

Supplemental Information for:

Chromosomal Evolution in Mole Voles *Ellobius* (Cricetidae, Rodentia): Bizarre Sex Chromosomes, Variable Autosomes and Meiosis

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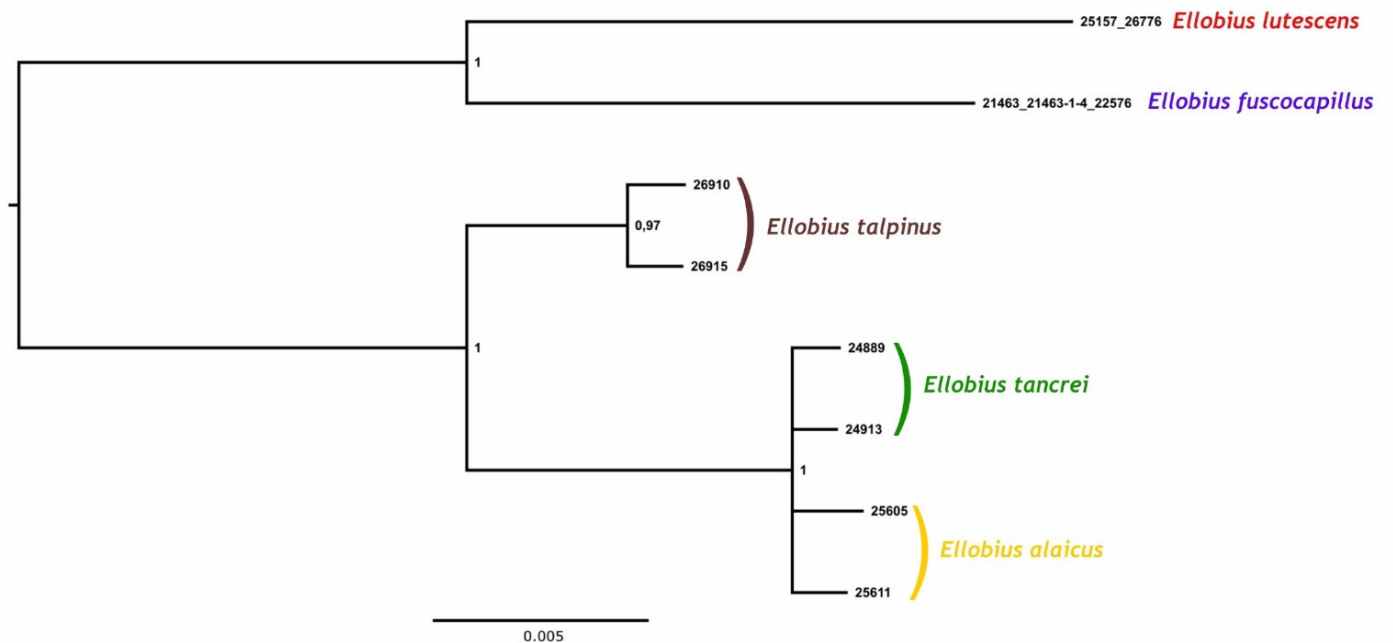


Figure S1. Bayesian inference for the data of the *Eif2s3y* sequences of five *Ellobius* species was evaluated in MrBayes ver. 3.2 (Ronquist et al. 2012). Final phylogenetic trees images were rendered in FigTree 1.4.3. The data were executed with 1 million generations, sampling every 1000 generations, with four independent chains and a burn-in of 25%. Bayesian inference revealed a well-supported tree for all *Ellobius* species, joined into two subgenera.

Reference

Ronquist, F.; Teslenko, M.; Van Der Mark, P.; Ayres, D.L.; Darling, A.; Höhna, S.; Larget, B.; Liu, L.; Suchard, M.A; Huelsenbeck, J.P. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic biology* **2012** 61(3), 539-542.

