

Description and DNA barcoding assessment of the new species *Deutonura gibbosa* (Collembola: Neanuridae: Neanurinae), a common springtail of Alps and Jura

DAVID PORCO¹, ANNE BEDOS² & LOUIS DEHARVENG²

¹Canadian Center for DNA Barcoding, University of Guelph, 50 Stone Road East, Guelph, Ontario, N1G 2W1 Canada.

E-mail: dporco@uoguelph.ca

²Museum National d'Histoire Naturelle, UMR7205 «Origine, Structure et Evolution de la Biodiversité», 45 rue Buffon, CP50, 75005 Paris, France. E-mail: deharven@mnhn.fr

Abstract

Deutonura gibbosa, a new species of the *phlegraea* group, is described. It is characterized by a large elongate uneven tubercle Di on Abd. V, with chaetae Di1 and Di2 shift backward. It has otherwise the same chaetotaxic pattern as the subspecies *sylvatica* of *D. deficiens*. *Deutonura gibbosa* **sp. nov.** is the most widespread *Deutonura* in the Alps and southern Jura. Its barcode sequence is provided and compared to those of four other *Deutonura* of the *phlegraea* group; it unambiguously differs from them, including from *D. deficiens sylvatica*, its closest relative according to current taxonomy. This is the most convincing example so far that barcode may help to discriminate taxa among closely related species in Collembola.

Key words: taxonomy, chaetotaxy, new taxon, DNA barcode, molecular discrimination, species complex

Introduction

With 53 species, *Deutonura* is the most speciose genus of the large subfamily Neanurinae. Distributed in the whole palaeartic region, it is particularly diversified in Southwestern Europe, where it has been studied in more details than anywhere else. A few species (like *Deutonura phlegraea*) are relatively widespread, but most have restricted range and many are narrow endemics. The present paper describes a new species of the *Deutonura phlegraea* group (*sensu* Deharveng 1979), *Deutonura gibbosa* **sp. nov.**, which is one of the most common species of the genus, widely distributed in Alps and southern Jura. The new species has a dorsal chaetotaxy identical to that of *Deutonura deficiens sylvatica* Deharveng, 1982, but arrangement of chaetae and development of hind body dorso-internal tubercles are different. Barcode sequences of this new species are used and compared with 4 other species of the same species-group, providing an additional genetic support to the validity of the new species.

Material and methods

Morphological terminology. The terminology used in the text and Tab. 1 are derived from that of Deharveng (1983), Deharveng and Weiner (1984), Smolis and Deharveng (2006) and Smolis (2008).

Abbreviations. Body parts : Abd.—abdomen, Ant.—antenna, Cx—coxa, Fe—femur, Scx2—subcoxa 2, Ti—tibiotarsus, Th.—thorax, Tr—trochanter, VT—ventral tube.

Groups of chaetae: Ag—antegenital, An—anal, Fu—furcal, Ve—ventroexternal, Vi—ventrointernal, VL—ventrolateral.

Tubercles: Af—antenna-frontal, CL—clypeal, De—dorsoexternal, Di—dorsointernal, DL—dorsolateral, L—lateral, Oc—ocular, So—subocular.

Types of chaetae: ML—long macrochaeta, Mc—short macrochaeta, me—mesochaeta, mi—microchaeta, ms—s-microchaeta, S—S-chaeta, or—organite of antenna IV, mou—blunt chaetae on Ant. IV (« soies mousses » of Ant. IV), x—labial papilla x.

MNHN— Muséum National d'Histoire Naturelle de Paris, France; ZIWU— Zoological Institute, Wrocław University, Poland.

Molecular analysis. 17 specimens from 5 species were used for genetic examination of the divergence within the genus (Tab. 2). All the specimens were processed for the campaign 'Barcoding Collembola' (BCCOL).

