
| ***C. elburzensis*** | Sabzevar, Khorasan-e-Raza | ZMFUM 4490 | KT884556 | KT884585 |
| ***C. elburzensis*** | Taft, Shirkuh, Godar-Nir, Yazd | ZMFUM 1 | KU042999 | KU043023 |
| ***C. elburzensis*** | Taft, Shirkuh, Godar-Nir, Yazd | ZMFUM4 | KU043000 | KU043024 |
| ***C. elburzensis*** | Taft, Shirkuh, Godar-Nir, Yazd | ZMFUM9 | KU043001 | KU043025 |

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|---|---|---|---|---|
| ***C. elburzensis*** | Taft, Shirkuh, Godar-Nir, Yazd | ZMFUM 10 | KU043002 | KU043026 |
| ***C. elburzensis*** | Taft, Shirkuh, Yazd | ZMFUM 2932 | KU043004 | KU043027 |
| ***C. elburzensis*** | Taft, Shirkuh, Cheshme, Yazd | ZMFUM 2948 | KU043007 | KU043029 |
| ***C. elburzensis*** | Taft, Shirkuh, Yazd | ZMFUM 2952 | KU043010 | KU043030 |
| ***C. elburzensis*** | Taft, Shirkuh, Tezerjan, Yazd | ZMFUM 3039 | KU043015 | KU043036 |
| ***C. elburzensis*** | Qeidar, Zanjan | ZMFUM 3925 | KU043020 | KU043037 |
| ***C. elburzensis*** | Qeidar, Zanjan | ZMFUM 3937 | KU043021 | KU043038 |
| ***C. elburzensis*** | Karkas, Isfahan | ZMFUM 3938 | KU043022 | KU043039 |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2144 | | |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2149 | | |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2172 | | |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2156 | | |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2169 | | |
| ***C. elburzensis*** | Neyshabur, Khorasan-e-Razavi | ZMFUM 2158 | | |
| ***C. elburzensis*** | Esfarayen, North Khorasan | ZMFUM 3224 | | |
| ***C. elburzensis*** | Saluk, Bojnurd, | ZMFUM 3085 | | |
| ***C. elburzensis*** | Bojnord, North Khorasan | ZMFUM 2616 | | |
| ***C. elburzensis*** | Esfaraien, North Khorasan | ZMFUM 3216 | | |
| ***C. elburzensis*** | Nishapur, Razavi Khorasan | ZMFUM 2176 | | |
| ***C. elburzensis*** | Shirkuh , Yazd | ZMFUM 2949 | | |
| ***C. elburzensis*** | Shirkuh , Yazd | ZMFUM 2968 | | |
| ***C. elburzensis*** | Shirkuh , Yazd | ZMFUM 2945 | | |
| ***C. elburzensis*** | Mahriz, Kuhe-Bakhtaki, Yazd | ZMFUM 3088 | | |
| ***C. elburzensis*** | Shirkuh , Yazd | ZMFUM 3057 | | |
| ***C. elburzensis*** | Dehaj, Kerman | ZMFUM 5410 | | |
| ***C. elburzensis*** | Dehaj, Kerman | ZMFUM 5411 | | |
| ***C. elburzensis*** | Dehaj, Kerman | ZMFUM 5414 | | |
| ***C. elburzensis*** | Dehaj, Kerman | ZMFUM 5416 | | |
| ***Calomyscus* sp. Group B** | BagheShadi, Yazd | ZMFUM3324 | KT878608 | KT878571 |
| ***Calomyscus* sp. Group B** | BagheShadi, Yazd | ZMFUM3327 | KT878609 | KT878572 |
| ***Calomyscus* sp. Group B** | BagheShadi, Yazd | ZMFUM3328 | KT878610 | KT878573 |
| ***Calomyscus* sp. Group B** | BagheShadi, Yazd | ZMFUM3333 | KT878611 | KT878574 |
| ***Calomyscus* sp. Group B** | BagheShadi, Yazd | ZMFUM3351 | KT878612 | KT878575 |
