A new species of Andean mouse of the genus *Thomasomys* (Cricetidae, Sigmodontinae) from the eastern Andes of Ecuador

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Abstract

We name and describe a new species of Andean mouse from the eastern slope of the Andes of central Ecuador (Sangay National Park). This rodent is large-bodied (head-body length 167–184 mm) inhabiting the wet montane forest between 3,400–3,900 m in elevation. A molecular phylogeny based on mitochondrial genes resolved the new species as a member of the “aureus” group, closely related to an undescribed species from north Ecuador. This finding increases the diversity of *Thomasomys* to 48 species, of which 18 species inhabit Ecuador. In addition, the species described herein is the largest species of the genus described in Ecuador.

Key words

Montane forest, Rodentia, Thomasomyini

Introduction

The genus *Thomasomys* contains the highest diversity of any Sigmodontinae genus (Patton et al. 2015; Pardiñas et al. 2017). The genus is mostly confined to the Andes of South America and is usually found above 2,500 m in elevation (Pacheco 2015). Within this genus are members that range in size from *Thomasomys hudsoni* with a head/body length of 88 mm (Brito and Argüero 2016) to *Thomasomys apeco* with head/body length over 235 mm (Gardner and Romo 1993; Ruelas and Pacheco 2021). The subfamily Sigmodontinae is the most species rich subfamily of Cricetidae (Pardiñas et al. 2017). Sigmodontinae has been the subject of many recent studies concerning both its systematics and what the subfamily can teach us about the last 7 million years of evolutionary and biogeographic history of South America and the Andes in particular (Patton et al. 2015, Pacheco 2015; Brito et al. 2019; Brito et al. 2021; Ruelas and Pacheco 2021).

Currently, 47 species of *Thomasomys* are recognized (Pacheco 2015; Brito et al. 2019; Brito et al. 2021; Ruelas and Pacheco 2021). Internal complexity of *Thomasomys* is high given that it contains, at least, 7 species groups (Pacheco 2003; Salazar-Bravo and Yates 2007; Brito et al. 2019): aureus, baeops, cinereus, gracilis, incanus, macrotis, and notatus. The aureus group contains...
the largest-bodied species of the genus, with members ranging from 135 to 238 mm in head-body length, and weighing from 68 to 335 g (Pacheco 2015). Using sequence data from the rapidly evolving cyt b gene and a detailed comparative examination of the morphology, we have discovered a previously undocumented taxon within the T. aureus group.

Materials and Methods

Studied specimens

We used Sherman traps with an accumulated trap effort of 5,675 trap/nights in very remote and difficult to access mountain regions of Sangay National Park, Ecuador (Lee et al. 2011; and collections by Jorge Brito). We followed the guidelines established by the American Association of Mammalogists (Sikes et al. 2016) for the capture, manipulation and preservation of specimens captured in the field. A qualitative morphological comparison was made based on 60 specimens of the species of the Thomasomys that are part of the T. aureus group present in Ecuador (Appendix 1). These specimens are deposited in the following collections: Abilene Christian University Natural History Collection (ACUNHC), Abilene, Texas, USA; Museo de Zoología de la Pontificia Universidad Católica del Ecuador, Quito, Ecuador (QCAZ); Escuela Política del Ecuador, Quito, Ecuador (MEPN), and Instituto Nacional de Biodiversidad, Quito, Ecuador (MECN; formerly known as Museo Ecuatoriano de Ciencias Naturales).

Anatomy, age criteria, and measurements

We followed the main concepts explained by Carleton and Musser (1989), Musser et al. (1998), Pacheco (2003), and Voss (1993) for the description of cranial anatomy. Our description of molar occlusal morphology was based on Reig (1977; upper and lower molars are identified as M/m, respectively). This study followed the terminology and definitions employed by Tribe (1996) and Costa et al. (2011) for age classes and restricted the term to those categorized as having molar wear pattern 3 and 4. We obtained the following external measurements in millimeters (mm), some of them registered in the field and reported on specimen tags, others recorded from specimens stored in the museum cabinets: head and body length (HB), tail length (TL), hind foot length (HF, including claw), ear length (E), and body mass (W, in grams (gr)). Cranial measurements were obtained with digital calipers, to the nearest 0.01 mm; we employed the following dimensions (see Tribe 1996; Voss 2003; and Musser et al. 1998, for illustrations): condylo-incisive length (CIL), length of upper diastema (LD), crown length of maxillary toothrow (LM), length of incisive foramina (BIF), breadth of rostrum (BR), length of rostrum (LR), length of nasals (LN), length of palatal bridge (LPB), breadth of first maxillary molar (BM1), breadth of bony palate (BBP), least interorbital breadth (LIB), zygomatic breadth (ZB), breadth of zygomatic plate (BZP), orbital fossa length (OFL), braincase breadth (CBB), depth of upper incisor (DI), bular breadth (BB), length of mandible (LMN), crown length of mandibular toothrow (LLM), and length of lower diastema (LLD).