Lysis of the tissues was carried out in 50µl volume of lysis buffer and proteinase K incubated at 56°C overnight. DNA extraction followed a standard automated protocol on 96-well glass fibre plates (Ivanova *et al.* 2006) and during this DNA extraction a voucher recovery specially designed for high-throughput work flow (Porco *et al.* 2010) was used. The 5' region of COI used as a standard DNA barcode was amplified using M13 tailed primers LCO1490 and HCO2198 (Folmer *et al.* 1994). A standard PCR reaction protocol was used for PCR amplifications and products were checked on a 2% E-gel 96Agarose (Invitrogen). Unpurified PCR amplicons were sequenced in both directions using M13 tails as primers. The sequencing reactions followed standard protocols of the Canadian Center for DNA Barcoding (Hajibabaei *et al.* 2005), with products subsequently purified using Agencourt CleanSEQ protocol (Agencourt) and processed using BigDye version 3.1 on an ABI 3730 DNA Analyzer (Applied Biosystems). Sequences were assembled with Sequencer 4.5 (GeneCode Corporation, Ann Arbor, MI, USA) and aligned by eye using BIOEDIT version 7.0.5.3 (Hall 1999); we observed no indels in this coding region of the mitochondrial genome and therefore all base positions were aligned with confidence in positional homology. Sequences are publicly available on BOLD (Ratnasingham & Hebert 2007; <http://www.barcodinglife.org>) within the project DGIBD and in GenBank (HM208624-HM208640). Distance analyses were conducted with MEGA4 (Tamura *et al.* 2007) using a Neighbor-Joining (Saitou & Nei 1987) algorithm and distances corrected with the Kimura-2 parameter (Kimura 1980). Kimura-2 parameter is the best metric when distances are low (Nei & Kumar 2000). The robustness of nodes was evaluated through bootstrap re-analysis of 1000 pseudoreplicates.

Deutonura gibbosa sp. nov.

Figs 1, 2–6, 8; Tab. 1

Type material. Holotype male and 90 paratypes, France, Isère, Montaud, along the road from Saint-Quentin-sur-Isère to Montaud. 3.xi.2007, mixed broadleaf forest, litter, berlese. L. Deharveng & A. Bedos leg. (38–036) (Alt. 500 m, X 5.557634, Y 45.276590). Deposited in MNHN (holotype, 80 paratypes) and in ZIWU (10 paratypes).

Other material. France. Ain: Angletfort, le Grand Colombier, 2 ex, eastern slopes, 13.v.2001, beech forest, litter, berlese, L. Deharveng & A. Bedos leg. (01–012); Culoz, le Grand Colombier, 4 ex., 13.v.2001, beech-fir forest, litter, berlese, L. Deharveng & A. Bedos (01–013).

Haute-Savoie: Cordon, 2 ex., 1xii.1977, beech forest, litter, L. Deharveng (74–160); Dingy-Saint-Clair, Nanoir, 3 ex., 10.v.1983, beech and oak forest, litter, L. Deharveng leg. (74–184); Les Clefs, La Tournette, 2 ex., 27.ix.1976, beech forest, litter, L. Deharveng leg. (74–151); Saint-Jorioz, montagne du Semnoz, 2 ex., 23.vii.1973, small shaft with névé, in daylight, (74–061); *ibid.*, crête du Tertère, 9 ex., 20.viii.1979, under *Sorbus*, litter, L. Deharveng leg. (74–169); *ibid.*, 14 ex., 1.ix.1980, on lapiez, spruce forest, litter, L. Deharveng leg. (74–170); Sillingy, Chaumontet, Montagne d'Age, at a small spring, 3 ex., 23.vii.1974, in moss, L. Deharveng leg. (74–148); Vallorcine, Col des Montets, 3 ex., 1.ix.1980, larch and *Rhododendron* forest, litter, L. Deharveng leg. (74–171).

Hautes-Alpes: Aspres-sur-Buech, 8 ex., 4.xi.2007, beech forest, litter, berlese, L. Deharveng & A. Bedos leg. (05–035); La Faurie, Bois de Longeagnes, 1 ex., 13.v.1981, fir forest, litter, J. Monbayé leg. (05–006); Le

Monetier-les-Bains, Le Casset, vallon du Petit Tabuc, 1 ex., 19.vii.1997, larch litter, berlese, F. Brouquisse leg. (05–027).

Isère: La Balme-les-Grottes, above the village, 2 ex., 13.v.2001, oak forest, litter, berlese, L. Deharveng & A. Bedos leg. (38–026); Le Sappey-en-Chartreuse, Col de Porte, 12 ex., 5.viii.1977, L. Deharveng leg. (38–038); Saint-Laurent-du-Pont, Pont Saint Bruno, 13 ex., 3.xi.2007, litter, berlese, L. Deharveng & A. Bedos leg. (38–028); Saint-Pierre-de-Chartreuse, Pont des Cottaves, 1 ex., 3.xi.2007, spruce forest, litter, berlese, L. Deharveng & A. Bedos leg. (38–032).

Savoie: Aillon-le-Jeune, Col des Près, 20 ex., 1.v.1982, beech forest, litter, berlese, L. Deharveng leg. (73–038); Bourg-Saint-Maurice, Beaufortin, vallon de la Neuva, 1 ex., 24.ix.1976, lichen, moss on rock, soil in the alpine zone, L. Deharveng leg. (73–021); Saint-Christophe, near grotte de Fontaine Noire, 1 ex., 12.vii.1984, beech forest, litter, berlese, L. Deharveng leg. (73–053).