Table S1. Specificity of the *Sry*, *Eif2s3x* and *Eif2s3y* genes in 5 species of *Ellobius* and GenBank accession numbers

Species	Voucher number	Sex	Genes			
			<i>Sry</i> full HMG-box predicted length 202 bp	<i>Sry</i> fragment of HMG-box, predicted length 144 bp	Fragment of <i>Eif2s3x</i> , predicted length 163 bp	Fragment of <i>Eif2s3y</i>
<i>E. talpinus</i>	26910	♂	—	—	+ 161 bp	452 bp PCR product was represented by two bands after visualization in gel: major fast, with predicted product size 160 bp and minor slow, with predicted product size 700 bp. The sequence is clearly divided into two parts, major is <i>Eif2s3y</i> , and minor is <i>Eif2s3y</i> with intron, like in <i>E. fuscocapillus</i> . Intron includes fragment of SINEs B2-B4. GenBank accession number MF796853
	26915	♀	—	—	+ 161 bp	521 bp PCR product looked as in 26910 GenBank accession number MF796852
<i>E. tancrei</i>	24913	♂	—	—	+ 161 bp	653 bp PCR product looked as in 26910 GenBank accession number MF796855
	24889	♀	—	—	+ 161 bp	589 bp PCR product looked as in 26910 GenBank accession number MF796854
<i>E. alaicus</i>	25611	♂	—	—	+ 161 bp	537 bp PCR product looked as in 26910 GenBank accession number MF796857
	25605	♀	—	—	+ 161 bp	397 bp BLAST to <i>Tokudaia muenninki</i> LC066213.1T, EIF2S3Y pseudogenes: 84.2 max score, 74% identity GenBank accession number MF796856

<i>E. lutescens</i>	26776	♂	—	—	+ 161 bp	616 bp The structure of PCR product was similar to that in 26910, but sequences of both parts had many changes GenBank accession number MF796851
	25155	♀	—	—	+ 161 bp	identical to 26776, 25157
	25157	♂	—	—	+ 161 bp	identical to 26776, 25155
<i>E. fuscocapillus</i>	22576	♀	+ 203 bp GenBank accession number MF787748	+ 138 bp	+ 162 bp	658 bp A specific PCR product about 700 bp divided into two fractions if annealing temperature decreased. An intron was sequenced together with testing fragment of <i>Eif2s3y</i> , about 160 bp. Intron included a fragment similar to SINEs B2-B4. GenBank accession number MF796850
	21463	♀	—	—	+162 bp	identical to 22576
	21463-1 embryo	♀ (?)	—	+ 138 bp	+ 162 bp	identical to 22576
	21463-2 embryo	♂ (?)	—	+	+ 162 bp	identical to 22576
	21463-3 embryo	♀ (?)	—	+ 138 bp	+ 162 bp	identical to 22576
	21463-4 embryo	♂ (?)	—	+ 138 bp	+ 162 bp	identical to 22576

Table S2. Fragments of sequences of *Sry* gene for sex-determining region Y protein and *Eif2s3x*, gene for eukaryotic translation initiation factor 2 subunit 3

Genes	Species, voucher numbers	Sequences
<i>Sry</i> -HMG box 138 bp	<i>E. fuscocapillus</i> 21463_1-4, 22576	GTTGTGGTCTCGTGGTCAGAGGCGCAAGTTGGCCCTGGAGAACCCCAGC ATGCAAAACACAGAAATCAGCAAACAACCTGGGATACCAGTGGAAACGCC TTACAGAAGCCGAAAAAAGGCCATTTTCCAGGAGGCACA
<i>Eif2s3x</i> 162 bp	<i>E. fuscocapillus</i> 21463, 21463_1-4, 22576	AGATCGACCCCACTTTGTGCAGAGCTGACAGGATGGTGGGTCAAGTGCT TGGTGCAGTTGGAGCTTTACCTGAAATATTCACGGAACCTGGAAATTTCC TATTTCTGCTGAGACGTCTCTTGGGTGTACGAACTGAAGGAGACAAGA AAGCAGCAAAGGTCC
<i>Eif2s3x</i> 161 bp	<i>E. lutescens</i> 26776, 25155, 25157 <i>E. talpinus</i> 26910, 26915 <i>E. tancrei</i> 24913, 24889 <i>E. alaicus</i> 25611, 25605	GATCGACCCCACTTTGTGCAGAGCTGACAGGATGGTGGGACAAGTGCTT GGTGCAGTTGGAGCTTTACCTGAAATATTCACGGAACCTGGAAATTTCTT ATTTCTGCTGAGACGTCTCTTGGGTGTACGAACTGAAGGAGACAAGAA AGCAGCAAAGGTCC