DNA extraction, amplification and sequencing

We extracted DNA from tissues (liver and dry skin) of four specimens identified as Thomasomys aureus (MEPN 6144, MECN 2720, MECN 2807, and MECN 5389). All genomic DNA was extracted using the guanidine thiocyanate protocol (Bilton et al. 1996). We amplified the gene cytochrome b (cyt b) using the forward primer MVZ05 and reverse primers MVZ16H to obtain approximately 500 to 1,000 base pairs. The thermal conditions for PCR are as described in Bonvicino and Moreira (2001).

Phylogenetic analysis

The sequences were edited in Geneious R11.5 (https://www.geneious.com) and aligned with CLUSTALW (Larkin et al. 2007). The evolutionary model for the analysis using Bayesian Inference (BI) and Maximum Likelihood (ML) were obtained using PartitionFinder 2.1 (Lanfear et al. 2016). For the Bayesian and Maximum Likelihood analyses, the best model was 1st position, 2nd position, 3rd position GTR+G+I. The BI analysis was carried out in the MrBayes V3.2 program (Ronquist et al. 2011), the BI analysis consisted of 2 independent runs, each with 4 Markov chains (3 hot and 1 cold); 10 million generations were run, sampling every 1,000 generations. The first 25% of trees were discarded as “burn-in” remaining trees were used to obtain the posterior probabilities (PP). The consensus tree was obtained using the 50% majority rule. Convergence was evaluated by the elective sample size (EES) and the potential scale reduction factor (PSRF). For most of the parameters the EES should be ≥ 200 and for the PSRF most of the values of the parameters should be between 1.0 and 1.2. The ML analysis was carried out in the IQ-Tree program (Trifinopoulos et al. 2016; http://iqtree.ebiv.univie.ac.at). We included 30 sequences from different species of Thomasomys from the “aureus” group and some species from other groups of Thomasomys (Appendix 2). The genetic distances among species of the “aureus” group were calculated with MEGAX (Kumar et al. 2018), using the Kimura 2-parameter correction model (K-2P) and uncorrected distances (p-distances). This allowed a comparison with the genetic distances obtained in other studies of the genus Thomasomys (Salazar-Bravo and Yates 2007; Lee et al. 2015, 2018; Brito et al. 2019, 2021; Ruelas and Pacheco 2021).
Results

Taxonomic accounts

The IB and ML analysis presented different topologies within the aureus group. The IB analysis failed to recover the monophyly of the aureus group because the sample DQ914653 (Thomasomys sp. Bolivia) was located outside the aureus group (Fig. 1A) forming a polytomy (PP=0.62) with other samples: (Thomasomys sp. + Thomasomys ka linowskii + notatus group + baeps group), while within the aureus group some interspecific relationships could not be resolved (Fig. 1A) [(Thomasomys sp.1 PE + T. apeco) + ((T. praetor + T. antonibracki + (T. pyrrhomotus + T. auricularis)) + (T. sp. Cajanuma + (T. aureus + T. pardignasi) + (Thomasomys sp. El Angel + (T. sp. Pichincha + Thomasomys sp. Sangay))]). In the ML analysis it was possible to recover the monophyly of the aureus group (Fig. 1B), where the main difference was the location of the sample DQ914653, (Thomasomys sp.1 Bolivia) and the resolution of the relationships of the samples identified as T. aureus. (From different locations in Ecuador). The sample DQ914653 was located within the “aureus” group (BS=99; Fig. 1B); [(Thomasomys sp.1 PE + T. apeco) + (Thomasomys sp.1 Bolivia + (T. antonibracki + ((T. praetor + (T. pyrrhomotus + T. auricularis)) + (T. sp. Cajanuma + (T. aureus + T. pardignasi) + (Thomasomys sp. El Angel + (T. sp. Pichincha + Thomasomys sp. Sangay))). The IB and ML analyzes recovered the samples of T. pardignasi and T. aureus (all samples), within the same monophyletic clade (1.00/100, Fig. 2) named aureus, this clade presented five internal clades defined and supported (BS>70 / PP>0.90, Fig. 2): Thomasomys sp. Cajanuma, T. aureus, T. pardignasi, Thomasomys sp. El Angel, T. sp. Pichincha, and T. sp. Sangay. Samples of Thomasomys sp. El Angel (98/0.93) were located outside the clade formed between Thomasomys sp. Pichincha, and Thomasomys Sangay (95/0.85, Fig. 2). The genetic variation within the aureus group was 10.68% ± 0.64. While the interspecific variation was from 4% to 14% (Table 1). Within the aureus clade the variation between the internal clades was from 2% to 8% (Table 1).

