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Morphological redescription and DNA barcoding of *Linevitshia prima* Makarchenko, 1987 (Diptera: Chironomidae: Diamesinae) from Amur River basin (Russian Far East), with notes on systematics of the genus

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Abstract

Additions and corrections to the diagnosis of the genus *Linevitshia* for male adult, pupa and larva are given, and systematic position of the genus is discussed. Illustrated redescription of adult male and first description of 4th instar larva of *L. prima* Makarchenko from Amur River basin are provided. Comparison of data based on a new material with those of *L. yezoensis* Endo showed that the latter name is a junior synonym of *L. prima*. The species-specificity of *L. prima* COI sequences is analyzed and the sequences are presented as diagnostic characters—molecular markers of *L. prima*.

Key words: Diptera, Chironomidae, *Linevitshia,* taxonomy, redescription, DNA barcoding, Russian Far East

Introduction

The genus *Linevitshia* Makarchenko was established for *L. prima* Makarchenko, the species described from the southern part of Russian Far East (Makarchenko 1987). First, the genus was placed in the subfamily Podonominae, partly due to the incompletely developed wing vein R_{2+3} in the freshly emerged specimens originally described. Later, however, K. Endo collected very similar midges in Hokkaido with distinct R_{2+3}. The male genitalia of these Japanese specimens differ slightly from *L. prima*, thus were described as *L. yezoensis* Endo, 2007, and consequently, the genus *Linevitshia* was provisionally transferred from the Podonominae to the Diamesinae (Endo *et al.* 2007). It was shown also that the genus *Linevitshia* and *Protanypus* Kieffer are closely related based on adult morphology, namely by complex of setae on pronotum (median and lateral Aps present) and mesonotum—Ac and Dc stripes connected in base, setae present on PAII and EII, and the presence of setae on alula of wing in adult males. This opinion was supported after examination of pupal morphology of *L. yezoensis* later (Makarchenko & Endo 2009).

In April 2014 we have got new materials consisted of adult males, pupae and larvae of *L. prima* from Amur River basin, including some males and larvae treated in DNA barcoding analysis. Characters of the *Linevitshia* larva, here described for the first time in the genus, confirm close relations to those of *Protanypus*, as was shown earlier for pupae and adults (Makarchenko & Endo 2009). Comparison of data based on a new material with those of *L. yezoensis* showed that the latter must be synonymized with *L. prima*. Additions and corrections to diagnoses for male adults, pupa and larva of the genus *Linevitshia* are also given, and systematics of the genus is discussed. The species-specificity of *L. prima* COI sequences is shown. These sequences could be used in future as diagnostic characters—molecular markers of *L. prima*.

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TABLE 1. Lengths (in μm) and proportions of leg segments of *Linevitshia prima* Makarchenko, male (n = 4).

	fe	ti	ta_1	ta_2	ta_3
P_1	1168–1336	1376–1520	960–1069	451–518	301–351
P_2	1152–1269	1269–1403	560–618	304–359	217–251
P_3	1376–1503	1664–1787	832–935	464–534	272–301

continued.

	ta_4	ta_5	LR	BV	SV
P_1	200–288	150–160	0.68–0.70	2.74–3.28	2.65–2.76
P_2	142–150	134–150	0.44–0.46	3.67–4.12	4.20–4.34
P_3	167–184	150–167	0.50–0.52	3.56–3.61	3.52–3.65

Results of DNA barcoding

The final alignment of the COI gene yielded 686 bp for 4 individuals of *L. prima* that were 4 haplotypes. The nucleotide composition of the studied sequences of *L. prima* COI gene fragments deviated from an equilibrium one, comprising 25.8 % of A, 36.6 % of T, 20.0 % of C, and 17.6 % of G. Total pairwise sequence divergence within *L. prima* ranged from 0.0015 to 0.0029, which is based on three nucleotide substitutions. All the substitutions were synonymous transitions (A-G) and observed only in the third codon positions. The HKY (Hasegawa, Kishino, & Yano 1985) model was the best-fit in describing the pattern of nucleotide variation in the *L. prima* COI sequences.

Average intergenus P-distance between *L. prima* and other genera of the subfamily Diamesinae showed the following results: *Potthastia* Kieffer (JF287767)—15.9%, *Pseudodiamesa* Goetghebuer (JF764760, JF764764, JF764771)—16.7%, *Pagastia* Oliver (JF287653)—17.2%, *Diamesa* Meigen (AB704934)—17.4%, *Sympotthastia* Pagast (JF288065)—18.2%. High differences between the groups can argue genus independence of *Linevitshia* (Ekrem *et al.* 2007).

Distribution and biology. East Palaearctic species, known from Japan, China and the Russian Far East (Kunashir Island, Primorye Territory, Amur River basin) (Wang 2000, Endo *et al.* 2007, Ashe & Connor 2009). Pupae and larvae from Amur River basin were collected in springs with water temperature 5–7°C, from gravel and stones covered with moss *Brachythecium rivulare* Bruch *et al.* Larvae in Kunashir Island were collected from small stones covered with moss in spring with water temperature 2°C.

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