

**Molecular phylogeny and classification of *Chelidurella* Verhoeff,  
stat. restit. (Dermaptera: Forficulidae)**

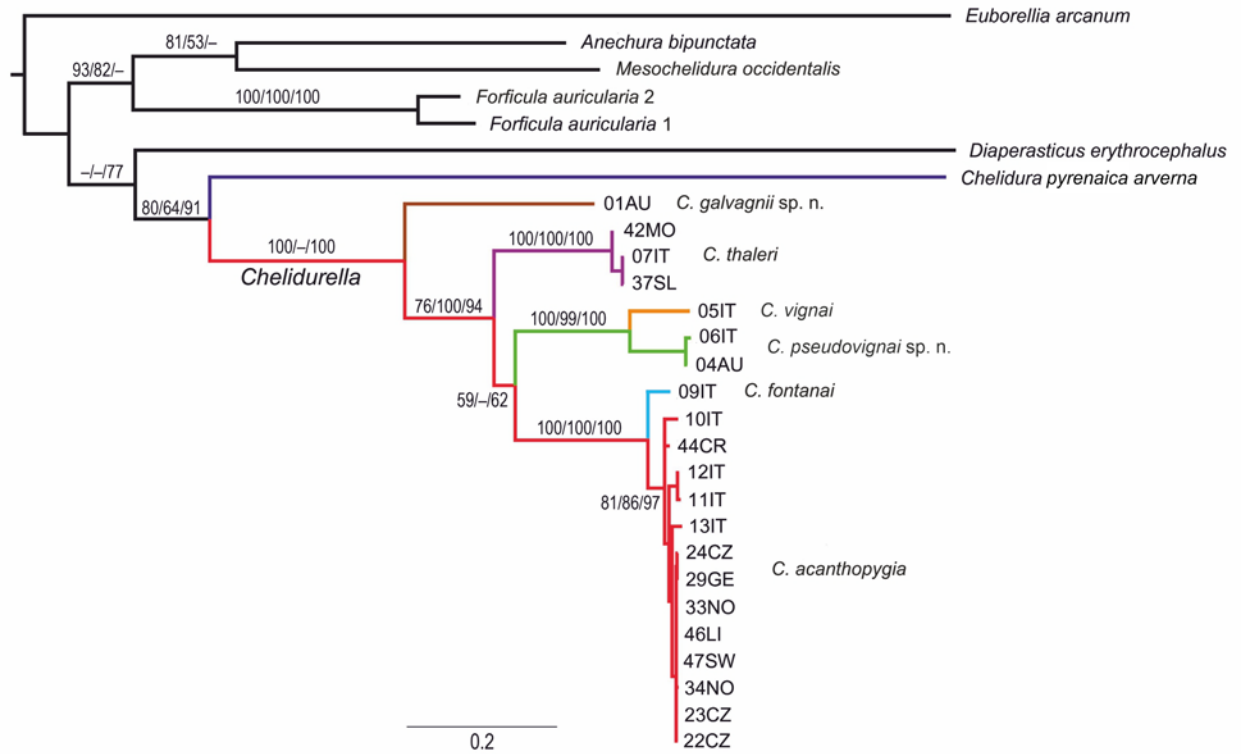
**Markéta Kirstová<sup>a</sup>, Robin Kandrata<sup>b</sup> and Petr Kočárek<sup>a,\*</sup>**

<sup>a</sup>Department of Biology and Ecology, and Institute of Environmental Technologies, Faculty of Science,  
University of Ostrava, Chittussiho 10, CZ 710 00 Slezská Ostrava, Czech Republic

<sup>b</sup>Department of Zoology, Faculty of Science, Palacky University, 17. Listopadu 50, CZ 779 00 Olomouc, Czech  
Republic

\*Corresponding author, e-mail: petr.kocarek@osu.cz

**Supplementary material**



**Fig. S1.** Phylogenetic hypothesis for the *Chelidurella acanthopygia* species complex inferred from the ML analysis of the MUSCLE alignment (28 terminals). Numbers at the branches indicate bootstrap values for the ML and MP analyses and posterior probabilities for the BI analysis, respectively. Only the values above 50% are shown.

