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Redescription of *Homeopronematus anconai* (Baker) (Acari, Iolinidae) and description of *Quasihomeopronematus nordestinus* n. gen. n. sp.

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Original research

ABSTRACT

In a survey of natural enemies of *Aculops lycopersici* (Tryon, 1917), we collected specimens of *Homeopronematus anconai* (Baker, 1943) in different European countries and redescribed the species based on specimens collected in Belgium. The newly collected specimens were measured and morphologically compared with USA specimens available from museum collections. We also measured collections' specimens previously identified as *H. staercki* from Hungary, and others, previously identified (but undescribed) as *Homeopronematus* cf. *staercki* sp. nov. from Serbia. *Quasihomeopronematus* n. gen., with its type species *Quasihomeopronematus nordestinus* n. gen. n. sp., are described based on specimens from Brazil. As the name suggests, this genus is similar to the genus *Homeopronematus*. Single female expansion lines were set-up with *H. anconai* specimens from Belgium, France, Germany and Hungary, and *Q. nordestinus* specimens from Brazil. With specimens of these lines, molecular analysis was performed to construct a phylogenetic tree including the results of previous studies with *Pronematus ubiquitous* (McGregor, 1932) and *P. duffelensis* De Vis & Ueckermann, 2024. The tree showed differences between origins of *H. anconai*, with one French line standing out. In a PCA analysis on morphological characters, the same French line separated from all other geographical origins albeit with some overlap. The molecular and morphological differences were assigned to intraspecific variation, and we consider all specimens studied as *H. anconai*. *Homeopronematus anconai* is morphologically different from *Q. nordestinus* but the latter separated similarly as that one French line from all other *H. anconai* lines. We conclude that the CO1-gene is not sufficient to separate genera in the family of the pronematinae. The specimens previously identified as *H. staercki* or *Homeopronematus* cf. *staercki* sp. nov. overlap in the PCA analysis with the specimens of *H. anconai*. Therefore, we synonymise *H. staercki* with *H. anconai*. The results are discussed and additionally both species' distribution, habitat, and feeding habits are presented.

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Introduction

Since 2016, *Aculops lycopersici* (Tryon, 1917) (Acari: Eriophyidae) has become a major pest in greenhouse tomato crops in Western Europe (Reybroeck *et al.* 2018; Vervaet *et al.* 2021). Therefore, a search for potential natural enemies was started in 2017 in Belgium and neighbouring countries during two successive projects funded by the Flemish vegetable auctions (LAVA) and Flanders region (DUCATO and BALTO) (Reybroeck *et al.* 2018; Vervaet *et al.* 2021; Vervaet *et al.* 2022). During that study, we found *Pronematus ubiquitous* (McGregor 1932) (Ueckermann & De Vis *et al.*, 2024) and *Duoparus hyeresensis* De Vis & Ueckermann 2024 (De Vis *et al.* 2024) and *Homeopronematus anconai* (Baker, 1943). Here we present the results of our taxonomic study of *H. anconai*.

At the same time, Marcossi *et al.* (2024) started research with an iolinid, initially identified as *H. anconai*, as biological control agent in Viçosa, Brazil. We received material to confirm the identity of the species they used but concluded it is a different species. This new species is described here, as it is closely related to *H. anconai*.

Currently, two *Homeopronematus* species are described: *H. anconai* and *H. staercki* (Schruff, 1972) [André (2021), <https://species.wikimedia.org/wiki/Pronematinae>, accessed on 22/05/2024]. The identification of these two species is, however, not trivial given that the descriptions do not present distinguishing characteristics and lack the (range of) measurements of individual characteristics. Baker (1943) described *Pronematus anconai* based on specimens collected from Mexico. His description is limited, not including species specific characteristics such as the leg and body chaetotaxy, the *ag* setae or the characteristics of the distal eupathidia on tarsus I. In his redescription (Baker 1968), he added detail on the relative length of the setae, without measurements, but mentions distinctive characteristics such as the partially smooth eupathidia with (*tc*) longer than tarsus I and (*p*) shorter than tarsus I, and the forked *ag*₃. However, he mentions that the striae are apparently without lobes.

Kuznetsov (1972) found *H. anconai* on a large number of trees, shrubs and grasses in the south coast and steppe regions of Crimea. His redescription is more detailed and gives general setal lengths, but not the range for each individual seta. Although described as a *Pronematus*, the leg chaetotaxy differs from that of the *Pronematus* genus description of Baker (1965) in having one seta more on each of trochanters I and II (one instead of zero), tarsi III and IV (six instead of five), and femur II (three instead of two). He mentioned two setae on genu IV. We suppose that this is a printing error as on his drawing he depicted only one seta (the leg chaetotaxy on the drawing coincides apart from this seta with that in the text) and no other species of the Pronematinae has two setae on genu IV. Another difference is the number of setae on tarsus I as most descriptions of genera or species do not mention the two tiny (*u*) setae, mentioning thus six setae instead of eight for that segment.

In the same year, Schruff (1972) described *Pronematus staercki* based on specimens collected in Schliengen, in the south-west tip of Germany. His description is more detailed, including leg chaetotaxy and immature stages (except tritonymph) but lacks measurements of individual setae and the shape of *ag*₃. The leg setation is the same as that described by Kuznetsov for *H. anconai* (with one seta on genu IV). He did not mention distinguishing characters to separate *H. staercki* from *H. anconai* or other Pronematinae. Based on his description, *H. staercki* cannot be distinguished from *H. anconai*. Schruff certainly omitted (as most authors at that time) the two tiny setae (*u*) on tarsus I mentioning 6 setae for that segment.

André (1980) erected several new genera to solve the inconsistencies in leg chaetotaxy in the genera descriptions of the Tydeidae and the species allocated in those genera. He erected the genus *Homeopronematus* with the leg setation of *P. staercki* and allocated therein besides *P. staercki* also *H. vidae* André 1980 a new species he described based on specimens from a

lab culture of M. Hoy from University of California, Berkeley, USA. He did not mention the redescription of *P. anconai* of Kuznetsov (1972) neither resolved the position of *Pronematus anconai* (Baker 1943). Three years later, Knop and Hoy (1983a) compared the Californian *P. anconai* with a type slide of *P. anconai* they obtained from Baker (containing two females) and concluded that the Californian are the same as the Mexican specimens and that they belong to the genus *Homepronematus*. They synonymised *H. vidae* with *H. anconai*, and transferred *Pronematus anconai* to the genus *Homepronematus*, stating that the types of *H. vidae* came from a lab culture of *H. anconai* of M. Hoy and that variability within the species is high. They redescribed *H. anconai* based on Californian specimens, adding the lobed striation as a distinguishing feature (that they could also distinguish on the types of *H. anconai*) but did not determine the variability of the characteristics.

No new species have been described within the genus *Homepronematus* but two authors mention undescribed, related species: *Homepronematus* cf. *staercki* in Serbia (Stojnić *et al.* 2002) and *Pronematus* cf. *anconai* in Iran (Daneshvar 1978).

Two papers suggest that *H. staercki* might be a junior synonym of *H. anconai* (Knop and Hoy 1983a; Ueckermann *et al.* 2019). However, André (1980) studied several individuals without specific label (from the Schuft's collection) of *H. staercki*, and found for this species a shorter *c*₂, a higher striation density and further different "shape and length of idiosomal setae" (sic), without describing the exact differences. Schruft (1972) did not mention the shape of setae *ag*₃ in the description of *H. staercki* while it is forked in *H. anconai* (Baker 1968; Kuznetsov 1972; Knop and Hoy 1983a). Ripka *et al.* (2022) stated that the tectal and proral eupathidia on tarsus I of *H. anconai* are all four equal in length while in *H. staercki*, the tectals are nearly twice as long as the prorals. This is, however, in contradiction with the redescription of *H. anconai* (Baker 1968; Kuznetsov 1972) or *H. vidae* (= syn. *H. anconai*) (André 1980), where the tectals are longer than the prorals with *p*"ζ the shortest. The figures of *H. staercki* of Schruft (1972) show indeed longer tectals than prorals.

Based on published reports, *H. anconai* has an almost worldwide distribution. It has been registered i.a. in Mexico, place of original description (Baker 1943), throughout USA (Baker 1968; Hessein and Perring 1986; Oatman 1971; Childers and Enns 1975; Knop and Hoy 1983a), Canada (Thistlewood 1991), Argentina (Baker 1968), Brazil (Johann *et al.* 2009; Klock *et al.* 2011; Horn *et al.* 2011; Sousa *et al.* 2015), Portugal (Maurício *et al.* 2009; Ferreira 2016), Spain (García González 2003), Italy (Liguori 1987), Hungary (Ripka *et al.* 2022), Crimea (Kuznetsov 1972), Türkiye (Yanar *et al.* 2013; Çobanoğlu and Kumral 2014), Iran (Darbemamieh *et al.* 2020), China (Xu 2011) and Japan (Kawai *et al.* 2001), but no references of its presence in Africa or Oceania were found. *Homepronematus staercki* has been registered in central Europe and the middle east, i.a. in Germany (Schruft 1972), Hungary (Ripka and Kaźmierski 1998; Ripka *et al.* 2005; Ripka *et al.* 2013; Tempfli *et al.* 2015; Tempfli 2019; Ripka *et al.* 2022), Türkiye (Ozman-Sullivan *et al.* 2005) and Iran (Darbemamieh *et al.* 2021). In Italy, Hungary, Türkiye and Iran both species have been reported.

The previous illustrates the need for a redescription of the *Homepronematus* spp to clear out differences and similarities as to ensure a correct identification. Because the material used for the description of *H. staercki* is lost [according to Schruft, personal communication, this material is at Musée Royal de l'Afrique Centrale, Tervuren, Belgium, MRAC (Zhang 2018), where we could not find them], We studied specimens of Ripka from Hungary that were identified as *H. staercki* (Ripka *et al.* 2022) and compared the results with the measurements of specimens from USA and western Europe.

Molecular techniques have shown that we can distinguish Pronematinae genera from each other using the CO1-gene (Ueckermann & De Vis *et al.*, 2024; De Vis *et al.*, 2024). However, it is not clear if closely related species can be distinguished using this method.

The objectives of this study are to redescribe *H. anconai*, to describe a new species from Brazil that is closely related with *H. anconai*, to morphologically compare the species studied, to answer the question if *H. anconai* and *H. staercki* are indeed different species and genetically compare *H. anconai* and the new species with other Pronematinae that are molecularly typified.

Material and methods

Collecting material

During the DUCATO (strain numbers labelled with a ‘D’) and BALTO (strain numbers labelled with a ‘B’) projects (Reybroeck *et al.* 2018; Aussems *et al.* 2021), a survey was done from summer 2017 until autumn 2019, mostly in Belgium and France (Survey permission nr. NOR TREL1902817S/165). Sampling was directed to wild or cultivated eriophyid susceptible plants [mostly *Rubus* spp (Rosaceae), but also grape (*Vitis vinifera* L., Vitaceae), fig (*Ficus carica* L., Moraceae), linden (*Tilia* sp., Malvaceae), maple (*Acer pseudoplatanus* L.), etc.] and wild or cultivated solanaceous plants (Solanaceae), bittersweet *Solanum dulcamara* L., *Brugmansia* sp., tomato *Lycopersicon esculentum* L., sweet pepper *Capsicum annuum* L., egg plant *Solanum melongena* L., *Physalis peruviana* L. Sampling was done in the surroundings of the research institutes or during travel in Belgium or abroad. Cultivated solanaceous plants were sampled on organic farms in Flanders or in gardens and for wild plants on sites where they were earlier found according to the site waarnemingen.be. Samples were transported to PSKW where they were screened for predatory mites under a stereo microscope (Leica DM16 or Leica M125 C) and slide mountings in Hoyer medium (Walter and Krantz 2009) were made of phytoseiids, iolinids and triophtydeids. At the same time, small lab colonies were set up with iolinids and transferred to Ghent University where cultures were increased, and single female lines (SFEL) were set up to provide material for the genetic study.

Finally, we studied slides from museum collections of USPB Museu de Zoologia “Luiz de Queiroz” at the Escola Superior de Agricultura “Luiz de Queiroz”, Universidade de São Paulo, Piracicaba, São Paulo, Brazil; of EMEC—Essig Museum of Entomology, University of California, Berkeley, California, USA, and of AMU, Department of Animal Morphology, Adam Mickiewicz University, Poznań, Poland.

Morphological examination and principal component analysis

Specimens were measured using a Leica DM750 with an eyepiece micrometer or a Leica Flexacam c3 camera and Leica LAS-X software. Line drawings were made with a Leica DM750 with a phototube or Wacom Cintiq 16 pen display and drawn using Adobe Illustrator 28.2. The environmental scanning electron microscope images were taken with Hitachi tabletop microscope TM-1000. Nomenclature of body parts and its organotaxy is that of Kaźmierski (1989) except for adoral setae where we use notation *or*, and that of André (1981) and Khaustov *et al.* (2020) for the legs. In the text, measurements in micrometres are given directly after each structure.

Principal component analysis (PCA) of the females measured in this work was done with PAST (version 4.03), cf. Ueckermann & De Vis *et al.* (2024); De Vis *et al.* (2024).

Phylogenetic analysis

The methodology of culturing mites, molecular analysis and construction of a phylogenetic tree is described in detail in Ueckermann & De Vis *et al.* (2024). Briefly, it consists first of the culture of progeny of single females to have sufficient homogenous genetic material (although it is possible with one female, three to four females for one DNA extraction increases the success rate). After DNA extraction of 1 to 4 mites, a 710-bp fragment of the cytochrome c oxidase subunit I gene (CO1, mtDNA) was amplified by PCR, using the same primers and conditions as in Ueckermann & De Vis *et al.* (2024) and sequenced. The consensus sequences were aligned online using MAFFT version 7, including CO1 sequences of *P. ubiquitous* (Ueckermann and De Vis *et al.* 2024), *P. duffelensis* De Vis & Ueckermann 2024 (De Vis *et al.*, 2024) and a set of gradually less related prostigmatid mites from previous studies, available at GenBank NCBI. Finally, a phylogenetic tree was constructed based on DNA sequences, using the software W-IQ-TREE with 1,000 ultrafast bootstrap combined with automatic model finding through ModelFinder (Trifinopoulos *et al.* 2016; Kalyaanamoorthy *et al.* 2017; Hoang *et al.*

2018). According to the Bayesian information Criterion, the best-fit model was determined to be K3Pu+F+I+G4, based on the likelihood scores for 88 different models. The resulting Maximum-likelihood consensus tree was rooted with the sequence of *Varroa destructor* Anderson and Trueman, 2000 and edited with iTOL version 5 (Letunic and Bork 2021).

Deposits of type material

Type material, holotype and paratypes, of *Q. nordestinus* n. gen. n. sp. are deposited at USPB—“Museu de Zoologia Luiz de Queiroz” at the Escola Superior de Agricultura “Luiz de Queiroz”, Universidade de São Paulo, Piracicaba, São Paulo, Brazil.

The COI-sequences of every collection location of *H. anconai* and *Q. nordestinus* n. gen. n. sp. obtained in this study have been deposited in the NCBI Genbank database. The accession numbers can be found in Table 1.

