

Fig. S1. The consensus of trees obtained in three approaches for the alignment of 16S rRNA. Numbers at nodes, in the order shown, correspond to: the number of the trees that contained a given node (NT), posterior probabilities estimated in MrBayes (MB) and PhyloBayes (PB) as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure (SH) and bootstrap method (BP) calculated in IQ-Tree. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-".

NT/MB/PB/SH/BP
3/1/0.99/99/97

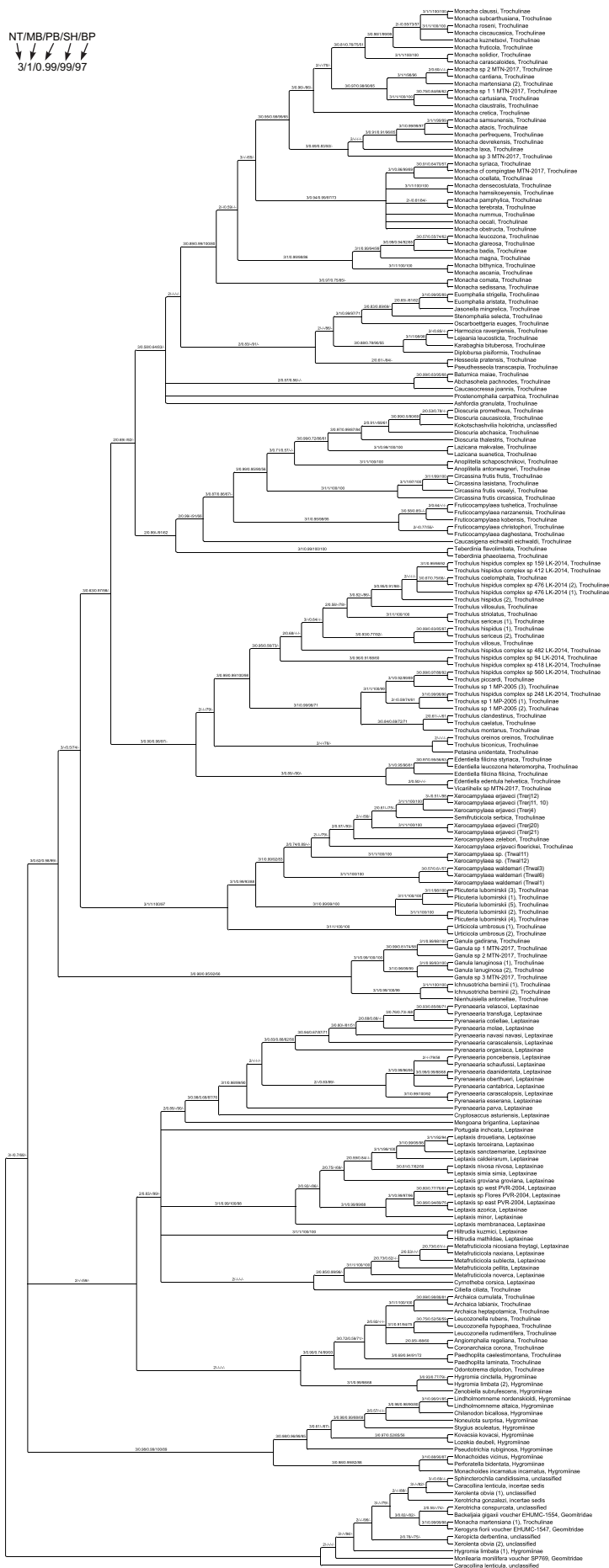
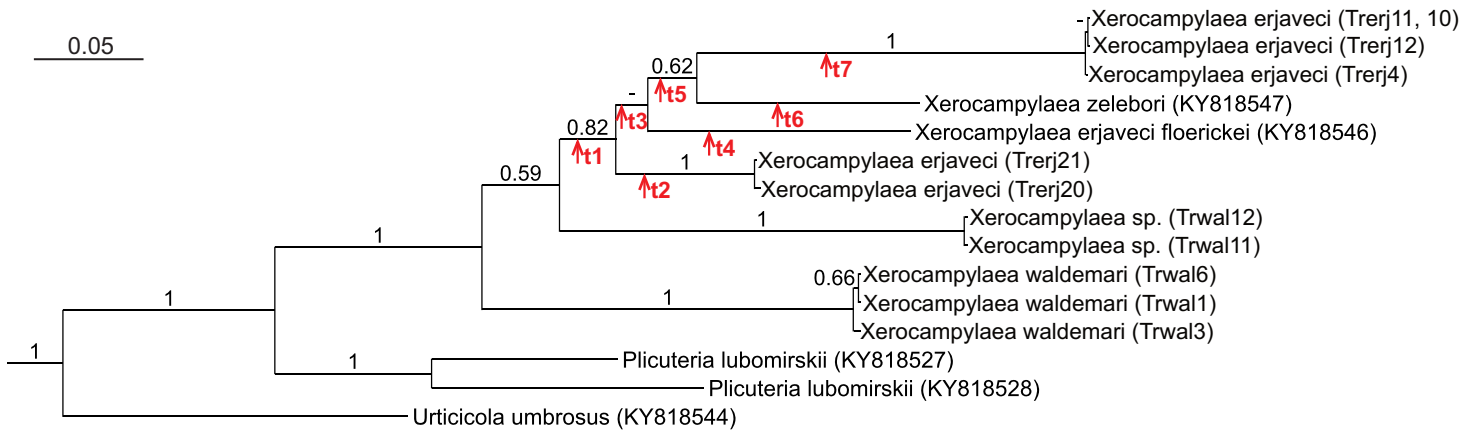