**Table S1.** Primers used for the PCR amplifications of the studied genes.

Gene	Code	-mer	Sequence (5' → 3')	Reference
ITS2	CAS5p8sFc	26	TGAACATCGACATTTYGAACGCACAT	Ji et al. 2003
	CAS28sB1d	30	TTCTTTTCCTCCGCCTATTAATATGCTTAA	Ji et al. 2003
12S	SR-J-14199	18	TACTATGTTACGACTTAT	Simon et al. 1994
	MZ-12S-R	20	GCCAGCATTGCGGTTATAC	Mantič & Ševčík 2017
COI	LCO1490	25	GGTCAACAAATCATAAAGATATTGG	Folmer et al. 1994
	HCO2198	26	TAAACTTCAGGGTGACCAAAAAATCA	Folmer et al. 1994

Ji, Y.-J., Zhang, D.-X. & He, L.-J. (2003) Evolutionary conservation and versatility of a new set of primers for amplifying the ribosomal internal transcribed spacer regions in insects and other invertebrates. *Molecular Ecology Notes* **3**: 581–585.

Simon, C., Frati, F., Beckenbach, A., Crespi, B., Liu, H. & Flook, P. (1994) Evolution, weighting and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. *Annals of Entomological Society of America* **87**: 651–701.

Mantič, M. & Ševčík, J. (2017) *Macrocera rohaceki* sp. nov. and other interesting records of Keroplatidae (Diptera) from southern and central Europe, with DNA sequence data. *Acta entomologica Musei Nationalis Pragae* **57**: 751–764.

Folmer, O., Black, M., Hoeh, W., Lutz, R. & Vrijenhoek, R. (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology* **3**: 294–299.

**Table S2.** Summary of the PartitionFinder results. Settings: branch lengths = linked, models of evolution = mrbayes, search algorithm = greedy. Partition scheme in PartitionFinder format = (Gene1\_pos1) (Gene2\_pos1) (Gene3\_pos1) (Gene4\_pos1) (Gene4\_pos2)\*. Criterion= AICc.

\*(Gene1\_pos1) = ITS2, (Gene2\_pos1) = 12S, [(Gene3\_pos1), (Gene3\_pos2), (Gene3\_pos3)] = COI.

Dataset (taxa/aln)	#parameters	#subsets	Model				
			Gene1 pos1	Gene2 pos1	Gene3 pos1	Gene3 pos2	Gene3 pos3
28/MAFFT	96	5	HKY+I	GTR+I+G	HKY+G	GTR+I	GTR+I+G
28/MUSCLE	95	5	HKY+I	GTR+I+G	F81+I+G	GTR+G	GTR+I

**Table S3.** Numbers and types of characters in the analysed datasets. \* COI mtDNA aligned only by MAFFT.

<b>Number of taxa/ Alignment type</b>	<b>Total characters</b>	<b>ITS2 rRNA</b>	<b>12S rRNA</b>	<b>COI mtDNA*</b>	<b>constant</b>	<b>parsimony</b>	
						<b>variable</b>	<b>informative</b>
28/MAFFT	1739	454	627	658	931	755	537
28/MUSCLE	1805	452	695	658	960	749	516

**Table S4.** Results of Xia's nucleotide substitution saturation test in DAMBE, Iss - index of substitution saturation; Iss.c<sup>S</sup> - critical value for symmetrical tree topology; Iss.c<sup>A</sup> - critical value for extremely asymmetrical tree topology; T - T value; DF - degrees of freedom; P<sup>S</sup>, P<sup>A</sup> - probability that Iss is significantly different from the critical value (Iss.c<sup>S</sup> or Iss.c<sup>A</sup>, respectively); P<sub>inv</sub> - proportion of invariable sites.