| ***Calomyscus* sp. Group B** | Anjerk, Kerman | ZMFUM2003 | KT878613 | KT878566 |
| ***Calomyscus* sp. Group B** | Anjerk, Kerman | ZMFUM2004 | KT878614 | KT878567 |
| ***C. baluchi*** | Pakistan, Sibi Dist | 980 (OUT-13) | | KT884596 |
| ***C. baluchi*** | FATA, North Waziristan, Pakistan | N/A | EU135591.1 | |
| ***C. baluchi*** | Balochistan., Pakistan | N/A | EU135586.1 | |
| ***C. baluchi*** | Balochistan, Kalat, Pakistan | N/A | AY288509.1 | |
| ***C. baluchi*** | Ziarat, Pakistan | ZTNH897 | | KT878579 |
| ***C. baluchi*** | Datta Khel, Pakistan | ZTNH1262 | | KT878580 |
| ***C. baluchi*** | Bamyan, Afghanistan | ZMFUM2798 | | |
| ***C. baluchi*** | Takhte Waras, Afghanistan | ZMFUM2782 | | |
| ***C. baluchi*** | Yakawlang, Afghanistan | ZMFUM2786 | | |
| ***C. baluchi*** | Bamyan, Afghanistan | ZMFUM2800 | | |
| ***C. baluchi*** | Yakawlang, Afghanistan | ZMFUM2787 | | |
| ***C. baluchi*** | Yakawlang, Afghanistan | ZMFUM2820 | | |

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| ***C. baluchi*** | Yakawlang, Afghanistan | ZMFUM2789 | | |
| ***C. baluchi*** | Surkh Joy, Afghanistan | ZMFUM2813 | | |
| ***C. baluchi*** | Afghanistan | ZMFUM 2718 | | |
| ***C. baluchi*** | Afghanistan | ZMFUM2821 | | |
| ***C. baluchi*** | Afghanistan | ZMFUM2810 | | |
| ***C. baluchi*** | Pitab-Joy, Afghanistan | ZMFUM2784 | | |
| ***C.hotsoni*** | Bashagard, Hormozgan | ZMFUM4739 | | |
| ***C.hotsoni*** | Khash, Sistan and Baluchestan | ZMFUM 3563 | | |
| ***C.hotsoni*** | Zahedan, Sistan and Baluchestan | ZMFUM3564 | | |
| ***C.hotsoni*** | Zahedan, Sistan and Baluchestan | ZMFUM3529 | | |
| ***C.hotsoni*** | Balouchestan, Sistan and Baluchestan | ZMFUM4409 | | |
| ***C.hotsoni*** | Saravan, Sistan and Baluchestan | ZMFUM3287 | | |
| ***C.hotsoni*** | Bashagard, Sistan and Baluchestan | ZMFUM19 | | |
| ***C.hotsoni*** | Bashagard, Sistan and Baluchestan | ZMFUM4785 | | |
| ***C.hotsoni*** | Bashagard, Sistan and Baluchestan | ZMFUM4761 | | |
| ***C.hotsoni*** | Birjand, South Khorasan | ZMFUM4024 | | |
| ***C.hotsoni*** | Birjand, South Khorasan | ZMFUM4012 | | |
| ***C.hotsoni*** | Birjand, South Khorasan | ZMFUM4013 | | |
| ***C. hotsoni*** | Saravan, Sistan-o-Baluchistan | ZMFUM2068 | KT884560 | KT878577 |
| ***C. hotsoni*** | Saravan, Sistan-o-Baluchistan | ZMFUM2069 | KT884561 | KT878578 |
| ***C. hotsoni*** | Saravan, Sistan-o-Baluchistan | ZMFUM2102 | KT884562 | KT884588 |
| ***C. hotsoni*** | Saravan, Sistan-o-Baluchistan | ZMFUM2103 | KT884563 | KT884589 |
| ***C. hotsoni*** | Saravan, Sistan-o-Baluchistan | ZMFUM3286 | KT884564 | KT884590 |
| ***C. hotsoni*** | Khash, Sistan-o-Baluchistan | ZMFUM3306 | KT884567 | KT884591 |
| ***C. hotsoni*** | Zahedan, Sistan-o-Baluchistan | ZMFUM3962 | KT884571 | KT884593 |
| ***C. hotsoni*** | Bagheran, Bijand, South Khorasan | ZMFUM4013 | KT884573 | KT884594 |
