

News from the Balkan refugium: Thrace has an endemic mole species (Mammalia: Talpidae)

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Abstract. We utilized 1084 bp sequences of the cytochrome *b* gene to assess the taxonomic status of small blind moles from eastern Thrace in Bulgaria and European Turkey. So far, these moles were classified either as *Talpa caeca* or as *T. levantis*. Our study showed them to be genetically closer to *T. europaea*, *T. aquitania*, and *T. occidentalis*, albeit not being part of any of these species. We describe them as a new species, *Talpa martinorum* n. sp. The new species differs from *T. europaea*, another mole occupying Thrace, by having a sealed palpebral fissure and a 1st upper molar with no parastyle, and by being smaller. The contemporary distribution range of *T. martinorum* n. sp. is small and restricted to the Black Sea coast between Burgas (Bulgaria) and Istanbul (Turkey). The species name is an eponym to the married couple Vladimir and Evgeniya Martino, two early students of Balkan mammals.

Key words. Balkans, cytochrome *b*, cryptic species, species delimitation, *Talpa martinorum* n. sp.

INTRODUCTION

Moles (family Talpidae, Lipotyphla) are widespread in temperate Eurasia, North America, and in Oriental Southeast Asia. The majority of species has adapted to a subterranean mode of life and displays convergent morphologies. Interspecific differences are usually slight and further obscured by morphologic plasticity. The traditional approach towards mole taxonomy, based solely on cranial and dental traits, frustrated early students and posed a long-lasting source of dispute and disagreement over a number of genera and species. Since 1758, when Linnaeus named the first mole species (Linnaeus 1758), about 180 species group names accumulated (Hutterer 2005) for over 50 currently valid species. In the past, the authors disagreed which of these names were valid and which were to be considered of subspecific value or just synonyms. For example, Schwarz (1948) synonymized five currently valid generic names from Asia with *Talpa*, and reduced the number of Eurasian fossorial moles to merely six species; Ellerman & Morrison-Scott (1951) further condensed these to four species in two genera.

Despite obvious taxonomic problems with moles, molecular tools were employed in talpid systematics relatively late (Colangelo et al. 2010; Bannikova et al. 2015; Feuda et al. 2015; He et al. 2016). It became immediately clear how incomplete our alpha taxonomic knowledge of the Eurasian moles was. He et al. (2016) proposed that talpid species richness is underestimated by nearly one third. Although the majority of these undescribed species occupy mountain areas in southern China, several cryp-

tic species were recently found also in the genus *Talpa* in Europe (Nicolas et al. 2017a) and south-western Asia (Bannikova et al. 2015).

In this paper we utilized molecular evidence in assessing the taxonomic status of small blind moles along the south-western Black Sea coast, specifically in Thrace of Bulgaria and European Turkey. Osborn (1964) was the first to realize that the region features two distinct mole species, a larger *T. europaea*, which is widespread in Europe, and a smaller one, which he took for *T. caeca*. In Osborn's times, *T. caeca* contained small blind moles of southern Europe, northern Anatolia, and the Caucasus (Ellerman & Morrison-Scott 1951, Grulich 1972), which are currently classified as distinct species (*T. davidiana*, *T. levantis*, *T. occidentalis*; Hutterer 2005). Doğramacı (1988, 1989c) applied the epithet *levantis* (*T. caeca levantis*) for small moles of Thrace and northern Anatolia. Following Pavlinov & Rossolimo (1987), Vohralík (1991) and Kefelioğlu & Gençoğlu (1996) accepted *T. levantis* as a species on its own right specifically for the European populations. As a result, four mole species are reported for south-east Europe (the Balkan Peninsula): *T. europaea* in the north and east, *T. caeca* and *T. stan-kovici* in the south-west, and *T. levantis* in the south-east (Hutterer 2005).

MATERIAL AND METHODS

Specimens. We studied 14 individuals of *T. martinorum* n. sp. (see below) and comparative material of 244

museum vouchers belonging to 11 species of *Talpa* (Appendix 1). Individuals of *T. martinorum* n. sp. were collected in Bulgaria in 2011 (one individual) and 2017 (the remaining 13). External measurements were scored before skinning to the nearest 0.1 mm (hind foot) or 1 mm (the rest): length of head and body (from snout tip to anus), length of tail (from anus to tail tip with exclusion of terminal hairs) and length of hind foot (without claws). Body mass was recorded to the nearest 0.5 grams. We examined the palpebral fissure using a 10x magnifying glass and photographed each mole captured in 2017. In part the individuals were immersed in ethanol and the rest were processed following standard mammalogical procedures (Kryštufek & Vohralík 2001). Skins were mounted on cardboard (carded skins) while skulls and postcranial skeletons were preserved in 95% ethanol, dried subsequently and cleaned by *Dermestes* beetles. Tissue samples for DNA analysis were placed in non-denaturated 96% ethanol and subsequently refrigerated. All field procedures involving handling of animals in this study were in compliance with guidelines approved by the American Society of Mammalogists (Sikes et al. 2011).

Molecular analysis. The cytochrome *b* (Cyt *b*) gene was sequenced for eight specimens of the new species. These sequences were analyzed together with 23 additional *Talpa* sequences (within 13 species), and three outgroup Talpinae sequences (*Urotrichus talpoides*, *Euroscaptor parvidens* and *Euroscaptor klossi*), all downloaded from GenBank. Collecting data for the new sequences and all GenBank numbers are given in Appendix 2.

For the new specimens, total genomic DNA was extracted from ethanol-preserved muscle tissue using silica membrane columns of the Blood and Tissue kit by Qiagen (Hilden, Germany). DNA extracts are available from the ZFMK Biobank, Bonn (DNA voucher IDs are listed in Appendix 2). For PCR amplifications, we used the Qiagen Multiplex PCR kit, following the manufacturer's specifications and based on 2 µl undiluted DNA template in 20 µl total reaction volumes. DNA fragments of 1084 bp were amplified with an Applied Biosystems GeneAmp PCR System 2700 (Life Technologies), applying the primers L14724ag (5'-ATGATATGAAAAC-CATCGTTG-3') and H15915ag (5'-TTTCCNTTCTG-GTTTACAAGAC-3') (Guillén-Servent & Francis 2006). PCR routine followed a 'touch-down' protocol: Taq activation: 15 min at 95°C; first cycle set (15 repeats): 35 s denaturation at 94°C, 90 s annealing at 60°C (−1°C per cycle) and 90 s extension at 72°C. Second cycle set (25 repeats): 35 s denaturation at 94°C, 90 s annealing at 50°C, and 90 s extension at 72°C.

After enzymatic cleanup, all PCR products were Sanger-sequenced at Macrogen Europe's commercial Sanger sequencing service (Amsterdam, NL). Sequences were assembled, inspected and aligned using Geneious vers. R7 (Biomatters, Auckland, New Zealand).

The Maximum Likelihood (ML) tree was inferred with RAxML-HPC vers. 8.1.24 (Stamatakis 2014). For the ML search, a GTR+Γ model of sequence evolution was applied following the program recommendations. The dataset was partitioned to treat 3rd codon positions separately from 1st and 2nd positions. The analysis used the “-f a” option (bootstrap analysis and search for best-scoring ML tree in one program run) and included 100,000 bootstrap replicates. Nodes with a bootstrap support of 50 or below were collapsed. To comparatively assess the topology delivered by the ML reconstruction, a Bayesian analysis was run for 5 million generations (assuming a GTR+Γ model and unlinking 3rd positions) in MrBayes vers. 3.2 (Ronquist & Huelsenbeck 2003), but results were very similar and hence not shown in a separate illustration.

Morphological analysis. Our study was based on visual examination of museum specimens, both macroscopically and under a stereomicroscope at different magnifications. Museum vouchers (skins, skulls and occasionally postcranial skeletons) are deposited in the following collections (acronym in parentheses): Field Museum of Natural History, Chicago (FMNH), National Museum of Bosnia and Herzegovina, Sarajevo (ZMBiH), National Museum of Natural History, Washington D. C. (NMNH), National Museum of Natural History Sofia (NMNHS), Natural History Museum London (NHML), Naturhistorisches Museum Wien, Vienna (NMW), Museum Nationale d'Histoire Naturelle, Paris (MNHN), Mammal Collection in the Ondokuz Mayıs University, Samsun, Turkey (OMU), Slovenian Museum of Natural History, Ljubljana (PMS), Zoologisches Forschungsmuseum Alexander Koenig, Bonn (ZFMK), and Zoological Institute and Zoological Museum, Russian Academy of Sciences, St. Petersburg (ZIN). Vouchers in ZFMK and PMS were directly compared to *T. martinorum* n. sp.. Material from the remaining collections was examined by BK prior to this study and records were compiled to contain measurement data, drawings and photographs.

Skull morphology was quantified using a set of six cranial variables which were scored using a Vernier caliper with accuracy to the nearest 0.1 mm (acronyms in parentheses): condylobasal length of skull (CbL), length of maxillary tooth row (MxT; canine to 3rd molar), breadth of braincase (BcB), height of braincase (BcH; bullae excluded), breadth of rostrum over canines (RoC), and breadth of rostrum over molars (RoM). We also measured the pelvis (greatest length and greatest anterior breadth) and the humerus (length and width). Length and width of 3rd upper molar were scored under a dissecting microscope fitted with an eyepiece graticule. Three morphotypes of the pelvis (sensu Grulich 1971, Popov & Miltchev 2001) were distinguished: (i) the caecoid morphotype lacked a bony anastomosis between the *os sacrum* and the *os ischii* posterior to the 4th *foramen sacrale*; (ii) the europaeoid morphotype had a well-developed and

ossified anastomosis and a closed 4th *foramen sacrale*; (iii) in the intermediate morphotype, the foramen was closed, the anastomosis, however, was thin and narrow, and the ischio-sacral suture was not ossified.

