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On the possible synonymy of two *Protracheoniscus* species (Isopoda: Oniscidea): molecular and morphological clues

О возможной синонимии двух видов *Protracheoniscus* (Isopoda: Oniscidea): молекулярные и морфологические аспекты

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КЛЮЧЕВЫЕ СЛОВА: молекулярные маркеры, морфология, разделение видов, синоним, наземные равноногие ракообразные, мокрицы.

ABSTRACT. Two morphologically similar terrestrial isopod species, *Protracheoniscus nogaicus* Demianovitcz, 1932 and *P. darevskii* Borutzky, 1975, are evaluated for possible conspecifity in term of available molecular data using the protein coding mitochondrial gene cytochrome c oxidase I (COI) based on the Iranian and Russian material. The two species are clustered in a same clade on phylogenetic trees. Moreover, the K2P genetic distance between these two nominative species (2.2%) placed within intraspecific variation achieved in congeneric species. Low interspecies genetic distance along with the shallow reported morphological variations, criticizing the distinct position of *P. darevskii*, rather suggested it as a potential synonym of *P. nogaicus*. However, for a firm taxonomic interpretation, fresh material from topotype of *P. nogaicus* has to be explored in an integrative manner.

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РЕЗЮМЕ. С помощью анализа COI по материалу из Ирана и России дана оценка возможной конспецифичности двух морфологически близких видов мокриц, *Protracheoniscus nogaicus* Demianovitcz, 1932 и *P. darevskii* Borutzky, 1975. Оба вида размещаются в одной и той же кладе филогенетических деревьев. Более того, генетическая дистанция K2P между этими видами (2,2%) укладывается во внутривидовую изменчивость, показанную для соседних видов рода. С учетом этого обстоятельства, а также морфологической изменчивости *P. darevskii*, скорее всего, является потенциальным младшим синонимом *P. nogaicus*. Для окончательного решения этого вопроса необходимо интегративное исследование свежего материала из типовой местности *P. nogaicus*.

Introduction

Terrestrial isopods of the genus *Protracheoniscus* Verhoeff, 1917 include 62 species [Boyko *et al*., 2008 onwards], broadly distributed in the Palearctic and Oriental regions [Kashani, Hamidnia 2016]. A major portion of the known isopods have been recorded only from their type localities, in contrast some species are intensively distributed (e.g. *P. major*, *P. politus*, etc.) occupying an over larger area [Schmalfuss, 2003].

During recent decades, a huge dynamic has been made in identification and classification of many animal taxa employing new techniques related with DNA markers [Pečnikar, Buzan, 2014]; however, little is done on the terrestrial isopods in Iran and adjacent territories.

Eight species of the genus *Protracheoniscus* have been previously reported from Iran [Kashani, 2018]. One of them, *Protracheoniscus darevskii*, originally was identified in Meghri district, southern Armenia [Borutzky, 1975] (Fig. 1) and further records were documented from Iran [Kashani, 2014]. Borutzky

Fig. 1. Sampling localities of the specimens examined in the present study. *Protracheoniscus darevskii* (triangles), *P. nogaicus* and *P. pokarzhevskii* (asterisk), *P. major* (rectangles) and *P. kryszanovskii* (circle). Hollow triangle indicates the type locality of *P. darevskii*.

Рис. 1. Местонахождения образцов, изученных в данной работе. *Protracheoniscus darevskii* (треугольники), *P. nogaicus* and *P. pokarzhevskii* (звездочка), *P. major* (прямоугольники) and *P. kryszanovskii* (кружок). Контурный треугольник обозначает типовое местонахождение *P. darevskii*.

[1975] noticed the similarity of *P. darevskii* and *P. nogaicus*; the latter has been described from Moldova [Demianovitcz, 1932], but assigned it to a distinct species concerning to the following demarcations: "the position of the noduli laterales on pereon-segments I–IV are a little further apart than those in *P. nogaicus*, and the structure of pleopod endopodite I of male, in which the apical lobe is not tender and transparent, but chitinized and equipped with stronger teeth on the inner edge; the outer edge is folded, not flat. In addition, pereopod VII meropodite of the male in *P. darevskii* contain a large rounded swelling, which is much less developed in *P. nogaicus*" (see Figs 2–4). Khisametdinova [2014] and Gongalsky *et al.* [2018] identified the specimens collected from the Rostov Region and Republic of Kalmykia, Russia as *P. nogaicus*; the latter authors submitted the COI sequence of one of the specimens as well as of some other species in GenBank.