| ***C. bailwardi*** | Ludab, Kohgiluyeh and Boyer-Ahmad | ZMFUM5348 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5174 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5175 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5176 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5177 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5178 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5179 | | |
| ***C. bailwardi*** | Sudejan , Chaharmahal and Bakhtiari | ZMFUM5180 | | |
| ***C. bailwardi*** | Sudejan, Chaharmahal and Bakhtiari | ZMFUM5181 | | |
| ***C. bailwardi*** | Sureshjan, Chaharmahal and Bakhtiari | ZMFUM5158 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5372 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5373 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5374 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5375 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5376 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5377 | | |
| ***C. bailwardi*** | Dorud, Lorestan | ZMFUM5378 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5412 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5413 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5415 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5417 | | |

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| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5418 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5419 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5420 | | |
| ***C. bailwardi*** | Semirom, Isfahan | ZMFUM5421 | | |
| ***C. bailwardi*** | Behbahan, Khuzestan | ZMFUM2536 | | |
| ***C. bailwardi*** | Izeh, Khuzistan | ZMFUM3569 | | |
| ***C. bailwardi*** | Izeh, Khuzistan | ZMFUM3570 | | |
| ***C. bailwardi*** | Izeh, Khuzistan | ZMFUM3571 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2514 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2516 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2522 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2524 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2529 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2536 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2700 | | |
| ***C. bailwardi*** | Behbahan, Khuzistan | ZMFUM2701 | | |
| ***C.bailwardi*** | Behbahan, Khuzistan | ZMFUM2702 | | |
| ***C. urartensis*** | Kordasht, Eastern Azerbaijan | ZMFUM2253 | KT878594 | KT878554 |
| ***C. uratensis*** | Kordasht, Eastern Azerbaijan | ZMFUM2908 | KT878595 | KT878555 |