Italy. Liguria: Imperia: Cossio di Arroscia, near Ponte di Nava, 2 ex., 15.xii.1982, beech forest, litter, L. Deharveng leg. (ITA–015).

Lombardia: Bergamo: Oneta, Valle de Seriana, Monte Alben, near Zambla, 31 ex., 14.viii.1997, beech mixed with a few spruce, litter, L. Deharveng & A. Bedos leg. (ITA–097, –098, –099); Brescia: Col de Vivione, northern slope, 42 ex., 14.viii.1997, *Pinus uncinata*, birch and *Rhododendron*, litter, berlese, L. Deharveng & A. Bedos leg. (ITA–100); Brescia, foot of Col de Vivione, Valle Paisco, 16 ex., 14.viii.1997, *Castanea*, litter, berlese, L. Deharveng & A. Bedos leg. (ITA–102).

Piemonte: Cuneo: Garessio, Capello, road to Pamparato, 23 ex., 15.xii.1982, beech forest, litter, L. Deharveng leg. (ITA–017); Pamparato, Valcasotto, 6 ex., 2.x.1979, beech forest, M. Curti leg. (ITA–002); Ponte di Nava, below Bricco, 120 ex., 15.xii.1982, chestnut forest, litter, L. Deharveng leg. (ITA–013).

Trentino-Alto Adige: Bolzano: above Ora, Castel Vetere hill, 1 ex., 15.viii.1997, oak forest, litter, berlese, L. Deharveng & A. Bedos leg. (ITA–121); Trento: Sdruzzina, Passo Fittanze della Sega, 27 ex., 12.ix.2002, beech forest, litter, berlese, L. Deharveng & A. Bedos leg. (ITA–139).

Veneto: Belluno: Cortina d'Ampezzo, Falcade, east of Passo San Pellegrino, 1 ex., 15.viii.1997, beech, by hand, L. Deharveng & A. Bedos leg. (ITA–124); Belluno: Bosco de Cansiglio, near Spert, 1 ex., 16.viii.1997, beech, litter, berlese, L. Deharveng & A. Bedos leg. (ITA–135).

Slovenia. Lokev: Divaca, Vilenica cave, 5 ex., 27.vi.1981, E. Christian leg. (SLN–Christ001).

Switzerland. Vaud: Bex, Solalex, massif des Diablerets, 1 ex., 1.viii.1982, fir and spruce forest, litter, L. Deharveng leg. (SUI–004).

Etymology. The species name *gibbosa* is a latine word meaning humped, in reference to the prominent Di tubercle of Abd. V of the new species.

Description. Length: 1–2 mm. Color : deep blue to light blue. Habitus usual for the genus, rather parallel. Abd. VI completely hidden under Abd. V, deeply bilobed. All tubercles well developed on tergites, indicated by reticulations and tertiary granules without papillae, but with strong secondary granules especially on Abd. V. All dorsal chaetae integrated in tubercles (no free chaetae). Dorsal ordinary chaetae of four types: long macrochaetae, short macrochaetae, mesochaetae and microchaetae. Long macrochaetae long, robust, thick, finely and sparsely rugose, sheathed, rounded-ogival at the apex, except the most lateral ones pointed apically. Short macrochaetae similar to long macrochaetae, but shorter. Mesochaetae similar to ventral chaetae, thin and acuminate, short, smooth. Microchaetae morphologically similar to mesochaetae but very short, limited to Oca in some specimens. S-chaetae of tergites thin and long but much shorter than neighbour long macrochaetae (slightly less than 1/2 as long as nearby macrochaeta on Abd. V). S-chaetae of thoracic tubercles De antero-internal to De1 and equally distant to De1 and De2.

Antennae typical of the genus. Ant. IV with S-chaetae thickened, S1 and S2 thinner than others; apical vesicle trilobed. Mouthparts reduced, mandible thin and tridentate, maxilla styliform. Labrum with ventro-distal sclerification rounded and truncated apically, with several minute denticles on apical edge. Labium chaetotaxy as in Fig. 4, with chaetae A and C subequal, three times as long as D. Eyes black, 2+2. Head chaetotaxy and tubercles as in Fig. 2 and Tab. 1. Tubercle Af with elementary tubercles DE and EE present, two elementary tubercles between chaetae A and no granular plate between chaetae A and B.

Tergite chaetotaxy and tubercles as in Fig. 2 and Tab. 1. Tubercles Di of Abd. V fused into a large, strongly bilobed axial tubercle overhanging Abd. VI. Chaetae Di1, Di2 and Di3 in elongated triangle with

Di1–Di2 about 2.5 times shorter than Di1–Di3. Di1: very long, bent macrochaeta, Di 2: long macrochaeta 2/3–3/4 as long as Di1, and Di3: short macrochaeta 3 times shorter than Di2 in adult. Tergite pseudopora (arranged as 0,1,1/1,1,1,1,?1,0 per half tergite) and muscular insertions shown on Fig. 2.