Fig. S2. The consensus of trees obtained in three approaches for the concatenated alignment of 16S rRNA+COI. Numbers at nodes, in the order shown, correspond to: the number of the trees that contained a given node (NT), posterior probabilities estimated in MrBayes (MB) and PhyloBayes (PB) as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure (SH) and bootstrap method (BP) calculated in IQ-Tree. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-". Some sequences annotated as *Monacha* and *Hygromia* are clustered with Geomitridae rather than within their tribes. They should be verified in terms of sample misidentification.

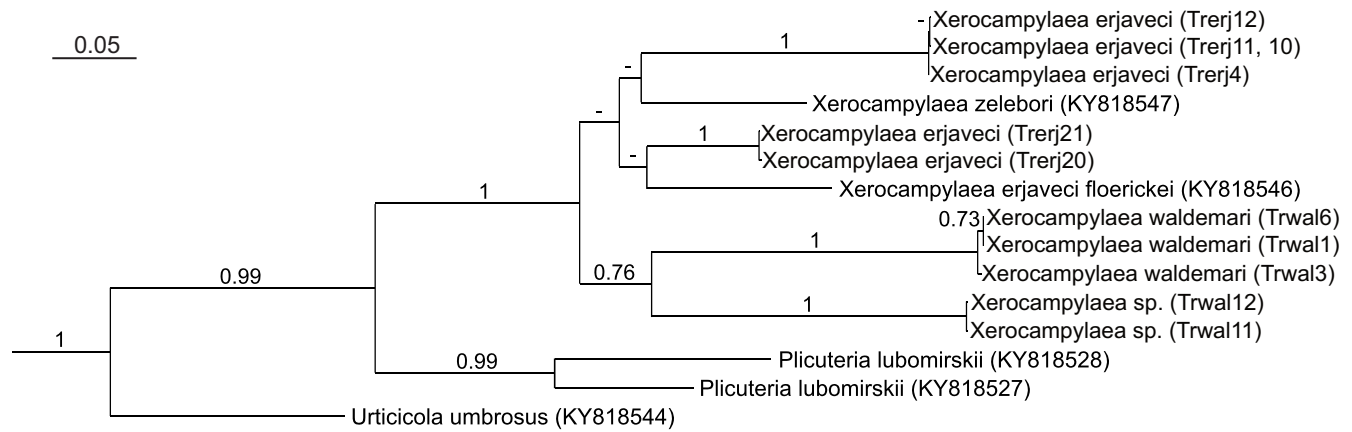
Tab. S3. Results of tests comparing 16S rRNA tree topologies presented in Fig. S3. The topology t0 corresponds to the best tree found in MrBayes and IQ-Tree. The table includes: p-values from an approximately unbiased test (AU), bootstrap probabilities calculated from all sets of scaled replicates (NP) and from one set of replicates (BP), Bayesian posterior probabilities calculated by BIC approximation (PP), p-values from Shimodaira-Hasegawa (SH) and weighted Shimodaira-Hasegawa (wSH) tests as well as Bayes factor (BF) expressed as differences in natural logarithm likelihood units from the best topology (t0). P-values smaller than 0.005 and BF > 3 were highlighted.