Heterogeneity between samples was assessed in one-way analysis of variance (Anova). To characterize the craniometric variation among species of moles and to find patterns in our high-dimensional data, we used principal components analysis (PCA), which was performed on the correlation matrix of \log_{10} -transformed cranial variables. The resulting principal components (PCs) are linearly uncorrelated; therefore, each PC measures different 'dimensions' of the original dataset. The first PC (PC1) is responsible for the largest possible variance and acts in morphometrics as a size vector (Kryštufek et al. 2015). Rates of correct classification of *a priori* defined species were evaluated by discriminant analysis (DA). To evaluate the performance of the DA and avoid the risk of overfitting the data, all analyses were cross-validated using the jackknife procedure, in which each specimen is classified into a group using the discriminant function derived from all specimens except the specimen being classified. Statistical tests were run in Statistica 7.0 (StatSoft Inc., OK, USA) and SPSS Statistics 2012 (IBM Analytics, NY).

RESULTS

Molecular results. Sequencing of the eight samples resulted in a single haplotype, with the exception of one alignment position (pos. 215) with ambiguous information ('N') in 3 sequences. No stop-codon insertions or deletions were observed in the alignment.

In the ML tree, our new samples of *T. martinorum* n. sp. clustered with *T. europaea*, *T. aquitania*, and *T. occidentalis* into a weakly supported clade (Fig. 1). The Bayesian analysis includes also *T. romana* and *T. caeca* in this cluster. Above species level, the ML branching pattern was poorly supported (the very similar topology in MrBayes had higher support – but see Douady et al. (2003), among others, on potentially misleading high posterior probability values). Therefore the tree topology offers only a meagre idea on phylogenetic relationships among species. At species level however, support values are usually much higher: the new species *T. martinorum* is recovered as monophyletic with maximal bootstrap support. Also the genetic metrics show that *T. martinorum* n. sp. is clearly separated from all other moles: the closest genetic matches to *T. martinorum* n. sp. were *T. europaea* and *T. occidentalis* with *p*-distances of more than 9% (i.e., distances well above the typical intraspecific range, see below). Maximal interspecific distances for *T. martinorum* n. sp. were registered towards *T. altaica* and *T. talyschensis* (both ca. 14%). Minimal interspecific distances among all *Talpa* species in the dataset were ca.

8%, maximal distances 15%. Intraspecific *p*-distances in *T. martinorum* n. sp. were 0.0 to 0.1% (the 0.1% divergence created through the position mentioned above), 0.4 to 1.9% in *T. europaea*, 2.6% in *T. aquitania*, 1.8% in *T. ognevi*, and 0.4 to 6.9% in *T. stankovici*. Conspicuously high distances within *T. stankovici* result from the inclusion of genetically highly divergent Greek populations (from Gravia and Chelmos; see Tryfonopoulos et al. 2010). The two specimens representing the two subspecies of *T. levantis* (i.e., *T. levantis levantis* and *T. levantis minima*) were separated by a distance of 7.5%.

Morphometric results. Secondary sexual dimorphism in size (SSD) is usually obvious in the genus *Talpa* (Niethammer & Krapp 1990). Our sample from Thrace contained nine males and four females, of which nine were clean skulls. We therefore tested SSD only on the external measurements. One-way analysis of variance detected significant heterogeneity between sexes only in length of hind foot ($F=9.45$, $p=0.012$) with males attaining a higher mean (17.21 ± 0.204 mm) than females (16.13 ± 0.289 mm). Since the remaining external traits showed no significant SSD ($F<2.8$, $p>0.12$), we pooled the sexes.

All cranial measurements retrieved highly significant interspecific heterogeneity ($F>18$, $p<0.001$) with highest *F*-values ($F>30$) for length of skull and breadth of rostrum. To visualize morphometric distances and similarity between species we ran PCA on 187 complete skulls belonging to 11 species. *Talpa caucasica* was excluded because the available skulls were damaged. The first two principal components (PC1 and PC2) in concert explained 87.7% of the variance in the original data set and were used to display morphometric relationships between species (Fig. 2). PC1 had high positive loadings for all measurements and sorted moles according to their overall size, from the smallest (negative scores on the left hand side of the PC1 axis) to the largest (positive scores on the right hand side of the axis). PC2 arranged moles in respect to breadth of rostrum over molars. Moles with high PC2 loadings had a broad rostrum and vice versa. There was considerable overlap in the centre of the plot between *T. martinorum* n. sp., *T. levantis*, *T. talyschensis*, *T. occidentalis*, and the larger individuals of *T. caeca*. *Talpa europaea* was well characterized by a combination of large skull size and relatively narrow rostrum; *T. aquitania* was less variable than *T. europaea* and on average had a narrower rostrum. The rostrum was most robust in *T. stankovici* and *T. davidiana*; *T. romana* was transitional in this respect towards *T. europaea*. *Talpa caeca* attained smaller dimensions than any other mole in our analysis. Noteworthy, all principal components showed significant heterogeneity between species ($F>2.5$, $p<0.072$).

Discriminant analysis performed on the same matrix of \log_{10} -transformed cranial variables (Wilks' $\lambda = 0.0248$, $F = 14.408$, $p<0.0001$) classified 65.6% (cross-validated 56.8%) of specimens to the correct species. All pair-

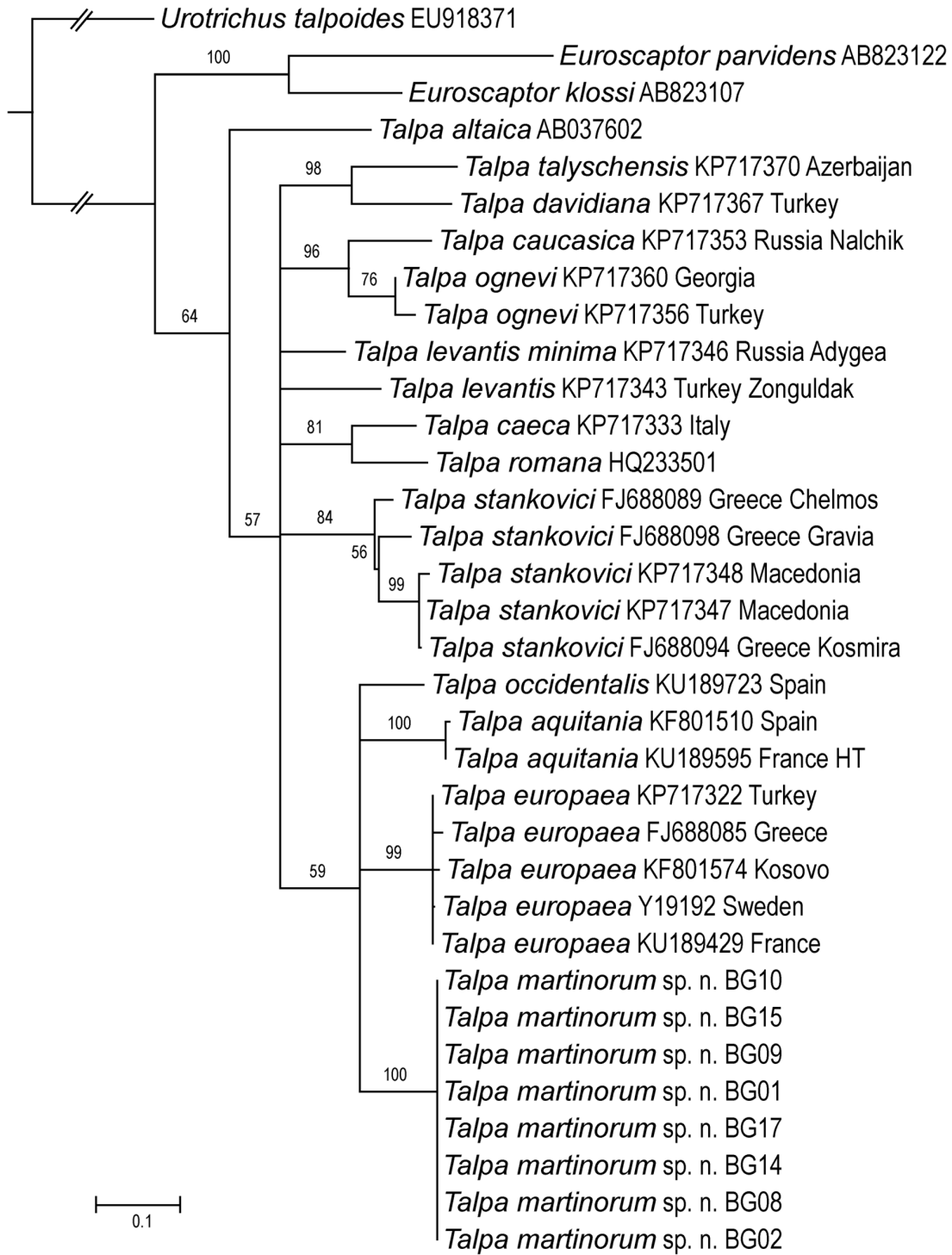


Fig. 1. Maximum likelihood tree inferred from 1084 bp of the mitochondrial cytochrome *b* gene for 14 species of the genus *Talpa*. Bootstrap values are shown on the nodes. The tree is rooted with *Urotrichus talpoides*, *Euroscaptor parvidens* and *Euroscaptor klossi*.