Sternite chaetotaxy as in Fig. 6 and Tab. 1.

Leg chaetotaxy as in Fig. 5 and Tab. 1. No ventral tenent hairs on tibiotarsi, B4 and B5 moderately long, not or slightly overpassing apex of tibiotarsi. Claw basally granulated, without inner tooth.

TABLE 1. Chaetotaxy of *Deutonura gibbosa* sp. nov.

Cephalic chaetotaxy

Group of chaetae	Tubercle	Number of chaetae	Type of chaetae	Name of chaetae
Cl	+	4	ML	F
			Mc	G
Af	+	10	ML	B
			Mc	A,C,D,E
Oc	+	3	ML	Ocm
			Mc	Ocp
			me or mi	Oca
Di + De	+	4	ML	Di1,De1
			Mc	Di2,De2
DL	+	6	ML	DL1,DL5
			Mc	DL2,DL3,DL4,DL6
L + So	+	8-(9)	ML	So1,L1,L4
			Mc or me	L2
			me	(L3),So3 to 6

Vi of head	6
Ve of head	10 or 11
Labrum	4/2,4
Labium	10, 0x
Ant. I	7
Ant. II	12
Ant. III	17+5s
Ant. IV dorsally	12 mou+or+i+8s

Postcephalic chaetotaxy

	Di	De	DL	L	Scx2	Cx	Tr	Fe	Ti
Th. I	1	2	1		0	3	6	13	19
Th. II	3	2+S	3+S+ms	3	2	7	6	12	19
Th. III	3	3+S	3+S	3	2	8	6	11	18
Abd. I	2	3+S	2	3	TV: 4				
Abd. II	2	3+S	2	3	Ve: 5*				
Abd. III	2	3+S	2	4	Ve: 4–5		Fu: 5–6 me, 0mi		
Abd. IV	2	2+S	3	8	Ve: 7–9		VL: 4		
Abd. V	3+3		7+S	1	Ag: 3		VL: 1		
Abd. VI			7		Ve: 14		An: 2 mi		