**Table S2.** Means and standard errors of craniodental measurements in *Calomyscus* groups: *C. baluchi* (BA), C. *elburzensis* (El), C. *grandis* (Gr), *Calomyscus* sp. from Kermanshah and Ilam (C), *Calomyscus* sp. group D (D), C. *bailwardi* (Bai), C. *hotsoni* (Ho).

| **Variables** | ***C. elburzensis*** | ***C. bailwardi*** | ***C. hotsoni*** | ***C. grandis*** | ***C. baluchi*** | ***Calomyscus* sp. (from Kermanshah and Ilam)** | ***Calomyscus* sp. Group D** | **T-test and Welch t-test result (size + shape)** | **Shape data** |
|---|---|---|---|---|---|---|---|---|---|
| **BL** | 79.29 ± 0.92 | 83.17 ± 1.13 | 74.78 ± 1.81 | 80.25 ± 3.52 | 77.75 ± 2.61 | 83.25 ± 0.89 | 79.5 ± 1.84 | Ho<C | |
| **TL** | 89.87 ± 1.09 | 90.44 ± 1.02 | 84.42 ± 1.62 | 91.5 ± 2.60 | 92.08 ± 2.47 | 92.25 ± 0.45 | 89.66 ± 1.54 | Ho<C | |
| **El** | 17.54 ± 0.39 | 19.64 ± 0.26 | 17.5 ± 0.59 | 13.75 ± 1.75 | 17.5 ± 0.66 | 18.08 ± 0.23 | 18.5 ± 0.43 | C<Bai | |
| **FL** | 20.16 ± 0.19 | 21.92 ± 0.26 | 19.07 ± 0.35 | 20.75 ± 0.48 | 20.66 ± 0.33 | 21 ± 0.28 | 20.83 ± 0.48 | C>Ho | |
| **LLD** | 3.81 ± 0.04 | 4.04 ± 0.06 | 3.61 ± 0.03 | 4.00 ± 0.03 | 3.90 ± 0.07 | 3.91 ± 0.08 | 3.98 ± 0.06 | Ho<C | |
| **HLD** | 2.29 ± 0.02 | 2.37 ± 0.03 | 2.29 ± 0.02 | 2.37 ± 0.05 | 2.4 ± 0.02 | 2.23 ± 0.04 | 2.38 ± 0.02 | Bai>C, D>C, BA>C | El>C, Bai>C, Ke>C,Ho>C, BA>C, D>C |
| **MH** | 5.86 ± 0.04 | 6.08 ± 0.04 | 6.01 ± 0.07 | 6.12 ± 0.07 | 6.07 ± 0.03 | 6.00 ± 0.06 | 6.30 ± 0.07 | D>C, C>El | Ho>C, D>C |
| **UDL** | 6.68 ± 0.03 | 6.97 ± 0.08 | 6.34 ± 0.08 | 7.29 ± 0.10 | 6.97 ± 0.06 | 6.92 ± 0.10 | 7.00 ± 0.15 | Ho<C, C>El | Ho<C |
| **NL** | 9.54 ± 0.09 | 10.01 ± 0.09 | 9.43 ± 0.17 | 10.67 ± 0.10 | 9.76 ± 0.08 | 9.56 ± 0.10 | 9.82 ± 0.11 | Bai>C, D>C, Gr>C | C<El ,Bai>C, Gr>C |
| **ZW** | 12.35 ± 0.06 | 12.69 ± 0.10 | 11.96 ± 0.09 | 12.67 ± 0.09 | 12.96 ± 0.09 | 12.61 ± 0.015 | 12.91 ± 0.13 | Ho<C, Ke<C | |
| **Forl** | 4.81 ± 0.04 | 4.89 ± 0.06 | 4.64 ± 0.07 | 5.31 ± 0.04 | 5.00 ± 0.05 | 4.71 ± 0.09 | 4.79 ± 0.09 | BA>C, Gr>C | C<El. Ke>C, Gr>C, BA>C |
| **NW** | 2.92 ± 0.03 | 3.09 ± 0.03 | 2.87 ± 0.06 | 3.41 ± 0.06 | 3.44 ± 0.07 | 3.12 ± 0.08 | 3.57 ± 0.07 | BA>C, Ho<C, Ke<C, C>El | Ke<C, Gr>C, BA>C, D<C |
| **Patl** | 11.58 ± 0.04 | 11.86 ± 0.12 | 11.26 ± 0.12 | 12.09 ± 0.12 | 12.04 ± 0.05 | 11.93 ± 0.12 | 12.02 ± 0.14 | Ho<C, Ke<C, C>El | Ke<C |
| **SH** | 7.89 ± 0.04 | 8.07 ± 0.04 | 7.76 ± 0.07 | 7.76 ± 0.12 | 7.91 ± 0.05 | 8.02 ± 0.07 | 7.95 ± 0.11 | Ho<C, Ke>C | Ke>C, BA<C, D<C |
| **Occl** | 25.05 ± 0.10 | 26.31 ± 0.22 | 24.80 ± 0.21 | 26.01 ± 0.23 | 25.98 ± 0.07 | 25.98 ± 0.19 | 26.25 ± 0.29 | Ho<C, C>El | C>El, Gr<C, BA<C |
| **CW** | 11.59 ± 0.04 | 11.82 ± 0.07 | 11.24 ± 0.08 | 11.80 ± 0.09 | 12.25 ± 0.08 | 11.60 ± 0.06 | 12.06 ± 0.08 | Bai>C, D>C, BA>C, Ho<C | C<El, Ke>C, BA>C |
| **INTW** | 4.0 ± 0.01 | 4.34 ± 0.03 | 4.05 ± 0.01 | 4.15 ± 0.08 | 4.25 ± 0.03 | 4.28 ± 0.02 | 4.44 ± 0.06 | D>C, Gr<C, C>El Ho<C, Ke<C | C>El, Gr<C |
| **BULL** | 5.70 ± 0.04 | 5.88 ± 0.05 | 5.65 ± 0.05 | 6.00 ± 0.00 | 5.71 ± 0.07 | 5.75 ± 0.05 | 6.04 ± 0.06 | D>C, Gr>C | Ke>C, Ho>C |