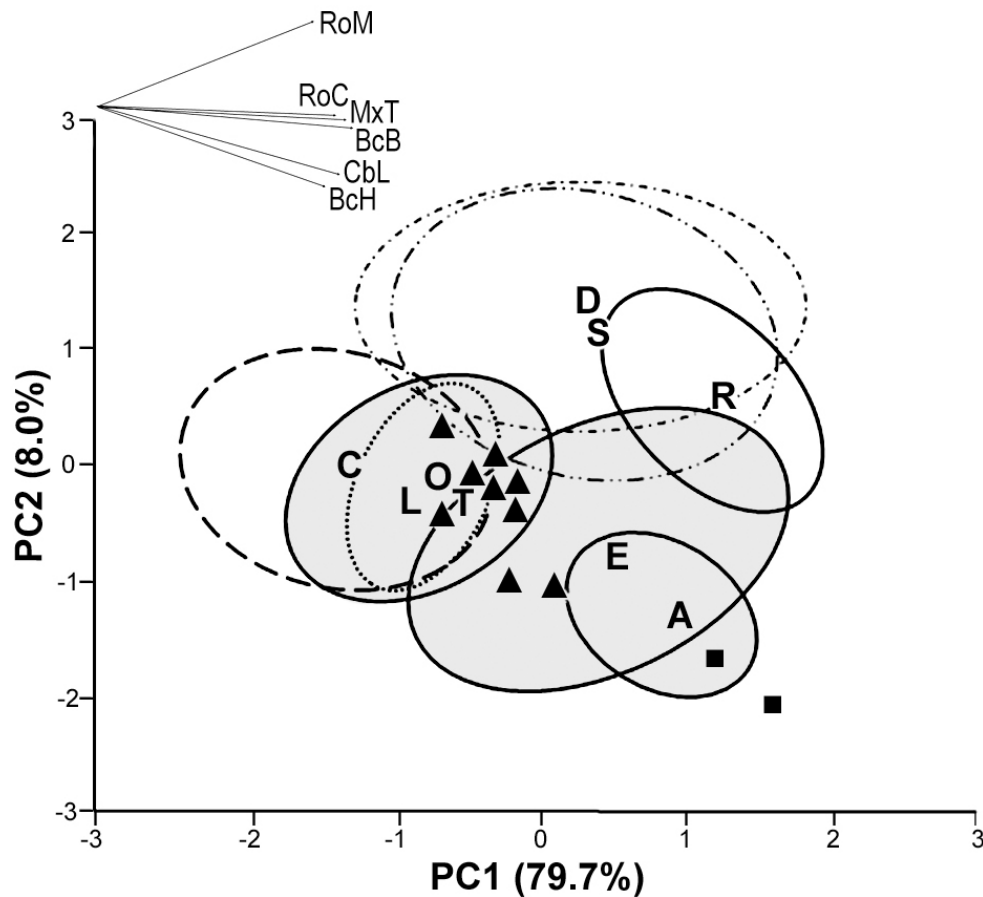


Fig. 2. Projection of group centroids (upper case letters) onto the two principal components (PCs) resulting from principal components analysis of six \log_{10} -transformed cranial variables (percentage of variance explained by each component is in parentheses) of 10 *Talpa* species. Ellipses are 95% confidence limits of the dispersion in each species except *T. martinorum* n. sp. (specimens shown by triangles), *T. altaica* (squares) and *T. talyschensis* (only group centroid is shown). Area inside the ellipses for *T. aquitania*, *T. europaea* and *T. occidentalis* are shaded grey. The character vector diagram illustrates the relative contribution of the original variables (see text for acronyms) to the principal components. Abbreviations for centroids: A – *T. aquitania*, C – *T. caeca*, D – *T. davidiana*, E – *T. europaea*, L – *T. levantis*, O – *T. occidentalis*, R – *T. romana*, S – *T. stankovici*.

wise-squared Mahalanobis distances (D^2) were significant except two (*T. talyschensis* against *T. occidentalis* and *T. martinorum* n. sp., respectively). Pairwise D^2 distances with *T. martinorum* n. sp. (mean \pm standard error = 10.72 ± 5.56) were low in comparison to the remaining pairwise distances ($20.21.87 \pm 2.62$), the difference however was not significant ($F=3.28$, $p=0.076$).

A new mole species from Thrace

***Talpa martinorum* n. sp.** (Figs. 3, 4, 5a, 6a)

Holotype and type locality. Skin mounted on cardboard, skull, postcranial skeleton, and tissue sample in ethanol of a young adult female (ZFMK-MAM-2017.1149; tis-

sue: ZFMK-TIS-23035), collected by B. Kryštufek and N. Nedyalkov on 27.04.2017 (field No. BG8) on the edge of a meadow near Zvezdets, Mt. Strandzha, Bulgaria. DNA of this specimen has been deposited (ZFMK-DNA-FC19476469) and the Cytochrome *b* sequence is available from GenBank (Accession number MH093593).

Measurements of holotype. Body mass 45 g, head and body 124 mm, tail 24 mm, hindfoot length 16.4 mm, condylobasal length of skull 30.4 mm, maxillary tooth row 11.6 mm, breadth of braincase 15.2 mm, height of braincase 9.2 mm, breadth of rostrum over canines 4.1 mm, breadth of rostrum over molars 8.3 mm, length of humerus 14.1 mm, width of humerus 9.7 mm, greatest length of pelvis 22.1 mm, breadth of pelvis 7.5 mm.

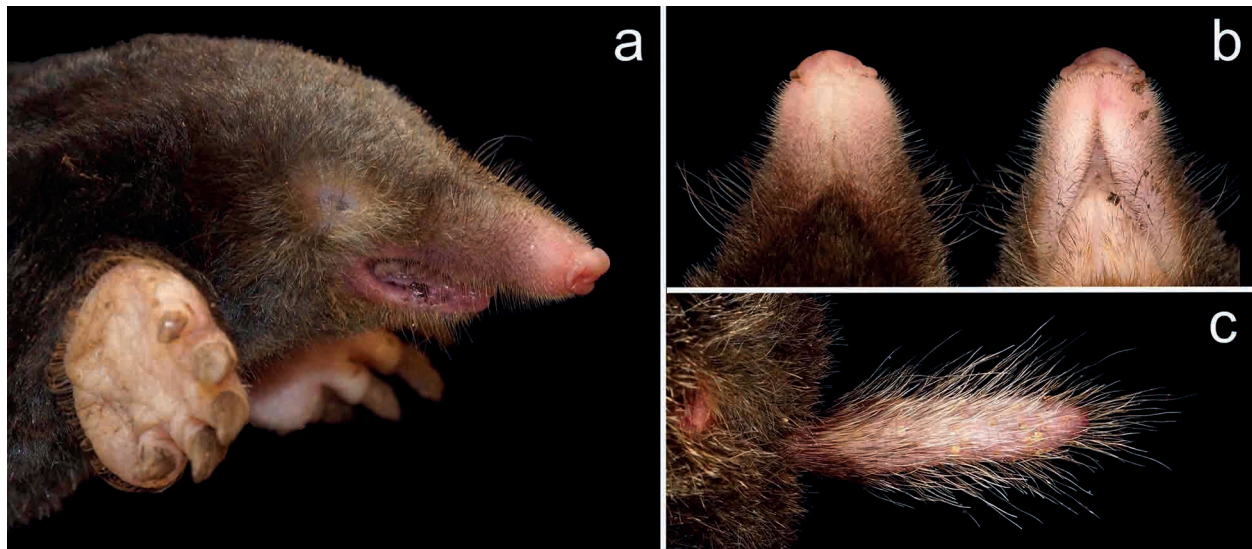


Fig. 3. Head (a) in lateral view, tip of nose (b) in dorsal (left) and ventral (right) views, and ventral side of tail in *Talpa martinorum* n. sp. Note that the palpebral fissure is covered by transparent skin (a). Museum vouchers PMS 25631 (a), ZFMK 2017.1152 (b) and ZFMK 2017.1151 (c). Not to scale.

Diagnosis. A member of the subgenus *Talpa*. Medium-sized species with palpebral fissure sealed by a transparent skin (Fig. 3a). First upper molar (M^1) lacks parastyle (Fig. 6a); the mesostyle is indistinctly bifurcate (Fig. 6a). Pairwise interspecific *p*-distances ($> 9\%$) are within the range observed between other species of moles (e.g., within *Talpa*, interspecific distances average ca. 12%).

Paratypes. Skins, skulls, postcranial skeletons, tissue samples in ethanol and isolated DNA; voucher NMNHS 1053 is represented by a skull and a tissue sample, and vouchers NMNHS 1049–1052 are submerged in ethanol. Specimens were collected on Mt. Strandzha, Bulgaria: Velika, 1 female, collected on 23.09.2011 by N. Nedyalkov (NMNHS 1053), 1 female, collected on 01.05.2017 by N. Nedyalkov & B. Kryštufek (PMS 25631); Gramatikovo, 2 males, collected on 25.04.2017 by N. Nedyalkov & B. Kryštufek (NMNHS 1047, 1048); Vizitsa, 1 male, collected on 27.04.2017 by N. Nedyalkov & B. Kryštufek (ZFMK-MAM-2017.1150); Kondolovo, 1 male, collected on 28.04.2017 by N. Nedyalkov & B. Kryštufek (ZFMK-MAM-2017.1151); Fazanovo, 1 male, collected on 30.04.2017 by N. Nedyalkov & B. Kryštufek (ZFMK-MAM-2017.1152); Pismenovo, 1 male, 1 female, collected on 01.05.2017 by N. Nedyalkov & B. Kryštufek (PMS 25632, 25633); Chengene skele, Burgas, 1 male, 1 female, collected on 19.11.2017 by Nedko Nedyalkov (NMNHS 1049, 1050), Uzungeren, Burgas, 2 males, collected on 19.11.2017 by Nedko Nedyalkov (NMNHS 1051, 1052). Paratype voucher numbers for ethanol-fixed tissue samples (ZFMK-TIS-23033 to -23037 and ZFMK-TIS-33755 to -33758), and for extracted DNA are given in Appendix 2.