The data presented in detail below suggest that the taxon discussed represents a new species. We provide below a description of the species, a comparison with other congener and a discussion of their morphology and phylogenetic relationships. Relevant summaries of qualitative diagnostic traits variation are provided in Table 2 and Fig. 3, respectively.
Table 1. Genetic distance in percentage (K-2P) between the described species of the *Thomasomys aureus* group. The values on the right represent the standard deviation.

<table>
<thead>
<tr>
<th>Taxa</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 T. apeco</td>
<td>1.04</td>
<td>1.12</td>
<td>1.13</td>
<td>1.19</td>
<td>1.05</td>
<td>1.03</td>
<td>1.00</td>
<td>1.30</td>
<td>1.18</td>
<td>1.58</td>
<td>1.57</td>
<td></td>
</tr>
<tr>
<td>2 T. sp. 1 PE Cusco</td>
<td>10.88</td>
<td>1.00</td>
<td>0.99</td>
<td>1.11</td>
<td>1.05</td>
<td>0.96</td>
<td>1.06</td>
<td>1.12</td>
<td>1.12</td>
<td>1.55</td>
<td>1.50</td>
<td></td>
</tr>
<tr>
<td>3 T. praetor</td>
<td>11.42</td>
<td>10.99</td>
<td>0.93</td>
<td>0.97</td>
<td>1.05</td>
<td>1.06</td>
<td>1.02</td>
<td>1.09</td>
<td>1.09</td>
<td>1.50</td>
<td>1.19</td>
<td></td>
</tr>
<tr>
<td>4 T. antoniobracci</td>
<td>10.96</td>
<td>11.09</td>
<td>8.55</td>
<td>0.99</td>
<td>1.04</td>
<td>1.02</td>
<td>0.96</td>
<td>0.85</td>
<td>1.06</td>
<td>1.48</td>
<td>1.33</td>
<td></td>
</tr>
<tr>
<td>5 T. aureus</td>
<td>12.06</td>
<td>12.24</td>
<td>10.17</td>
<td>10.17</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1.14</td>
<td>0.86</td>
<td>0.89</td>
<td>1.38</td>
</tr>
<tr>
<td>6 T. pyrrhonotus</td>
<td>11.53</td>
<td>12.54</td>
<td>10.37</td>
<td>9.65</td>
<td>9.91</td>
<td>1.02</td>
<td>1.00</td>
<td>1.34</td>
<td>1.09</td>
<td>1.45</td>
<td>1.52</td>
<td></td>
</tr>
<tr>
<td>7 T. burneoi sp. nov</td>
<td>10.72</td>
<td>12.48</td>
<td>10.41</td>
<td>8.88</td>
<td>4.69</td>
<td>9.47</td>
<td>0.44</td>
<td>1.10</td>
<td>0.72</td>
<td>1.06</td>
<td>1.04</td>
<td></td>
</tr>
<tr>
<td>8 T. sp. Pichincha</td>
<td>10.93</td>
<td>11.61</td>
<td>10.07</td>
<td>8.66</td>
<td>5.76</td>
<td>9.45</td>
<td>2.15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9 T. auricularis</td>
<td>11.17</td>
<td>11.64</td>
<td>8.42</td>
<td>5.86</td>
<td>9.74</td>
<td>8.15</td>
<td>10.07</td>
<td>8.78</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10 T. pardignasi</td>
<td>12.49</td>
<td>12.65</td>
<td>10.50</td>
<td>9.06</td>
<td>4.73</td>
<td>10.00</td>
<td>5.26</td>
<td>5.51</td>
<td>7.48</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11 T. sp. El Angel</td>
<td>13.34</td>
<td>12.60</td>
<td>10.53</td>
<td>11.41</td>
<td>7.42</td>
<td>10.77</td>
<td>4.05</td>
<td>4.67</td>
<td>5.45</td>
<td>6.30</td>
<td></td>
<td></td>
</tr>
<tr>
<td>12 T. sp. Cajanuma</td>
<td>12.33</td>
<td>12.02</td>
<td>10.20</td>
<td>10.61</td>
<td>6.59</td>
<td>11.23</td>
<td>4.75</td>
<td>5.87</td>
<td>6.85</td>
<td>5.29</td>
<td>7.09</td>
<td></td>
</tr>
</tbody>
</table>

Figure 2. Extension of the clade aureus of the phylogenetic tree of the aureus group. A Bayesian inference phylogenetic tree, numbers represent posterior probability values, PP>0.90 are considered high supports. B Maximum likelihood phylogenetic tree, numbers represent bootstraps values, BS>70 are considered high supports.