As a general trend in modern taxonomy, combination of various types of information has led researchers intensively to define the taxonomic status of the specimens under study, precisely [Song *et al*., 2020]. Therefore, a preexisting taxonomic name could truly be assigned to the individuals of a given species [Mahmoudi, Kryštufek, 2020]. In this study, specimens of *P. darevskii* from Iran were explored both for morphology and COI gene, then were compared with morphological information for *P. nogaicus* obtained from its original description [Demianovitcz, 1932] and COI sequence downloaded from GenBank (cf. Gongalsky *et al*. [2018]). The aim of the present study was to provide pieces of morphologic and molecular evidences about taxonomic position of *P. darevskii* and *P. nogaicus*; whether they are really distinct species or belong to a single species.

Material and methods

The morphologically studied isopods here come from different localities in northwestern Iran. For accurate identification of the isopods, almost twenty male specimens from different localities were explored under stereomicroscope, prepared into microscopic slides and compared with all characteristic variables presented in the literatures for *P. darevskii* and its most similar species, *P. nogaicus* [Demianovitcz, 1932; Borutzky, 1975; Kashani, 2014] (for detail comparison cf. Figs 2–4).

For molecular analysis, two specimens from Uremia and Bostanabad identified as *P. darevskii* were used (Fig. 1, Table 1). Genomic DNA was extracted from the isopod's legs preserved in 96% ethanol using the Qiagen method (DNeasy tissue kit, Qiagen, Hilden, Germany). The partial mitochondrial cytochrome oxidase c subunit I (COI) gene was amplified using the universal primers; HCO2198/LCO1490 [Folmer *et al*., 1994] under following condition: initial denaturation for 3 min at 95 °C, followed by 34 cycles of 30, 40 and 50 seconds at 94 °C, 46 °C and 72 °C, respectively, and a final extension step of 72 °C for 10 min. PCR products were purified using QIA quick PCR purification Kit (Qiagen), following manufacturer's instructions, and were sequenced using a dye-labelled dideoxy terminator cycle sequencing with Big Dye V.3.1 (Applied Biosystems, Inc).

The raw sequences of the forward and reverse primers were checked by CodonCode Aligner software (CodonCode Corp.) in order to solve the ambiguous sites and obtain the consensus alignment. The final alignment of 682bp of COI gene was performed using Clustal X algorithm implemented in BioEdit v.7 [Hall, 1999]. The sequences were checked for the absence of premature stop-codons, insertion and deletion using MEGA v7.0 [Kumar *et al*., 2016]. Genetic divergence between and within species were estimated assuming both Pure (P-distance) and Kimura 2-parametr (K2P) models. The General Time-Reversible (GTR+I+G) model was determined as the most appropriate model for DNA substitution based on the Akaike Information Criterion (AIC) using jModeltest 0.1.1 [Posada, 2008]. Phylogenetic tree was constructed using two probabilistic algorithms, Bayesian inference (BI) and Maximum Likelihood (ML) analyses. BI analysis was conducted in MrBayes v3.2 [Ronquist *et al*., 2012]. Two independent analyses were performed with a four Markov Chain Monte Carlo (MCMC) model, which started from random trees and were run for 2×10^6 generations. The trees were sampled every 100th generation after the first 20% of trees were discarded as burn-in. The ML analysis was performed using RAxML v.8.2.10 [Stamatakis, 2014] with the bootstrap values (ML-BS) obtained from 1000 replicates. Nodal supports for ML analysis were estimated using 1000

Table 1. List of specimens, locality and accession numbers of the sequences for COI mtDNA. References are given for sequences obtained from GenBank.
Таблица 1. Список образцов, местонахождений и номеров сиквенсов COI мДНК, полученных из GenBank.