* Vel present, sometimes as an uneven mesochaeta

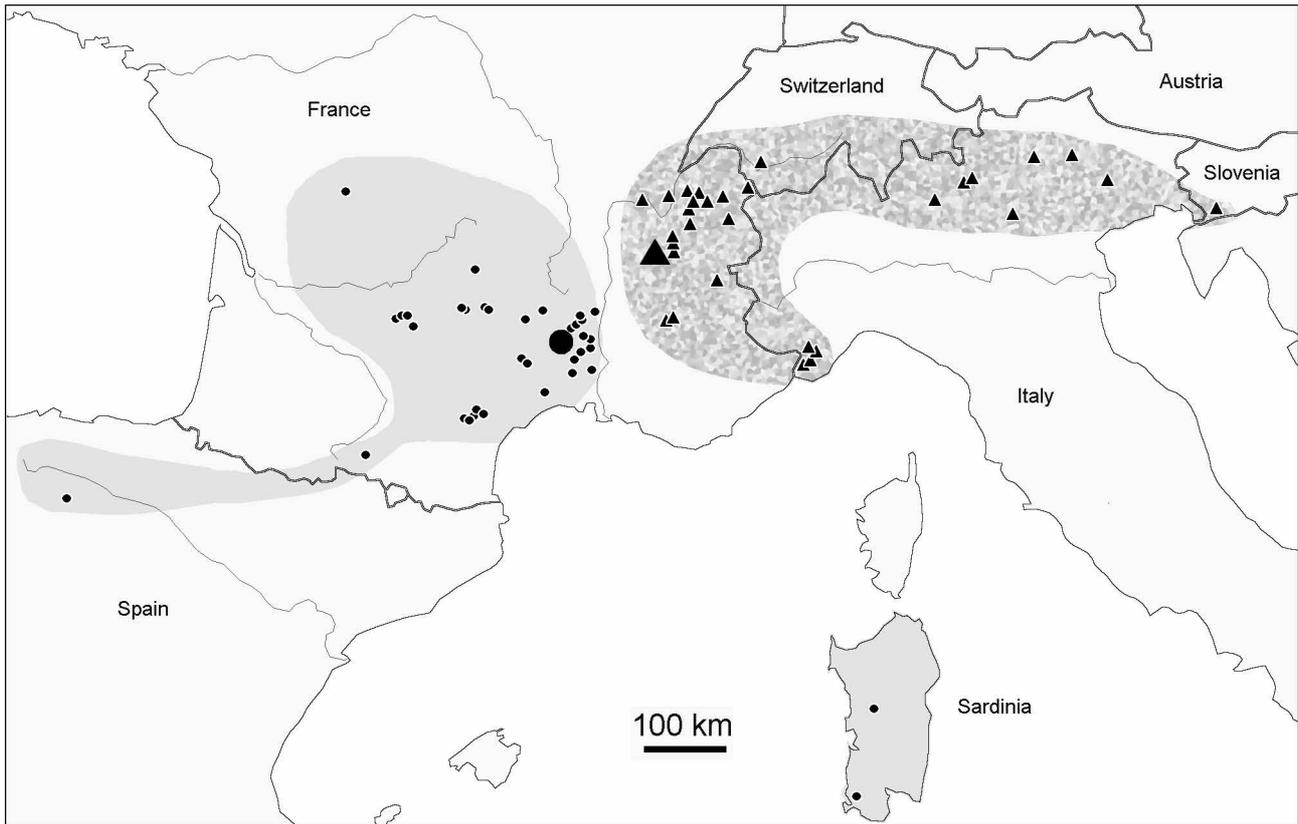
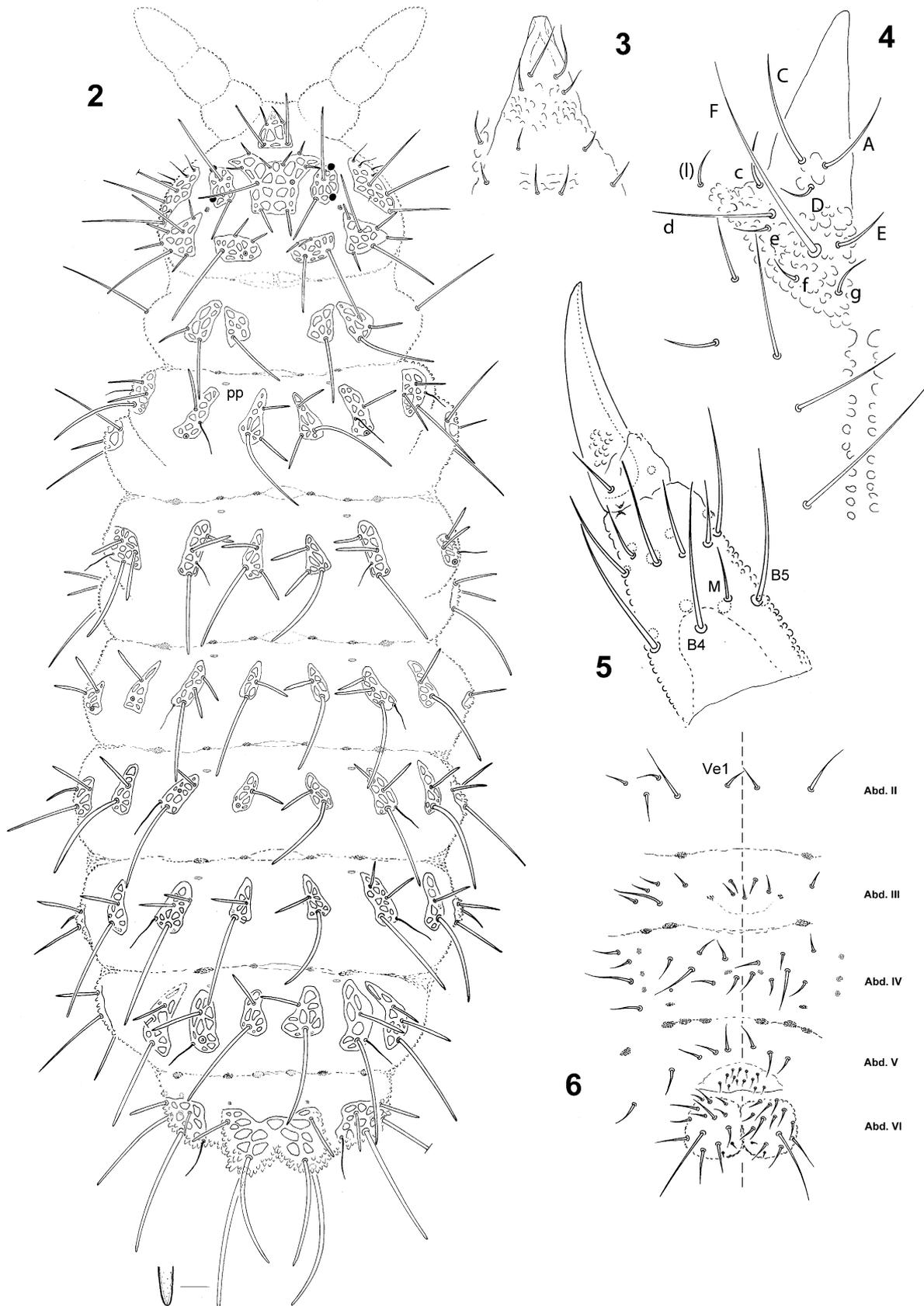


FIGURE 1. Distribution map of *Deutonura gibbosa* sp. nov. (triangles, Alps and southern border of Jura) and *D. deficiens sylvatica* (circles, western France, northwestern Spain and Sardinia). Large triangle and large circle: type localities; only localities from which we have examined specimens are represented for Sardinia.