Voucher specimens of the COI sequences (i.e., slide mountings of specimens originating from the same origin as the respective COI sequence) of *H. anconai* and *Quasihomeopronematus nordestinus* De Vis & Ueckermann n. gen. n. sp. are deposited at CBGP, INRAE, Montpellier, France. The COI-sequences of the single female lines of the following samples were identical for each origin/sample: *Q. nordestinus* Brazil (SFEL 1.1, 1.3, 1.4 and 1.5); *H. anconai* Belgium D21 (SFEL 21.1 and 21.2), Belgium B25 (SFEL 25.1 and 25.4), France B46 (SFEL 46.2, 46.5 and 46.3) and Germany B176 (SFEL 176.2 and 176.3); for each of these origins, several voucher specimens were deposited under the same COI-sequence. Of sample B175.1 no voucher specimens were available. Slide labels of the voucher specimens at CBGP can be found in Table 1.

Results

Collecting material

Homeopronematus anconai

In Europe, a total of 338 samples were collected mainly in Belgium (271) and France (50) (Survey permission UGent nr. NOR TREL1902817S/165) but also some in The Netherlands (2), Germany (4), Czech Republic (3), Switzerland (3) and Hungary (1). From these, 63 samples from 103 localities in Belgium, 14 samples from 47 localities in France, 2 samples from 2 localities in The Netherlands, 2 samples from 2 localities in Germany, 3 samples from 3 localities in Czech Republic, and 3 samples from 3 localities in Switzerland, and 1 sample from 1 locality in Hungary contained *H. anconai*. We studied and measured specimens of the following slide mounts: **Belgium:** 17/7/2017, Sint-Katelijne-Waver, 51.077141, 4.526659, *Viburnum x burkwoodii* Burkwood & Skipwith (Adoxaceae), Raf De Vis, 1 female, D18; 26/7/2017, Sint-Katelijne-Waver, 51.059258, 4.495511, *Rubus* sp., Raf De Vis, 1 female, D23.2; 1/3/2018, Sint Truiden, raspberry, Rik Cleymans, 1 female, D66.1; 18/08/2018, Hofstade, 50.99639, 4.51389,

Table 1 Characterisation of COI-sequences as deposited in the Genbank database.

Species	Isolate	Sequence ID	Collector	Collection date (yyyy-mm-jj)	Country	Latitude, longitude	Isolation source	Voucher specimen source*	Mounting date (yyyy-mm-jj)	Slide labels **	GenBank accession number
<i>Q. nordestinensis</i>	BRA	Seq1	Italo Marcossi	2022-01-24	Brazil	-20.7598, -42.8829	<i>Solanum lycopersicum</i> Tomato	single female lines BRA1.1, 1.3, 1.4 & 1.5	2024-04-04	CBGP-ACARI 2511–2521	PQ630653
<i>H. anconai</i>	B83	Seq2	Lore Vervae	2018-10-14	France	44.5120, 4.7796	<i>Rubus</i> sp.	single female line 83.2	2018-12-14	CBGP-ACARI 2522	PQ630654
<i>H. anconai</i>	B83	Seq3	Lore Vervae	2018-10-14	France	44.5120, 4.7796	<i>Rubus</i> sp.	single female line 83.5	2018-12-14	CBGP-ACARI 2523	PQ630655
<i>H. anconai</i>	B176	Seq4	Ute Perkons	2023-09-18	Germany	51.0020, 6.8488	<i>Solanum lycopersicum</i> Tomato	single female line B176.2, 176.3	2024-05-15	CBGP-ACARI 2524–2526	PQ630656
<i>H. anconai</i>	B174	Seq5	Anton van der Linden	2018-09-27	Hungary	47.9569, 20.6132	<i>Rosa</i> sp.	single female line B174.1	2018-02-22	CBGP-ACARI 2527–2528	PQ630657
<i>H. anconai</i>	B46	Seq6	Dieter Foqué	2018-09-29	France	46.3628, 2.3494	<i>Solanum lycopersicum</i> Tomato	single female line 46.4	2018-12-14	CBGP-ACARI 2529	PQ630658
<i>H. anconai</i>	B46	Seq7	Dieter Foqué	2018-09-29	France	46.3628, 2.3494	<i>Solanum lycopersicum</i> Tomato	single female lines B46.3, 46.5, 46.2	2018-12-14	CBGP-ACARI 2530–2531	PQ630659
<i>H. anconai</i>	B31	Seq8	Raf De Vis	2018-09-16	Belgium	50.9395, 4.1348	<i>Rubus</i> sp.	single female line 31.6	2018-12-14	CBGP-ACARI 2532	PQ630660
<i>H. anconai</i>	B25	Seq9	Lore Vervae	2018-09-05	Belgium	50.4323, 5.2482	<i>Rubus</i> sp.	single female lines B25.4, 25.1	2018-12-14	CBGP-ACARI 2533–2535	PQ630661
<i>H. anconai</i>	B175	Seq10	Markus Knapp	2018-10-07	Germany	48.5830, 8.1670	<i>Rubus</i> sp.	single female lines B175.1	-	no slide available	PQ630662
<i>H. anconai</i>	D21	Seq11	Raf De Vis	2017-07-07	Belgium	51.0771, 4.5266	<i>Viburnum x burkwoodii</i>	mass rearing	2017-08-20	CBGP-ACARI 2536–2537	PQ630663

*COI-sequences of single female lines on the same line are identical

**Collection Centre de Biologie pour la Gestion des Populations, Univ Montpellier, CIRAD, INRAE, Institut Agro, IRD, Montpellier, France “CBGP - Continental Arthropod Collection”, <https://doi.org/10.15454/D6XAKL>

Rubus sp., Raf De Vis, 1 female, B4.4; 20/8/2018, Schoten, 51.268127, 4.5169, *Rubus* sp., Kevin Van Puyvelde, 1 female, B12.4; 30/08/2018, Machelen a/d Leie, 50.945049, 3.487808, fig, Justine Dewitte, 1 female, B16.3; 30/08/2018, Kruishoutem, 50.904045, 3.528591, *Rubus* sp., Justine Dewitte, 1 female, B17.2; 16/09/2018, Meldert, 50.939477, 4.134792, *Rubus* sp., Raf De Vis, 10 females from rearing, B31.6; 30/09/2018, Maasmechelen, 50.982184, 5.639674, *Rubus* sp., Raf De Vis, 1 female, B42.1; 17/10/2018, Borgloon, 50.801239, 5.290275, grape, Eva Reybroeck, 1 female, B67.5; 03/2019, Gent, 51.053635, 3.706242, *Rubus* sp., Lore Vervaet, 3 females from rearing, B25; 27/07/2020, Pailhe, 50.432287, 5.248216, *Rubus* sp., Raf De Vis, 1 female, B164.2; **France**: 29/09/2018, Treignat, 46.362778, 2.349167, tomato, Dieter Foqué, 2 female B44.1-44.2; 29/09/2018, Treignat, 46.362778, 2.349444, tomato, Dieter Foqué, 1 wild female and 3 females from rearing, B46.2; 29/09/2018, Treignat, 46.366944, 2.344167, *Rubus* sp., Dieter Foqué, 1 female B52.3; 14/10/2018, Hyères, 43.1181, 6.1621, *Rubus* sp., Lore Vervaet, 16 females from rearing, 1 wild specimen B83.1; 17/10/2018, Allan, 44.5120, 4.7796, *Rubus* sp., Lore Vervaet, 2 females B89.2.1-2; 22/07/2019, Landrecies, 50.128817, 3.643396, bittersweet, Raf De Vis, 1 female, B100.1; 22/07/2019, Fontain-au-Bois, 50.128817, 3.643396, *Rubus* sp., Raf De Vis, 1 female, B109.2; 28/12/2019, Kaysersberg, 48.141464, 7.266328, *Rubus* sp., Raf De Vis, 2 females, B146.1 & D147.2; **The Netherlands**: 19/10/2019, Mechelen, 50.783623, 5.940681, *Rubus* sp., Raf De Vis, 4 females, B141.4; B141.5.1-2, B141.6; 30/8/2021, Mook, 51.762295, 5.911216, grape, Felix Wäckers, 1 female, B172.1; **Germany**: 07/10/2018, Seebach, 48.582689, 8.167126, *Rubus* sp., Markus Knapp, for rearing and CO1-sequences, no voucher specimen were mounted, B175.1; 18/09/2023, Auweiler, 51.001925, 6.848739, tomato, Ute Perkons, 5 females from rearing mounted on 15/5/2024, B176.1-5; **Czech Republic**: 27/11/2019, Prague, 50.085085, 14.307956, *Rubus* sp., Raf De Vis, 4 females, B144.5.1-2 & B144.7.1-2; 27/11/2019, Prague, 50.084640, 14.309172, *Rubus* sp., Raf De Vis, 3 females, B145.1 & B145.2.1-2; **Switzerland**: 13/9/2017, Oppens, *Rubus* sp., Hans Claes, 2 females, D56.1 & D56.2; 13/9/2017, Bavois-Orny, *Rubus* sp., Hans Claes, 1 female, D57.5; 13/9/2017, Pailly, *Rubus* sp., Hans Claes, 1 female, D58.6; **Hungary**: 27/09/2018, Kács, *Rosa* sp (Rosaceae), Anton van der Linden, 5 females from rearing, B174.1.

We studied the following slides from museums: **from EMEC**: 20 slides mounted on 12/10/1969 from a culture of *H. anconai* from unknown origin (we did not include measurements of these specimens in this study because the origin is not known); **from AMU**: **Hungary**: 3 slides from with 5 females and 1 male previously identified as *H. staercki* (Ripka *et al.* 2022): 17/07/2019, Lövvö, *Rubus caesius*, Geza Ripka, 1 female, slide 1479; 12/06/2020, Nagylózs, *Rubus Seebergensis*, Geza Ripka, 2 slides with 4 females, slides 1499-1 and 1499-2; 27/09/2018; **Serbia**: 2 slides with 1 female each, previously identified as *Homeopronematus* cf. *staercki* sp. nov. (Stojnić *et al.* 2002): 18/06/1996, Kolekcija Boleč, Boleč, *Malus* sp., Stojnić, 1 female, slide 28; 28/07/1996, Kolekcija Boleč, Boleč, *Malus* sp., Stojnić, 1 female, slide 34. **from USPB**: **USA**: 29/10/1977, U.C.R. Campus Riverside Co-CA, grape, Gilberto de Moraes, 1 female, 356; 14/10/1977, U.C.R. Campus Riverside CA, *Malva* sp. (Malvaceae), Gilberto de Moraes, 2 females, 359 MZQL 2199 C=994; 29/10/1977, Oakglen, San Bernardino, *Cedreila* ?, Gilberto de Moraes, 1 female, 356 MZQL 2206 C=997.

In this study, we found *H. anconai* on grape, *Malva* sp. and *Cedreila* (?) on slides with specimens from USA. In Europe, we found it on *Rubus* sp., raspberry, *Brugmansia* sp., bittersweet, Solanaceae sp., tomato, cucumber, grape and fig.

***Quasihomeopronematus nordestinus* n. gen. n. sp.**

Brazil: we received 7 slides From Ítalo Marcossi mounted 24/01/2022, Viçosa, MG, -20.7598, -42.8829, tomato, and additional material from the same culture in alcohol which we mounted in Hoyer. From museum USPB we studied three females on two slides: 11/06/1993, Amontada, CE, Campo 24, cassava *Manihot esculenta* Crantz (Euphorbiaceae), I.A. Almeida, 1 female, MZQL 4471 C=2941; 15/06/1993, 'Gov. De Ze Rosado' (we suppose Governador dix-sept Rosado) RN, Campo 27 *Macroptilium* sp., (Fabaceae) I.A. Almeida, 2 females, MZQL 4480 C= 2950.

Quasihomeopronematus nordestinus n. gen. n. sp. has been found on tomato, casava and *Macroptilium* sp.

Morphological descriptions

Family Iolinidae Pritchard, 1956

Subfamily Pronematinae André, 1979

Genus *Homeopronematus* André, 1980

Type species — *Homeopronematus vidae* by original designation André (1980: 114).

Description — Adult female. Aspidosoma procurved with four pairs of setae *bo*, *ro*, *la* and *ex*; opisthosoma with 11 pairs of setae, *cl*, *c2*, *dl*, *el*, *fl*, *f2*, *hl*, *h2*, *ps1*, *ps2* and *ps3*. Poroidotaxy: *ia*, *im*, *ip*, *ih*. Eye spots absent. Four pairs of aggenital setae. Empodium and claws absent on leg I, each of other legs with ciliate empodium and two claws, without empodial hooks. Leg chaetotaxy: I (9+ ω -3+k+ φ -3-3-1), II (6+ ω -2-3-3-1), III (6-2-2-2-1), IV (6-2-1-2-0). Epimeral formula 3-1-4-1. Body setae finely serrate. Poroidotaxy: *ia*, *im*, *ip*, *ih*. Adult male as female, but with only one pair of ag setae, however, in some specimens a second unpaired ag seta, anterior to the paired setae, has been found.

Immatures can be recognised by the following chaetotaxy (difference with adult in bold): opisthosoma same as adult for all stages; epimeral formula adult, tritonymph and deutonymph (3-1-4-2), protonymph (3-1-**3-0**), larva (3-1-2). Aggenital setae: female and tritonymph: 4; male: 1; deutonymph: **2** in female, unknown in male; protonymph and larva **absent**. Leg chaetotaxy: tritonymph: I (9+ ω -3+ κ + φ -3-3-1), II (6+ ω -2-3-3-1), III (6-2-2-2-1), IV (**5-2-1-2-0**); deutonymph: I (9+ ω -3+ κ + φ -3-3-**0**), II (6+ ω -2-3-3-**0**), III (**5-2-2-2-1**), IV (**5-2-1-2-0**); protonymph: I (9+ ω -3+ κ + φ -3-3-**0**), II (6+ ω -2-3-3-**0**), III (**5-2-2-2-1**), IV (**5-0-0-0-0**); and larva: I (6+ ω -3+ κ + φ -3-3-**0**), II (6+ ω -2-3-3-**0**), III (**5-2-2-2-0**).

Remark — We add seta homologous to *s* (see Ueckermann & De Vis *et al.*, 2024) on tarsus I in all stases, except larva to the genus description of André (1980). Although we could not study the type material, which is lost or faded away (personal observation of the last author), all material we studied, including the US material, clearly showed this small seta homologous to *s*.

Homeopronematus anconai (Baker, 1943)

Homeopronematus anconai (Baker), Knop and Hoy 1983a: 2.

Pronematus anconai Baker, 1943:188-9; Baker, 1968: 1094-5; Kuznetsov, 1972: 11

Senior synonym of *Homeopronematus vidae* André, 1980: 116; *Pronematus staercki* Schruft, 1972: 129

(Figures 1-8)

Redescription

Measurements — Measurements of different structures are shown in Table 2.

Adult female

Idiosoma — (Figures 1, 4a–b & 6a). Ovaloid, tapering posteriorly. Completely striated; striae in general continuous, fine and lobed. Dorsal setae clearly barbed, ventral setae apparently smooth, except *3c* and *3d*, which are finely serrated.

Dorsum — (Figure 1 & 6a). Aspidosoma with subparallel striae, converging anteriorly; dorsum of opisthosoma with striae converging posteriorly *dl*, becoming transverse between *dl-fl* and then divergent toward posterior edge. Idiosomal setae aciculate, serrated (Figures 5e, g); trichobothrial seta *bo* finally serrated over entire length (Figure 5c). Trichobothrial seta *bo* the longest, followed by *ex*, *la* and *ro*; *la* somewhat finer than others of similar thickness. Setae *cl*, *dl*, *el* and *fl* not reaching base of *dl*, *el*, *fl* and *hl*, respectively. Lyrifissure *ia* situated

Table 2 Dimension of characteristics of *Homeopronematus anconai* (Baker) of different origins and *Quasihomeopronematus nordestinus* n. gen. n. sp. (mean ± standard error (min-max) n).