Species	Locality	Accession number	Reference
Protracheoniscus major (Dollfus, 1903)	Iran, Qeydar, 25 km to Zarrin-Rood (35.949N, 48.570E) 8.09.2016, leg. G.M. Kashani		This study
Protracheoniscus major (Dollfus, 1903)	Iran, Malayer, Saman City (34.217N, 48.711E) 9.09.2016, leg. G.M. Kashani		This study
Protracheoniscus major (Dollfus, 1903)	Russia, Republic of Kalmykia, 1 km N of Bolshoy Tsaryn (47.9040N, 45.3929E) 29.04.2017, leg. K. Gongalsky	MH400726	Gongalsky *et al*. [2018]
Protracheoniscus darevskii Borutzky, 1975	Iran, Urmia, 58 km to Mahabad (37.132N, 45.440E) 4.10.2008, leg. G.M. Kashani		This study
Protracheoniscus darevskii Borutzky, 1975	Iran, Bostanabad, Oshdologh village (38.013N, 46.980) 30.07.2016, leg. G.M. Kashani		This study
Protracheoniscus nogaicus Demianowicz, 1932	Russia, Republic of Kalmykia, 1 km N of Bolshoy Tsaryn (47.9040N, 45.3929E) 29.04.2017, leg. K. Gongalsky	MH400724	Gongalsky *et al*. [2018]
Protracheoniscus kryszanovskii Borutzky, 1957	Russia, Republic of Kalmykia, 1 km W of Tsagan Nur, bank of lake Sarpa (47.362N, 45.201E), 27.04.2017, leg. K. Gongalsky	MH400727	Gongalsky *et al*. [2018]
Protracheoniscus politus (C. Koch, 1841)	Hungary, Budapest, Janos Hegy Mt. (47.5158N, 18.9602E) 29.08.2017, leg. K. Gongalsky	MG696252	Gongalsky *et al*. [2018]
Protracheoniscus pokarzhevskii Gongalsky and Turbanov, 2018	Russia, Republic of Kalmykia, 1 km N of Bolshoy Tsaryn (47.9040N, 45.3929E) 29.04.2017, leg. K. Gongalsky	MG696253 MH400723	Gongalsky *et al*. [2018]
Burmoniscus kathmandius (Schmalfuss, 1983)	Nepal	LC075192	Karasawa [2016]
Ligia baudiniana Milne-Edwards, 1840	Colombia	KF555872	Santamaria *et al*. [2014]

non-parametric bootstrap (BP) replicates, and Bayesian posterior probabilities (BPP) were used to assess branch support of the BI tree.

To assess the phylogenetic relationships of *P. darevskii* (present study; accession number: pending) within the genus *Protracheoniscus* accurately, eight more COI sequences belonging to five species were downloaded from GenBank and/or obtained from the present study: *P. nogaicus* (MH400724), *P. kryszanovskii* (MH400727), *P. major* (MH400726 and present study; accession number: pending), *P. politus* (MG696252) and *P. pokarzhevskii* (MG696253, MH400723) [Gongalsky *et al*., 2018]. *Ligia baudiniana* (KF555872) and *Burmoniscus kathmandius* (LC075192) were used as outgroups (Table 1).