Figure 3. Scatterplots illustrating selected metric comparisons between *Thomasomys burneoi* sp. nov., with *T. aureus* and *T. pardignasi*.
**Taxonomy**

Family Cricetidae Fischer, 1817

Subfamily Sigmodontinae Wagner, 1843

Tribe Thomasomyini Steadman & Ray, 1982

Genus *Thomasomys* Coues, 1884

*Thomasomys burneoi* sp. nov.

*Thomasomys praetor* : Lee et al. 2011:9; part no *Thomasomys praetor* (Thomas, 1900)

*Thomasomys princeps* : Lee et al. 2015:10; part no *Thomasomys princeps* (Thomas, 1895)

*Thomasomys aureus* : Brito et al. 2019:9; par not *Thomasomys aureus* Tomes, 1860

**Burneo’s Olfield Mouse**

**Ratón andino de Burneo** (in Spanish)

http://zoobank.org/F47D0CE6-4E92-4712-9E8C-95EA07A859FF

**Holotype.**

MECN 5662 (field number JBM [Jorge Brito Molina] 1812), an adult female captured on August 18, 2017, by Jorge Brito, Jenny Curay, Rocío Vargas, and Erika Beltrán, preserved as dry skin, skull, postcranial skeleton, and muscle and liver biopsies in 95% ethanol.

**Paratopotype.**

MECN 5666 (JBM 1822), an adult female collected next to the holotype, on August 18, 2017, by J. Brito, J. Curay, R. Vargas and E. Beltrán.

**Paratype.**

ACUNHC 1548 (field number TEL 2394); 1560 (TEL 2378); QCAZ 11937, adult male captured on July 20, 2010, by Thomas Lee, Carlos Boada, and Amy Scott; QCAZ 11938 (TEL 2295), and adult male captured on October 06, 2010, by Thomas Lee, Carlos Boada, and Amy Scott; QCAZ 11939 (TEL 2296), and Paratypes. MECN 5666, MECN 5239, and MECN 5240 are paratypes.

**Type locality.**

Ecuador, Provincia de Morona Santiago, cantón Morona, parroquia Zúñac, Parque Nacional Sangay

**Table 2.** Selected morphological differences with species that could be confused with *Thomasomys burneoi* sp. nov., compiled from Pacheco (2015), Brito et al. (2021), and our own observations.