Measurements of paratypes. Reported are mean \pm standard deviation (minimum–maximum, sample size). Linear measurements are in mm, body mass in grams. Body mass 58.31 ± 4.06 (52.5–65, 8), head and body 126.75 ± 3.196 (124–134, 8), tail 27.88 ± 3.137 (24–32, 8), hind foot 16.91 ± 0.861 (15.0–17.4, 7), condylobasal length of skull 31.80 ± 0.747 (30.3–33.1, 9), maxillary tooth row 12.07 ± 0.224 (11.8–12.4, 9), breadth of braincase 15.47 ± 0.300 (14.9–15.9, 9), height of braincase 9.028 ± 0.323 (8.6–9.5, 9), breadth of rostrum over canines 4.41 ± 0.088 (4.3–4.5, 9), breadth of rostrum over molars 8.50 ± 0.158 (8.3–8.8, 9), greatest length of pelvis 23.98 ± 0.564 (23.3–24.7, 6), breadth of pelvis 7.82 ± 0.366 (7.4–8.3, 6), length of humerus 13.93 ± 0.186 (13.7–14.2, 6), width of humerus 10.42 ± 0.132 (10.2–10.6, 6).

Description. *Talpa martinorum* n. sp. is of about the same external appearance and body proportions as *T. europaea* (Miller 1912). The tail is rather short (18–26% of head and body length) and densely covered by up to 6.5 mm long bristles (Fig. 3c). Pelage is dense and velvety, 7.0–8.0 mm long on the back, 4.5–6.0 mm ventrally. Fur is blackish dorsally and slightly lighter and with slate shades ventrally. A skin PMS 25632 has an irregular buff strike (21 mm long and up to 3.5 mm wide) on the posterior abdomen. Hairs around the eye are short and lighter, whitish or buff. The tip of the snout is pink to grey, covered by short hairs. There is a reverse triangle of bare skin behind the rhinarium. The tail is usually blackish. Fore foot is 12.6–14.3 mm broad. The skull (Fig. 4, 5a) shows no peculiarities and is of average size and shape overall. Rostrum is moderately robust; width across the canines accounts for 13.3–14.5% and across the molars for 25.4–27.7% of condylobasal length. Maxillary tooth

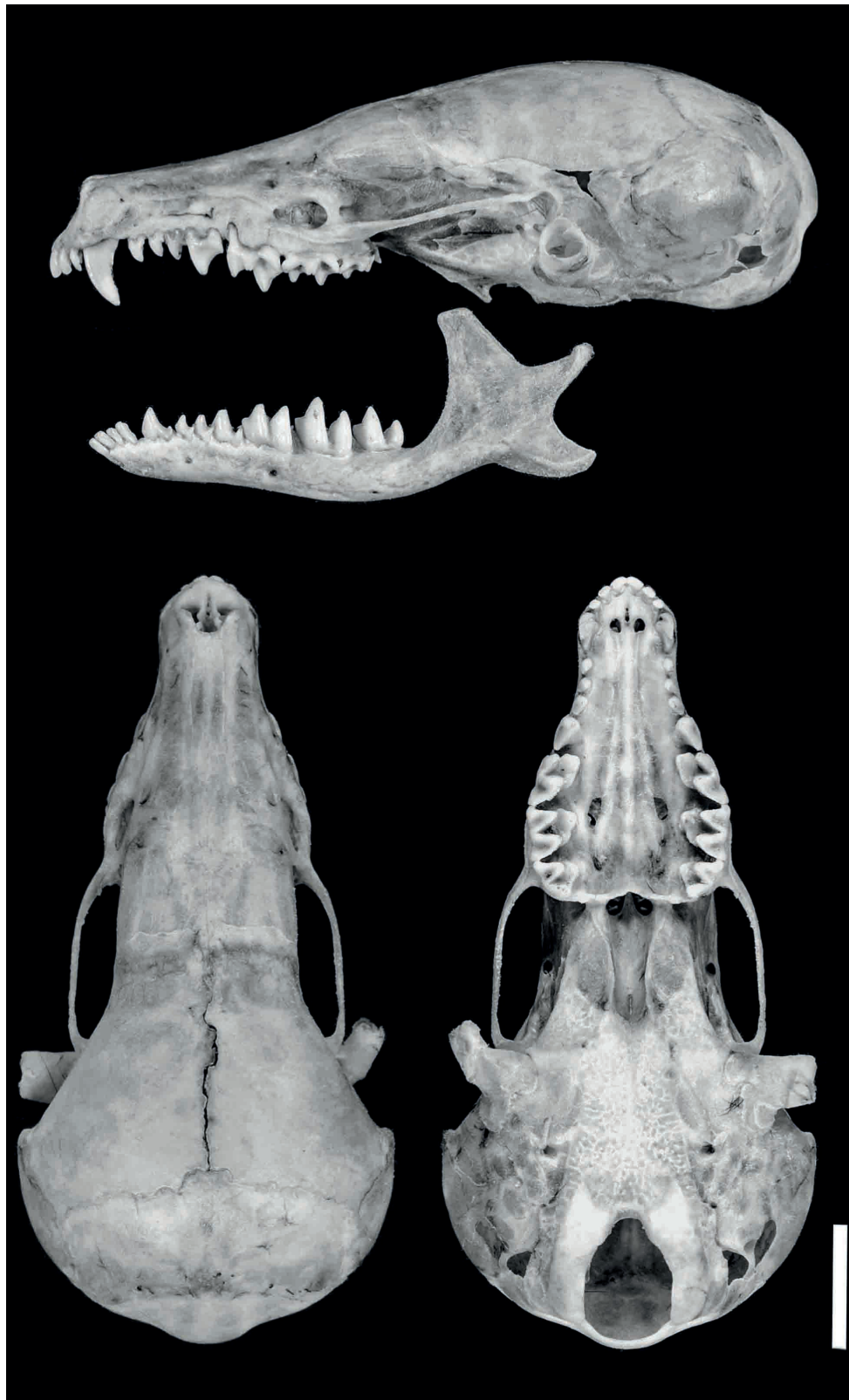


Fig. 4. Skull and mandible of the type specimen of *Talpa martinorum* sp. n. ZFMK 2017.1149. Scale bar = 5 mm.