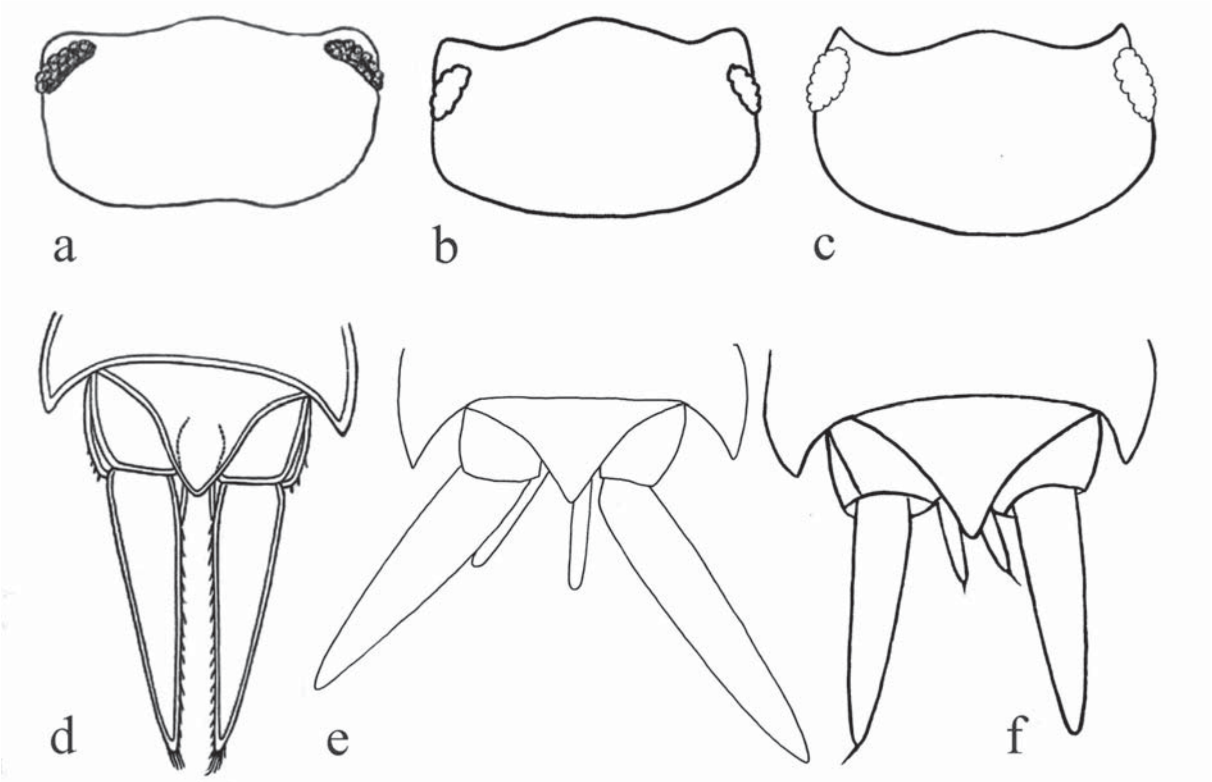

Fig. 2. *Protracheoniscus nogaicus* / *darevskii*: a–c — head, dorsal view; d–f — telson and uropods. Sources: a — Borutzky [1975]; b, e — Kashani [2014]; d — Demianovitcz [1932]; c, f — original.

Рис. 2. *Protracheoniscus nogaicus* / *darevskii*: a–c — голова, дорсально; d–f — тельсон и уроподы. Источники: a — Боруцкий [Borutzky, 1975]; b, e — Kashani [2014]; d — Demianovitcz [1932]; c, f — ориг.

Results

Comparing morphologic diagnostic characters of the specimens from different localities in Iran [Kashani, 2014 and the present study] with those presented in the original descriptions and illustrations for *P. darevskii* and *P. nogaicus* in Borutzky [1975] and Demianovitcz [1932] revealed no distinctive differences (Figs 2–4). Due to the vicinity of some sampling sites in Iran to the type locality of *P. darevskii* in Armenia (Fig. 1 and unpublished data), the specimens from Iran assigned to *P. darevskii*.

In molecular analysis, the BI and ML trees gave very similar topologies; therefore only the ML tree is shown (Fig. 5). The specimens from Uremia and Bostanabad, identified as *P. darevskii*, were clustered in a same clade with *P. nogaicus* from Russia, and did not hold a specific position on its own. Accordingly, the COI gene analyses did not support *P. darevskii* (Iran) and *P. nogaicus* (Russia) distinct positions (Fig. 5). The intraspecies K2P genetic distance for the analyzed *Protracheoniscus* species in the present study varied between 0.2–4.2%, while interspecies K2P distance ranged from 16.0–26.0%. Genetic divergence between *P. darevskii* and *P. nogaicus* (2.2%) was really low, being at least eight times smaller than the ranges observed between congeneric species (Table 2).