Species	USA	Europe	Belgium	France	France 85	The Netherlands	Switzerland	Germany	Czech Republic	Serbia	Hungary	Belgium
Country	female	male	female	male	female	female	female	female	female	female	female	female
Subs	4	86	23	14	17	5	4	5	7	2	9	7
<i>length</i>	1367.5 ± 45.1 (121.1-1621.1)	3863.5 ± 165.1 (1975.5-2201.36)	3075.2 ± 107.5 (220.1-3280.1)	1865.2 ± 200.0 (200.0-317.15)	1601.5 ± 51.2 (103.2-1663.5)	1893.2 ± 47.0 (14.2-186.64)	1851.4 ± 157.0 (102.3-2308.5)	1445.2 ± 24.0 (136.6-158.7)	1445.2 ± 24.0 (136.6-158.7)	1487.7 ± 45.1 (103.2-1663.5)	188.4 ± 56.4 (13.8-186.219)	111.4 ± 1.0 (108.2-115.57)
<i>width</i>	1241.1 ± 38.1 (106.1-1421.0)	4091.0 ± 182.0 (2000.0-4991.0)	1228.8 ± 103.8 (149.0-1475.2)	1216.6 ± 221.0 (109.4-181.13)	1234.9 ± 75.1 (113.6-1473.4)	1052.2 ± 57.0 (104.5-128.24)	1051.1 ± 102.0 (136.3-1463.5)	1001.1 ± 16.0 (103.5-113.7)	1001.1 ± 16.0 (103.5-113.7)	121.4	178.8 ± 56.4 (12.0-170.318)	30.2 ± 1.6 (16.6-36.047)
<i>h</i>	27.5 ± 0.6 (2.6-30.5)	187.8 ± 16.8 (135.5-189.9)	31.7 ± 0.2 (34.2-38.2)	36.0 ± 0.7 (37.1-39.1)	33.9 ± 0.4 (30.0-37.3)	34.4 ± 0.8 (31.9-38.2)	37.5 ± 0.7 (35.9-40.5)	35.3 ± 0.9 (32.3-39.5)	35.3 ± 0.9 (32.3-39.5)	35.2	36.6 ± 0.7 (32.9-39.2)	30.2 ± 0.5 (19.9-32.7)
<i>h₁</i>	35.6 ± 0.3 (32.2-38.2)	35.6 ± 0.3 (32.2-38.2)	35.6 ± 0.3 (32.2-38.2)	35.9 ± 0.2 (31.7-38.0)	37.4 ± 0.3 (33.6-39.5)	37.4 ± 0.3 (33.6-39.5)	37.5 ± 0.8 (35.9-40.5)	37.5 ± 0.8 (35.9-40.5)	37.5 ± 0.8 (35.9-40.5)	35.2	36.6 ± 0.7 (32.9-39.2)	30.2 ± 0.5 (19.9-32.7)
<i>h₂</i>	21.3 ± 0.2 (16.7-23.5)	201.1 ± 0.6 (15.1-23.9)	21.3 ± 0.2 (16.7-23.5)	206.0 ± 0.2 (17.6-22.6)	20.6 ± 0.2 (17.6-22.6)	20.6 ± 0.2 (17.6-22.6)	20.6 ± 0.2 (17.6-22.6)	20.6 ± 0.2 (17.6-22.6)	20.6 ± 0.2 (17.6-22.6)	21.7	19.8 ± 0.4 (17.8-21.3)	13.5 ± 0.4 (12.5-15.8)
<i>ro</i>	23.1 ± 0.2 (20.9-25.9)	23.1 ± 0.2 (20.9-25.9)	23.1 ± 0.2 (20.9-25.9)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	21.7	24.1 ± 0.5 (21.8-26.4)	16.3 ± 0.3 (15.1-17.5)
<i>ro₁</i>	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	18.9 ± 0.3 (17.4-21.4)	19.9	19.9 ± 0.5 (15.4-19.9)	14.7 ± 0.3 (12.6-16.9)
<i>ro₂</i>	40.1 ± 0.3 (38.4-43.7)	40.1 ± 0.3 (38.4-43.7)	40.1 ± 0.3 (38.4-43.7)	39.9 ± 0.3 (37.4-43.1)	38.3 ± 0.3 (36.1-41.5)	39.3 ± 0.7 (38.4-41.5)	41.6 ± 0.5 (40.2-43.0)	41.6 ± 0.5 (40.2-43.0)	41.6 ± 0.5 (40.2-43.0)	39.2	41.3 ± 0.8 (37.3-44.3)	30.4 ± 0.3 (29.5-32.7)
<i>la</i>	121.1 ± 1.0 (116.0-126.1)	352.4 ± 10.1 (312.0-392.4)	121.1 ± 1.0 (116.0-126.1)	121.1 ± 1.0 (116.0-126.1)	121.1 ± 1.0 (116.0-126.1)	121.1 ± 1.0 (116.0-126.1)	121.1 ± 1.0 (116.0-126.1)	121.1 ± 1.0 (116.0-126.1)	121.1 ± 1.0 (116.0-126.1)	121.1	121.1 ± 1.0 (116.0-126.1)	20.1 ± 0.4 (18.5-21.7)
<i>la₁</i>	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2 ± 0.2 (18.8-21.6)	20.2	20.2 ± 0.2 (18.8-21.6)	11.5 ± 0.3 (10.8-12.4)
<i>la₂</i>	18.5 ± 0.2 (14.8-20.2)	18.5 ± 0.2 (14.8-20.2)	18.5 ± 0.2 (14.8-20.2)	17.3 ± 0.1 (15.1-19.2)	16.6 ± 0.2 (15.1-19.2)	17.9 ± 0.4 (16.9-19.4)	16.9 ± 0.3 (16.1-18.5)	16.2 ± 0.3 (14.8-17.6)	16.2 ± 0.3 (14.8-17.6)	16.9	17.2 ± 0.6 (14.7-19.9)	11.5 ± 0.3 (10.8-12.4)
<i>cl</i>	40.7 ± 0.9 (37.2-47.9)	40.7 ± 0.9 (37.2-47.9)	40.7 ± 0.9 (37.2-47.9)	38.1 ± 1.4 (34.9-46.1)	35.4 ± 0.9 (33.1-37.6)	35.4 ± 0.9 (33.1-37.6)	35.4 ± 0.9 (33.1-37.6)	35.4 ± 0.9 (33.1-37.6)	35.4 ± 0.9 (33.1-37.6)	32.1	32.1 ± 1.6 (25.8-34.5)	27.8 ± 0.5 (25.9-30.7)
<i>cl₁</i>	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3 ± 0.2 (21.3-27.3)	24.3	24.3 ± 0.2 (21.3-27.3)	13.6 ± 0.3 (12.7-14.8)
<i>cl₂</i>	36.3 ± 0.8 (28.4-44.2)	36.3 ± 0.8 (28.4-44.2)	36.3 ± 0.8 (28.4-44.2)	34.7 ± 1.1 (31.5-42.1)	33.7 ± 1.1 (31.2-42.1)	34.7 ± 1.1 (31.5-42.1)	33.7 ± 1.1 (31.2-42.1)	33.7 ± 1.1 (31.2-42.1)	33.7 ± 1.1 (31.2-42.1)	33.2	33.2 ± 0.9 (30.5-36.3)	18.1 ± 0.2 (16.9-19.1)
<i>cl₃</i>	23.1 ± 0.4 (19.1-26.8)	23.1 ± 0.4 (19.1-26.8)	23.1 ± 0.4 (19.1-26.8)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2 ± 0.3 (21.9-25.6)	23.2	23.2 ± 0.3 (21.9-25.6)	11.4 ± 0.3 (10.1-12.8)
<i>cl₄</i>	32.7 ± 0.9 (27.6-39.4)	32.7 ± 0.9 (27.6-39.4)	32.7 ± 0.9 (27.6-39.4)	32.0 ± 0.3 (30.0-34.0)	34.6 ± 0.3 (32.3-37.5)	32.5 ± 0.3 (31.8-33.6)	32.5 ± 0.3 (31.8-33.6)	32.5 ± 0.3 (31.8-33.6)	32.5 ± 0.3 (31.8-33.6)	29.7	34.5 ± 0.6 (32.7-37.8)	24.0 ± 0.2 (23.3-25.9)
<i>cl₅</i>	21.2 ± 0.2 (18.3-23.1)	21.2 ± 0.2 (18.3-23.1)	21.2 ± 0.2 (18.3-23.1)	20.2 ± 0.3 (18.3-23.1)	19.7 ± 0.2 (18.3-23.1)	19.9 ± 0.8 (16.9-19.6)	20.7 ± 0.3 (19.9-21.5)	18.8 ± 0.5 (17.2-21.0)	18.8 ± 0.5 (17.2-21.0)	21.1	20.9 ± 0.1 (17.2-21.0)	9.9 ± 0.2 (8.1-11.7)
<i>cl₆</i>	30.2 ± 0.4 (26.2-33.8)	30.2 ± 0.4 (26.2-33.8)	30.2 ± 0.4 (26.2-33.8)	29.6 ± 0.4 (26.2-33.8)	28.1 ± 0.2 (26.2-33.8)	28.1 ± 0.2 (26.2-33.8)	28.1 ± 0.2 (26.2-33.8)	28.1 ± 0.2 (26.2-33.8)	28.1 ± 0.2 (26.2-33.8)	30.2	30.2 ± 0.4 (26.2-33.8)	15.6 ± 0.4 (14.2-17.3)
<i>cl₇</i>	20.6 ± 0.2 (18.4-22.2)	20.6 ± 0.2 (18.4-22.2)	20.6 ± 0.2 (18.4-22.2)	18.4 ± 0.2 (16.1-21.1)	18.4 ± 0.2 (16.1-21.1)	18.4 ± 0.2 (16.1-21.1)	18.4 ± 0.2 (16.1-21.1)	18.4 ± 0.2 (16.1-21.1)	18.4 ± 0.2 (16.1-21.1)	18.5	18.5 ± 0.2 (16.1-21.1)	8.3 ± 0.1 (7.4-9.3)
<i>cl₈</i>	23.4 ± 0.2 (20.8-25.9)	23.4 ± 0.2 (20.8-25.9)	23.4 ± 0.2 (20.8-25.9)	23.7 ± 0.5 (20.9-28.1)	21.9 ± 0.2 (20.8-25.9)	21.9 ± 0.2 (20.8-25.9)	21.9 ± 0.2 (20.8-25.9)	21.9 ± 0.2 (20.8-25.9)	21.9 ± 0.2 (20.8-25.9)	21.9	21.9 ± 0.2 (20.8-25.9)	11.2 ± 0.3 (9.8-12.9)
<i>cl₉</i>	11.4 ± 0.4 (10.8-12.6)	11.4 ± 0.4 (10.8-12.6)	11.4 ± 0.4 (10.8-12.6)	12.1 ± 0.3 (10.3-14.1)	12.1 ± 0.3 (10.3-14.1)	12.1 ± 0.3 (10.3-14.1)	12.1 ± 0.3 (10.3-14.1)	12.1 ± 0.3 (10.3-14.1)	12.1 ± 0.3 (10.3-14.1)	12.1	12.1 ± 0.3 (10.3-14.1)	6.6 ± 0.1 (6.1-7.3)
<i>cl₁₀</i>	15.2 ± 0.2 (12.7-17.6)	15.2 ± 0.2 (12.7-17.6)	15.2 ± 0.2 (12.7-17.6)	16.2 ± 0.2 (14.1-17.8)	14.6 ± 0.6 (12.4-16.5)	14.6 ± 0.6 (12.4-16.5)	14.6 ± 0.6 (12.4-16.5)	14.6 ± 0.6 (12.4-16.5)	14.6 ± 0.6 (12.4-16.5)	15.2	15.2 ± 0.2 (12.7-17.6)	9.9 ± 0.1 (9.4-10.7)
<i>lc</i>	16.8 ± 0.5 (13.6-19.6)	16.8 ± 0.5 (13.6-19.6)	16.8 ± 0.5 (13.6-19.6)	16.5 ± 0.2 (14.6-18.7)	17.4 ± 0.2 (15.5-19.1)	16.9 ± 0.4 (16.8-17.7)	16.9 ± 0.4 (16.8-17.7)	16.9 ± 0.4 (16.8-17.7)	16.9 ± 0.4 (16.8-17.7)	16.9	16.9 ± 0.4 (16.8-17.7)	6.5 ± 0.4 (5.4-8.7)
<i>lc₁</i>	15.0 ± 0.3 (13.1-16.8)	15.0 ± 0.3 (13.1-16.8)	15.0 ± 0.3 (13.1-16.8)	14.2 ± 0.2 (13.3-16.4)	15.3 ± 0.3 (13.6-16.8)	14.9 ± 0.3 (14.2-15.9)	15.4 ± 0.1 (14.9-15.9)	15.4 ± 0.1 (14.9-15.9)	15.4 ± 0.1 (14.9-15.9)	15.4	15.4 ± 0.1 (14.9-15.9)	12.2 ± 0.2 (10.5-11.8)
<i>lc₂</i>	18.9 ± 0.6 (15.7-22.4)	18.9 ± 0.6 (15.7-22.4)	18.9 ± 0.6 (15.7-22.4)	18.1 ± 0.4 (16.7-19.4)	18.1 ± 0.4 (16.7-19.4)	18.1 ± 0.4 (16.7-19.4)	18.1 ± 0.4 (16.7-19.4)	18.1 ± 0.4 (16.7-19.4)	18.1 ± 0.4 (16.7-19.4)	18.5	18.5 ± 0.2 (16.7-19.4)	10.5 ± 0.4 (10.1-13.6)
<i>lc₃</i>	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2 ± 0.2 (15.7-18.7)	17.2	17.2 ± 0.2 (15.7-18.7)	13.1 ± 0.3 (12.4-14.8)
<i>lc₄</i>	11.8 ± 0.4 (10.9-13.4)	11.8 ± 0.4 (10.9-13.4)	11.8 ± 0.4 (10.9-13.4)	10.5 ± 0.1 (9.1-11.5)	10.3 ± 0.3 (9.4-11.5)	10.3 ± 0.3 (9.4-11.5)	10.3 ± 0.3 (9.4-11.5)	10.3 ± 0.3 (9.4-11.5)	10.3 ± 0.3 (9.4-11.5)	10.3	10.3 ± 0.3 (9.4-11.5)	7.4 ± 0.2 (6.6-8.3)
<i>lc₅</i>	34.6 ± 3.8 (25.7-43.9)	34.6 ± 3.8 (25.7-43.9)	34.6 ± 3.8 (25.7-43.9)	26.1 ± 1.1 (21.1-31.6)	26.8 ± 2.3 (22.4-32.8)	22.4 ± 0.4 (21.6-23.2)	37.4 ± 1.1 (32.4-39.5)	15.9 ± 0.5 (12.8-17.4)	15.9 ± 0.5 (12.8-17.4)	23.8	34.8 ± 3.8 (26.7-48.4)	9.4 ± 0.4 (6.4-20.7)
<i>lc₆</i>	18.8 ± 0.7 (17.1-20.3)	18.8 ± 0.7 (17.1-20.3)	18.8 ± 0.7 (17.1-20.3)	17.2 ± 0.2 (15.6-18.7)	17.2 ± 0.2 (15.6-18.7)	17.2 ± 0.2 (15.6-18.7)	17.2 ± 0.2 (15.6-18.7)	17.2 ± 0.2 (15.6-18.7)	17.2 ± 0.2 (15.6-18.7)	17.2	17.2 ± 0.2 (15.6-18.7)	12.4 ± 0.2 (11.6-13.6)
<i>lc₇</i>	17.3 ± 0.6 (16.1-18.7)	17.3 ± 0.6 (16.1-18.7)	17.3 ± 0.6 (16.1-18.7)	20.2 ± 0.4 (16.3-23.2)	20.2 ± 0.4 (16.3-23.2)	20.2 ± 0.4 (16.3-23.2)	20.2 ± 0.4 (16.3-23.2)	20.2 ± 0.4 (16.3-23.2)	20.2 ± 0.4 (16.3-23.2)	20.2	20.2 ± 0.4 (16.3-23.2)	14.8 ± 0.4 (13.1-16.3)
<i>lc₈</i>	20.7 ± 1.0 (18.1-23.2)	20.7 ± 1.0 (18.1-23.2)	20.7 ± 1.0 (18.1-23.2)	22.5 ± 0.2 (18.2-23.8)	22.5 ± 0.2 (18.2-23.8)	22.5 ± 0.2 (18.2-23.8)	22.5 ± 0.2 (18.2-23.8)	22.5 ± 0.2 (18.2-23.8)	22.5 ± 0.2 (18.2-23.8)	22.5	22.5 ± 0.2 (18.2-23.8)	15.7 ± 0.2 (15.1-17.7)
<i>lc₉</i>	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2 ± 0.2 (8.5-9.9)	9.2	9.2 ± 0.2 (8.5-9.9)	6.8 ± 0.2 (5.7-10.7)
<i>lc₁₀</i>	13.9 ± 0.1 (12.4-15.4)	13.9 ± 0.1 (12.4-15.4)	13.9 ± 0.1 (12.4-15.4)	14.1 ± 0.3 (13.1-15.5)	14.1 ± 0.3 (13.1-15.5)	14.1 ± 0.3 (13.1-15.5)	14.1 ± 0.3 (13.1-15.5)	14.1 ± 0.3 (13.1-15.5)	14.1 ± 0.3 (13.1-15.5)	14.1	14.1 ± 0.3 (13.1-15.5)	9.9 ± 0.2 (8.5-11.8)
<i>lc₁₁</i>	8.8 ± 0.2 (6.9-10.8)	8.8 ± 0.2 (6.9-10.8)	8.8 ± 0.2 (6.9-10.8)	8.7 ± 0.2 (7.2-10.2)	8.7 ± 0.2 (7.2-10.2)	8.7 ± 0.2 (7.2-10.2)	8.7 ± 0.2 (7.2-10.2)	8.7 ± 0.2 (7.2-10.2)	8.7 ± 0.2 (7.2-10.2)	8.7	8.7 ± 0.2 (6.9-10.8)	5.9 ± 0.2 (5.2-7.1)
<i>lc₁₂</i>	8.6 ± 0.5 (6.6-10.3)	8.6 ± 0.5 (6.6-10.3)	8.6 ± 0.5 (6.6-10.3)	8.5 ± 0.1 (6.9-9.2)	8.5 ± 0.1 (6.9-9.2)	8.5 ± 0.1 (6.9-9.2)	8.5 ± 0.1 (6.9-9.2)	8.5 ± 0.1 (6.9-9.2)	8.5 ± 0.1 (6.9-9.2)	8.5	8.5 ± 0.1 (6.9-9.2)	7.4 ± 0.2 (6.6-8.3)
<i>lc₁₃</i>	4.4 ± 4.2 (3.5-7.9)	4.4 ± 4.2 (3.5-7.9)	4.4 ± 4.2 (3.5-7.9)	4.2 ± 0.1 (3.1-5.1)	4.9 ± 0.9 (5.1-5.1)	4.4 ± 0.1 (3.5-4.4)	4.8 ± 0.2 (4.4-5.8)	4.8 ± 0.2 (4.4-5.8)	4.8 ± 0.2 (4.4-5.8)	4.6	4.4 ± 0.1 (3.5-7.9)	4.2 ± 0.1 (3.5-7.9)
<i>lc₁₄</i>	13.8 ± 4.3 (10.5-16.3)	13.8 ± 4.3 (10.5-16.3)	13.8 ± 4.3 (10.5-16.3)	12.8 ± 0.3 (10.5-15.1)	13.1 ± 0.3 (11.1-17.1)	12.2 ± 0.3 (11.1-13.4)	13.5 ± 0.3 (12.6-16.3)	12.4 ± 0.3 (11.6-13.9)	12.4 ± 0.3 (11.6-13.9)	13.8	13.8 ± 4.3 (10.5-16.3)	9.3 ± 1.2 (1.7-10.9)
<i>lc₁₅</i>	6.4 ± 4.8 (7.1-13.8)	6.4 ± 4.8 (7.1-13.8)	6.4 ± 4.8 (7.1-13.8)	6.1 ± 0.5 (5.5-6.8)	6.0 ± 0.5 (5.5-6.8)	6.0 ± 0.5 (5.5-6.8)	6.0 ± 0.5 (5.5-6.8)	6.0 ± 0.5 (5.5-6.8)	6.0 ± 0.5 (5.5-6.8)	6.2	6.2 ± 0.1 (5.4-7.1)	5.1 ± 0.4 (4.8-5.4)
<i>lc₁₆</i>	10.5 ± 4.9 (8.6-13.4)	10.5 ± 4.9 (8.6-13.4)	10.5 ± 4.9 (8.6-13.4)	10.9 ± 1.6 (9.2-11.5)	10.9 ± 1.6 (9.2-11.5)	10.9 ± 1.6 (9.2-11.5)	10.9 ± 1.6 (9					