Topology	AU	NP	BP	PP	SH	wSH	BF
t0	0.695	0.456	0.456	0.544	0.851	0.862	NA
t1	0.612	0.355	0.354	0.38	0.819	0.807	0.11
t2	0.396	0.085	0.04	0.037	0.662	0.699	3.69
t3	0.151	0.046	0.047	0.001	0.212	0.273	4.36
t4	0.04	0.01	0.01	3.0E-04	0.174	0.269	7.41
t5	0.411	0.084	0.035	0.037	0.663	0.718	8.2
t6	0.15	0.055	0.055	0.001	0.268	0.317	8.85
t7	0.046	0.004	0.004	0.001	0.211	0.284	11.74

MrBayes (t0)



PhyloBayes



IQ-Tree (t0)

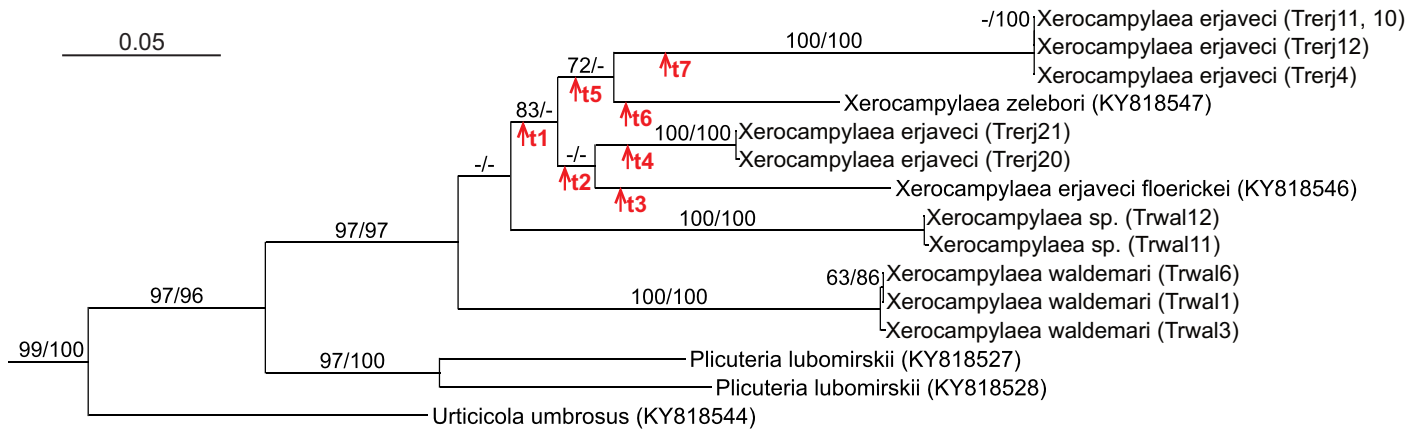


Fig. S3. Selected subtrees obtained in three approaches based on 16S rRNA and showing relationships between analysed samples and their close relatives from tribe Urticicolini. Numbers at nodes correspond to posterior probabilities in MrBayes and PhyloBayes phylogenies as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method in IQ-Tree phylogeny. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-". The arrows indicate the alternative placement of the monophyletic clade including the sequences assigned to *X. waldemari* (Trwal1, 3, 6) and *Xerocampylaea* sp. (Trwal11, 12), which were subjected to statistical testing. The results of this testing are shown in Table S3.

Tab. S4. Results of tests comparing 16S rRNA+COI tree topologies presented in Fig. S4. The topology t0 corresponds to the best tree found in MrBayes and IQ-Tree. The table includes: p-values from an approximately unbiased test (AU), bootstrap probabilities calculated from all sets of scaled replicates (NP) and from one set of replicates (BP), Bayesian posterior probabilities calculated by BIC approximation (PP), p-values from Shimodaira-Hasegawa (SH) and weighted Shimodaira-Hasegawa (wSH) tests as well as Bayes factor (BF) expressed as differences in natural logarithm likelihood units from the best topology (t0). P-values smaller than 0.005 and BF > 3 were highlighted.