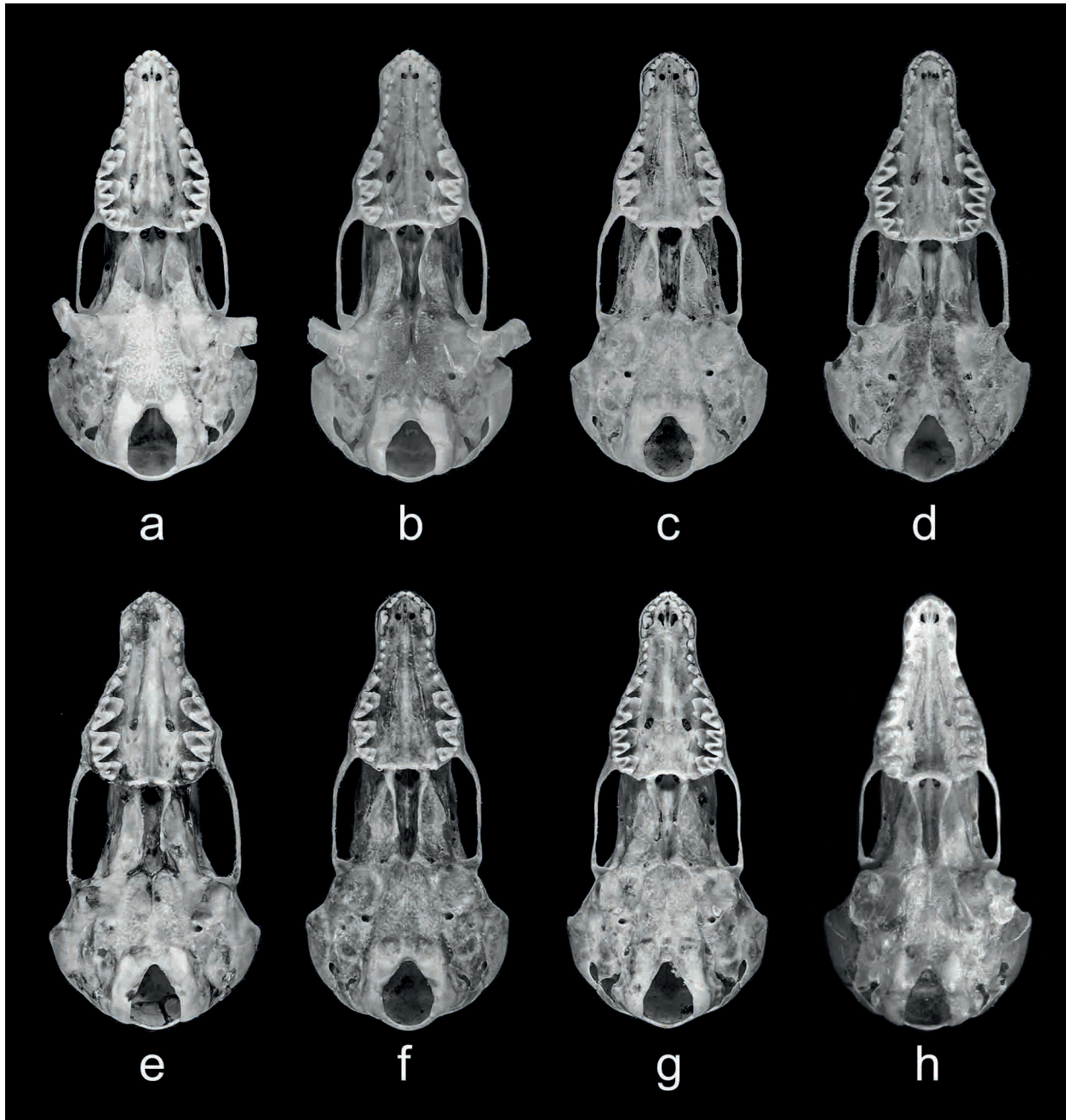


Fig. 5. Ventral cranium of species of *Talpa*: (a) *T. martinorum* n. sp. ZFMK 2017.1149 (greatest length of skull = 31.2 mm), (b) *T. europaea* ZFMK 2014.748 (35.8 mm), (c) *T. aquitania* ZFMK 2005.194 (35.6 mm), (d) *T. occidentalis* ZFMK 2005.301 (33.4 mm), (e) *T. romana* ZFMK 66.304 (37.7 mm), (f) *T. caeca* ZFMK 2005.268 (31.2 mm), (g) *T. stankovici* ZFMK 98.709 (34.1 mm), (h) *T. levantis* PMS 21658 (30.8 mm).

row equals to 37.3–38.9% of condylobasal length. The braincase is rather deep and the height of neurocranium makes up 26.9–30.3% of condylobasal length. The posterior margin of palatine is usually anterior to the imaginary line connecting the posterior alveolar margins of 3rd

upper molars, and the anterior border of the infraorbital foramen is above the 2nd upper molar (Fig. 4).

All three morphotypes of the pelvis were recorded in *T. martinorum* n. sp. The most frequent is the intermediate morphotype (n=13; own material combined with data in Popov & Milchev 2001), followed by the cae-

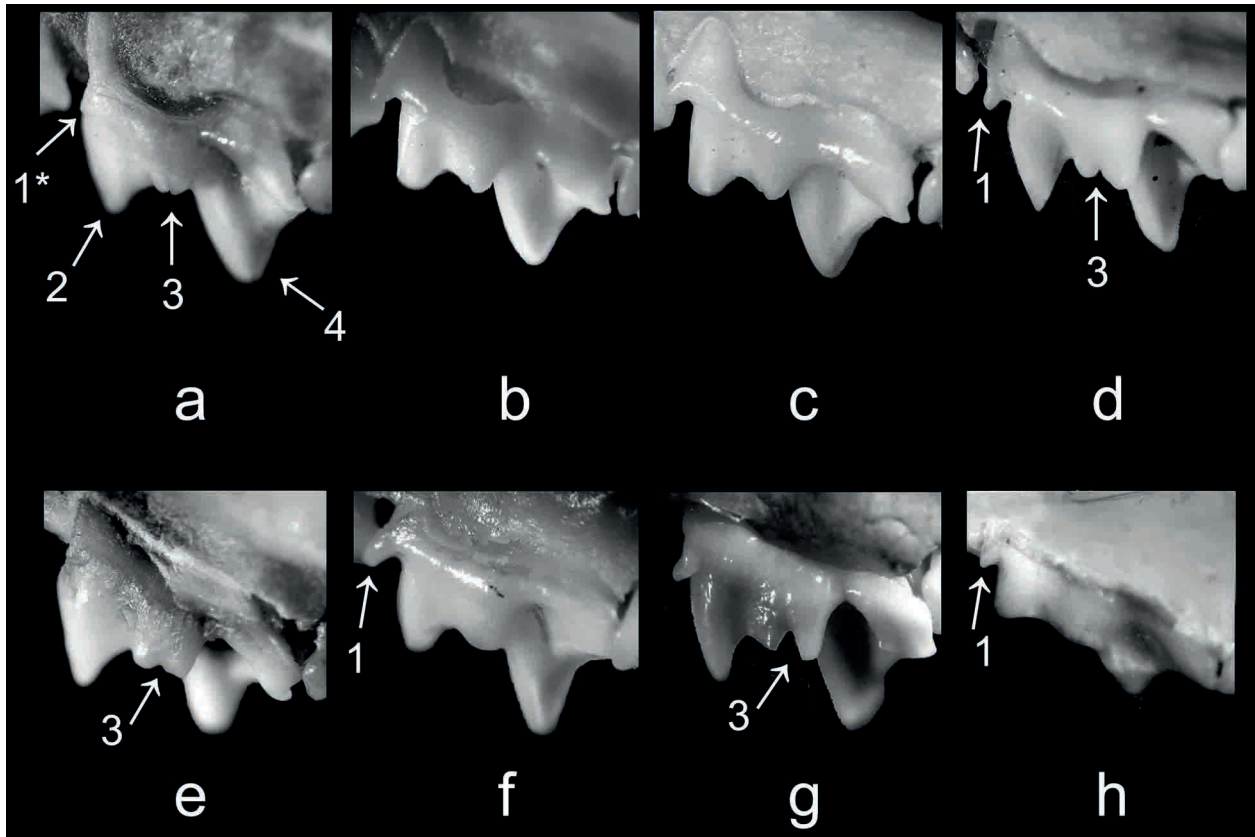


Fig. 6. Lateral view of left upper molar in species of *Talpa*: (a) *T. martinorum* n. sp. ZFMK 2017.1149, (b) *T. europaea* ZFMK 2007.006, (c) *T. aquitania* ZFMK 2005.160, (d) *T. occidentalis* ZFMK 2005.303, (e) *T. romana* ZFMK 1972.202, (f) *T. caeca* ZFMK 1966.310, (g) *T. stankovici* ZFMK 2005.326, (h) *T. levantis* PMS 10650. Anterior is to the left. Not to scale. 1 – parastyle, 2 – paracone, 3 – mesostyle, 4 – protocone. Note that the parastyle is missing in *T. martinorum* sp. n. (1*).

coidal morphotype (n=10) and the europaeoid morphotype (n=2). The sezamoidal *os falciformis* is robust in its proximal part.

Incisors are of decreasing size with 1st incisor being nearly twice as large as 3rd incisor, which is the smallest. The molars are robust, and the 3rd molar is particularly large. The 1st upper molar entirely lacks the parastyle (Fig. 6a). The 1st lower premolar has a prominent distal cusp; the 4th lower premolar lacks metaconid, and the 3rd lower molar is always without hypoconulid while the entocristid is present only exceptionally. Oligodonties were present on three skulls out of nine studied: both 1st upper premolars are missing in ZFMK-MAM-2017.1150, left 1st upper premolar is missing in PMS 25632, and left 1st upper and 2nd lower premolars are missing in PMS 25631.

Comparison. Morphologically, *T. altaica* (subgenus *Asioscalopus*) is peculiar by its large size, short tail, slim skull (Fig. 2) and weak dentition with a reduced 1st upper molar (Stroganov 1957; Zaytsev et al. 2014). Differences between *Asioscalopus* and the subgenus *Talpa* are so

obvious that no comparison with *T. martinorum* n. sp. is required.

In Thrace, *T. martinorum* n. sp. can be safely differentiated from *T. europaea* by (i) a sealed palpebral fissure (open in *T. europaea*), (ii) absence of parastyle on 1st upper molar (present in *T. europaea*; Fig. 6b), and (iii) smaller size. Ranges for the two species overlap only marginally; dimensions of *T. europaea* are from Thrace in Bulgaria and Turkey (Osborn 1964; Doğramacı 1989a,b; Vohralík 1991; Popov & Miltchev 2001): body mass (in grams) 43–65 in *T. martinorum* n. sp. (own material and data in Doğramacı 1988) vs. 60–105 in *T. europaea*; condylobasal length (in mm) 29.3–33.1 in *T. martinorum* n. sp. (own material and data in Osborn 1964; Doğramacı 1988; Popov & Miltchev 2001) vs. 32.4–37.0 in *T. europaea*; length of pelvis (in mm) 21.5–25.0 in *T. martinorum* n. sp. (own material and data in Doğramacı 1989b; Vohralík 1991; Popov & Miltchev 2001) vs. 24.9–30.1 in *T. europaea*; length of humerus (in mm) 12.9–14.9 in *T. martinorum* n. sp. (own material and data in Vohralík 1991; Popov & Miltchev 2001) vs. 14.5–17.8 in *T. europaea*. Molars