<table>
<thead>
<tr>
<th>T. burneoi</th>
<th>T. pardignasi</th>
<th>T. aureus ss</th>
<th>T. auricularis</th>
</tr>
</thead>
<tbody>
<tr>
<td>Head and body length</td>
<td>Head and body length</td>
<td>Head and body length</td>
<td>Head and body length</td>
</tr>
<tr>
<td>between 167–184 mm</td>
<td>between 137–145 mm</td>
<td>between 120–173 mm</td>
<td>between 138–155 mm</td>
</tr>
<tr>
<td>Tail ~ 119–136 % head-body length</td>
<td>Tail ~ 125–141 % head-body length</td>
<td>Tail ~ 122–134 % head-body length</td>
<td></td>
</tr>
<tr>
<td>Tail with 12-13 rows of scales per cm on the axis</td>
<td>Tail with 16 rows of scales per cm on the axis</td>
<td>Tail with 12 rows of scales per cm on the axis</td>
<td></td>
</tr>
<tr>
<td>Genal 1 vibrissae present</td>
<td>Genal 1 and 2 vibrissae present</td>
<td>Genal 1 vibrissae present</td>
<td>Genal 1 vibrissae present</td>
</tr>
<tr>
<td>Postauricular patch present</td>
<td>Postauricular patch present</td>
<td>Postauricular patch present</td>
<td>Ochraceous postauricular patch present</td>
</tr>
<tr>
<td>Upper maxillary row 7.72–8.30 mm</td>
<td>Upper maxillary row 6.4–6.6 mm</td>
<td>Upper maxillary row 6.90–7.42 mm</td>
<td>Upper maxillary row 6.6–7.4 mm</td>
</tr>
<tr>
<td>Wide and robust presphenoid</td>
<td>Narrow presphenoid</td>
<td>Narrow presphenoid</td>
<td>Narrow presphenoid</td>
</tr>
<tr>
<td>Auditory bullae small and inflated</td>
<td>Auditory bullae small and uninfated</td>
<td>Auditory bullae large and inflated</td>
<td>Auditory bullae small and inflated</td>
</tr>
<tr>
<td>Eustachian tube short and wide</td>
<td>Eustachian tube long and narrow</td>
<td>Eustachian tube long and wide</td>
<td>Eustachian tube short and narrow</td>
</tr>
<tr>
<td>Moderately developed dorsolepticals</td>
<td>Moderately developed dorsolepticals</td>
<td>Moderately developed dorsolepticals</td>
<td>Moderately developed dorsolepticals</td>
</tr>
<tr>
<td>Additional anterior edge on procotyl of M1 present</td>
<td>Additional anterior edge on procotyl of M1 present</td>
<td>Additional anterior edge on procotyl of M1 present</td>
<td>Additional anterior edge on procotyl of M1 present</td>
</tr>
<tr>
<td>M1 with deep anteroflexus</td>
<td>M1 with shallow anteroflexus</td>
<td>M1 with deep anteroflexus</td>
<td>M1 with deep anteroflexus</td>
</tr>
<tr>
<td>M1 with narrow anteroloph</td>
<td>M1 with wide anteroloph</td>
<td>M1 with wide anteroloph</td>
<td>M1 with wide anteroloph</td>
</tr>
<tr>
<td>M1-M2 with narrow mesoloph</td>
<td>M1-M2 with wide mesoloph</td>
<td>M1-M2 with wide mesoloph</td>
<td>M1-M2 with wide mesoloph</td>
</tr>
<tr>
<td>M3 with distinct mesoloph</td>
<td>M3 with indistinct mesoloph</td>
<td>M3 with indistinct mesoloph</td>
<td>M3 with indistinct mesoloph</td>
</tr>
<tr>
<td>m1 with distinct anterolophid</td>
<td>m1 with indistinct anterolophid</td>
<td>m1 with indistinct anterolophid</td>
<td>m1 with indistinct anterolophid</td>
</tr>
<tr>
<td>Ectolophid present in m1</td>
<td>Ectolophid present in m1 and m2</td>
<td>Ectolophid absent</td>
<td>Ectolophid absent</td>
</tr>
<tr>
<td>m1-m2 with ectostyloid</td>
<td>m1-m2 lack ectostyloid</td>
<td>m1-m2 with ectostyloid</td>
<td>m1-m2 with ectostyloid</td>
</tr>
<tr>
<td>m1-m2 with wide hypoflexid</td>
<td>m1-m2 with narrow hypoflexid</td>
<td>m1-m2 with narrow hypoflexid</td>
<td>m1-m2 with narrow hypoflexid</td>
</tr>
<tr>
<td>m3 equals m2</td>
<td>m3 slightly longer than m2</td>
<td>m3 longer than m2</td>
<td>m3 equals m2</td>
</tr>
</tbody>
</table>
Diagnosis. A species of *Thomasomys* from the aureus group described by the following character combinations: large size (combined head and body length 167–184 mm); postauricular patch present; wide metatarsal patch; hind foot large 40 mm; M1 with broad and deep anteroflexus; additional anterior edge on procingulum of M1 present; M3 with metaflexus large and mesoloph distinctive; m1 with small and distinctive anterolophid; m1 with ectolophid; m2–m3 with hypoflexid wide; m3 size equals m2.
Measurements of the holotype (in mm). Head and body length = 172, Tail length = 232, Hind foot length = 43, Ear length = 27, Body mass = 105, Condylo-incisive length = 38.28, Zygomatic breadth = 22.04, Least interorbital breadth = 5.16, Length of rostrum = 13.14, Length of nasals = 14.53, Breadth of rostrum = 7.91, Orbital fossa length = 13.87, Length of upper diastema = 10.87, Crown length of maxillary toothrow = 7.8, Length of incisive foramina = 8.95, Breadth of incisive foramina = 3.13, Breadth of first maxillary molar = 2.84, Length of palatal bridge = 6.96, Breadth of bony palate = 3.34, Bulbar breadth = 5.43, Depth of upper incisor = 2.05, Breadth of zygomatic plate = 3.98, Braincase breadth = 17.26, Length of mandible = 22.7, Crown length of mandibular toothrow = 8.2, Length of lower diastema = 5.17. External and craniodental of additional specimens are presented in Table 3.