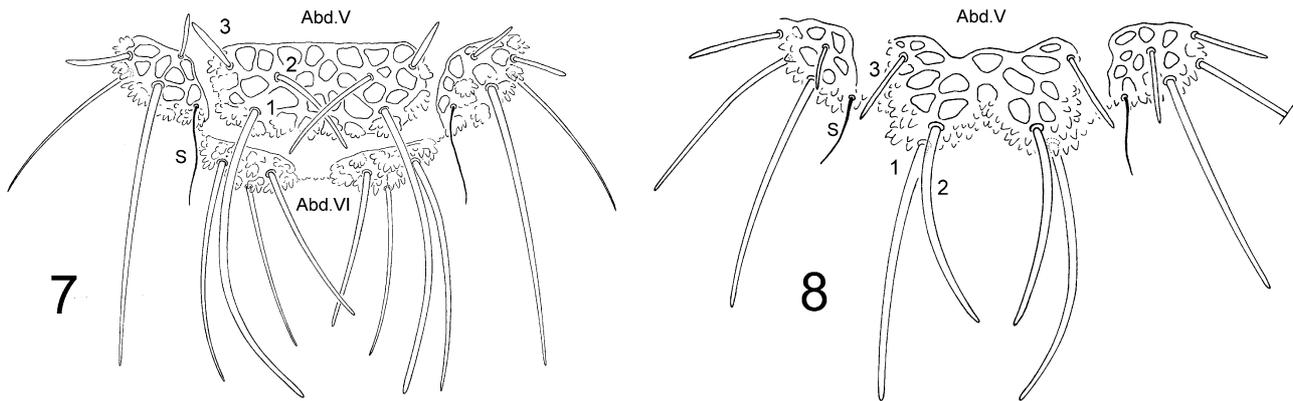
Male without modified chaetae ventrally.

Remarks. Deharveng (1979) recognized three forms in the subspecies *Deutonura plena plena* (Stach, 1951), that was subsequently renamed *D. deficiens sylvatica* Deharveng, 1982 after it was clearly shown that *D. plena* was actually a species of northeastern Europe. The type material from Ardèche near the Rhône valley in France corresponds to the form B characterized by a pigmented body and the presence of 8 chaetae L on Abd. IV. Specimens from Alps cited by Deharveng (1979), which are now placed in the new species *D. gibbosa*, also correspond to the form B. Indeed, *D. gibbosa* sp. nov. shares most chaetotaxic and tuberculation features with the form B of *D. deficiens sylvatica*, widespread in southwestern France and northwest of the Iberian peninsula, and recorded from Sardinia by Dallai (1983). The new species is readily separated from it by the morphology of the dorso-internal tubercle of Abd. V, conspicuously bilobed, larger and more elongate, hiding most of Abd. VI in dorsal view. This development of dorso-internal tubercle of Abd. V is associated to a chaetotaxic re-arrangement, with Di1 and Di2 shift backwards in the new species compared to *D. d. sylvatica* (Figs. 7, 8). This difference holds for all specimens of the form B examined from the cited regions, including those from Sardinia. The ratio of chaetae Di on Abd. V is also different, with Di2 2/3–3/4 as long as Di1 and almost 3 times as long as Di3, versus Di2 about half as long as Di1 or less, and about 2 times as long as Di3 in types of *D. d. sylvatica*.

Distribution and ecology. With a distribution ranging from southwest to eastern Alps and southern Jura, *D. gibbosa* sp. nov. is one of the most widespread species of the genus. It replaces *D. deficiens sylvatica* to the east of the Rhône valley (Fig. 1). Given the frequency of the new species in the Alps, it is surprising that the species seems to have been overlooked by previous authors. For instance, none of the *Deutonura* cited from Austria by Christian (1987) could correspond to *D. gibbosa* sp. nov. It might be that the species, while present in the whole massif, may be replaced in some large areas like Austria by other *Deutonura* species, as it seems to be the case in the most southwestern regions of the Alps.