Discussion

The present study is the first attempt on molecular justification of *P. darevskii* and *P. nogaicus*; two species that were considered the most similar within the genus *Protracheoniscus* [Borutzky, 1975]. The COI phylogenetic tree did not support distinct position of *P. darevskii* haplotypes from Iran comparing to a single haplotype of *P. nogaicus* available in GenBank [Gongalsky *et al*., 2018], rather showed the two species belong to a same clade (BPP=1.00, BP=100) (Fig. 5). The shallow pairwise genetic distance between *P. darevskii* from Iran and *P. nogaicus* from Russia (0.8–3.7%) placed within the range of intraspecific divergence in terrestrial isopods (e.g. Cooper *et al*. [2008]; Hurtado *et al*. [2010, 2013]; Eberl *et al*. [2013]; Lee *et al*. [2014]; Niikura *et al*. [2015]; Zimmermann *et al*. [2015]; Santamaria *et al*. [2017]). These findings clearly demonstrated that the analyzed specimens from Russia and Iran belong to the same species. However, one should take into account that there could be two scenarios for explaining these results: i) the single COI sequence (MH400724) from Russia might belong to *P. darevskii*, but misidentified/mislabeled as *P. nogaicus*; ii) *P. nogaicus* and *P. darevskii* belong to the same species with some usual character variability expected to be present in broadly distributed species. As we