Morphological description of the holotype and variation. Large body size (head and body length combined with a range between 128 and 184 mm). Cinnamon-brown dorsal fur (Fig. 4, 5), with a faint dark dorsal band; long hairs (medium length on the back = 18–20 mm) dark gray at the base. Light tan dark ventral coat, hairs with (medium length = 10–12 mm) dark gray base, and pale yellowish tips (Fig. 5). Black periocular ring. Mystacial vibrissae long, thick at the base and remain thin towards the tip, exceeding the ear when they are tilted back; 1 supraciliary vibrissae present and 1 genal vibrissae present. Ears (between 24–28 mm from notch to margin) externally covered by short orangebrown hairs, pale pink inner surface, dark pale brown margin. Large and wide foot (Fig. 6) with 5 digits ending in thin semi-curved claws. Long white ungueal tufts that slightly exceed the claws. Wide and brown metatarsal patch, that extends to the base of the palanges. Plantar surface with 6 pads, including 4 interdigitalis of similar size to each other (Fig. 6), slightly larger than hypothenar and with very small space between them. Digit I exceeds the base of digit II; digit II and III are the same size and slightly shorter than digit IV; digit V (apparently opposable) reaches the beyond the middle of digit IV. Long tail (207–232 mm; ~127% of HB), ground cinnamon (color 270) and unicolor; square flow scales with three hairs each, which extend over 2.5 to 3 rows of scales in the dorsal basal sector; with 12–13 scales per cm on the shaft. Hirsute tail, even to the rear, hair increasing in length to the apex of the tail. Protuberant anus prominent. Females present six mammary pairs in pectoral, abdominal and inguinal position (sensu Pacheco 2003). The details of soft and genitalia anatomy are unknown.

The cranium is large for the genus (38.2–40.13 mm of CIL). The rostrum is long, somewhat acuminate and narrow, with the nasal bones exceeding the anterior face of the incisors; poorly developed gnathic process (Fig. 7). Posterior margin of the nasal bone slightly exceeds the plane of the lachrymal bone. Moderately deep zygomatic notch (Fig. 8). Small and rounded lacrimal bones. Narrow interorbital region with poorly developed supraorbital ridges, the alveolar maxillary processes well exposed in dorsal view. Supraorbital region with divergent posterior borders (sensu Steppan 1995). Frontoparietal suture V-shaped. Broad and rounded braincase, slightly flattened at the outer edges. Large and concave exoccipital. In the lateral view, small nasolacrimal fissures can be seen in the rostral region and internally, no further development in the ethmoturbinals is distinguishable. Developed and oblique lambdoidal crest. Zygomatic arches sturdy and robust with jugals spanning a short segment of each midarch but distinctly separating zygomatic processes of the maxillary and squamosal bones. Alisphenoid strut wide and robust. Carotid circulatory pattern type 2, derived...
Figure 7. Dorsal, ventral and lateral view of the cranium, lateral view of the jaw, occlusal view of the right upper and left lower toothrow of *Thomasomys burneoi* sp. nov. (MECN 5662, holotype) from Sangay National Park, Ecuador. Scale = 10 mm.

Figure 8. Composed figure illustrating selected differences in the cranial anatomy of *Thomasomys burneoi*, sp. nov. (MECN 5662, holotype; left half cranium), *T. pardignasi* (MECN 5852, holotype; right half cranium A, C, and *T. aureus* sensu stricto (MEPN 6144; right half cranium B, D. Acronyms: if = incisive foramen, nl = nasolacrimal capsule, m = molars, mf = mesopterygoid fossa, zn = zygomatic notches.
sensu Voss 1988); carotid canal large (Fig. 9), stapedial foramen and anterior alar fissure small. Postglenoid foramen narrower as the subsquamosal fenestra (Fig. 10); hamular process of squamosal thin, long, but without going beyond the edge on the mastoid capsule. Lightly square tegmen tympanic is superimposed over the suspensory process of the squamosal. Lateral expressions of parietals present (Fig. 10); bullae small and inflated; pars flaccida of tympanic membrane present, large; orbicular apophysis of malleus well developed, the manubrium of malleus is blade like with a cup at the distal end. Parasphenoidal process large. Hill foramen small; long and narrow incisive foramen with curved edges that subsequently exceed the plane defined by the anterior face of M1 (Fig. 7). Premaxillary capsule slightly widened in the middle and narrow at the ends, maxillary septum of incisive foramen robust and long. Short and narrow palate (sensu Hershkovitz 1962), with the narrow mesopterygoid fossa that enters between the molars reaching the hypoflexus of M3 or 50% of M3, without a medium process. Posterior palatal pit small and inconspicuous. Thin and inconspicuous sphenopalatine vacuities covered by the roof of the palate. The basisphenoid is wide, with a small ovale foramen and the middle lacerate foramen is narrow. Auditory bullae small and inflated with short and wide Eustachian tube. Petrosal little exposed (Fig. 9).

