Supplementary Materials S2: Results

A molecular phylogeny of *Stylodipus* (Dipodidae, Mammalia): a small genus with a complex history

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Figure S2. Bayesian ultrametric tree reconstructed in BEAST for all codon positions of *cytb* gene for 93 sequences of *Stylodipus* spp. and two outgroups produced in newick format.

*((Chimaerodipus_BH06:0.0014557879431881249,Chimaerodipus_BH01:0.00145578794318812
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5,m15_82:6.82825912681484E-5):1.318242022993188E-4,m15_108:2.001067935674672E-
4):2.698017974306077E-4,((m15_92:7.475784590219026E-5,m15_94:7.475784590219026E-
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4):4.860943006339963E-4,((((m15_83:7.487408536341333E-
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5):3.511690804271217E-5):2.0983885017274162E-4):4.536066248897741E-
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4):7.11556711953068E-4):3.928517228856121E-4):1.38312395558865E-
4):5.112464849048176E-4):4.813407075665993E-4,(k19_29:7.474851925748371E-
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4,S69276:9.918724432109172E-
4):0.0018616333254445339):0.001684361831578815):0.0016104684548791381,(k16_22:0.004
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4,X1:1.5384452701147633E-
4):0.004347782025167474):0.0010574954072623821,(((X3:0.00132445826392 5632,Rx1:0.001*

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Figure S4. Bayesian ultrametric tree reconstructed in BEAST from concatenated alignment of fragments of four nuclear loci for 57 specimens of *Stylodipus* spp. including all specimens of *S. t. karelini* and three outgroups produced in newick format.
(Jaculus:0.0291995224,Dipus:0.0355702543,(Chimaerodipus:0.0167150791,((((((((((((((((((St_k13_85:2.0697E-6,St_k13_86:2.0697E-6):2.39E-6,St_k12_64:2.4714E-6):2.5381E-6,St_k12_65:2.6662E-6):0.0022541177,((Ss_m11_96:2.8102E-6,Ss_M15_031:2.5745E-6):3.769665E-4,(((Ss_m15_84:3.733369E-4,Ss_m11_95:2.0697E-6):2.0408E-6,Ss_m11_94:2.5272E-6):2.9918E-6,Ss_M15_102:2.013E-6):2.1272E-6):0.0014816471):2.1058E-6,Ss_M15_32:3.808915E-4):0.0015167275,((((Ss_M15_53:2.0697E-6,Ss_m15_94:2.0697E-6):1.237E-6,Ss_m15_54:2.2914E-6):2.3938E-6,Ss_M15_108:2.0697E-

6):2.7693E-6,Ss_m11_141:2.0697E-6):7.06863E-4):0.0031966296,St_S148037:4.098603E-4):0.0024888505,St_k16_05:2.5619E-6):0.0014805915,((((St_Kalmykia:5.650772E-4,St_X1_Tzimla:2.7783E-6):5.601637E-4,St_RX3:3.753163E-4):2.6915E-6,St_X2_Kherson:2.0697E-6):2.5558E-6,(St_X3_Kherson:3.736844E-4,St_RX4:2.0697E-6):1.4809E-6):7.511576E-4):0.0011314751,((St_k12_238:7.507624E-4,((St_k22_26:2.8207E-6,St_k22_28:1.4693E-6):3.770749E-4,St_k22_27:3.783512E-4):3.76688E-4):3.664469E-4,St_K12_270:2.0697E-6):1.2229E-6):1.2544E-6,St_k22_29:2.0697E-6):3.686894E-4,St_K19_09:3.963539E-4):1.4568E-6,St_k19_10:1.8546E-6):2.9008E-6,St_k16_04:2.0697E-6):2.6691E-6,St_K16_16:3.801273E-4):7.454287E-4,(St_k16_22:3.729311E-4,St_K19_08:2.5783E-6):3.738692E-4):2.27902E-4,(St_K12_260:3.73492E-4,St_k19_12:2.2045E-6):5.172335E-4):0.0023032755,(St_S148039:0.0025512116,St_S148041:3.787768E-4):0.0028624469):0.004041127,((((((((((((Sa_m11_51:2.0697E-6,Sa_m13_2:2.0697E-6):2.0697E-6,Sa_m13_183:2.0697E-6):1.5783E-6,((Sa_m11_53:2.0697E-6,Sa_m17_163:2.0697E-6):1.6417E-6,Sa_m17_235:2.0697E-6):1.4681E-6):1.4236E-6,Sa_m14_187:2.0697E-6):2.1793E-6,Sa_m14_190:2.0697E-6):1.5048E-6,Sa_m17_164:2.0697E-6):1.726E-6,Sa_m17_234:2.0697E-6):1.4443E-6,Sa_m13_04:2.0697E-6):1.3924E-6,Sa_m13_3:2.0697E-6):1.424E-6,Sa_m13_5:2.0697E-6):3.620374E-4,Sa_m14_191:2.0697E-6):1.2428E-6,Sa_m14_188:2.5597E-6):3.880394E-4,(Sa_m15_176:2.7178E-6,Sa_m17_230:2.0697E-6):3.619585E-4):0.0089505878):0.0072314687):0.004172692);

Individual nuclear trees and networks

Part of the sequences was used only for the reconstruction of the ML trees due to their insufficient length. Besides, among the phased sequences, alleles with posterior probabilities below 0.8 were excluded from the network reconstruction in PopArt (Table S9).