FIGURES 2–6. *Deutonura gibbosa* sp. nov.: 2, dorsal chaetotaxy and tubercles (represented by their undercuticular reticulations); 3, labrum; 4, labium (l—lateral chaeta of labrum); 5, tibiotarsus and claw of leg I (dotted line: limit of secondary granules on dorsal side); 6, ventral chaetotaxy of abdomen. Muscular insertions as punctuated areas; pp: pseudopora.



FIGURES 7–8. Arrangement of tubercles and chaetae on the tergite of Abd. V–VI in a paratype of *Deutonura deficiens sylvatica* (Fig. 7) and in a paratype of *D. gibbosa* **sp. nov.** (Fig. 8, Abd. VI not visible in dorsal view); 1, 2, 3: chaetae Di1, Di2 and Di3 on Abd. V.

D. gibbosa **sp. nov.** is frequent in forest litter and rotten wood of any kind of forest, even disturbed, from 300 to 1500 m a.s.l.

Molecular characterization

Tab. 2–4, Fig. 9

In the course of the campaign ‘Barcoding Collembola’ (BCCOL), we sequenced 17 specimens of 5 closely related species of *Deutonura* of the *phlegraea* group, including 3 from the Alps (*D. gibbosa* **sp. nov.**, *D. caerulescens* Deharveng, 1982 and *D. decolorata* (Gama & Gisin, 1964 in: Gisin 1964)), 1 from Eastern Pyrenees (*D. vallespirensis* Deharveng, 1982) and 1 from western Massif Central (*D. deficiens sylvatica* Deharveng, 1982) (Tab. 2, Fig. 9).

TABLE 2. List of barcoded species. N—number of sequences available.

Species	N	Localities (all from France)	Sampling date
<i>Deutonura caerulescens</i>	6	Mont Faron, Toulon, Var	17.xii.2008
<i>Deutonura deficiens sylvatica</i>	4	Saint-Sylvestre, Haute-Vienne	8.ix.2004
	1	Sainte-Mondane, Dordogne	18.iv.2005
<i>Deutonura decolorata</i>	1	Montaud, Isère	3.xi.2007
<i>Deutonura gibbosa</i> sp. nov.	1	Montaud, Isère	3.xi.2007
	3	Aspres-sur-Buech, Hautes-Alpes	4.xi.2007
<i>Deutonura vallespirensis</i>	1	Argelès-sur-Mer, Pyrénées-Orientales	3.vii.2007

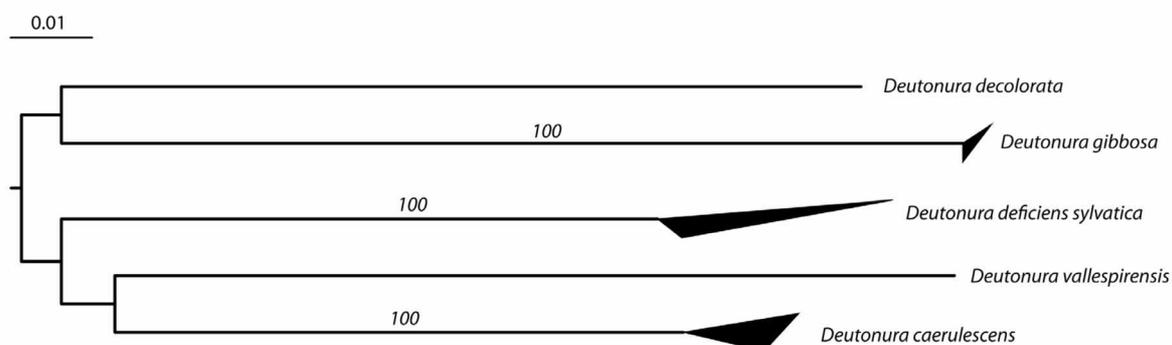
The barcodes obtained exhibited 0.2025 mean value for interspecific K2P distances among species of the genus (Tab. 3). The lowest value was 0.174 between *D. deficiens sylvatica* and *D. caerulescens*, and the highest was 0.2272 between *D. vallespirensis* and *D. gibbosa* **sp. nov.** (Tab. 3). By contrast intraspecific values were low (mean 0.0115) ranging from 0.0198 for *D. deficiens sylvatica* to 0.0006 for *D. gibbosa* **sp. nov.**. These values confirm the ‘barcoding gap’ described by Hebert *et al.* (2003) as a general principle of DNA barcoding and are consistent with the distance within genus previously found in arctic Collembola (Hogg & Hebert 2004) (Tab. 4). The neighbor joining tree built from this dataset shows the clear cut between the different barcode clusters corresponding to the different species (Fig. 9).