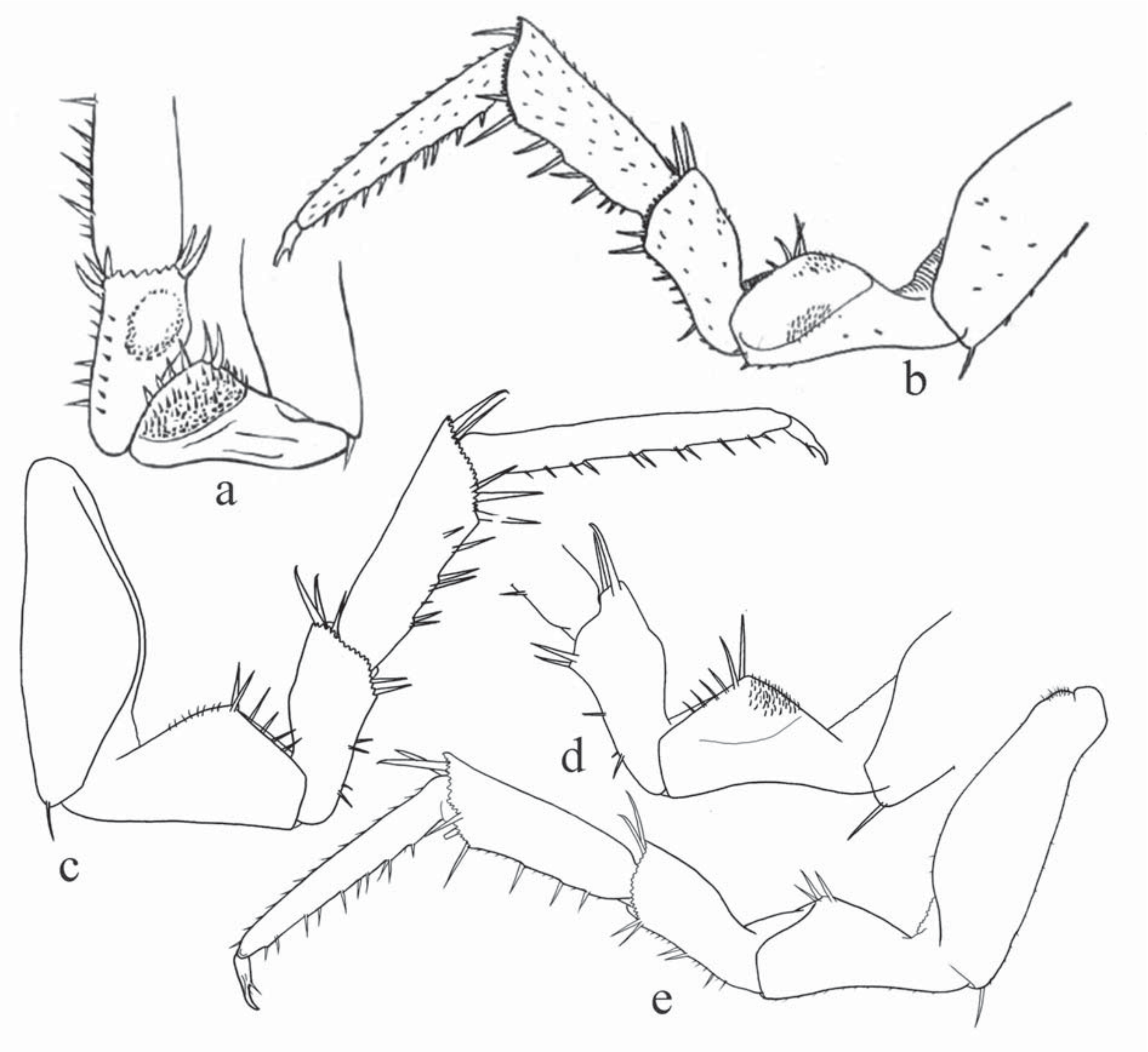

Fig. 3. *Protracheoniscus nogaicus* / *darevskii*, pereopod VII. Sources: a — Borutzky [1975]; b — Demianovitcz [1932]; c, d — Kashani [2014]; e — original.

Рис. 3. *Protracheoniscus nogaicus* / *darevskii*, переопод VII. Источники: a — Боруцкий [Borutzky, 1975]; b — Demianovitcz [1932]; c, d — Kashani [2014]; e — ориг.

were not able to provide sequences neither from the type series nor from topotypes for *P. nogaicus*, here we do not advocate any of the interpretations, rather suggesting a