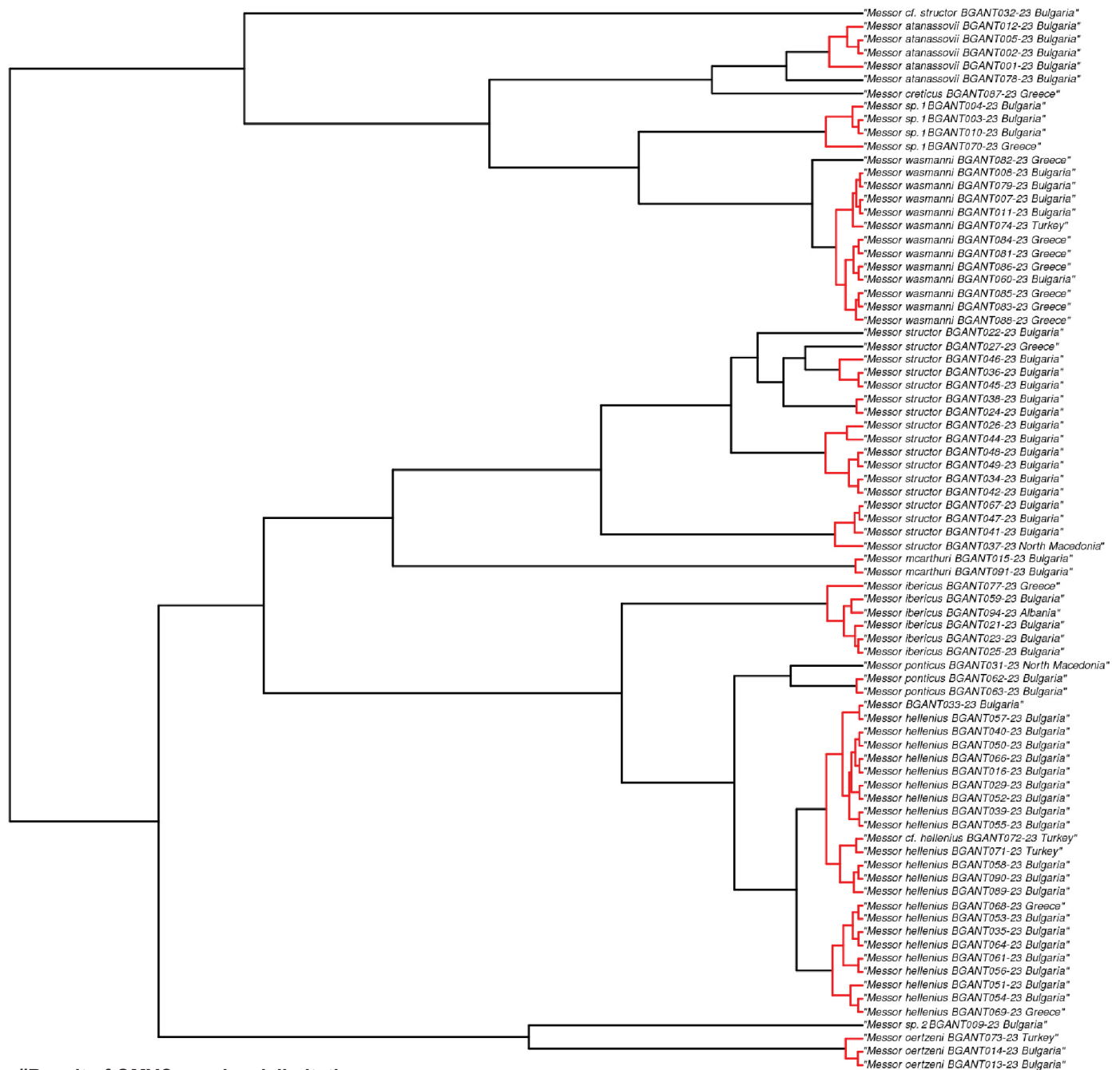
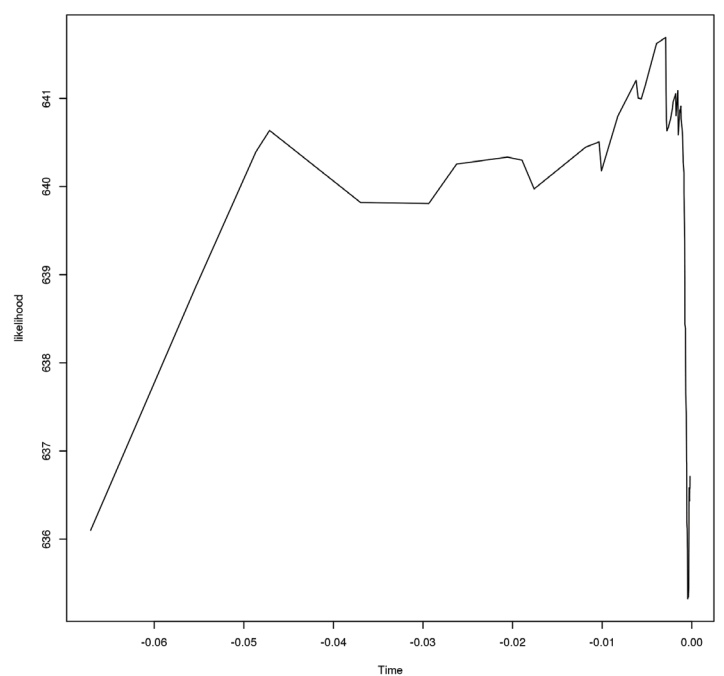