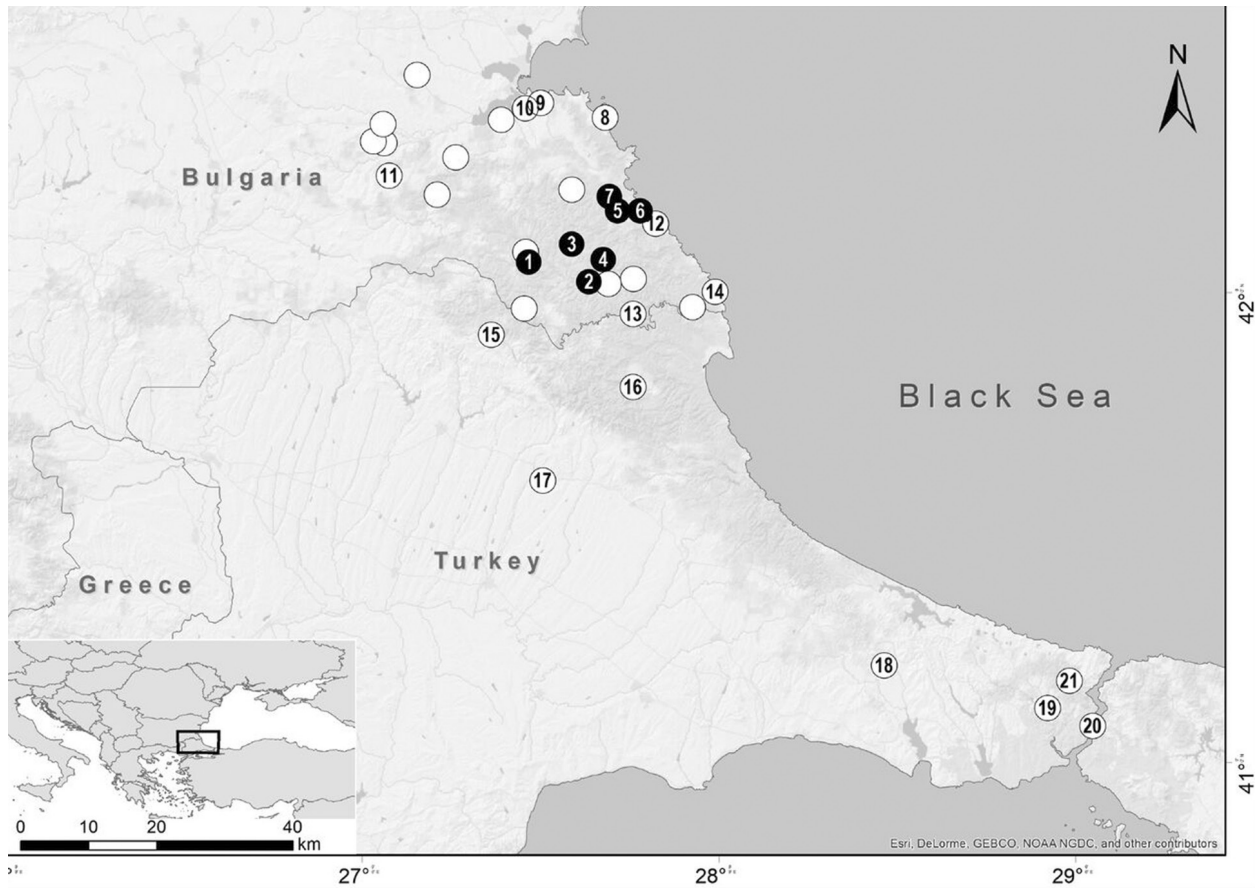


Fig. 7. Records of *Talpa martinorum* n. sp. in Bulgaria (BG) and Turkey (TR). Localities with known mitochondrial genetic identity are shown as black circles. Elevation is parenthesized. Legend: 1 – BG, Mt. Strandzha, Zvezdets (295 m); 2 – BG, Mt. Strandzha, Gramatikovo (210 m); 3 – BG, Mt. Strandzha, Vizitsa (274 m); 4 – BG, Mt. Strandzha, Kondolovo (298 m); 5 – BG, Mt. Strandzha, Fazanovo (106 m); 6 – BG, Mt. Strandzha, Velika (54 m); 7 – BG, Mt. Strandzha, Pismenovo (9 m); 8 – BG, Sozopol (50 m); 9 – BG, Burgas, Chengene skele (sea level); 10 – BG, Burgas, Tvarditsa, Uzungeren (4 m); 11 – BG, Valchanovo (300 m); 12 – BG, Tsarevo (40 m); 13 – BG, Lopushna Reserve (250 m); 14 – BG, Sinemorets, Silistar (40 m); 15 – TR, Kırklareli, Dereköy; 16 – TR, Kırklareli, Demirköy; 17 – TR, Kırklareli, Pınarhisar; 18 – TR, Subaşı; 19 – TR, Kagithane Dere; 20 – TR, Rumeli Hisar; 21 – TR, Bahçeköy. Corresponding references: localities 1–7, 9, 10, 12: own data; 8: Vohralík (1991); 11, 13, 14: Popov & Miltchev (2001); 15–17, 21: Doğramacı (1988); 18 – Collection H. Vierhaus (ZFMK); 19, 20 – NMNH. Localities with no numbers are unspecified in Popov & Miltchev (2001). Museum vouchers from the localities 18–20 are labelled as *T. caeca*; published records were classified as *T. caeca levantis* (pts. 15–17) or *T. levantis* (the remaining).

are relatively larger in *T. martinorum* n. sp. (dimensions of 3rd upper molar: 1.46–1.61 × 1.96–2.17 mm) than in *T. europaea* (1.29–1.59 × 1.77–2.24 mm; specimens from various parts of Europe). Pelvis in *T. europaea* is either europaeoid or intermediate but never caecoid (Petrov 1971b; Popov & Miltchev 2001).

Talpa martinorum n. sp. is well characterized by the absence of a parastyle on the 1st upper molar (Fig. 6a). Parastyle is present in the majority of species of *Talpa*, specifically in *T. europaea* (Fig. 6b), *T. aquitania* (Fig. 6c), *T. occidentalis* (Fig. 6d), *T. caeca* (Fig. 6f), *T. stankovici* (Fig. 6g), *T. levantis* (Fig. 6h), *T. davidiana*, *T. talyschensis*, and *T. caucasica*. *Talpa romana*, which clearly lacks

the parastyle (Fig. 6e), can be reliably differentiated from *T. martinorum* n. sp. by the robust rostrum (Fig. 5e) and large 3rd upper molar (1.67–2.20 × 1.87–2.72 mm).

Talpa martinorum n. sp. can be unambiguously set apart from all the remaining species of the genus *Talpa* by the nucleotide sequence of the Cyt *b* gene.

Distribution. The distribution range of *T. martinorum* n. sp. extends along the south-western Black Sea coast from Burgas in Bulgaria to Istanbul in European Turkey, covering Mt. Strandzha (also Strandja in Bulgarian; Istranca in Turkish) in Bulgaria and Turkey, and the forested coastal belt between the southern foothills of Mt. Istranca and the city of Istanbul (Fig. 7). Records

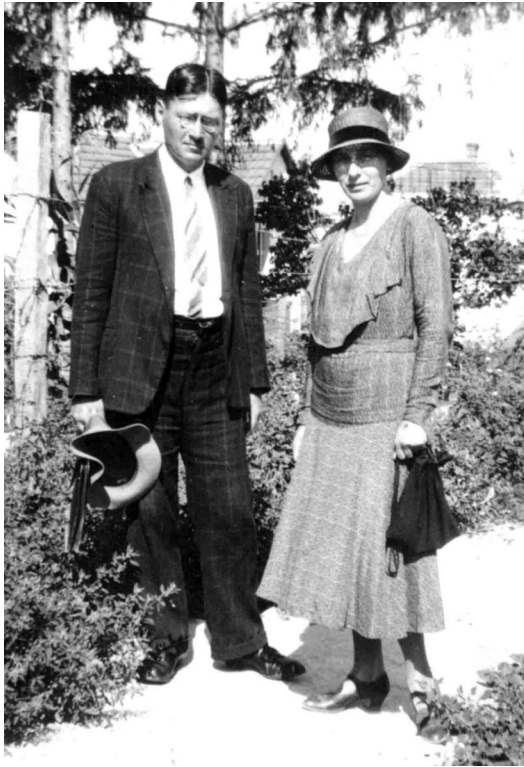


Fig. 8. Vladimir and Evgeniya Martino near their home in Topčidersko Brdo (part of the city of Belgrade), Serbia, in early 1930s. Courtesy by Georgy Bakhtadze.

associated with published Cyt *b* sequences are all from Strandzha in Bulgaria. *Talpa martinorum* n. sp. is parapatric or allopatric with respect to *T. europaea* which is widespread in the lowlands further west. For the distribution range of *T. europaea* see Osborn (1964), Dođramaci (1989a), Vohralík (1991), and Popov & Miltchev (2001). The identity of small blind moles on the Asiatic side of the Bosphorus strait (Osborn 1964) is not known. All moles from north-western Anatolia sequenced so far have the molecular profile of *T. levantis* (vicinity of Zonguldak; Bannikova et al. 2015) and show a distinct parastyle on 1st upper molar (vicinity of Bolu and Bursa).

Habitat. *Talpa martinorum* n. sp. is a fossorial mole of similar habitat requirements as other species of the subgenus *Talpa* (cf. Niethammer & Krapp 1990). Characteristic mounds of unearthed soil (molehills) are a common feature in Mt. Strandzha. Specimens were captured in mesic meadows, pastures and orchards on deep medium-textured and well-drained soils (zheltozem and cinnamonic forest soils; Shishkov & Kolev 2014) in hilly regions, on the edges of arable land and on abandoned fields, in light black soil on low alluvial plains, in oak woodland and forests of river floodplains (own data as well as Osborn 1964 and Popov & Miltchev 2001). Altitudinal range is from near sea level up to at least 445 m.