Dentary moderately short, robust, with long and wide coronoid process that exceeds the upper edge of the condylar process, (Fig. 9); deep sigmoid notch. Semilunar recess is symmetrical, whose lower edge is wide. Capsular projection of the root of the incisor small.

Opistodont incisors with orange front enamel; brachydont and pentalophodont molars (sensu Hershkovitz 1962). Maxillary molar rows parallel and hypsodont; coronal surfaces crested; main cusps slightly opposite and sloping backwards when viewed from side. The outline of M1 is rectangular with procingulum divided by anteromedian flexus deep into subequal anterolabial and anterolingual conules; additional anterior edge on procingul-
A new species of Thomasomys

Thomasomys burneoi sp. nov. is characterized by the following traits:

- **Upper Molars**: M1 square in outline; mesoloph and posteroloph showing the same condition as in M1. M3 rounded in outline with narrow anteroloph; deep paraflexus; metaflexus large; mesoloph distinctive. Lower molars with main cusps alternated and sloping forward when viewed from side.

- **Lower Molars**: m1 with anteromedian flexid that divides the procingulum into subequal anterolabial and anterolingual conules; anterolophid distinctive; mesolophid narrow; ectolophid and ectostylid present (Fig. 11). M2 with narrow mesoloph (Fig 11). M3 with distinctive mesoloph (indistinct); m1 with ectolophid (present in m1 and m2); m1–m2 with ectostylid (lack ectostylid); m3 equals m2 (m3 is slightly shorter than m2).

**Comparisons.** Thomasomys burneoi sp. nov., apart from being large (Fig. 11; Table 2), differs from T. pardignasi Brito et al. (2021) (traits in parentheses) by dorsal unif rom color (presenting a dim dark band on the back); back hairs of 18–20 mm (15.53); ventral hairs long, 10–12 mm (9.92 mm); long tail ~127% of HB (~152%); genal vibrissae 2 absent (genal vibrissa 2 absent). Craniodentally, qualitative differences between both species are conspicuous. Additional anterior edge on procingulum of M1 present in T. burneoi (absent); M1 with narrow anteroloph (wide); M3 with distinctive mesoloph (indistinct); m1 with distinctive anterolophid (indistinct); m1 with ectolophid (absent); m3 equals m2 (m3 is longer than m2). Further comparisons among all the recognized species of Thomasomys from the aureus group present in Ecuador are provided in Table 2.

**Etymology.** Named for Santiago F. Burneo, of the Pontificia Universidad Católica del Ecuador, Quito, Ecuador in recognition of his teaching and support of mammalogists both in Ecuador and the United States of America. The specific epithet is a noun in the genitive case formed by the addition of an “i” to the stem of the name.

**Distribution.** Known only from Sangay National Park, Chimborazo Province and Morona Santiago Province, Ecuador, 3,400–3,900 m in elevation (Fig. 12).

**Natural history.** Thomasomys burneoi sp. nov., has been recorded in the Altoandino floor (Albuja et al. 2012), in the montane evergreen forest plant formation in the

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**Figure 11.** Occlusal view of the right upper (A–C) and right lower (D–F) tooth row of: A, D Thomasomys burneoi sp. nov. (MECN 5662, holotype), B, E Thomasomys pardignasi (MECN 5852, holotype) and C, F Thomasomys aureus (MEPN 6144). Acronyms: anf = anteroflexus, al = anteroloph/id, am = anterior mure, ec = ectostylid, hy = hypoflexid, mf = metaflexus, ml = mesoloph/id, ecl = ectolophid. Scale = 2.5 mm.
southern Cordillera Oriental of the Andes (Ministerio Del Ambiente Del Ecuador 2013). According to the capture data, it is associated with primary elfin forests and páramo (Fig. 13), where the trees are covered by mosses and epiphytes. The specimens were generally collected on thick trunks or branches. In October (dry season), a pregnant female with an embryo was discovered. *Thomasomys burneoi* was found in sympathy with other small mammals *Akodon mollis, Caenolestes sangay, Cavia patzelti, Cryptotis montivagus, Microyzomys altissimus, M. minutus, T. baeops, T. cinnameus, T. hudsoni, T. paramorum and T. taczanowskii*.