comprehensive study with adding some specimens from type material to the analyses to provide a clear cut off regarding the species boundaries and taxonomic affiliations of given species.

In conclusion, performing molecular analyses would possibly trigger huge taxonomic dynamics within isopods which is of upmost importance both for taxonomic and conservation concerns.

Disclosure statement

No potential conflict of interest was reported by the authors.

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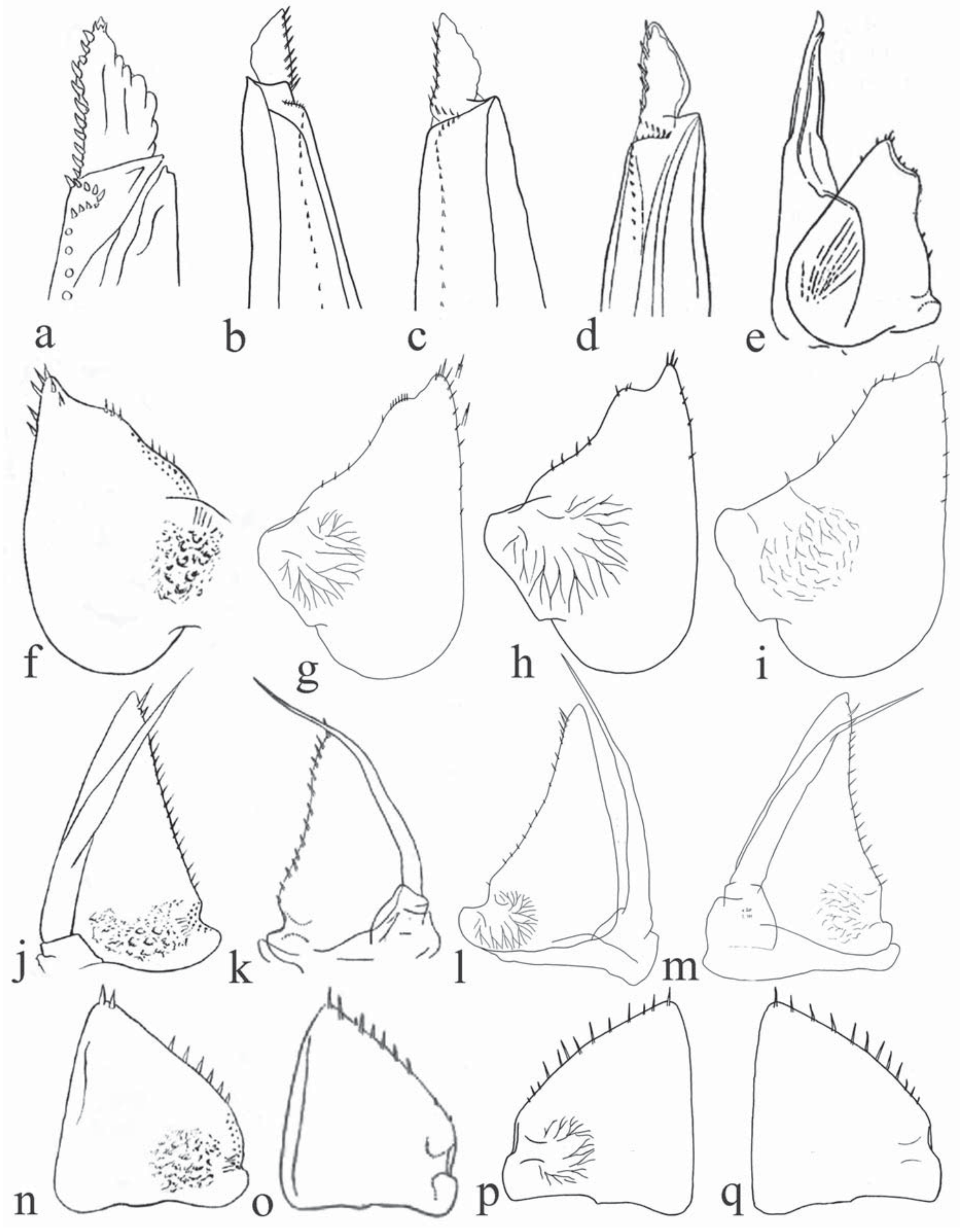