Etymology. *Talpa martinorum* n. sp. is an eponym to Vladimir Emmanuilovich Martino (Владимир Эммануилович Мартино, 1888–1961) and Evgeniya Veniaminovna Martino (Евгения Вениаминовна Мартино, 1894–1979) née Stepanova (Степанова), ethnic Russians who in 1920 escaped the October Revolution by emigrating to the Kingdom of Serbs, Croats and Slovenes (Kingdom of Yugoslavia since 1929). In politically insecure and frequently violent Eastern Europe of the 20th century, the Martinos were refugees for more than three decades. In 1949 they moved to Bulgaria and in 1955 returned to Russia (at that time still Soviet Union). Inspired by G. S. Miller's (1912) "Catalogue of the Mammals of Western Europe" they initiated mammal research in south-eastern Europe and named, among others, two Balkan endemics: *Dinaromys bogdanovi* (V. Martino & E. Martino, 1922) (Martino & Martino 1922: 413) and *Talpa stankovici* V. Martino & E. Martino, 1931 (Martino & Martino 1931: 53) (Fig. 8). While Vladimir had a degree in Biology from the University in Novorossiysk (1913), Evgeniya had no formal academic education. Despite this, she attained competency in mammalogy and successfully collaborated with her spouse, both in the field and cabinet. Although they published several joint papers (as V. and E. Martino), the contribution by Evgeniya is mainly ignored and she is nearly anonymous today (cf. Beolens et al. 2009). At least nine subspecific names for mammals with the epithet *martinoi* (see Appendix 3) were proposed by mammalogists between 1935 and 1971, and all are eponyms to Vladimir Martino. With the name *martinorum* n. sp. we stress the equal share by Evgeniya in the tandem "V. et E. Martino" and correct the injustice done to her contribution in the past decades. Along with Dorothea Bate (1878–1951) and Gabriele Neuhäuser (1911–1998) Evgeniya was one of the early women who studied the taxonomy of Palaearctic mammals already between the two great wars. In addition to their publications, a renowned legacy of Vladimir and Evgeniya Martino is their meticulously prepared and carefully labelled mammal collection, deposited primarily in the Natural History Museum London and the Zoological Institute and Museum of the Russian Academy of Sciences in St. Petersburg. For biographies of Vladimir Martino, see Mezentsev (1961), Paspalev (1962), Pusanov (1962), Zimmermann (1962), Gus'kov (1965), Taranenko (1999), and Boreiko (2001).

DISCUSSION

During the Pleistocene climatic changes over the last ca. 2.6 My, temperate species have endured glacial maxima in geographically restricted refugial areas. A legacy of the repeated extinctions of northern populations on the one hand, and the long-term persistence in southern refugia on the other hand is a number of taxa with restricted

distributions in the former glacial refugia (Hewitt 2000). Contemporary biogeographic pattern of the genus *Talpa* obviously results from the allopatric evolution in such constrained refugia. Only two mole species (*T. altaica* and *T. europaea*) have extensive distribution ranges in temperate and southern boreal regions of Europe and western Asia, while the remaining ten or so species occupy small areas along the southern edge of the distribution range of the genus (Bannikova et al. 2015). The new species from Thrace, with its small distribution range, is therefore well nested within a broader biogeographic pattern of the western Palaearctic.

Mammals endemic to the Balkan Peninsula, which include a mole *T. stankovici* and several rodents, are restricted to the topographically rough south-west Balkans (Kryštufek 2004). *Talpa martinorum* n. sp. therefore provides the first evidence on speciation of a mammal in the extreme eastern part of the peninsula. Besides, our new evidence also corroborates an earlier assumption on the persistence of multiple independent refugia inside the topographically complex Balkan refugium (cf. Kryštufek et al. 2007).

The new species shows no close phylogenetic links with the Balkan endemic *T. stankovici* nor with the Balkan-Italian *T. caeca*. Instead, *T. martinorum* n. sp. forms a (weakly supported) clade in the Cyt-*b* tree containing also the widespread *T. europaea* and two endemics from Western Europe, *T. aquitania* and *T. occidentalis*. Biogeographically, it is straightforward to interpret this finding. Inside the Balkan refugium there was no evolutionary divergence of an ancestral mole to *T. martinorum* n. sp. and either *T. stankovici* or *T. caeca*. Instead, *T. martinorum* putatively originated from a small peripheral fragment population of a taxon ancestral also to *T. europaea*. The process replicates itself in each of the three major southern European refugia, namely with *T. aquitania* and *T. occidentalis* in the west, with a deeply divergent phylogeographic lineage of *T. europaea* in northern Italy (Feuda et al. 2015), and finally in the eastern part of the Balkan refugium with *T. martinorum* n. sp. (this study). The observed pattern fits well the hypothesis by Bilton et al. (1998) on Mediterranean refugia as areas of endemism rather than sources of postglacial northward recolonizations. Based on molecular clock estimates of divergences between *T. europaea*, *T. aquitania* and *T. occidentalis* (1.88–3.71 Mya; Bannikova et al. 2015; Feuda et al. 2015; Nicolas et al. 2017b), the most recent common ancestor to *T. martinorum* n. sp. and *T. europaea* must be of Early Pleistocene age or older. Late Pliocene small moles from Varshets in north-western Bulgaria, classified as *T. cf. levantis*, closely resemble *T. martinorum* n. sp. by their small size and the 3rd upper molar with no parastyle and with an undivided mesostyle (Popov 2004). Middle Pleistocene strata of Yarimbargaz Cave near Istanbul, i.e., inside the contemporary range of the new species, also yielded a small species of mole

tentatively identified as *T. levantis* (Santel & Königswald 1998). Fossil evidence therefore provides strong support for a long persistence in the eastern Balkan refugium of a mole most similar to the current *T. martinorum* n. sp.

Molecular evidence (Bannikova et al. 2015; this study) so far did not yield any support for the earlier assumption that moles colonized southeast Europe via an intermittent Bosphorus land bridge during one of the low sea level phases (Vohralík 1991; Kryštufek & Vohralík 2001). The alternative submergences and emergences of the Bosphorus Strait enabled migrations of mammals from Europe to Asia (e.g., *Glis glis*; Helvaci et al. 2012), from Asia to Europe (e.g., *Microtus hartingi*; Kryštufek et al. 2009), or in both directions (*Crocidura leucodon*; Dubey et al. 2007). As shown by sedimentological evidence, however, the Bosphorus land bridge emerged as a permeable barrier only in the Middle Pleistocene (Kerey et al. 2004) and therefore postdates the postulated split between *T. martinorum* n. sp. and *T. europaea* (see discussion above). Therefore, even if moles from Asia would colonize Europe via the Bosphorus land bridge, they would face an established congeneric species in the new habitats. However, such speculations should be taken with a grain of salt. So far, none of the moles in the Bosphorus region on either side of the strait have been screened genetically. A denser sampling in that particular part of Turkey is therefore a necessity for a more holistic understanding of mole evolution in this biogeographically dynamic region.

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APPENDIX 1

Comparative museum vouchers

Listed are museum vouchers with the appropriate collection numbers; see text for collection acronyms. Material is itemized by country and sorted alphabetically according to locality.

***Talpa altaica* Nikol'skiy, 1883** (Nikol'skiy 1883: 165). Russian Federation – ZFMK-MAM-1987.751 and 1987.752 from Akademgorodok, Novosibirsk Oblast.

***Talpa aquitania* Nicolas, Martínez-Vargas & Hugot, 2017** (Nicolas et al. 2017a: 641). France – ZFMK-MAM-2005.242 from Arles-sur-Tech, Département Roussillon. ZFMK-MAM-2005.156 to 2005.159 from vicinity of Blaye, Département Gironde. Spain – ZFMK-MAM-2005.203 to 2005.205 from vicinity of Barbadillo de Pez, Province of Burgos. ZFMK-MAM-2005.201 from Burguete, Province of Navarra. ZFMK-MAM-2005.202 from Cameros, Sierra de Cebollera, Province of Logroño. ZFMK-MAM-2005.189 to 2005.200 from vicinity of Corconte, Province of Santander. ZFMK-MAM-2005.160 to 2005.166, 2005.169 to 2005.175, 2005.177 to 2005.179, and 2005.181 from Ramales de la Victoria, Province of Cantabria. ZFMK-MAM-2005.176 and 2005.180 from Lanetosa, Province of Vizcaya.

***Talpa caeca* Savi, 1822** (Savi 1822: 265). Bosnia and Herzegovina – PMS 7239 from Čemerno. PMS 7478 from Lake Boračko jezero, Mt. Prenj. ZMS 293 (type of *Talpa hercegovinensis* Bolkay, 1925; Bolkay 1925: 1) from Stolac. Greece – NHML 31.11.11.24 to 31.11.11.26 and 31.11.11.27 (type of *Talpa olympica* Chaworth-Musters, 1932; Chaworth-Musters 1932: 166), 31.11.11.28 to 31.11.11.31 from eastern slope of Mt. Olympus. Italy – ZFMK-MAM-2005.260 to 2005.263, 2005.268, and 2005.269 from Abetone Pass, Province of Pistoia. PMS 9813 from Caramanico, Province of Pescara. ZFMK-MAM-2005.266 and 2005.267 from vicinity of Colle di Nava, Province Imperia. ZFMK-MAM-2005.264 and 2005.265 from Osiglia, Province of Savona. Kosovo – PMS 7473 from Pavlov kamen, Mt. Šar planina. Macedonia – PMS 7475 from Derven Pass above Prilep. PMS 7474 from Magarevo, Bitola. Montenegro – PMS 7485 from Mt. Kom Vasojević. ZFMK-MAM-1966.310 from Mt. Lovćen. PMS 7523 from Morača. PMS 8131 from

Nikšić. Switzerland – ZFMK-MAM-1965.065 from Bergell, Canton Graubünden.

***Talpa caucasica* Satunin, 1908** (Satunin 1908: 5). Russian Federation – NMW 19943 to 19945 from Psebaj, Krasnodar krai, north-western Caucasus.