IRBP. In the the network (Figure 3) both in the ML tree of unphased sequences (Figure S3, A), sequences of *S. andrewsi* and *S. t. karelini* are substantially divergent from sequences of all other *Stylodipus* spp. *S. t. birulae* appears inside the clade of *S. sungorus* dividing it paraphyletic. The Western lineage (*S. telum* from SE Europe) shares some alleles with Eastern lineage but *S. t. karelini* and *S. t. birulae*, and some alleles are specific.

CHY. Both in the network of alleles (Figure 3) and in the ML tree of unphased sequences (Figure S3, B), the *S. andrewsi* appeared the most compact and homogeneous group which is far distant from other *Stylodipus* spp., while *S. telum* is the most heterogeneous. Most specimens of the western lineage of *S. telum* share one allele with other *S. telum* (but *S. t. karelini* and *S. t. birulae*), and one allele is specific. *S. t. birulae* and *S. t. karelini* tend to group with *S. sungorus* and both have common alleles with it in addition to specific.

THY. *S. andrewsi* appeared the most divergent and demonstrates a tendency to subdivide into two subgroups. *S. t. birulae* grouped with *S. sungorus*. The haplotypes of

Western lineage of *S. telum* and *S. t. karelini* do not form a separate groups and mixed with haplotypes of Eastern lineage except of *S. t. birulae* (Figure 3, Figure S3, C). *DMPI. S. andrewsi* is divergent from all other branchers of *Stylodipus*. *S. t. birulae* groups with *S. sungorus* which shares alleles with *S. t. karelini* (Figure 3). The last one is very polymorphic, it has common alleles not only with *S. sungorus* but also with the West lineage of *S. telum* (see the ML tree of unfased genotypes, Supporting Information Figure S3, D).

Table S7. Sample size and length of alighment used in ML and network reconstructions, and results of allelic phase reconstruction.

gene	Alighment (bp)		N of sequences			N of haplotypes reconstructed by PHASE	N of genotypes found by PHASE
	MI trees	networks	MI trees	networks			
				Sample 1	Sample 2		
IRBP	1152	1058	72	58	42	18	20
CHY	551	459	70	62	61	11	12
THY	547	547	77	75	68	12	17
DMPI	539	539	77	77	64	26	27

Notes: Sample 1: N of sequences used in the allelic phase reconstruction

Sample 2: N of sequences for which allelic phase were determined with adequate posterior probability (>0.8)

Table S8. Number of occurrence points and bioclimatic variables used in modeling in each node and estimation of model's quality.

Node	N records	Bioclimatic variables included in analyses												AUC
		1	2	3	5	6	9	10	11	12	13	15	18	
0	614		+	+	+	+				+		+		0,916
1	608		+	+	+	+				+		+		0,917
2	486		+	+	+	+					+	+		0,922
3	35	+				+	+	+				+	+	0,962
4	451		+	+	+				+		+	+		0,922

Table S9. External and cranial measurements of *Stylodipus* species (modified from Sokolov & Shenbrot, 1987 [42]).

Stylodipus subspecies and locality	Number of measurements (n)	L	C	Pl	Au	M	Number of measurements (n)	CBL	BCWb	IOW	BULL	BULW	M1M3L	m2W
S. andrewsi (Gobi Lakes valley)	37	125.4 0.7	150 1.0	53.1 0.3	17.2 0.1	75.3 1.4	17	31.6 0.2	22.88 0.14	10 0.09	13.65 0.12	11.3 0.08	5.5 0.03	1.95 0.02
S. telum (NE part of Aral region)	20	118.7 1.3	153.7 2.0	49.0 0.3	17.5 0.5	59.5 2.0	25	28.3 0.11	18.97 0.08	8.54 0.09	11.82 0.06	8.49 0.05	5.18 0.02	1.82 0.01
S. sungorus (Mongolian Dzungaria)	7	127.1 1.0	158.3 2.5	56.1 0.4	18.7 0.4	88.1 1.9	24	30.76 0.09	21.12 0.09	9.39 0.08	12.77 0.05	10.19 0.05	5.95 0.03	2.24 0.02
S. birulae (Zaisan basin)	7	119.3 4.3	150.9 2.5	53.6 0.4	16.3 0.5	70.6 4.1	16	29.74 0.13	20.07 0.14	8.55 0.14	12.14 0.1	9.04 0.09	5.42 0.03	1.94 0.01

Notes: Mean values are listed above and standard errors, below. External measurements: L, head&body length; C, tail length; Pl, hind foot length; Au, ear length; M, body mass. Cranial measurements: CBL, condylobasal length; BCWb, braincase breadth (at the front edge of meatus acusticus); IOW, interorbital length; BULL, auditory bulla length; BULW, auditory bulla width; M1M3L, upper molar toothrow length; m2W, m2 width.