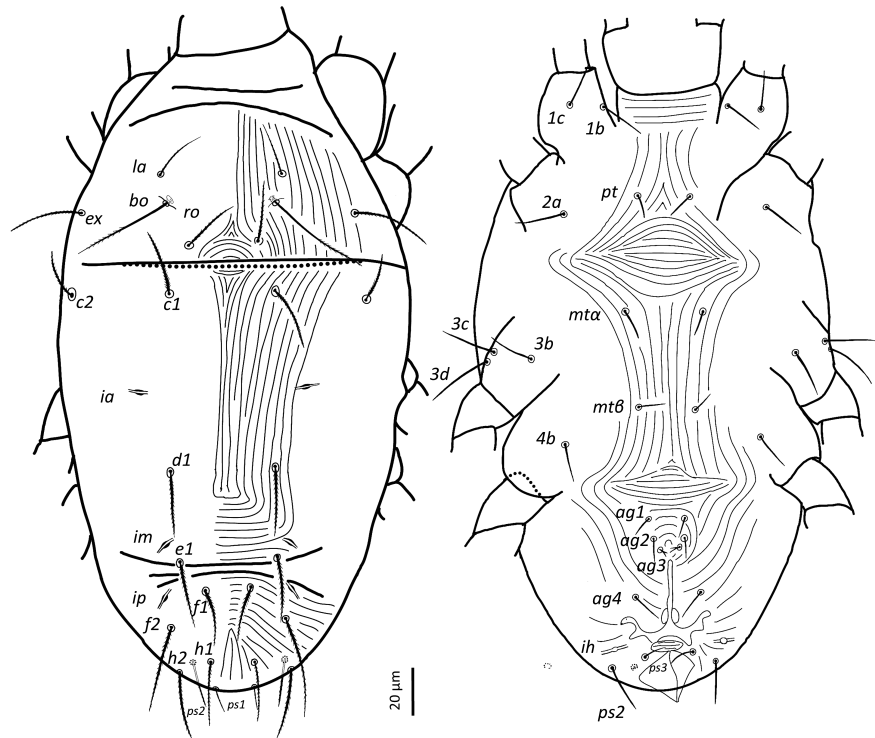


Figure 1 *Homeopronematus anconai* (Baker). Dorsum (left) and venter (right) of female.

half distance between setae *c1* and *d1* and far apart from imaginary line *c1-d1*. Lyrifissures *im* anterior to and closely associated with setae *e1*, slightly apart from imaginary line *d1-e1*. Lyrifissures *ip* situated approximately half distance between *e1* and *f2*, slightly apart from imaginary line *e1-f2*. Setae *ps2* dorsolaterally.

Venter — (Figure 1 & 4c). Transition area between idiosoma and gnathosoma with transverse striation, elsewhere longitudinal; constricted between legs I-II and legs III-IV; transverse for short median sections anterior to setae *mta* and anterior to setae *ag1*, constituting two spindle-shaped patterns, both wider than the distance between setae *mta* and setae *ag1*, respectively; striae convergent to genital opening. Setae *ps3*, antierad anal opening in area of striae that circumventing anal opening. Setae *ag3* small and bifurcated. In several slides kept at Essig Museum from a rearing from unknown origin and mounted in 1969, several females appear with *ag3* trifurcated. Genital opening in form of inverted “T”. With one pair of genital papillae. Lyrifissure *ih* laterad genital opening.

Gnathosoma — (Figure 2). Chelicera with parallel diagonal striation; dorsally with sclerotised tip and ventral stylet. Subcapitulum with longitudinal striation, two pairs of subcapitular setae, *sc1* 10.8 and *sc2* 13.1, and two pairs of adoral setae, *or1-2* ~ 5. Palpal tarsus terminating with distally bifurcate eupathidium, solenidion ω and seta *ba* minute; dorsal seta *d* bifurcate (not always visible), ventral seta *v* stouter and smooth; femorogenu 21.5 long and 9.7 wide. Palpal chaetotaxy (6+ ω -1-2).

Legs — (Figures 3 & 6b-d). Setae on legs fine and filiform and most of them are finely barbed or serrated, although hardly visible, except for ventral setae on tibiae and dorsal setae on femora and seta on trochanter III, which are stouter and more clearly barbed (only these have been drawn as such on Figure 3). Ventral setae of tibiae I to IV longer than their respective dorsals. **Leg I** with ω not surpassing tip of segment (Figures 3a, 6 a-c), five eupathidia of which abaxial fastigial and pair of tectals subequal; prorals shorter of which *p''*ζ shortest (Figures 3a & 6b); eupathidia barbed for about 2/3 at their base (Figures 3a, 5a & 6b), prorals and tectals

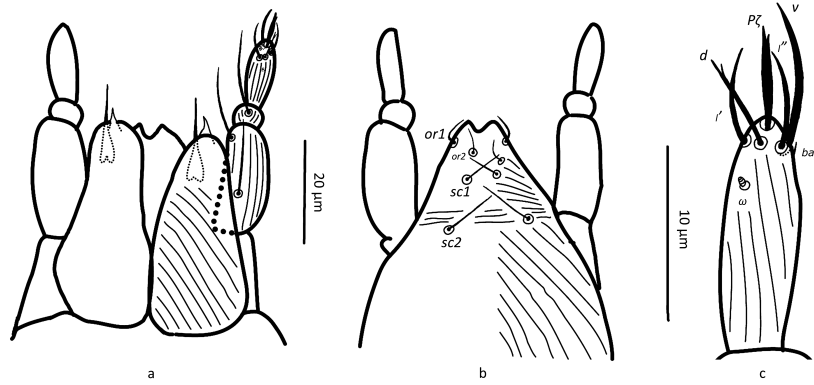


Figure 2 *Homeopronematus anconai* (Baker): a – Dorsal view of gnathosoma, b— ventral view of gnathosoma; and c – palptarsus.

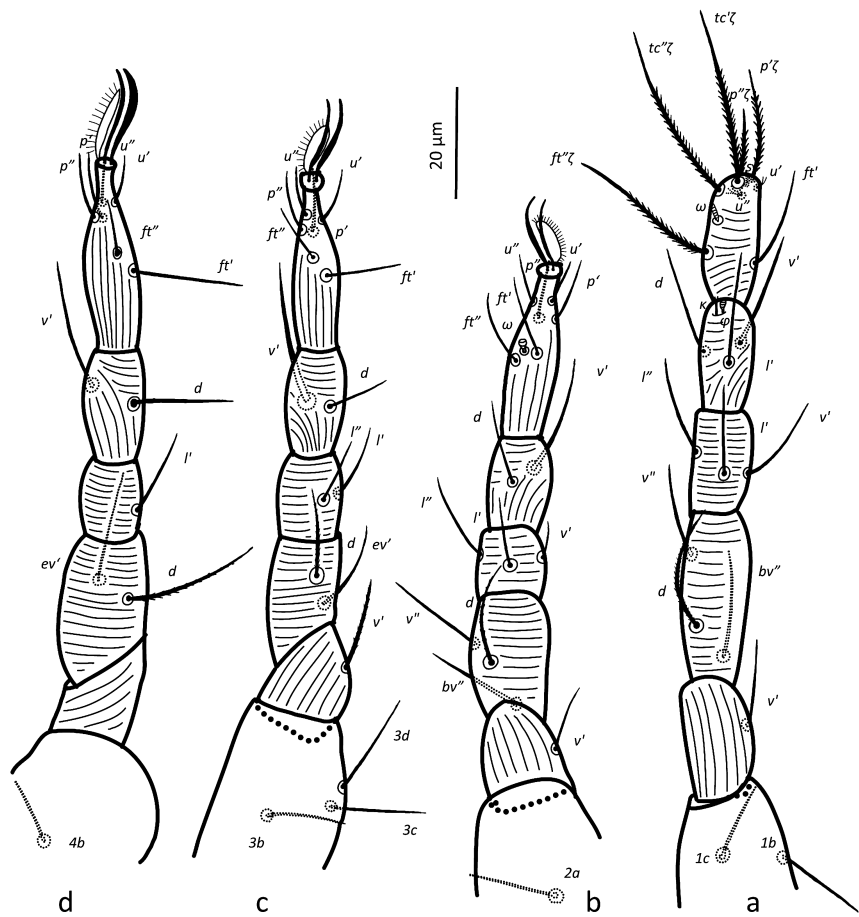


Figure 3 *Homeopronematus anconai* (Baker). Legs of female: a – Leg I, b – Leg II, c – leg III and d – leg IV.

in form of bow, fastigial $ft''\zeta$ slightly sigmoid; with two bifurcated unguinals adjacent and proximal to prorals; seta homologous to $s \sim 2.5$ between prorals (Figures 6c, d); ventral seta v' on tibia 30.5, famulus bifurcated at tip (Figure 6b) with common base of both forks (mostly only