Topology	AU	NP	BP	PP	SH	wSH	BF
t0	0.612	0.409	0.409	0.626	0.836	0.839	NA
t1	0.598	0.266	0.265	0.324	0.897	0.898	3.07
t2	0.406	0.107	0.106	0.025	0.871	0.876	7.59
t3	0.396	0.187	0.186	0.026	0.789	0.771	7.66
t4	0.09	0.01	0.01	5.0E-06	0.404	0.394	13.7
t5	0.014	0.001	0.001	5.0E-08	0.24	0.202	16.38
t6	0.005	3.0E-04	3.0E-04	6.0E-10	0.132	0.118	19.17
t7	2.0E-04	4.0E-05	4.0E-05	1.0E-21	0.005	0.003	20.13
t8	0.08	0.023	0.023	3.0E-08	0.255	0.242	19.74
T9	0.004	7.0E-05	6.0E-05	2.0E-09	0.156	0.155	22.29

For the topology t1, Bayes factor is 3.07, i.e. only slightly above the assumed threshold 3 indicating a strong evidence for the better tree found than its alternative (Kass & Raftery, 1995). However, it is not very strong evidence, for which BF > 5 is assumed.

Kass, R. E., & Raftery, A. E. (1995). Bayes Factors. *Journal of the American Statistical Association*, 90, 773–795.