TABLE 3. Genetic distances between species within the *Deutonura* genus (K2P-pairwise).

species	1	2	3	4
1 <i>Deutonura caerulescens</i>				
2 <i>Deutonura deficiens sylvatica</i>	0.174			
3 <i>Deutonura decolorata</i>	0.198	0.1941		
4 <i>Deutonura gibbosa</i> sp. nov.	0.2124	0.2074	0.2104	
5 <i>Deutonura vallespirensis</i>	0.1864	0.1959	0.2193	0.2272

TABLE 4. Intraspecific genetic distances (d); n—number of specimens; na—non applicable.

species	d	n
<i>Deutonura caerulescens</i>	0.014	6
<i>Deutonura deficiens sylvatica</i>	0.0198	5
<i>Deutonura decolorata</i>	na	1
<i>Deutonura gibbosa</i> sp. nov.	0.0006	4
<i>Deutonura vallespirensis</i>	na	1

**FIGURE 9.** Neighbor joining tree (K2P) of five species of the *phlegraea* group of the genus *Deutonura* based on the COI 5' 'barcoding fragment'. Bootstrap support values showed on the branches. The upper and lower side of the triangle represent respectively the maximum and minimum of genetic distances within the species.

D. gibbosa **sp. nov.** exhibits the lowest intraspecific value in the genus for the species examined (0.0006) and its nearest neighbor is *D. deficiens sylvatica* with a K2P distance of 0.2074. Those intra/interspecific values and the distances observed among the other species of the genus bring a genetic support to the delineation of this new species which appears as a well individualized mitochondrial lineage.

Conclusions

In the present study, dorsal tubercle arrangement and number of chaetae on each tubercle, the characters most widely used to separate species of *Deutonura*, are identical in *D. gibbosa* **sp. nov.** and *D. deficiens* ssp. *sylvatica*. The only difference between them is the elongation and bilobation of the unpaired dorso-internal tubercle of Abd. V, associated to modification in chaetal arrangement and chaeta length ratio on the same tubercle. The fact that barcode clearly discriminates between such closely related species illustrates its power as a complementary tool in the characterization of Collembolan species. It also brings support to the use of chaeta insertion pattern on Abd. V for the taxonomy of Neanurinae.

The sequences obtained for the new species were yield from one paratype specimen and 3 specimens from another site, 82 km to south (sample 05–035). This allows to link the species name *gibbosa* to COI sequences of type specimens and thus to the corresponding barcode cluster, making possible the assignation of a new

name to sibling species if detected in the future. Although it is sometimes possible to get the sequence from old museum material for this purpose (Hausmann *et al.* 2009), it is much easier and cheaper to barcode fresh type material at the same time as the species is described. Furthermore, the voucher recovery protocol designed for high-throughput processing of specimens often allows to observe the finest morphological characters in Collembola of this size (Porco *et al.* 2010), so the DNA extraction will not interfere with the morphological description of the specimens.

In the pioneer works of Hogg and Hebert (2004), three species of *Folsomia*—*F. quadrioculata* (Tullberg, 1871), *F. regularis* Hammer, 1953 and *F. sexoculata* (Tullberg, 1871)—and two species of *Hypogastrura*—*H. concolor* Carpenter, 1900 and *H. sensilis* Folsom, 1919—were unambiguously discriminated by barcode sequences. However, these species, though congeneric, were not closely related (see: Fjellberg 1985 and Potapov 2001). Further on, Stevens *et al.* (2006) showed that divergence in COI between different forms and populations of the *Cryptopygus antarcticus* group reached species level. Other markers repeatedly suggested unusually high genetic divergence between congeneric species of Collembola (Fрати *et al.* 2000, Cicconardi *et al.* 2010), as well as between populations of a same species (Fanciulli *et al.* 1991). We retrieved here high interspecific divergences for COI among closely related species of the *Deutonura phlegraea* group, already well documented morphologically. Such levels of divergence in COI sequences is an interesting finding which is currently being assessed across a wide range of Collembolan groups within the context of the "Barcoding Collembola" campaign.

Through its ability to clearly discriminate species considered as very similar on morphological ground, barcoding provides therefore a very powerful tool to address taxonomic problems of sibling species, like the West-European subspecies and forms of *Deutonura deficiens* (Rougerie *et al.* 2006). The garbled taxonomy of several very common Collembolan "species" in Europe, that have been shown or suggested to be species complexes (Deharveng 2004), would deserve as well to be re-assessed in the light of standard barcode approaches.

Acknowledgements

This work was funded by NSERC, Genome Canada and the Ontario Genomics Institute. Prof. Romano Dallai (Siena) kindly lend us specimens of *Deutonura deficiens sylvatica* from Sardinia. We are indebted to two referees for significant improvement of the manuscript.

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