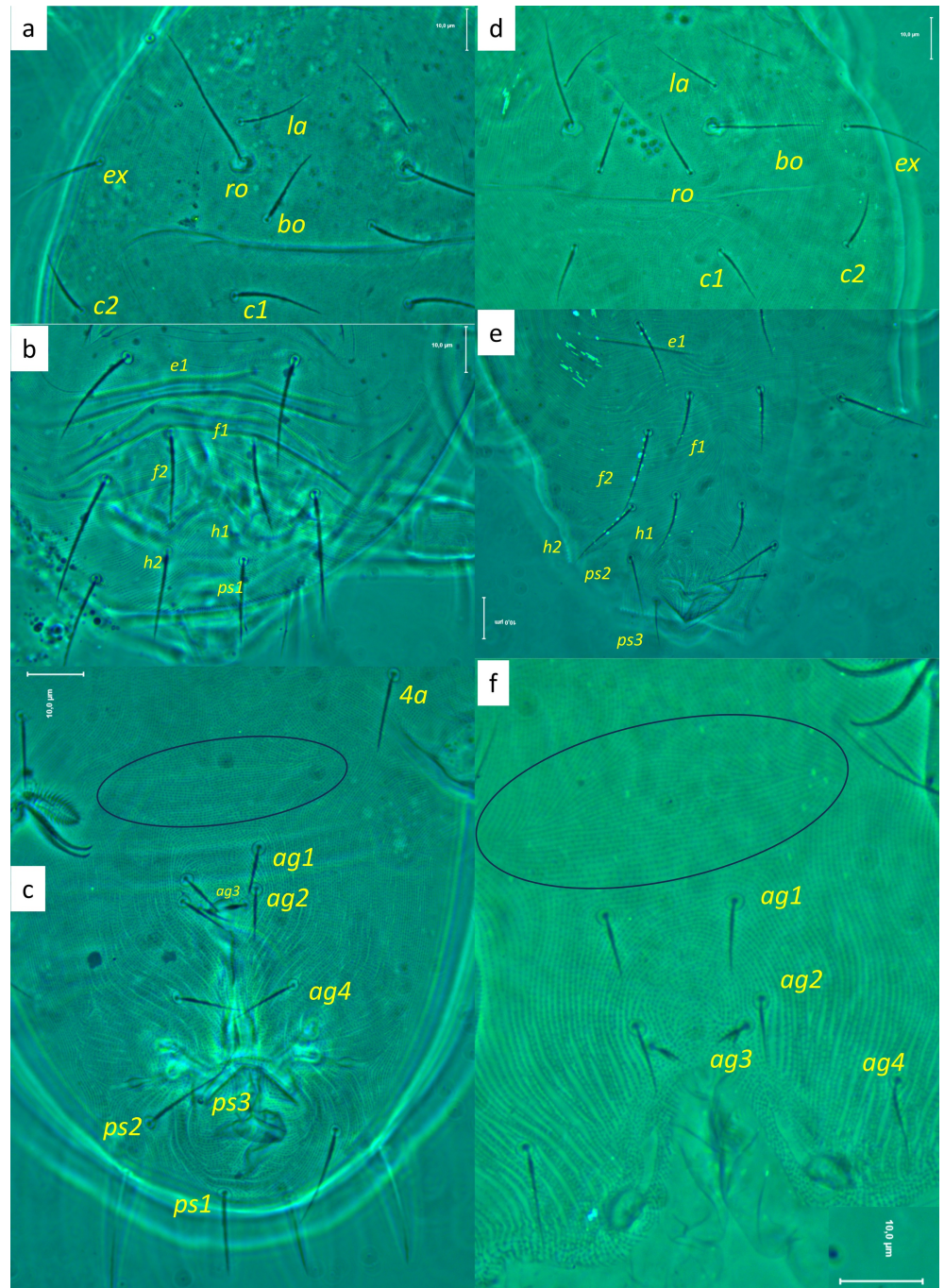


Figure 4 a-c *Homeopronematus anconai* (Baker): a – aspidosoma, b – posterior region of dorsum, c – posterior region of venter with transversal spindle-shaped striae (within ellipse) and genital area; d–f *Quasihomeopronematus nordestinus* n. gen. n. sp.: d – aspidosoma, e – posterior region of venter, f – posterior region of venter with transversal spindle-shaped striae (within ellipse) and genital area. Bar on each image = 10 µm.

this is visible) shorter than solenidion ϕ ; dorsal seta d on femur 30.7. **Leg II** with solenidion ω slender 2.2; tibia with ventral seta v' 29.2 and dorsal seta d 17.8; femur with dorsal setae d 22 and 18.4 and posterolateral/ventral seta v'' 18.4. **Leg III** with ventral seta v' 27.4 and dorsal seta d 15.9 on tibia; seta $3c$ of coxae shorter than $3b$ and $3d$. **Leg IV** with ventral seta v' 27.1 and dorsal seta d 19.7 on tibia; femur with ventral seta ev' 27.7 and dorsal d 27.9.

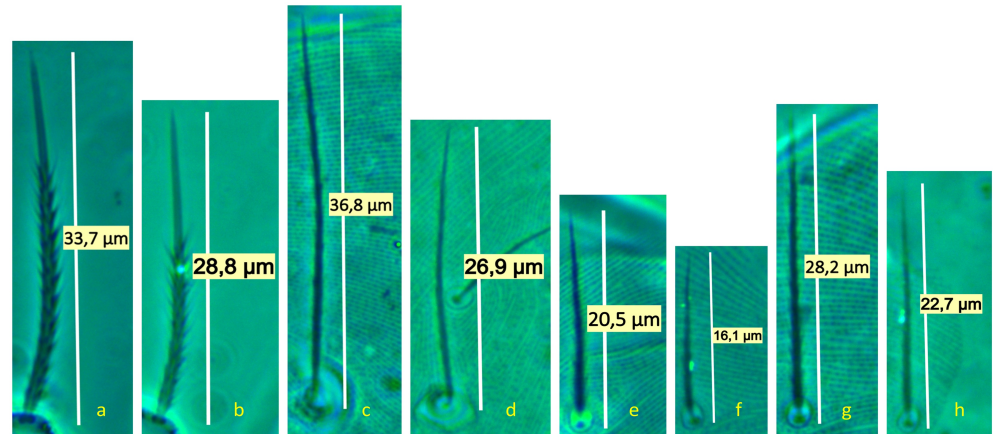


Figure 5 Different setae of respectively *Homeopronematus anconai* (Baker) and *Quasihomeopronematus nordestinus* n. gen. n. sp.: a–b $tc''\zeta$, c–d bo , e–f $f1$ and g–h $f2$.



Figure 6 Environmental scanning electron microscope images (ESEM) of *Homeopronematus anconai* (Baker) female. a – dorsal view, b – right leg I, c – dorsal view of tip of tarsus of leg I, d – ventral of tarsus of leg I with seta homologous to s .

Adult male

(Figure 7)

Idiosoma — Most of characters same as in female with exception of following: dorsal setae shorter, serrate; with only one pair of aggenital setae, although in one specimen a second, unpaired ag seta, posterior to one of $ag1$ setae was found; femur IV with distal, dorsal, adaxial, small and pointed spur (Figure 7). Two round spots, diameter 8, visible dorsally, posteriad $d1$ setae. Ventrally, genital opening forms a tube, as wide as distance $ps2-ps2$, above anal opening

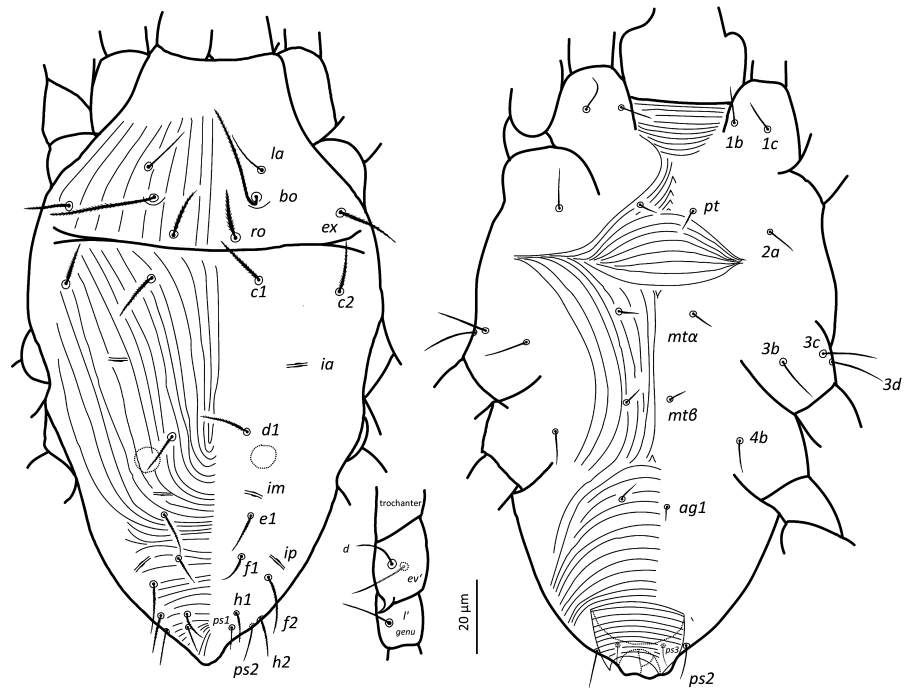


Figure 7 *Homeopronematus anconai* (Baker). Dorsum (left), venter (right) and leg IV (middle) of male.

and *ps3* setae. The dimensions of the Hungarian male fall within the range of the Belgian males.

Tritonymph

(Figure 8)

Idiosomal chaetotaxy like adults. Leg chaetotaxy like adults except for five setae on tarsus IV instead of six (seta *tc''* missing). Epimeral formula like in female. Setae *ag3* 4.7 not forked and shorter than *ag1* 5.3, *ag2* 5.6 and *ag4* 7.1; genital pore bivalved, situated medially and posterior to (*ag2*) and anterior to (*ag3*). Dehiscence line anterior to setae *la*.

Deutonymph

Idiosomal chaetotaxy like in female but with two pairs of aggenital setae instead of four, anterior to genital pore. Epimeral formula like in female. Leg chaetotaxy like in female but with five setae on each of tarsus III and IV instead of six, and no setae on each of trochanters I and II instead of one. Hence, deutonymph with the following chaetotaxy: I (9+ω-3+ κ+φ-3-3-0), II (6+ω-2-3-3-0), III (5-2-2-2-1), IV (5-2-1-2-0). Seta *ft''ζ* eupathid-like.

Protonymph

Idiosomal chaetotaxy like in female, but all aggenital setae missing. With only two setae on coxae III (*3d* missing) and *mtβ* and *4b* missing, hence epimeral formula 3-1-3-0. Leg chaetotaxy like in deutonymph but leg IV without setae except on tarsus which is equal deutonymph. Hence, protonymph with the following chaetotaxy: I (9+ω-3+ κ+φ-3-3-0), II (6+ω-2-3-3-0), III (5-2-2-2-1), IV (5-0-0-0-0). Seta *ft''* not eupathid-like.

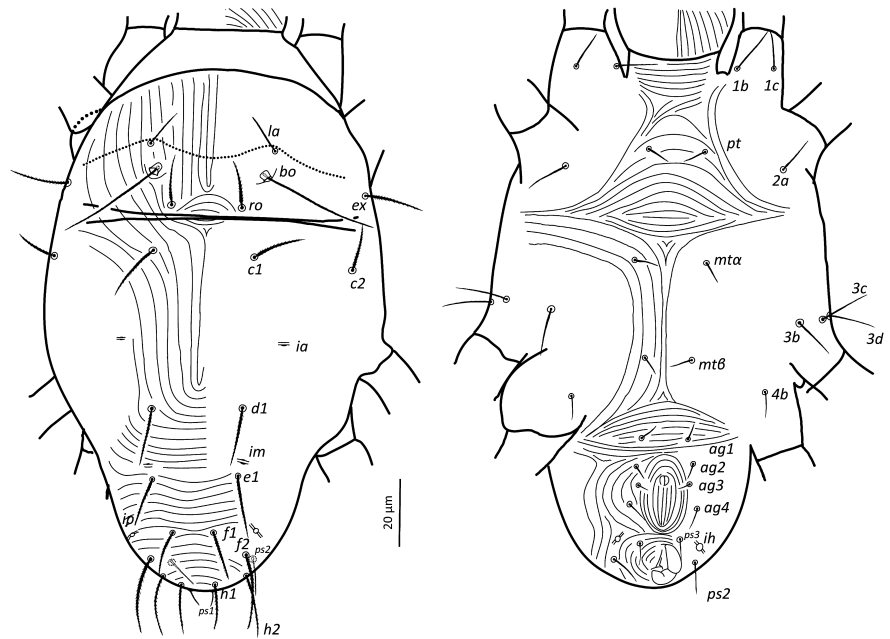


Figure 8 *Homeopronematus anconai* (Baker). Dorsum with dehiscent line anterior to setae *la* (left) and venter of tritonymph (right).

Larva

Idiosomal chaetotaxy like in protonymph. Coxae III with one seta (*3c* and *3d* missing) and leg IV missing, hence epimeral formula 3-1-2. Leg chaetotaxy like in protonymph but tarsus I with small pad-like empodium, without claws (*om*), setae (*p*) and setae (*fi*) not eupathid-like setae and setae (*tcζ*) eupathid-like, setae (*u*) and homologous to *s* missing; seta on trochanter III missing. Hence, larva with the following chaetotaxy: I (6+ω-3+κ+φ-3-3-0), II (6+ω-2-3-3-0), III (5-2-2-2-0).

Remarks

Chaetotaxy of body and legs as in André (1980) with the addition of seta homologous to *s* on tarsus I in adult, tritonymph, deutonymph and protonymph, but not in larva; moreover, in protonymph: epimeral formula 3-1-3-0 instead of 3-1-4-0; and in tritonymph five setae on tarsus IV instead of six.

Schruff (1972) did not describe the tritonymph of *H. staercki* but we suppose he confounded the deutonymph with a tritonymph as he found for his deutonymph 5 setae on tarsus IV and “two pairs of aggenital and two pairs of genital setae” (= 4 pairs of aggenital setae), which are characteristics of the tritonymph. He noted two unpaired genital pores, but we only found one bivalved genital pore. Furthermore, he noted for the female four pairs of ventral setae (we suppose *pt*, *mta*, *mtb* and *ag1*), two pairs of aggenital setae (we suppose the forked *ag3* considered as two setae), two pairs of genital setae (we suppose *ag2* and *ag4*) and one pair of anal setae (we suppose *ps3*). Unfortunately, he did not draw the venter of *H. staercki*, which could have cleared out the status of *ag3*. For all nymphal stages he did not note setae (*u*) on tarsus I and *κ* on tibia I and he also did not describe *κ* on tibia I in larval stage.

Genus *Quasihomeopronematus* n. gen. De Vis & Ueckermann

Zoobank: 312955B1-8AA8-4F42-B941-E1F61AE01C54

Description

Adult female — Aspidosoma procurved with four pairs of setae *bo*, *ro*, *la* and *ex*; opisthosoma with 10 pairs of setae, *c1*, *c2*, *d1*, *e1*, *f1*, *f2*, *h1*, *h2*, *ps2* and *ps3*; *ps1* absent. Poroidotaxy: *ia*, *im*, *ip*, *ih*. Eye spots absent. Four pairs of aggenital setae. Empodium and claws absent on leg I, each of other legs with ciliate empodium and two claws, without empodial hooks. Leg chaetotaxy: I (9+ ω -3+k+ ϕ -3-3-1), II (6+ ω -2-3-3-1), III (6-2-2-2-1), IV (6-2-1-2-0). Epimeral formula 3-1-4-1. Body setae finely serrate. Poroidotaxy: *ia*, *im*, *ip*, *ih*.

Etymology

The Latin prefix quasi- means “almost, having some of the features but not all”. So, the genus name refers to the similarity with the genus *Homeopronematus*, which differs only in the presence of *ps1*.

Type species

Quasihomeopronematus nordestinus n. gen. n. sp.

Differential diagnosis

The genus resembles *Homeopronematus* but differs in the absence of *ps1*.