***Talpa davidiana* (Milne-Edwards, 1884)** (Milne-Edwards 1884: 1143). Iran – FMNH 111007 from 1 mile south of Divandarreh, Kurdistan. FMNH 96421, 96423 and 96424 (type of *Talpa streeti* Lay, 1965; Lay 1965: 227) from Hezar Darreh, Kurdistan. Turkey – FMNH 82136 and 82137, PMS 21503 from Bitlis, Tatvan. OMU 231 from Megabuti yaylası, Hakkari. NMW 20326 and 20327 from Cilo-Sat-Mts., Mergan Zoma, Hakkari. MNHN 1883.469 (type of *Scaptochirus davidianus* Milne-Edwards, 1884) from Meydanekbez, Gaziantep. OMU 166 and 232 from Otluca köyü, Hakkari. Israel – NHML M15277 (type of *Talpa chthonia* Bate, 1937; Bate 1937: 399), M16092 from the Upper Pleistocene layers of Tabun Cave.

***Talpa europaea* Linnaeus, 1758** (Linnaeus 1758: 52). Austria – ZFMK-MAM-2005.143, 2005.146, and 2005.185 from Kleinalm, Lower Tauern, Styria. Bosnia and Herzegovina – PMS 21511 from Gornji Malovan. Bulgaria – ZFMK-MAM-1938.146 from Bansko, Mt. Pirin. Germany – ZFMK-MAM-2005.342 from Bonn-Kessenich, NRW. ZFMK-MAM-2005.334 from Bonn-Lengsdorf, NRW. ZFMK-MAM-2007.006 from vicinity of Münster, NRW. ZFMK-MAM-2009.021 from Wahner Heide, Niederrheinische Bucht, NRW. ZFMK-MAM-2014.748 from Welldorf, Dueren, NRW. ZFMK-MAM-2002.138 from Wesseling-Urfeld, North Rhine-Westphalia (NRW). ZFMK-MAM-2005.139 from Angeln, Schleswig-Holsteinisches Hügelland, Schleswig-Holstein. ZFMK-MAM-2005.153 from Großhansdorf, Schleswig-Holstein. France – ZFMK-MAM-2005.084 and 2005.085 from St. Tropez, Pampelonne, Département Var. Italy – ZFMK-MAM-2005.086 from vicinity of Albenga, Province of Savona. ZFMK-MAM-2005.089 from Dego, Province of Savona. ZFMK-MAM-2005.066, 2005.074, 2005.075, and 2005.328 from Merano, Province of South Tyrol. ZFMK-MAM-2005.090 to 2005.093 from Pass Colle di Nava, Province of Imperia. ZFMK-MAM-2005.087 from Pass Col di Sistrere, the Cottian Alps (Alpi Cozie), Region of Piedmont. ZFMK-MAM-2005.088 from Pietralunga, Province of Perugia. Montenegro – PMS 393 from Lubnice, Mt. Bjelasica. Serbia – ZIN 33974 (Type of *Talpa europaea pančići* V. Martino, 1930; Martino 1930: 60) from Kraljevo. Slovenia – PMS 25634 from Mt. Pohorje.

***Talpa levantis* Thomas, 1906** (Thomas 1906: 416). Turkey – NHML 25.11.1991 (type of *Talpa caeca levantis*) from Altindere, Trabzon. NHML 6.5.1.1 to 6.5.1.4 from Çosandere, Trabzon. NHML 6.3.6.6 from Euthey, Trabzon. NHML 6.3.6.4; NMNH 327252 and 327253 from Meryemana, Trabzon. OMU 233, 234, and 236 to 242 from Bitlis, Tatvan. NMW 13042 and 13043 from Bolu. PMS 10299 from Kürtler, Samsun. PMS 21658 from 10 km east of Şavşat, Ardahan. NMW 19858 from Ulubey, Ordu. NMW 19859 from Yavuz-Kemal, Bıcık, Giresun. PMS 11372 from Şehitler Geçidi, Mts. Giresun Dağları, Tamdere. NMNH 327263 and 327264, PMS 10650 from Mt. Ulu Dağ, Bursa.

***Talpa occidentalis* Cabrera, 1907** (Cabrera 1907: 212). Spain – ZFMK-MAM-2005.304 from 4 km south-west of Cantoral, Province of Burgos. ZFMK-MAM-2005.279 and 2005.280 from 1 km north-east of Cazorla, Province of Jaén. ZFMK-MAM-2005.271 to 2005.275 from Espinama, National Park Picos de Europa, Province of Cantabria. ZFMK-MAM-2005.290 to 2005.294, 2005.297, and 2005.298 from vicinity of Espinosa de los Monteros, Province of Burgos. ZFMK-MAM-2005.276 to 2005.278 from 7 km south-west of Lanetosa, Puerto de los Tomos, Province of Santander. ZFMK-MAM-2005.308 and 2005.309 from vicinity of Las Rozas, Province of Santander. ZFMK-MAM-2005.281 to 2005.286 from 10 km south of Rascafria, Province of Segovia. ZFMK-MAM-2005.299 to 2005.301 from Llánares de la Reina, Province of León. ZFMK-MAM-2005.301 and 2005.302 from 10 km south of Riano, Province of León. ZFMK-MAM-2005.314 from near Samosierra, Province of Segovia. ZFMK-MAM-2005.310 to 2005.313 from Sierra de Gredos, Province of Ávila. ZFMK-MAM-2005.270 from Paso di Samosierra, Sierra de la Guadarrama, Province of Segovia.

***Talpa romana* Thomas, 1902** (Thomas 1902: 516). Italy – PMS 9855 from Caramanico, Province of Pescara. ZFMK-MAM-1977.675 from Catanzano, Province of Calabria. ZFMK-MAM-1966.291 to 1966.302, 1966.305, 1966.306, and 2005.335 from Monte Gargano, Province of Puglia. ZFMK-MAM-1966.303 from the National Park Abruzzo. ZFMK-MAM-1966.304 from Pescasseroli, Province of L'Aquila.

***Talpa stankovici* V. Martino & E. Martino, 1931** (Martino & Martino 1931: 53). Greece – ZFMK-MAM-2005.322 to 2005.326 from Corfu, Ionian Islands. ZFMK-MAM-205.327 from 7 km south of Ioannina, Epirus. ZFMK-MAM-1963.680 and 1977.031 from Mt. Olympus. Macedonia – ZIN 34014 (type of *Talpa romana stankovici*) from Magarevo, Bitola. PMS 7488 from Derven Pass above Prilep. PMS 7491 to 7493 and 7502 from Mt. Galičica. ZFMK-MAM-1998.709 and PMS 7497 from Mt. Bistra. PMS 7499 from Mt. Kajmakčalan. PMS 7486 and 7487 from Prilep. PMS 7496 and 7503 from Popova šapka, Mt. Šar planina. PMS 7504, 7505, and 7507 from Resen. PMS 7495 and 7497 from Struga. Montenegro – PMS 3202, 3203, 3205 (type of *Talpa stankovici montenegrina* Kryštufek, 1994; Kryštufek 1994: 14) and 3207 from Ulcinj.

***Talpa talyschensis* Vereschchagin, 1945** (Vereschchagin 1945: 67). Iran– Ghilan, FMNH 96416 to 96419 from 12 km west of Chalus.

APPENDIX 2

GenBank accession numbers. Specimens of *Talpa martinorum* n. sp. sequenced in this study. List includes collecting data for the new sequences and GenBank accession numbers. See text for collection acronyms and Fig. 7 for locality numbers (Loc. No.).

Collection No.	Loc. No.	Latitude	Longitude	Field number	DNA voucher Tissue voucher	GenBank No.
NMS BG1	3	42.04736	27.64744	BG1	ZFMK-DNA-FC19476453 ZFMK-TIS-23033	MH093591
NMS BG2	3	42.04697	27.64782	BG2	ZFMK-DNA-FC19476461 ZFMK-TIS-23034	MH093592
ZFMK-MAM- 2017.1149	2	42.09068	27.47637	BG8	ZFMK-DNA-FC19476469 ZFMK-TIS-23035	MH093593
ZFMK-MAM- 2017.1150	1	42.12798	27.59862	BG9	ZFMK-DNA-FC19476382 ZFMK-TIS-23036	MH093594
ZFMK-MAM- 2017.1151	4	42.09424	27.68921	BG10	ZFMK-DNA-FC19476390 ZFMK-TIS-23037	MH093595
ZFMK-MAM- 2017.1152	6	42.19826	27.73069	BG14	ZFMK-DNA-FC19476398 ZFMK-TIS-33755	MH093596
PMS 25631	7	42.19739	27.79592	BG15	ZFMK-DNA-FC19476406 ZFMK-TIS-33756	MH093597
PMS 25633	5	42.2287	27.70733	BG17	ZFMK-DNA-FC19476422 ZFMK-TIS-33758	

APPENDIX 3

Eponyms to (Vladimir) Martino

Names are arranged chronologically. Species name as is currently in use (ex Wilson & Reeder 2005) is in square brackets when appropriate.

Pitymys subterraneus martinoid Éhik, 1935 (Éhik 1935: 60) [*Microtus subterraneus*]
Sumeriomys guentheri martinoid Petrov, 1939 (Petrov 1939: 363) [*Microtus guentheri*]
Rhinolophus ferrumequinum martinoid Petrov, 1940 (Petrov 1940: 59)
Arvicola terrestris martinoid Petrov, 1949 (Petrov 1949: 186) [*Arvicola amphibius*]

Mustela erminea martinoid Ellerman & Morrison-Scott, 1951 (Ellerman & Morrison-Scott 1951: 256)
Citellus citellus martinoid Peshev, 1955 (Peshev 1955: 290) [*Spermophilus citellus*]
Glis glis martinoid Mirić, 1960 (Mirić 1960: 36)
Spalax leucodon martinoid Petrov, 1971 (Petrov 1971a: 13P)
Lynx lynx martinoid Mirić, 1978 (Mirić 1978: 30)