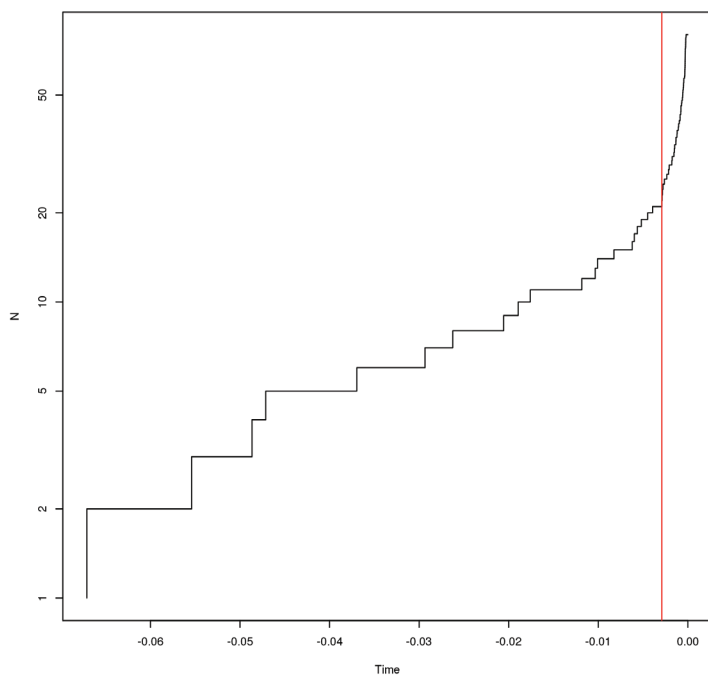