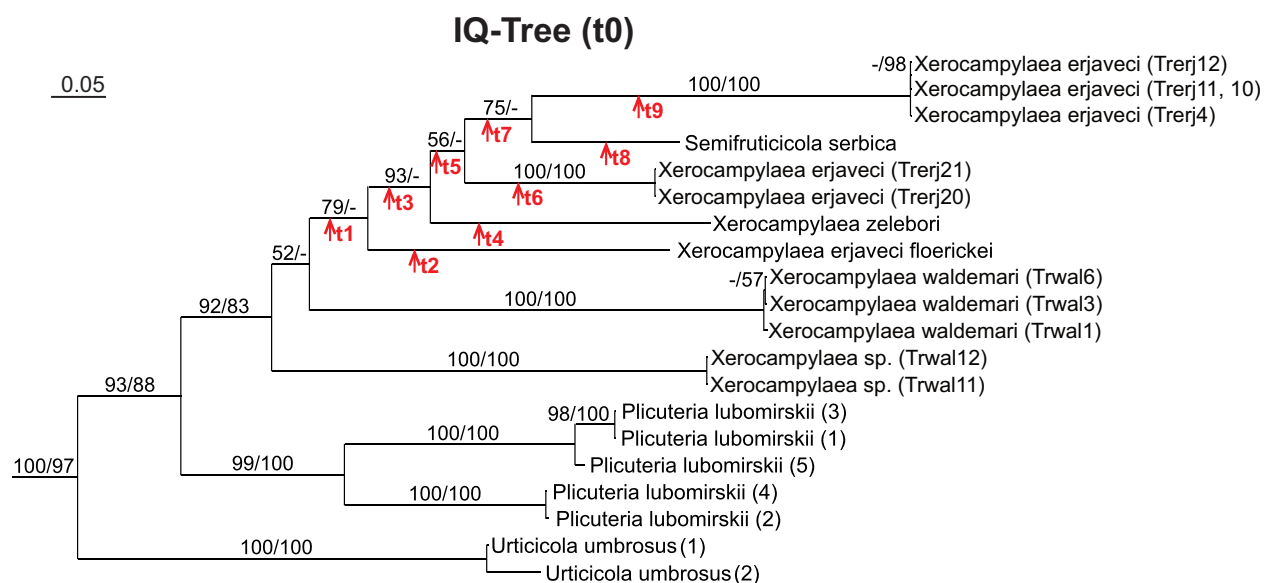
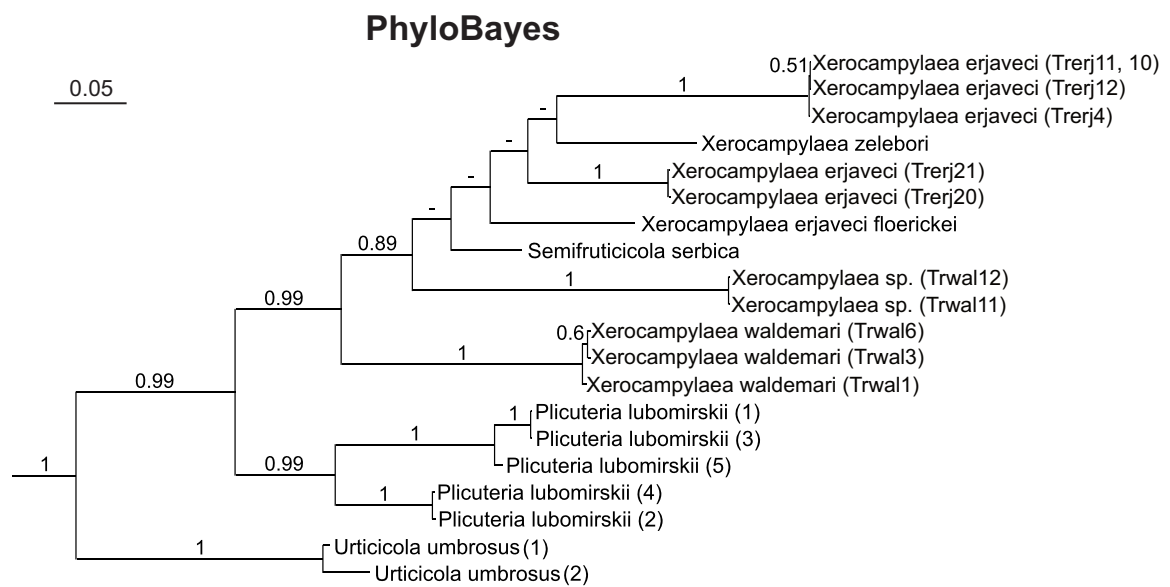
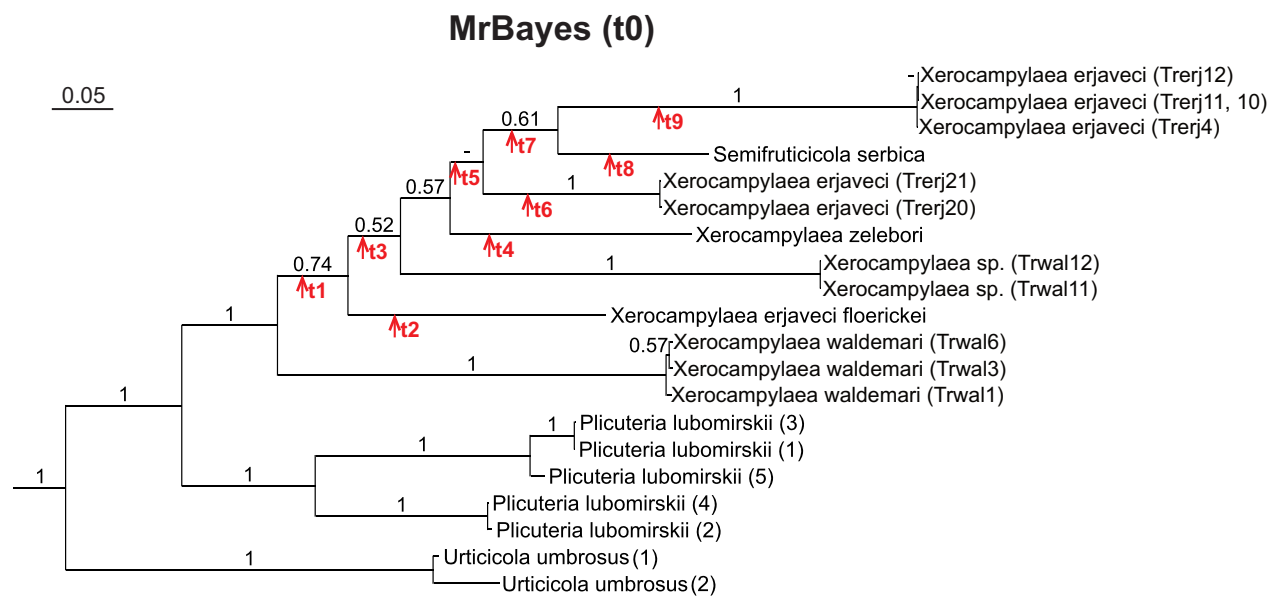


Fig. S4. Selected subtrees obtained in three approaches based on the concatenated alignment of 16S rRNA+COI and showing relationships between analysed samples and their close relatives from tribe Urticicolini. The arrows indicate the alternative placement of the monophyletic clade including all *X. waldemari* samples, which were subjected to statistical testing. The results of this testing are shown in Table S4. Other explanations as in Fig. S3.