Fig. 4. *Protracheoniscus nogaicus* / *darevskii*: a–d — pleopod endopodite I, enlarged apex; e–i — pleopod exopodite I, j–m — pleopod II; n–q — pleopod exopodite V. Sources: a, f, j, n — [1975]; b, g, h, l, p — Kashani [2014]; c, i, m, q — original; d, e, k, o — Demianovitcz [1932]. Note the variability in the shape of pleopod exopodite I outer lobe.

Рис. 4. *Protracheoniscus nogaicus* / *darevskii*: a–d — эндоподит плеопода I, увеличенное окончание; e–i — экзоподит плеопода I, j–m — плеопод II; n–q — экзоподит плеопода V. Источники: a, f, j, n — Боруцкий [Borutzky, 1975]; b, g, h, l, p — Kashani [2014]; c, i, m, q — ориг.; d, e, k, o — Demianovitcz [1932]. Обратите внимание на изменчивость формы внешней лопасти экзоподита плеопода I.

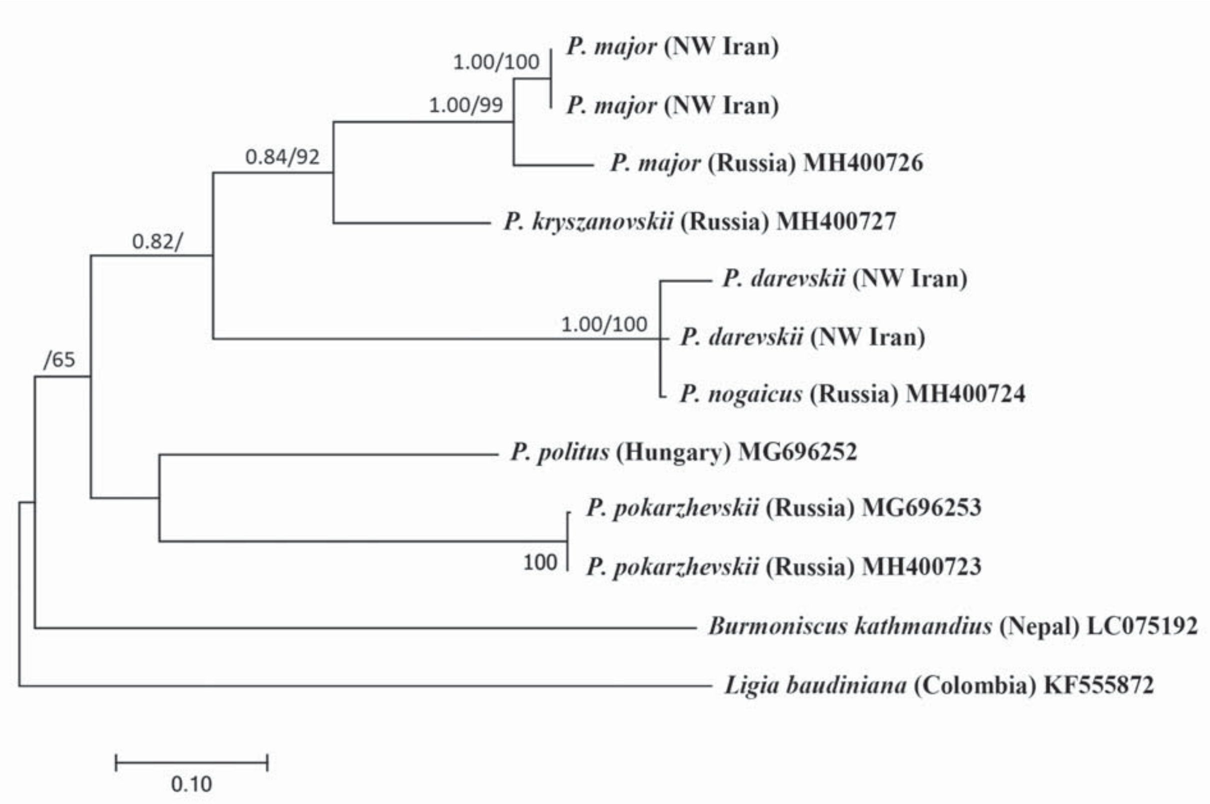

Fig. 5. Maximum Likelihood tree summarizing phylogenetic relationships of *Protracheoniscus* based on COI sequences. The first and second numbers on the branches correspond to posterior probability (BPP) and bootstrap (BP) values in the BI and ML tree analyses, respectively (supports <65 are not shown).

Рис. 5. Дерево, построенное по принципу максимального правдоподобия (Maximum Likelihood), суммирующее филогенетические отношения видов *Protracheoniscus* на основании сиквенсов COI. Первые и вторые номера на ветвях соответствуют оценкам апостериорной вероятности (BPP) и бутстрепа (BP), соответственно, в BI- и ML-анализе деревьев (поддержки менеех <65 не показаны).

Table 2. The K2P inter-species genetic divergence among the nominative species of the analyzed isopods is shown below the diagonal. Uncorrected p-distance is shown on above diagonal. Numbers on diagonal refer to the intra-species divergence in bold.

Таблица 2. Межвидовое генетическое расстояние K2P между проанализированными видами изопод показано под диагональю. Нескорректированная p-дистанция показана над дианональю. Показатели по диагонали отражают внутривидовую изменчивость (даны полужирным шрифтом).

Species	**1**	**2**	**3**	**4**	**5**	**6**
1. *P. darevskii*	**3.7±0.7**	2.1±0.4	19.1±1.4	20.9±1.6	20.5±1.5	21.7±1.4
2. *P. nogaicus*	2.2±0.4	***	19.3±1.5	20.6±1.6	20.3±1.5	21.3±1.4
3. *P. major*	22.4±1.9	22.6±1.9	**4.2±0.7**	14.2±1.3	21.1±1.4	20.9±1.5
4. *P. kryszanovskii*	24.7±2.2	24.4±2.1	16.0±1.7	***	18.8±1.4	19.6±1.5
5. *P. politus*	24.2±2.1	23..8±2.0	25.1±2.1	21.8±2.0	***	19.3±1.5
6. *P. pokarzhevskii*	26.0±2.1	25.4±2.1	24.7±2.1	22.8±2.4	22.5±2.2	**0.2±0.02**

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