Supplementary materials. COI genetic distance (%) within studied *Messor* species

species	n	min	max
<i>Messor atanassovii</i>	5	0	1.41
<i>Messor</i> sp. 1 (near <i>M. wasmanni</i> )	4	0	0.61
<i>Messor wasmanni</i>	13	0	0.81
<i>Messor oertzeni</i>	3	0	0.15
<i>Messor structor</i>	17	0	5.07
<i>Messor mcarthuri</i>	2	0	0.00
<i>Messor hellenius</i>	24	0	0.99
<i>Messor ponticus</i>	4	0	1.38
<i>Messor ibericus</i>	7	0	0.46

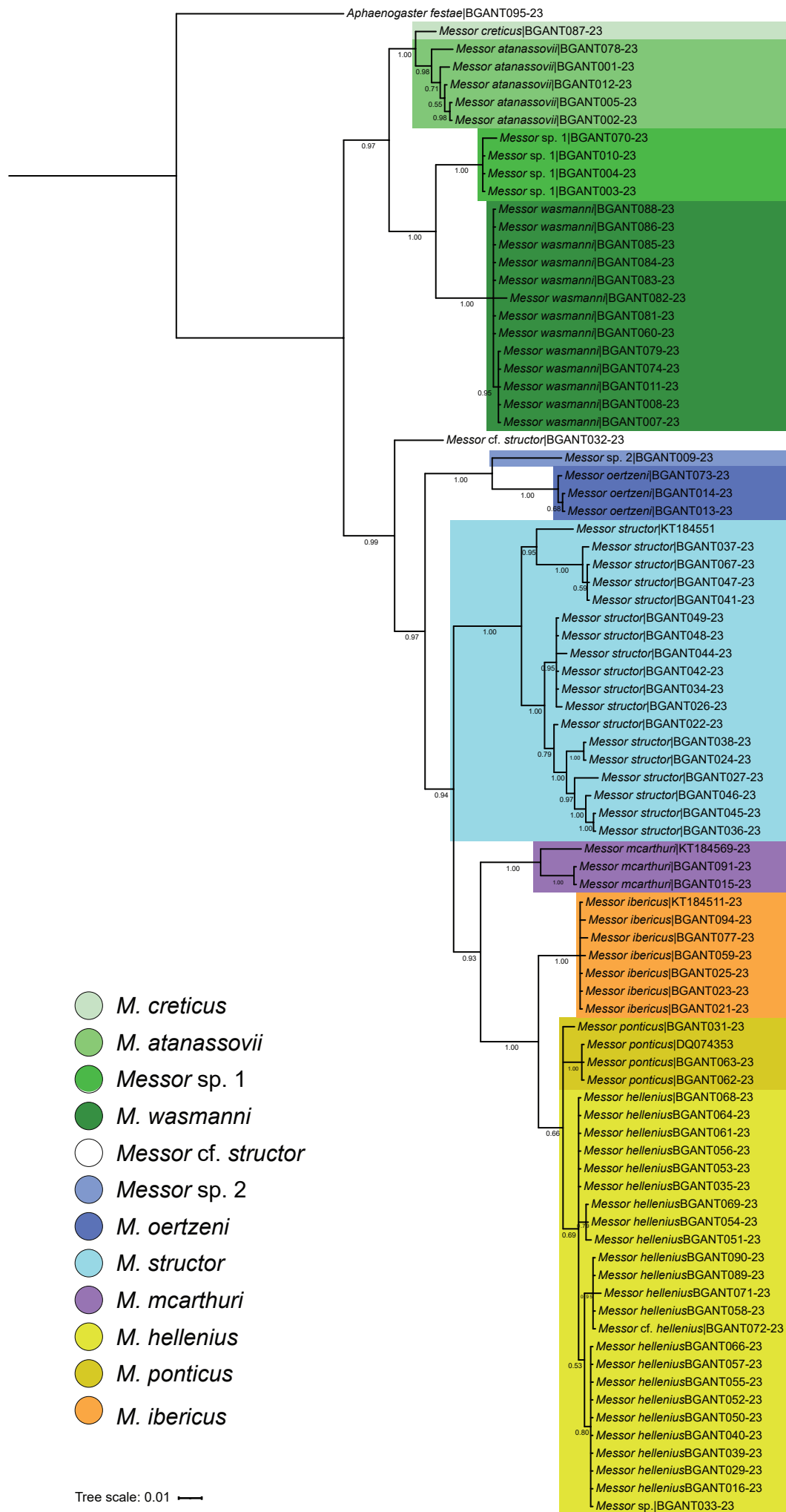
COI genetic distance (%) between *Messor* species under the Kimura 2-parameter model. Values in brackets represent the mean within species distance. NA/n.a.: not available.

N	species	1	2	3	4	5	6	7	8	9	10	11	12
1.	<i>M. creticus</i>	NA (n.a)											
2.	<i>M. atanassovii</i>	1.92	NA (0.74)										
3.	<i>Messor</i> sp. 1 (near <i>M. wasmanni</i> )	5.98	6.28	NA (0.31)									
4.	<i>M. wasmanni</i>	5.80	9.58	5.00	NA (0.18)								
5.	<i>M. oertzeni</i>	9.05	9.40	10.71	10.24	NA (0.10)							
6.	<i>M. structor</i>	8.99	9.18	10.20	10.18	9.22	NA (2.57)						
7.	<i>M. mcarthuri</i>	9.73	9.98	10.14	11.55	8.89	8.49	NA (0)					
8.	<i>M. hellenius</i>	9.50	9.66	10.12	10.88	9.13	8.48	6.47	NA (0.35)				
9.	<i>M. ponticus</i>	9.56	9.64	10.67	11.28	9.40	8.57	7.01	1.63	NA (0.83)			
10.	<i>M. ibericus</i>	9.26	9.48	10.29	10.72	8.93	8.40	6.73	3.20	3.30	NA (0.20)		
11.	<i>Messor</i> cf. <i>structor</i>	7.00	7.61	8.83	9.50	7.94	7.79	7.37	6.19	6.39	6.50	NA (n.a)	
12.	<i>Messor</i> sp. 2 (near <i>M. oertzeni</i> )	10.61	10.64	11.62	11.73	5.72	9.81	9.11	8.88	8.84	9.21	7.38	NA (n.a)



### #Result of GMYC species delimitation

method: single; likelihood of null model: 636.1001; maximum; likelihood of GMYC model: 641.692; likelihood ratio: 11.1838  
 result of LR test: 0.003727933\*\*; number of ML clusters: 13; confidence interval: 3-23; number of ML entities: 21;  
 confidence interval: 3-42; threshold time: -0.002905204



**Phylogenetic tree based on Bayesian inference (BI) analysis of COI gene fragment.**  
 Nodal support is given as posterior probability values. We considered significantly high nodal support for posterior probabilities (PP) > 0.95, and moderately good support for PP > 0.90–0.94.