We describe this new genus, following André (1980) who introduced the principle that new combinations of idiosomal or leg chaetotaxy lead to genera. However, we could also have described a subgenus for species having the characteristic of losing *ps1*. References can be found for both options. However, if we apply this principle to establish a subgenus based only on the absence of *ps1*, this leads to confusion with other genera:

- *Ueckermaniella* would be a subgenus of *Metapronematus*, both have the same leg chaetotaxy, but the former has four *ag* and 11 dorsals (3 *ps*), the latter three *ag* and 10 dorsals (2 *ps*). The loss of an *ag* and a *ps* seta goes together in this case.

- We have several species or genera with the leg chaetotaxy of *Neopronematus* but with 10 or 11 dorsals instead of nine in *Neopronematus* (*h2* and *ps2* missing, but we interpret as *ps1* and *ps2* missing): *Dasilcoferla nadirae* (Silva, Da-Costa & Ferla, 2017)(Da Silva *et al.* 2017; De Vis *et al.* 2024) with 10 dorsals (*ps1* lacking) and a new Brazilian species with 11 opisthosomals (De Vis *et al.* in preparation).

On the other hand, we find examples where a new genus was not erected:

- The subgenus *Neotydeolus* of *Proctotydaeus* lacks *ps2*, while the other subgenera do not (Kaźmierski 1998).

- *Pausia litchiae* lacks one *ps* (Da Silva *et al.* 2017) while *Pausia* described by Kuznetsov and Lifshitz (1972) does not.

André (1980) evidently did not follow the synonymy of *Pausia* with *Naudea* (Baker and Delfinado 1976), because besides the opisthosomal chaetotaxy also the leg chaetotaxy is different. *Pausia* has 11 opisthosomals, six setae on tarsus II and III and five on tarsus IV while *Naudea* has 10 opisthosomals and seven setae on tarsi II to IV.

We also see other characteristics that might be considered for separating genera:

- The short forked *ag3* can be found in *Quasihomeopronematus* as in *Homeopronematus* (Baker 1968; Knop and Hoy 1983a) but also in all but one species of *Neopronematus* (*N. aegae* Panou, Emmanouel & Kaźmierski, 2000) (Panou *et al.* 2000; Darbemamieh *et al.* 2015).

In conclusion, to avoid increasing genera confusion, we follow André (1980) and create a new genus. Future studies might reorganise the genera in the Pronematinae based on an analysis of all relevant genus characteristics. However, the genus descriptions might need amplification as in most cases they are limited to chaetotaxy, and other characteristics that might be generic are only mentioned in species descriptions.

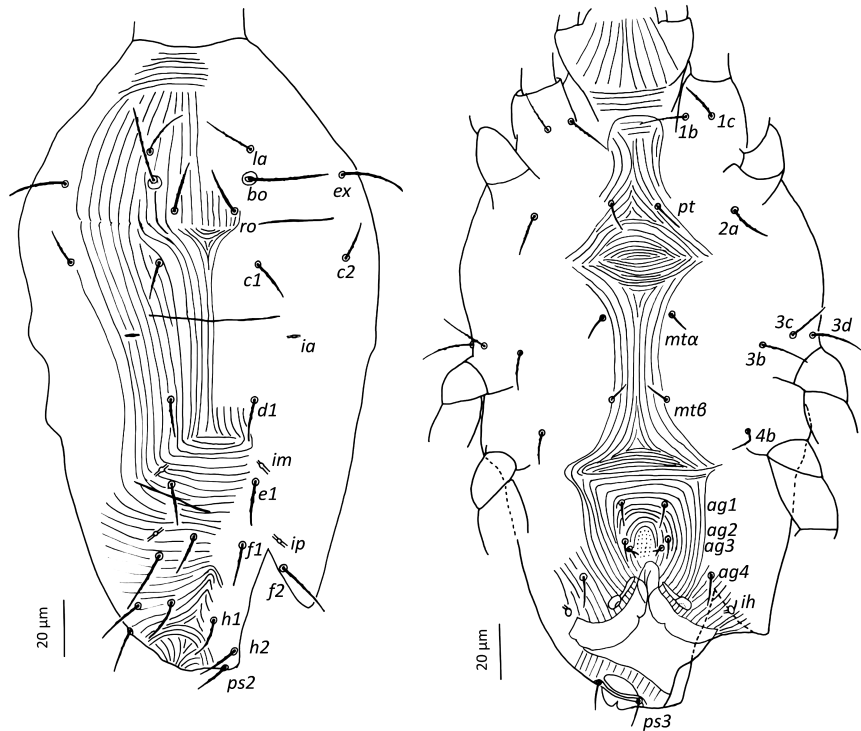


Figure 9 *Quasihomeopronematus nordestinus* De Vis & Ueckermann n. gen. n. sp. dorsum (left) and venter (right) of holotype female.

***Quasihomeopronematus nordestinus* De Vis & Ueckermann n. sp.**

Zoobank: [7D5C0FFF-66DA-4F1C-865E-1195D5D980C2](https://doi.org/10.24349/cu4t-4h6v)

(Figures 4-5 & 9-12)

Measurements

Measurements of different structures are shown in Table 2.

Adult female (holotype + paratypes 1-2)

Idiosoma — (Figure 9). Ovaloid, tapering posteriorly; procurved. Eye spots absent. Completely striated; striae in general continuous, fine and lobed. Dorsal setae finely barbed, ventral setae apparently smooth.

Dorsum — (Figure 9). Aspidosoma with subparallel striae, converging anteriorly; dorsum of opisthosoma with striae converging posteriorly *d1*, becoming transverse between *d1-f1* and then divergent toward posterior edge. Idiosomal setae aciculate, with very short serrations, *la* somewhat finer than others of subequal thickness (Figure 5f, h); trichobothrial seta *bo* with short serrations over entire length (Figure 5d). Trichobothrial seta *bo* the longest, followed by *ex*, *la* and *ro*; *la* somewhat finer than others of similar thickness. Most dorsal setae short, except *bo*, *f2* and *h2* which are longer. Setae *c1*, *d1*, *e1* and *f1* not reaching base of *d1*, *e1*, *f1* and *h1*, respectively. Lyrifissure *ia* situated half distance between setae *c1* and *d1* and far apart from imaginary line *c1-d1*. Lyrifissures *im* anterior to and closely associated with setae *e1*, slightly apart from imaginary line *d1-e1*. Lyrifissures *ip* situated approximately half distance between *e1* and *f2*, slightly apart from imaginary line *e1-f2*. Setae *ps2* dorsolaterally.

Venter — (Figure 9). Transition area between idiosoma and gnathosoma with transverse striation, elsewhere longitudinal; constricted between legs I-II and legs III-IV; transverse for

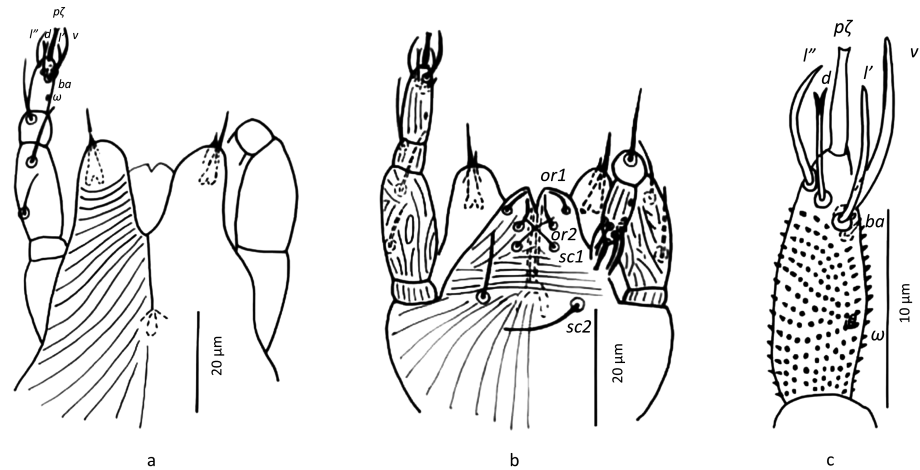


Figure 10 *Quasihomeopronematus nordestinus* De Vis & Ueckermann n. gen. n. sp. a – Dorsal view of gnathosoma, b – ventral view of gnathosoma and c – palptarsus.

short median sections anterior to setae *mta* and anterior to setae *agl*, constituting two spindle-shaped patterns, both wider than the distance between setae *mta* and setae *agl*, respectively; striae convergent to genital opening. Setae *ps3*, antierad anal opening in area of striae that circumventing anal opening. With four pairs of *ag* setae, *ag3* small and bifurcated. Genital opening in form of inverted “T”. With one pair of genital papillae and smooth longitudinal area anterior to each of them. Lyrifissure *ih* laterad genital opening.

Gnathosoma — (Figure 10). Chelicera with parallel diagonal striation; with dorsally sclerotised tip and ventral stylet. Subcapitulum with longitudinal striation, two pairs of subcapitular setae, *sc1* 8 and *sc2* 10.6, and two pairs of adoral setae, *or1-2* ~ 4. Palpal tarsus terminating with distally bifurcate eupathidium, solenidion ω and seta *ba* minute; dorsal seta *d* bifurcate, ventral seta *v* stouter and smooth; femorogenu 21.5 long and 9.7 wide. Palpal chaetotaxy (6+ ω -1-2).

Legs — (Figure 11). All setae on legs smooth, ventral setae of *v'* tibiae I to IV stouter and longer than their respective dorsals. **Leg I** with ω not surpassing tip of the segment, five eupathidia of which abaxial fastigial and pair of tectals subequal; prorals shorter of which *p''zeta* shortest; eupathidia barbed for about 2/3 at their base (Figure 5b); with two bifurcated unguinals adjacent and proximal to prorals; seta homologous to *s* ~2.5 between the prorals; ventral seta on tibia *v'* 26.8, famulus bifurcated at tip, shorter than solenidion φ ; dorsal seta *d* on femur 25. **Leg II** with solenidion ω slender 2.5; tibia with ventral seta *v'* 27.1 and dorsal seta *d* 15.6; femur with dorsal setae *d* 20.4 and *v''* 17 and posterolateral/ventral seta *bv''* 17.5. **Leg III** with ventral seta *v'* 24.5 and dorsal seta *d* 14.3 on tibia; seta *3c* of coxae shorter than *3b* and *3d*. **Leg IV** with ventral seta *v'* 23 and dorsal seta *d* 16.7 on tibia; femur not divided with ventral seta *21 ev'* and dorsal *d* 22.9.

Adult male

(Figure 12)

Idiosoma — Most of characters same as in female with exception of following: a pair of opisthosomal discs abaxial of setae *d1* (see also Ripka *et al.* 2013; Akbari *et al.* 2015), dorsal setae shorter, dorsal seta finely serrate, ventral setae apparently smooth; only 1 pair of aggenital setae, in some specimens only one unpaired *ag* seta; femur IV with a distal, dorsal, adaxial, small and pointed spur (Figure 11).

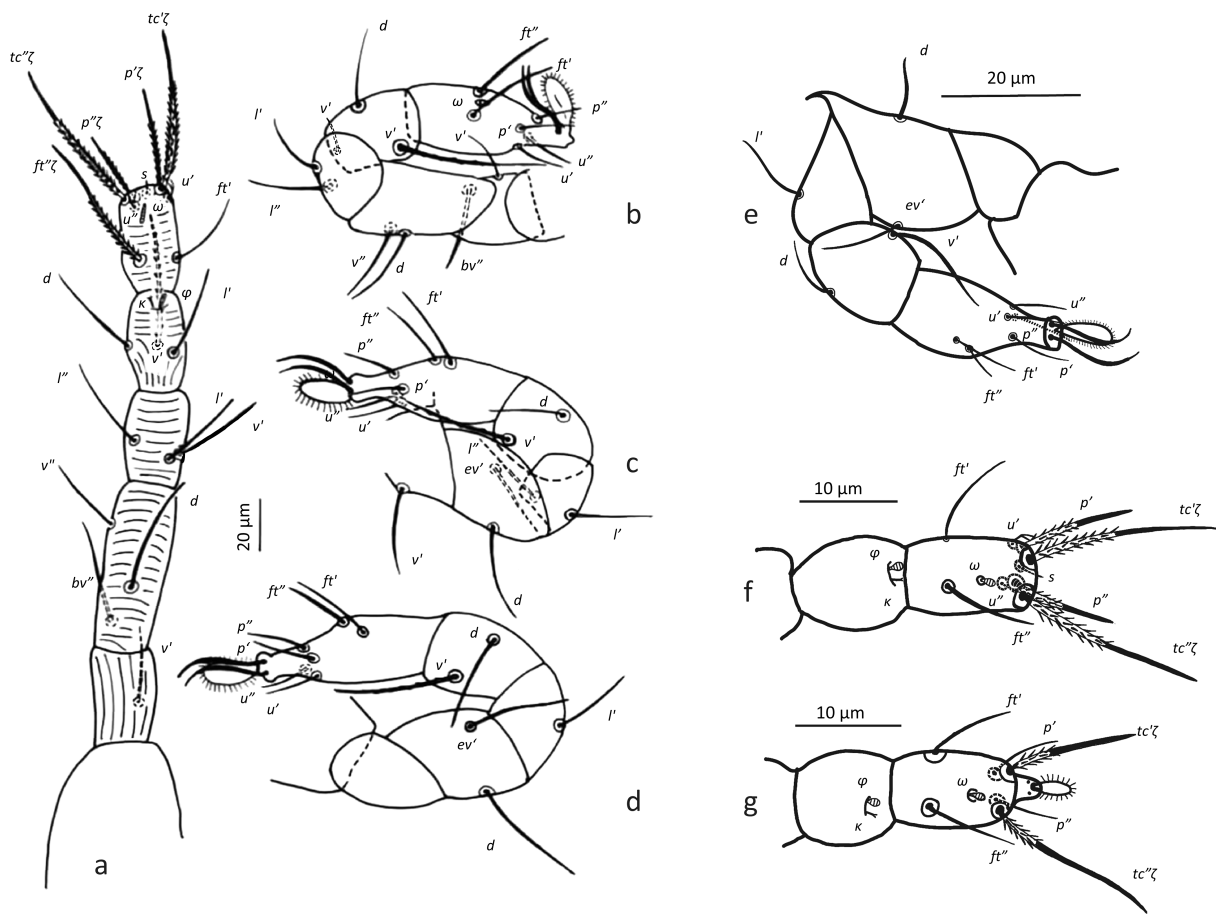


Figure 11 *Quasihomeopronematus nordestinus* De Vis & Ueckermann n. gen. n. sp. Legs of holotype female: a – leg I, b – leg II, c – leg III and d – leg IV; e – leg IV of male; f – tibia I and tarsus I of protonymph; and g – and tibia I and tarsus I of larva.

Tritonymph

Idiosomal chaetotaxy like in adults. Leg chaetotaxy like in adults except for five setae on tarsus IV instead of six. Epimeral formula like in female. Hence, tritonymph with the following chaetotaxy: I (9+ω-3+κ+φ-3-3-1), II (6+ω-2-3-3-1), III (6-2-2-2-1), IV (5-2-1-2-0). Female tritonymph with four pairs of aggenital setae, *ag1* 5.3, *ag2* 5.6, *ag3* 4.7 not forked and shorter than other *ag* setae, and *ag4* 7.1; genital pore bivalved, situated mesad and posterior to setae (*ag2*) and anterior to setae (*ag3*). Male tritonymph with one pair of aggenital setae.