| **CBL** | 22.09 ± 0.10 | 23.09 ± 0.17 | 21.69 ± 0.18 | 23.24 ± 0.17 | 23.22 ± 0.08 | 22.91 ± 0.12 | 23.45 ± 0.24 | D>C, BA>C, Ho<C, Ke<C, C>El | C>El, Ho>C |
| **DB2M** | 8.10 ± 0.06 | 8.26 ± 0.06 | 7.99 ± 0.08 | 8.89 ± 0.11 | 8.81 ± 0.04 | 8.16 ± 0.06 | 8.41 ± 0.14 | BA>C, Gr>C | Ho>C, Gr>C, BA>C |
| **Mxl** | 3.40 ± 0.02 | 3.42 ± 0.03 | 3.41 ± 0.03 | 3.32 ± 0.04 | 3.51 ± 0.04 | 3.50 ± 0.04 | 3.45 ± 0.07 | Gr<C, Ke<C, C>El | |
| **Mnl** | 3.37 ± 0.02 | 3.33 ± 0.03 | 3.37 ± 0.04 | 3.33 ± 0.04 | 3.47 ± 0.06 | 3.47 ± 0.02 | 3.54 ± 0.04 | Bai<C, Gr<C, Ho<C, Ke<C, C>El | Ke<C, Bai<C, Ho<C, D>C |
| **Mndl** | 12.92 ± 0.06 | 13.42 ± 0.09 | 12.61 ± 0.08 | 13.51 ± 0.14 | 13.43 ± 0.04 | 13.50 ± 0.05 | 13.70 ± 0.08 | D>C, Ho<C, Ke<C, C>El | C>El ,Bai<C, Ke<C, Ho<C, BA<C |
| **M1L** | 1.68 ± 0.01 | 1.67 ± 0.02 | 1.69 ± 0.02 | 1.61 ± 0.03 | 1.76 ± 0.01 | 1.69 ± 0.01 | 1.62 ± 0.02 | D<C, BA>C | Ke>C, BA>C, D<C |
| **M1W** | 1.13 ± 0.01 | 1.11 ± 0.01 | 1.15 ± 0.01 | 1.13 ± 0.01 | 1.19 ± 0.01 | 1.11 ± 0.01 | 1.10 ± 0.01 | BA>C | C<El ,C<Bai, Ke>C, Ho<C, Gr>C, BA>C |
| **M2L** | 1.27 ± 0.01 | 1.23 ± 0.01 | 1.24 ± 0.02 | 1.27 ± 0.02 | 1.32 ± 0.02 | 1.28 ± 0.02 | 1.27 ± 0.04 | Bai<C, Ho>C, Ke<C | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **M2W** | 1.07 ± 0.01 | 1.07 ± 0.01 | 1.09 ± 0.01 | 1.12 ± 0.01 | 1.15 ± 0.01 | 1.09 ± 0.01 | 1.12 ± 0.01 | BA>C, Ke<C | Gr>C |
| **M3L** | 0.62 ± 0.01 | 0.64 ± 0.01 | 0.64 ± 0.01 | 0.61 ± 0.03 | 0.66 ± 0.01 | 0.66 ± 0.02 | 0.71 ± 0.02 | Gr<C, C>El | Ke<C, BA>C |
| **M3W** | 0.72 ± 0.01 | 0.72 ± 0.01 | 0.72 ± 0.02 | 0.74 ± 0.01 | 0.75 ± 0.01 | 0.77 ± 0.01 | 0.79 ± 0.02 | Bai<C, Ho<C, Ke<C, C>El | C>El, Bai<C, Ho<C |
| **m1l** | 1.44 ± 0.01 | 1.46 ± 0.02 | 1.49 ± 0.02 | 1.47 ± 0.03 | 1.48 ± 0.01 | 1.49 ± 0.02 | 1.50 ± 0.02 | | |
| **m1W** | 0.96 ± 0.01 | 1.00 ± 0.01 | 1.01 ± 0.01 | 0.97 ± 0.01 | 1.01 ± 0.01 | 0.99 ± 0.01 | 1.00 ± 0.01 | C>El | Ke>C, Bai>C, Ho>C |
| **m2l** | 1.25 ± 0.01 | 1.25 ± 0.01 | 1.27 ± 0.02 | 1.24 ± 0.02 | 1.28 ± 0.01 | 1.25 ± 0.00 | 1.30 ± 0.02 | D>C, BA>C, Ke<C | C<El ,Bai>C, Ho>C, Gr>C, D>C |
| **m2W** | 1.05 ± 0.01 | 1.10 ± 0.01 | 1.08 ± 0.01 | 1.06 ± 0.01 | 1.11 ± 0.01 | 1.07 ± 0.01 | 1.06 ± 0.02 | BA>C, C>El | Ke>C ,Bai>C, Gr>C, BA>C |
| **m3L** | 0.79 ± 0.01 | 0.79 ± 0.01 | 0.79 ± 0.01 | 0.72 ± 0.02 | 0.76 ± 0.02 | 0.82 ± 0.01 | 0.86 ± 0.01 | BA<C, Gr<C, Ke<C | Ke<C, Ho>C, Gr<C, BA<C, D>C |
| **m3w** | 0.71 ± 0.01 | 0.72 ± 0.01 | 0.71 ± 0.01 | 0.70 ± 0.02 | 0.74 ± 0.01 | 0.72 ± 0.02 | 0.75 ± 0.01 | | |
| **Dental size** | 6.14 ± 0.03 | 6.13 ± 0.04 | 6.17 ± 0.06 | 6.06 ± 0.06 | 6.35 ± 0.04 | 6.28 ± 0.04 | 6.3 ± 0.08 | C>El, Ke<C, Gr<C | |
| **Skull size** | 45.86 ± 0.16 | 47.72 ± 0.33 | 45.03 ± 0.33 | 48 ± 0.32 | 47.83 ± 0.16 | 47.22 ± 0.28 | 48.13 ± 0.42 | C>El, C>Ho | |