**Discussion**

The genus *Thomasomys* evolved into 48 recognized taxa, and most of these species are endemic to the Andes (Pacheco 2015; Brito et al. 2019, 2021; Ruelas and Pacheco 2021; this study). The genus seems to have diverged from a Cricetid ancestor about 6 mya when the Andes were raising to elevations that are conducive to the formation of cloud forests, paramo, and *Polylepis* forest ecosystems (Leite et al. 2014). *Thomasomys* is not common nor does
the genus show great diversity below 2,500 m is elevation (Brito et al. 2021).

Based on molecular data T. burneoi falls into the T. aureus group (Fig. 1). This finding is not surprising because T. burneoi is a large member of the genus Thomasomys and shares morphological characters with this group. These characteristics include the large size and the orange-rufous color described above. Thomasomys burneoi is sister taxa with some members some of T. aureus group (including the recently described T. pardignasi) from Pichincha and Carchi Provinces Ecuador (Brito et al. 2017; Fig. 1).

The distribution of T. burneoi is poorly known, but we do know that it occurs in Sangay National Park; the elevation where these specimens were collected is around 3,400–3,900 m on the eastern slope of the Andes along the Cordillera Real or Oriental (Fig. 10). The geology of the Lagunas de Atíllo is the Tarqui Formation that consists of rhyodacitic pyroclastics and lavas (Longo and Baldock 1982). The type and paratypes were caught in a heterogeneous habitat of mixed páramo and temperate forests (Fig. 11). The páramo component consisted of grasses (Stipa ichu), Asteraceae, and Bromeliaceae (Puya). The forests were dominated by Polyplepis trees and plants of the families Calceolariaceae, Passifloraceae, Fabaceae, Onagraceae, Orchidaceae, Polypodiaceae (ferns), and Valerianaceae (Lee et al. 2011). Poorly drained areas of the paramo had thick beds of mosses. These animals were caught on steep slopes or at the base of rock cliffs (Fig. 11). All of these habitats are in the vicinity of the Lagunas de Atíllo and Cubillines which are deep, cold, oligotrophic, lakes with marshes of reeds along parts of their banks. In addition, we managed to acquire specimens of Amblyopinus colombiae which are beetles that were found living on the skin of T. burneoi usually on the dorsum of the neck (Lee et al. 2011).

Recent expeditions to previously unexplored areas in Sangay National Park have resulted in the discovery of sanctuaries of diversity, from which numerous species new to science have been described (eg, Ojala-Barbour et al. 2013; Brito et al. 2017a, b; Páez and Ron et al. 2019). During the eighteen expeditions made to Sangay National Park (2009–2018), and despite the extreme logistical difficulties, it was possible to collect around 1,000 samples of mammals from ca. 120 taxa (Lee et al. 2011; Brito and Ojala-Barbour 2016; Brito in prep.), three of which were described as new (Caenolestes sangay Ojala-Barbour et al. 2013), Rhipidomys albuja Brito et al. (2017), and Thomasomys salazari Brito et al. (2019) an additional four are also possibly new to science. Thomasomys burneoi sp. nov. is just one example of the still overlooked Ecuadorian diversity.

Conflict of Interest

The authors declare no conflict of interest.

Acknowledgements

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References


### Appendix I

*Thomasomys* sp. Pichincha (n=22). *Pichincha*, Lloa, Atacazo: MECN 2711 (0°18′26.996″ S, 78°40′52.855″ W, 2,743 m), Solaya River: MECN 2720–21 (0°1′45.040″ S, 78°49′0.0114″ W, 2,527 m), Nono, Rio Verde Cocha: MECN 2807 (0°7′39.939″ S, 78°35′28.640″ W, 3,562 m), Reserva Geobotánica Pululahua: MECN 5503, 5208 (0°1′12.9″ N, 78°29′35.29″ W, 3,190 m), Mejía, Tambillo Alto: MECN 5389 (0°24′26.607″ S, 78°35′14.987″ W, 3,553 m), Reserva Podocarpus: MECN 5662, 5666, QCAZ 11939–40 (2°47′13.99″ S, 78°50′54″ W, 1,750 m).


### Appendix II

We included 30 sequences from different species of *Thomasomys* from the “aureus” group and some species from other groups of *Thomasomys*:

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