Deutonymph

Idiosomal chaetotaxy like in female but with two pairs of aggenital setae instead of four, anterior to genital pore. Epimeral formula like in female. Leg chaetotaxy like in female but with five setae on each of tarsus III and IV instead of six, and no setae on each of trochanters I and II instead of one. Hence, deutonymph with the following chaetotaxy: I (9+ω-3+κ+φ-3-3-0), II (6+ω-2-3-3-0), III (5-2-2-2-1), IV (5-2-1-2-0). Seta *ft''ζ* eupathidial.

Protonymph

Idiosomal chaetotaxy like in deutonymph, but all aggenital setae missing. With only two setae on coxae III (*3d* missing) and *mtβ* and *4b* missing, hence epimeral formula 3-1-3-0. Leg chaetotaxy like in deutonymph but leg IV without setae except on tarsus which is equal to

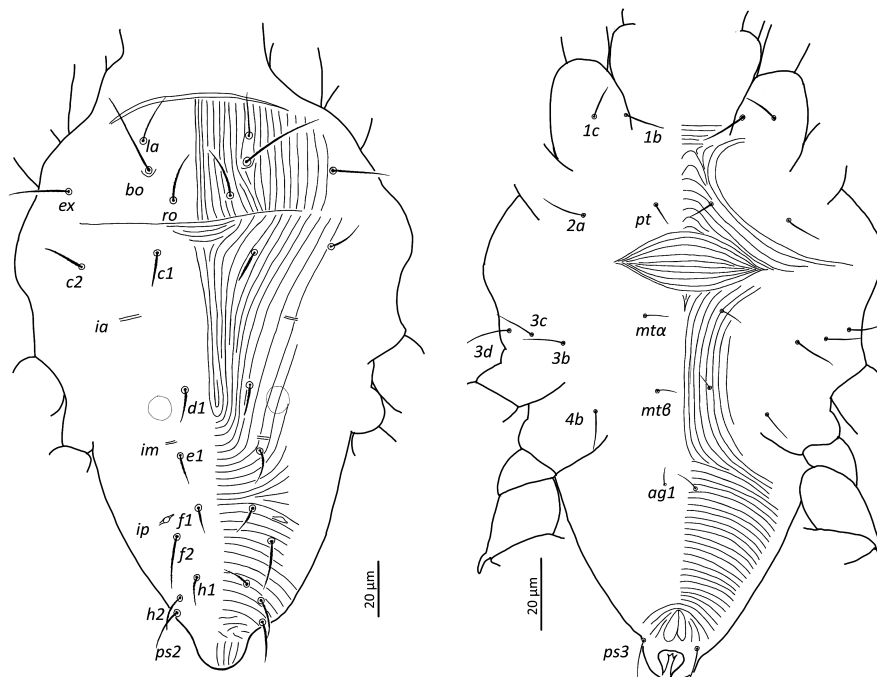


Figure 12 *Quasihomeopronematus nordestinus* De Vis & Ueckermann n. gen. n. sp. Dorsum (left) and venter (right) of male.

deutonymph. Hence, protonymph with the following chaetotaxy: I (9+ ω -3+ κ + ϕ -3-3-0), II (6+ ω -2-3-3-0), III (5-2-2-2-1), IV (5-0-0-0-0). Seta *ft*'' not eupathidial (Figure 11f).

Larva

Idiosomal chaetotaxy like in protonymph, all aggenital setae missing. Coxae III with 1 seta (3c and 3d missing) and leg IV missing, hence epimeral formula 3-1-2. Leg chaetotaxy like protonymph but tarsus I with small pad-like empodium, without claws (*om*), setae (*p*) and (*ft*) not eupathid-like, setae (*tc*ζ) eupathid-like, unguinal setae (*u*) and seta homologous to *s* missing and seta on trochanter III missing (Figure 11g). Hence, larva with the following chaetotaxy: I (6+ ω -3+ κ + ϕ -3-3-0), II (6+ ω -2-3-3-0), III (5-2-2-2-0).

Type locality and habitat

Quasihomeopronematus nordestinus has been found on tomato, casava, *Macroptilium* sp., in several states of the north-east of Brazil but also in the state of Minas Gerais (see collecting material in results section).

Type repository

All types deposited at Mite Reference Collection of Departamento de Entomologia e Acarologia, Escola Superior de Agricultura "Luiz de Queiroz" (ESALQ), Universidade de São Paulo (USP), Piracicaba, São Paulo state, Brazil, USPB (Zhang 2018).

Etymology

The species name refers to the North-East of Brazil, the region where the species was found for the first time in 1993.

Differential diagnosis

Quasihomeopronematus nordestinus **n. gen. n. sp.** resembles *H. anconai* but lacks dorsal setae *ps1* and all idiosomal setae are considerably shorter and finer (Figure 5). Except for the lack of *ps1*, the body and leg chaetotaxy of *Q. nordestinus* **n. gen. n. sp.** and *H. anconai* are the same in adults and immatures.

Molecular analysis

Homeopronematus anconai — For Belgium, 3 lab colonies (D21, B31 and B25) were set up. From these, 10 SFEL (D21.1, D21.2; B31.1, B31.6; B95.1-6) could be established and 6 DNA extractions (D21.1, D21.2; B31.6; B25.1, B25.3, B25.4;) were successful. For France, 2 lab colonies (B46 & B83) were set up, 12 SFEL (B46.1-6; B83.1-6) could be established and 9 DNA extractions (B46.1-6; B83.2, B83.3, B83.5) were successful. For Hungary, 1 lab colony (B174) was set up, 1 SFEL (B174.1) could be established, and 1 DNA extraction (B174.1) was successful. For Germany, 2 lab colonies (B175; B176) were set up, 3 SFEL (B175.1; B176.2-3) could be established, and 3 DNA extractions (B175.1; B176.2-3) were successful.

Quasihomeopronematus nordestinus **n. gen. n. sp.** — From Brazil, 1 lab colony (1) was set up in Brazil, and 13 SFEL (1.1-13) could be established, and 4 DNA extractions (1.1, 1.3-5) were successful.

We aligned 657 nucleotides of the sequences for analysis. The translation of the mtDNA CO1 nucleotide sequences resulted in a polypeptide of 219 amino acids in length.

As is generally the case in insects and mites, base pair frequencies showed that the region is A+T-rich. The G+C composition of the entire data set ranged from 20.70 to 36.07%. For *Q. nordestinus* **n. gen. n. sp.** this was 33.79% for all samples and for *H. anconai* the G+C content ranged from 33.03 to 34.09%.

Ueckermann & De Vis et. al. (2024) and De Vis et. al. (2024) defined CO1 sequences of *P. ubiquitous* and *P. duffelensis* and compared them with those of gradually less related species. Here we add sequences for *H. anconai* and *Q. nordestinus* **n. gen. n. sp.** and constructed a new maximum likelihood consensus tree. *Q. nordestinus* **n. gen. n. sp.** and *H. anconai* B83 separate in similar way from all other *H. anconai* (Figure 13). *Q. nordestinus* **n. gen. n. sp.** and *H. anconai* separate from *P. duffelensis* and *P. ubiquitous*.

Comparison of different origins and principal component analysis (PCA)

The measurements of reared (mass rearing or SFEL) females fell within the range of the wild specimens except for SFEL 83 from France. So, for constructing Table 2 and the PCA analysis all specimens for each country were pooled, except for SFEL 83 from France. A total of 84 measured specimens were included: for *Q. nordestinus* **n. gen. n. sp.** Brazil: 13; for *H. anconai*: USA-California: 4; Belgium: 23, The Netherlands: 5, France: 21, Germany: 5 (from Biobest) and XX from Markus Knapp (we hope to find at the site of first collection); Switzerland: 4, Czech Republic: 7 and Hungary 10. The PCA analysis was done with PAST (version 4.03). Based on 41 morphological measurements (see loading plot, Figure 8A), convex hulls were created (Figure 8B).

As in Ueckermann & De Vis et al. (2024), we could not find a good separation between the different origins using all 62 parameters. Similarly, we excluded in a second run also in this analysis the parameters that are susceptible to measurement errors and retained only the setal lengths (41 parameters) in the final PCA analysis. The loading of component 1 (63.3% of the variation) was highest for the dorsal setae with *bo*, *ex*, *c1*, *d1*, *e1*, *f1*, *f2*, *h1* and *3d* having a loading higher than 0.2, followed by *la*, *ro*, *c2*, *h2*, *3c*, and the eupathidia *ft''ζ*, *ft'''ζ*, *tc''ζ*, *tc'''ζ* and *p''ζ* on tarsus I, having a loading between 0.1 and 0.2. Most ventral setae as well as the small setae on leg I and the solenidia are characterized by a low loading (Figure 14A). The loading of component 2 with 6.6% was about tenfold lower than that of component 1.

Quasihomeopronematus nordestinus **n. gen. n. sp.** from Brazil clustered apart from all *H. anconai* origins. In *H. anconai*, the Californian (USA) and France SFEL 83.3 clustered apart

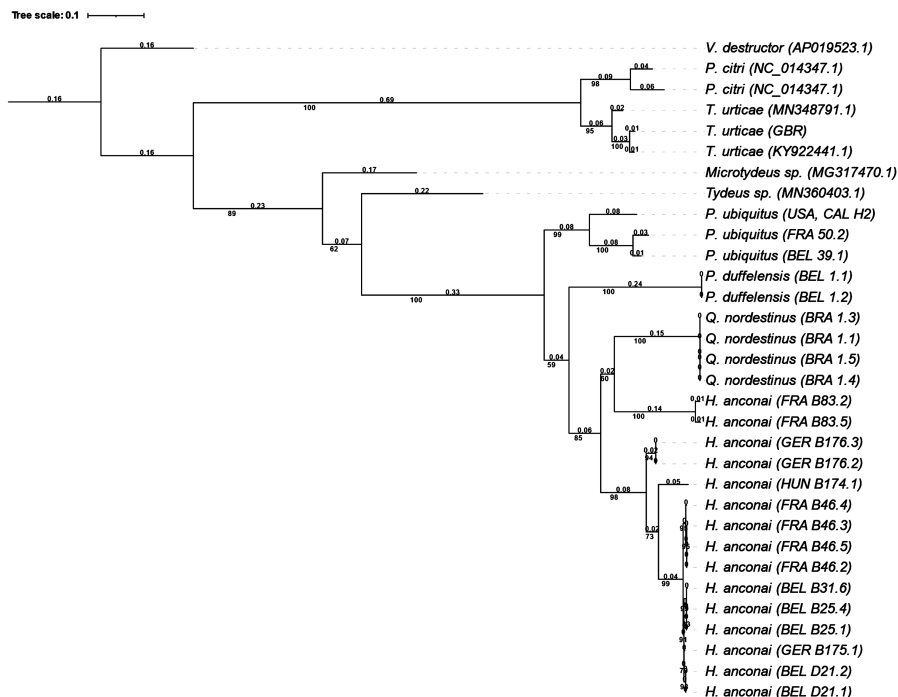


Figure 13 Maximum likelihood consensus phylogenetic tree of *Quasihomeopronematus nordestinus* n. gen. n. sp. and *Homeopronematus anconai* (Baker) and gradually less related species. Bootstrap values and branch lengths are shown respectively below and above the branches.

from all other origins, albeit with some overlap. All other origins show considerable overlap.

For Hungary, we studied five specimens identified as *H. staercki* [slides 1479, 1499-1 and 1499-2, Ripka *et al.* (2022)] apart from five specimens from our rearing originating from Hungary. We could not find morphological differences between these specimens and specimens of *H. anconai*. They did not cluster apart from *H. anconai* specimens of different countries.

For Serbia, the measurements of two specimens identified as “*Homeopronematus cf. staercki* sp. nov., Kazmierski” (see Stojnić *et al.* 2002) fall in the range of the European *H. anconai* specimens (Table 2 and Figure 14). We therefore consider the specimens of all countries as *H. anconai* (Figure 14B).

Discussion

Taxonomy

American and European *Homeopronematus anconai* are the same species.

We consider, based on our data and literature that they are indeed the same species. Knop and Hoy 1983a were the first to draw the American specimens. They studied types of Baker and concluded that *H. vidae* and *H. anconai* are synonyms. They did a thorough study. We could also study a series of slides with specimens coming from a rearing from the lab of M. Hoy in 1969, of unknown origin, held at Essig Museum and these specimens have both setae *u* and seta homologous to *s* present. The specimens we could study did not differ in such a way that we can consider them as different species (Table 2 and Figure 14). We are aware that studying topotypes (from type locality) would have been better, but we were unable to get this material, despite our efforts.

Homeopronematus staercki is junior synonym of *H. anconai* and “*Homeopronematus*

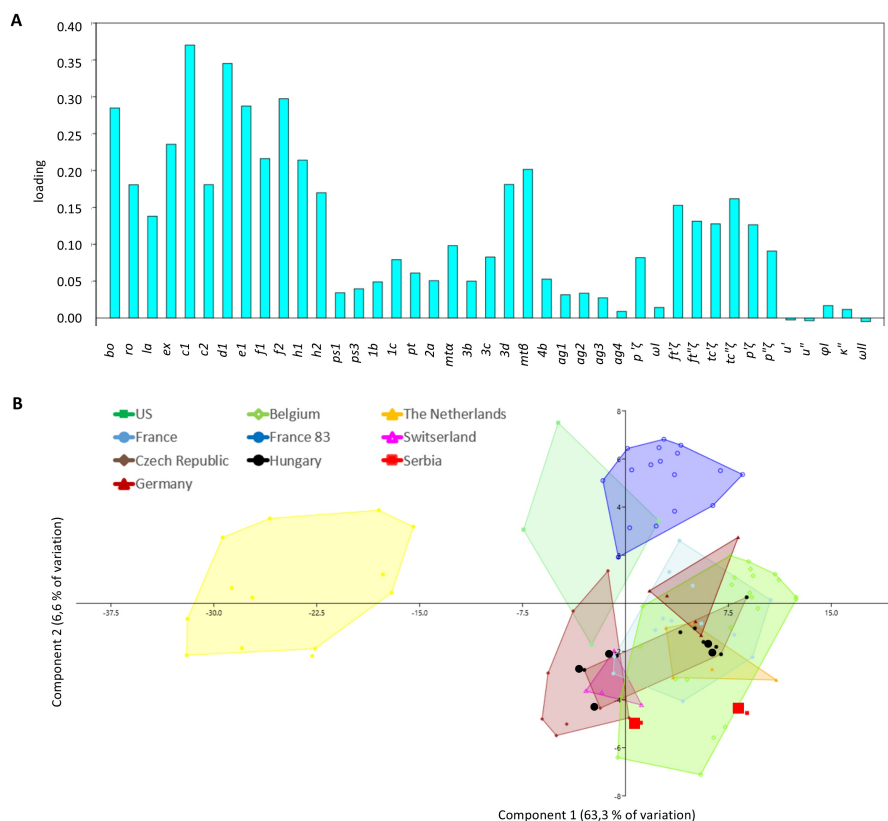


Figure 14 Principal component analysis (PCA) of morphometric characters measured on females of *Homeopronematus anconai* (Baker) from different countries and *Quasihomeopronematus nordestinus* n. gen. n. sp. from Brazil. A – loading of axis 1 for different characters B – Polygon graph. Each polygon refers to a different origin of *H. anconai* except the yellow one which refers to *Q. nordestinus* n. gen. n. sp. The bold black dots indicate Hungarian *H. anconai* specimens that were previously identified as *Homeopronematus staerki* n. syn. (see Ripka *et al.* 2022), and the two bold red squares to two Servian *H. anconai* specimens previously identified as *Homeopronematus* cf. *staercki* (see Stojnić *et al.* 2002).

cf. staercki sp. nov., Kazmierski” is *H. anconai*

As stated in the introduction, the literature is ambiguous in the description of the two species, *H. anconai* and *H. staercki*. The description of *H. staercki* (Schruff 1972) is so poor that the species could be synonymized with any species of the genus and no redescription has ever been proposed to clear out eventual differences with *H. anconai*. Schruff (1972) does not mention the shape of seta *ag3* in his description of *H. staercki* while it is forked in *H. anconai* (Baker 1968; Kuznetsov 1972; Knop and Hoy 1983a; this study). As the material used for the description *H. staercki* is lost, we cannot check this.