Marker	/codon pos.	Iss	Iss.c <sup>S</sup>	T	DF	P <sup>S</sup>	Iss.c <sup>A</sup>	T	DF	P <sup>A</sup>	P <sub>inv</sub>
<i>All sites</i>											
ITS2 rRNA	0.322	0.732	10.399	407	0.000	0.606	7.198	407	0.000	0.100	
12S rRNA	0.637	0.731	1.781	563	0.075	0.438	3.785	563	0.000	0.101	
COI mtDNA/1 <sup>st</sup>	0.579	0.613	1.274	215	0.204	0.386	7.268	215	0.000	0.019	
COI mtDNA/2 <sup>nd</sup>	0.180	0.623	13.990	150	0.000	0.413	7.349	150	0.000	0.312	
COI mtDNA/3 <sup>rd</sup>	0.645	0.672	0.537	15	0.560	0.505	2.767	15	0.014	0.929	
<i>Fully resolved sites</i>											
ITS2 rRNA	0.097	0.720	39.120	303	0.000	0.595	31.288	303	0.000	0.100	
12S rRNA	0.282	0.674	14.653	301	0.000	0.385	3.855	301	0.000	0.101	
COI mtDNA/1 <sup>st</sup>	0.572	0.595	0.823	192	0.412	0.378	6.832	192	0.000	0.019	
COI mtDNA/2 <sup>nd</sup>	0.137	0.609	14.952	135	0.000	0.407	8.547	135	0.000	0.312	
COI mtDNA/3 <sup>rd</sup>	0.383	0.668	2.006	13	0.066	0.507	0.869	13	0.401	0.929	

**Table S5.** Maximum uncorrected pairwise distances in *Chelidurella acanthopygia* species complex (%). Clade II = *Chelidura pyrenaica arverna* plus *Chelidurella* complex; *Chelidurella* = Clade II minus *C. aptera*; *C. vignai* = *C. vignai* (05IT) plus *C. pseudovignai* sp. nov. (04AU and 06IT); *C. thaleri* = 42MO, 37SL, 07IT; *C. fontanai* = *C. acanthopygia* including *C. fontanai*. \*distances computed only for 37SL and 07IT.

<b>Taxon</b>	<b>ITS2</b>	<b>12S</b>	<b>COI</b>
Clade II	17.8	33.3	20.8
<i>Chelidurella</i>	4.1	14.9	19.0
<i>C. vignai</i>	0.9	6.5	6.9
<i>C. thaleri</i>	0.0	0.9	0.2*
<i>C. fontanai</i>	0.6	3.9	6.3
<i>C. acanthopygia</i>	0.3	2.7	4.2

**Table S6.** Species entity delimitation of *Chelidurella* genus using the bPTP approach.

<b>PTP entities (support)</b>	<b>Morphological species, geographic origin</b>	<b>Voucher numbers</b>	
1 (0.719)	<i>C. fontanai</i> , Italy, ♂	09IT	
2 (0.715)	<i>C. acanthopygia</i> , Italy, ♂	10IT	
	<i>C. acanthopygia</i> , Italy, ♂	11IT	
	<i>C. acanthopygia</i> , Italy, ♂	12IT	
	<i>C. acanthopygia</i> , Czech Republic, ♂	22CZ	
	<i>C. acanthopygia</i> , Lithuania, ♂	46LI	
	<i>C. acanthopygia</i> , Norway, ♂	33NO	
	<i>C. acanthopygia</i> , Czech Republic, ♂	23CZ	
	<i>C. acanthopygia</i> , Czech Republic, ♂	24CZ	
	<i>C. acanthopygia</i> , Germany, ♂	29GE	
	<i>C. acanthopygia</i> , Switzerland, ♂	47SW	
	<i>C. acanthopygia</i> , Norway, ♂	34NO	
	<i>C. acanthopygia</i> , Italy, ♂	13IT	
	<i>C. acanthopygia</i> , Croatia, ♂	44CR	
	3 (0.856)	<i>C. thaleri</i> , Montenegro, ♂	42MO
		<i>C. thaleri</i> , Slovakia, ♂	37SL
<i>C. thaleri</i> , Italy, ♀		07IT	
4 (1.000)	<i>C. galvagnii</i> sp. nov., Austria, ♂	01AU	
5 (1.000)	<i>C. vignai</i> , Italy, ♂	05IT	
6 (0.961)	<i>C. pseudovignai</i> sp. nov., Austria, ♂	04AU	
	<i>C. pseudovignai</i> sp. nov., Italy, ♂	06IT	