The specimens previously identified as *H. staercki* we could study are not different from *H. anconai*: they have identical body and leg chaetotaxy, no differences in the form of the setae could be distinguished, *ag3* is forked, the length of the eupathidia coincide with those of *H. anconai*, the striae are lobed. In the PCA they fall within the ‘cloud’ of *H. anconai* (Figure 14A). No differences could be detected in the shape of the setae, or the striation density. The dimensions of the Hungarian male we measured fall within the range of the Belgian males. Despite the large number of specimens from different origins we studied, we could not find one specimen that can be clearly distinguished from *H. anconai*. According to Knop and Hoy (1983a), the variability within the species is high which is confirmed in this study.

The differences as discussed by other authors are very small and are not sufficiently supported by descriptions with (range of) measurements and/or drawings: André (1980)

studied the types of *H. staercki* and found for this species a shorter *c*2, a higher striation density and further different “shape and length of idiosomal setae” (sic). We found that the variability in the length of *c*2 of *H. anconai* is indeed very high, varying between 15 and 21 µm. The striation leaves us with some doubt but also variability of this characteristic can be observed. Moreover, the density might be influenced by mounting or the state of the specimens at mounting. Finally, the shape and length of the setae are not described in detail.

Ripka *et al.* (2022) stated that the tectal and proral eupathidia on tarsus I of *H. anconai* are all four equal in length, while in *H. staercki* the tectals are nearly twice as long as the prorals. Our data show that in *H. anconai* tectals are nearly twice as long as the prorals, confirming descriptions of other authors (Baker 1968; Kuznetsov 1972; André 1980).

So based on our data and the previous arguments, we synonymise *H. staercki* with *H. anconai* as previously suggested by other authors (Knop and Hoy 1983a; Ueckermann *et al.* 2019).

Similarly, the specimens identified as “*Homeopronematus cf. staercki sp. nov.*, Kazmierski” (see Stojnić *et al.* 2002) are *H. anconai*. The measurements of these specimens fall in the range of the European *H. anconai* specimens (Table 2 and Figure 14).

Unguinals and seta *s*. As for *P. ubiquitous*, we found two forked unguinals and a seta homologous to *s*. We confirm that this seta *s* is erroneously named *u'* in Figure 1a & 1b in Knop and Hoy (1983a), as the position of *u'* is ventral and proximal to *p'ζ* and the depicted *u'* in Knop and Hoy (1983a) is in between the two prorals, which is the positions of seta homologous to *s*. Additionally, it is not forked, while both (*u*) are forked (Figures 3 & 6c, d). As in *H. anconai*, seta homologous to *s* is also present in all stages of *Q. nordestinus n. gen. n. sp.*, except in the larval stage, as well as that both unguinals are forked.

DNA barcoding or morphological identification

Not all 13 *H. anconai* sequences form one cohesive cluster. The French strain B83, clusters separately from the other *H. anconai* strains and forms a cluster higher up with the *Q. nordestinus n. gen. n. sp.* sequences from Brazil. It seems that the two species are closely related. However, it must be noted that the distance found between *Q. nordestinus n. gen. n. sp.* and *H. anconai* B83 with 0.31 is equal to the two most distant *H. anconai* strains (strain B83 and the Hungarian strain B174.1) and less compared to more closely related *H. anconai* strains in the phylogenetic tree.

We cannot separate the *H. anconai* specimens of different countries because we cannot find distinguishing characters among their origins. Most characters overlap with other origins and if no overlap is present in a character, the difference is small (Table 2) and certainly not sufficient to distinguish as a different species. This can also be seen in the PCA analysis (Figure 14A). Surprisingly, the specimens of B83 (including 1 wild specimen) from France separate from all other French origins in the PCA, although the distance is not large. When comparing the data in Table 2, also in this case no distinguishing character can be found between the measurements of both French origins. Additionally, the area covered by the Belgian specimens is similar to the area covered by the combined area of all French specimens. About 50% of the measured specimens are coming from an SFEL. So, to have a good overview of real diversity in the field, more wild samples coming from all over each country should be analysed. When we overlook the large area that covers *H. anconai* on Figure 14A we conclude that it is a species with high variability as also stated by Knop and Hoy (1983a).

Although the French strain B83 differentiates similarly as *Q. nordestinus n. gen. n. sp.*, from the other *H. anconai* strains in the PCA (Figure 14A), no significant morphological differences were found, so we cannot separate strain B83 as a distinct species. *Q. nordestinus n. gen. n. sp.*, on the contrary, is morphologically clearly different from *H. anconai* with *psI* lacking and shorter setae in general.

We must conclude that a phylogenetic tree based on the CO1-sequence only, is not sufficient to identify the closely related iolinids to species level.

Similarly, as for *P. ubiquitous* (Ueckermann *et al.* 2024), we found high similarity of the sequences originating from one locality which could be explained by the limited genetic basis as the laboratory cultures were started with few females.

To date, no CO1 sequences were available for *H. anconai* and *Q. nordestinus* **n. gen. n. sp.** and the unique CO1 sequences reported here constitute the first barcode for these species. However, DNA sequencing of more species, and as shown above, with more than one marker gene is required to elucidate relationships and distinguish species clearly. Studies have shown that when CO1 is combined with other marker genes such as 28r-RNA, clade structure can change (Duarte *et al.* 2023). This underscores the importance of additional research, integrating barcoding with morphological identification as to make the species delimitation more reliable (Puillandre *et al.* 2012). Preferably such research should be performed using confirmed and distinct species of the same genus, subpopulations of the same species and/or combined with crossbreeding studies to identify those subpopulations (Anderson and Trueman 2000; Tixier *et al.* 2008).

An explanation for the separation of the SFEL B83 is the small genetic basis with which the first rearing was set up (possibly with only one female). If a deviant female were present in sample B83, this would also be reflected in its offspring. One wild specimen of sample B83 falls within the range of the SFEL specimens. There is variation in the offspring of 83.1 but specimens of the other SFEL from Belgium and France did not separate from the wild specimens. And although, the specimens of sample/SFEL B83 separate in the PCA (Figure 14A), we cannot find distinguishing characters in Table 2.

We had only four USA specimens available in this study, but also here, no distinguishing characters could be found and overlap with European specimens can be seen in the PCA analysis (Figure 14B). Whether the observed genetic and morphological differences between or among European and non-European specimens are due to geographic separation is not proven. Therefore, much more independent samples, spread throughout each country or region should be analysed.

Distribution

Homeopronematus anconai is almost cosmopolitan not being found in Africa and Oceania (see introduction). As for *P. ubiquitous*, we also suppose that this mite has been travelling throughout the world on traded plant material, where it might not always have been found by the plant inspection authorities because of its small size, especially that of the eggs.

For *Q. nordestinus* **n. gen. n. sp.** the distribution at this moment is limited to Brazil. The presence of *H. anconai* in Brazil and by extension in other South American countries should be confirmed given that they might have been misidentified.

Habitat and feeding habits

In previous studies, *H. anconai* (including *H. staercki* **n. syn.**) was found on a wide spectrum of wild plants: *Buddleja sessiliflora* Kunth. (Scrophulariaceae) (Baker 1943); 17 associated plants in citrus orchards mainly *Thelypteris dentata* (Forssk.) E.P. St. John (Thelypteridaceae); *Solidago chilensis* Meyen (Asteraceae), *Ageratum conyzoides* L. (Asteraceae) and *Solanum americanum* (Solanaceae) (Horn *et al.* 2011); bittersweet (Ripka and Kaźmierski 1998; Ripka *et al.* 2013); *Elaeagnus angustifolia* L. (Elaeagnaceae), *Koelreuteria paniculata* Laxm. (Sapindaceae), *Rosa canina* L. (Rosaceae), *Sambucus nigra* L. (Adoxaceae) and *Ulmus laevis* Pall. (Ulmaceae) (Ripka and Kaźmierski 1998); a variety of trees, shrubs, and herbaceous plants (Kuznetsov 1972); and bark and foliage of several tree and shrub species (Ripka and Kaźmierski 1998).

But it was also frequently found on cultivated plants: tomato ((Hessein and Perring 1986; Kawai *et al.* 2001; García González 2003; Xu 2011; Çobanoğlu and Kumral 2014); strawberry (*Fragaria* × *ananassa* (Weston) Duchesne ex Rozier, Rosaceae) (Oatman 1971); blackberry (*Rubus vitifolia* Cham & Schlecht, *Rubus* sp., Rosaceae) (Knop and Hoy 1983a; Ripka *et al.*

2005; Ferreira 2016); *Ribes rubrum* L. (Grossulariaceae) (Ripka and Kaźmierski 1998); grape (Schruff 1972; Liguori 1987; Maurício *et al.* 2009; Johann *et al.* 2009; Klock *et al.* 2011; Tempfli *et al.* 2015; Tempfli 2019); Valencia orange (*Citrus sinensis* (L.) Osbeck, Rutaceae); apple (*Malus domestica* Borkh.) and pear *Pyrus communis* L. (Rosaceae) (Childers and Enns 1975; Thistlewood 1991; Ripka and Kaźmierski 1998); almond (*Prunus sect. amygdalus* (L.) Benth. & Hook.f., Rosaceae); hazelnut (*Corylus avellana* L., Betulaceae) (Ozman-Sullivan *et al.* 2005); *Juglans nigra* L. (Juglandaceae), (Ripka and Kaźmierski 1998); orchards (Darbemamieh *et al.* 2021); as well as in leaf litter of hedge plants (Ozman-Sullivan *et al.* 2005) or soil (Darbemamieh *et al.* 2020).

We want to draw attention to the registrations of *H. anconai* in Brazil (Johann *et al.* 2009; Klock *et al.* 2011; Horn *et al.* 2011; Sousa *et al.* 2015). The identifications should be confirmed as it might have been confounded with *Q. nordestinus* **n. gen. n. sp.**

In this study, we found *H. anconai* both on wild and cultivated plants. It was present in about every sample of *Rubus* sp. but furthermore, we found it on grape, *Malva* sp. and *Cedreila* (?), on raspberry, *Brugmansia* sp., bittersweet, tomato, cucumber (*Cucumis sativus* L. Cucurbitaceae), and fig. *Homeopronematus anconai* was much more common on wild plants than *P. ubiquitous* (Ueckermann & De Vis *et al.* 2024) while *P. ubiquitous* was more commonly found on cultivated plants such as tomato, sweet pepper, cucumber, grape and fig.

Horn *et al.* (2011) suggest that the associated plants, *T. dentata* and *S. chilensis* had the largest number of predatory mites including *H. anconai* and that these plants could serve as banker plants, as a beneficial host in citrus IPM programs in Brazil.

Homeopronematus anconai needs plant tissue such as blackberry, grape, bean (*Phaseolus vulgaris* L. Fabaceae) or tomato (Knop and Hoy 1983a; Vervae *et al.* 2022) and pollen or prey to reproduce. It cannot reproduce on leaf tissue, pollen or prey alone (Knop and Hoy 1983a; Hessein and Perring 1988b). In most research, cattail pollen (*Typha latifolia* (L.)) is used to culture *H. anconai* (e.g. Hessein and Perring 1988b; Vervae *et al.* 2022) but it can also reproduce on pollen from bottlebrush [*Callistemon citrinus* (Curtis) or *Melaleuca hypericifolia* Smith, both Myrtaceae), *Carpobrotus chilensis* (Mol.), ice plant (*Mesembryanthemum crystallinum* L., Aizoaceae), California poppy (*Eschscholzia californica* Cham., Papaveraceae), *Magnolia* sp. (Magnoliaceae) or aerial pollen that deposits on plants (Flaherty and Hoy 1971; Knop and Hoy 1983a; Hessein and Perring 1986) but not on bee-collected pollens (Flaherty and Hoy 1971) or pollen of *Cosmos* sp (Asteraceae), *Dahlia* sp (Asteraceae), or pine (Pinaceae) (Knop and Hoy 1983a).

Several authors have studied its potential use in biological control of *A. lycopersici* (Hessein and Perring 1986; Brodeur *et al.* 1997; Kawai and Haque 2004; Xu 2011; Vervae *et al.* 2022) and found a high predation capacity (Hessein and Perring 1986; Xu 2011; Vervae *et al.* 2022) and showed that it can control that mite below economic threshold levels (Hessein and Perring 1986; Kawai *et al.* 2001; Kawai and Haque 2004) whereas Brodeur *et al.* (1997) found that *H. anconai* could not develop to adulthood when fed solely with *A. lycopersici*. Additional food (pollen) enhances the reproduction of *H. anconai* (Hessein and Perring 1988b; Vervae *et al.* 2022) and can improve the biological control of *A. lycopersici* by *H. anconai* (Hessein and Perring 1988b).

Homeopronematus anconai preys also citrus flat mite *Brevipalpus lewisi* McGregor 1949 (Tenuipalpidae) (Hessein and Perring 1988a). Similarly *Pronematus brasiliensis* De Vis & Ueckermann 2024 can reproduce and survives well on a diet of *Brevipalpus phoenicis* (Geijskes, 1939) or *Tenuipalpus heveae* Baker, 1945 (De Vis *et al.* 2006). *Homeopronematus anconai* can also reproduce on eggs of Pacific mite *Tetranychus pacificus* McGregor, 1919 or Willamette mite *Eotetranychus willamettei* (McGregor 1917) (Knop and Hoy 1983a).

The high sensitivity of *H. anconai* to pesticides, including sulphur might reduce its potential use in practice (Knop and Hoy 1983b), but recent studies with *P. ubiquitous* and *H. anconai* (Pijnakker *et al.* 2022) and *Q. nordestinus* **n. gen. n. sp.** (Marcossi *et al.* 2024) show that these Iolinidae can also control powdery mildew besides *A. lycopersici*, so they might be alternative for sulphur which is used for both phytosanitary problems. We hypothesise that

more Pronematinae might have this potential, but some probably more than others, or it might be dependent of climatic conditions, which can be the subject of further research. Additionally, the combined release of *Q. nordestinus* **n. gen. n. sp.** and the phytoseiid *Amblyseius herbicolus* (Chant, 1959) might also control whiteflies (Marcossi *et al.* 2024).

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Distribution of work

Raf De Vis coordinated the survey, started initial rearings, made the redescription and took pictures, and measured the specimens and wrote the major part of this work; Lore Vervaeet set up SFEL and performed the molecular study and recorded the ESEM pictures; In Brazil, Ítalo Marcossi reared *Q. nordestinus* **n. gen. n. sp.**, Caio Henrique Binda de Assis set up SFEL and Angelo Pallini supervised their work. Eva Reybroeck coordinated the survey in Belgium and made a lot of slides, Wendy Vanlommel participated in the survey; Thomas Van Leeuwen supervised the work of Lore Vervaeet; Edward A. Ueckermann supervised the work as senior acarologist.

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