



A new *Aceria* species (Acari:Trombidiformes: Eriophyoidea) from West Asia, a potential biological control agent for the invasive weed camelthorn, *Alhagi maurorum* Medik. (Leguminosae)

Biljana Vidović, Hashem Kamali, Radmila Petanović, Massimo Cristofaro, Philip Weyl, Asadi Ghorbanali, Tatjana Cvrković, Matthew Augé, Francesca Marini

► **To cite this version:**

Biljana Vidović, Hashem Kamali, Radmila Petanović, Massimo Cristofaro, Philip Weyl, et al.. A new *Aceria* species (Acari:Trombidiformes: Eriophyoidea) from West Asia, a potential biological control agent for the invasive weed camelthorn, *Alhagi maurorum* Medik. (Leguminosae) . *Acarologia*, 2018, 58 (2), pp.303-312. <10.24349/acarologia/20184243>. <hal-01715268>

HAL Id: hal-01715268

<https://hal.science/hal-01715268v1>

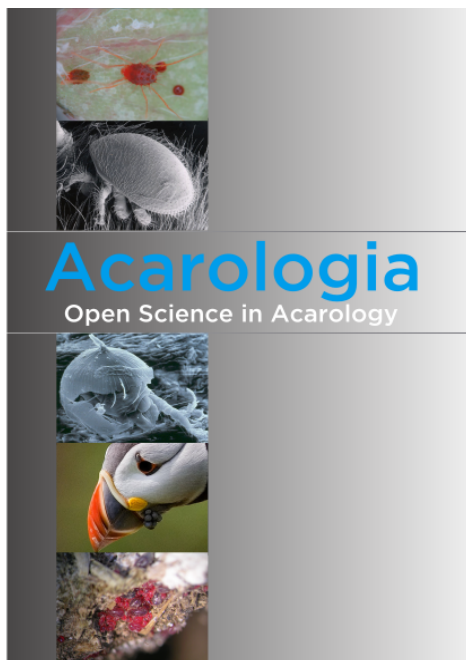
Submitted on 22 Feb 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons CC BY-ND 4.0 - Attribution - No Derivative Works - International License



Acarologia

A quarterly journal of acarology, since 1959
Publishing on all aspects of the Acari

All information:



<http://www1.montpellier.inra.fr/CBGP/acarologia/>
acarologia@supagro.inra.fr



**Acarologia is proudly non-profit,
with no page charges and free open access**

Please help us maintain this system by
encouraging your institutes to subscribe to the print version of the journal
and by sending us your high quality research on the Acari.

Subscriptions: Year 2018 (Volume 58): 380 €

<http://www1.montpellier.inra.fr/CBGP/acarologia/subscribe.php>

Previous volumes (2010-2016): 250 € / year (4 issues)

Acarologia, CBGP, CS 30016, 34988 MONTFERRIER-sur-LEZ Cedex, France

The digitalization of Acarologia papers prior to 2000 was supported by Agropolis Fondation under the reference ID 1500-024 through the « Investissements d'avenir » programme (Labex Agro: ANR-10-LABX-0001-01)



Supporting agricultural research
for sustainable development

Acarologia is under **free license** and distributed under the terms of the Creative Commons-BY-NC-ND which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original author and source are credited.

A new *Aceria* species (Acari:Trombidiformes: Eriophyoidea) from West Asia, a potential biological control agent for the invasive weed camelthorn, *Alhagi maurorum* Medik. (Leguminosae)

Biljana Vidović^a, Hashem Kamali^b, Radmila Petanović^a,
Massimo Cristofaro^c, Philip Weyl^d, Asadi Ghorbanali^e, Tatjana Cvrković^f,
Matthew Augé^g, Francesca Marini^g

^a Department of Entomology and Agricultural Zoology, Faculty of Agriculture, University of Belgrade, Nemanjina 6, 11080 Belgrade-Zemun, Serbia.

^b Khorasan Razavi Agricultural and Natural Resources Research and Education Center, P.O. Box 91735-488, Mashhad, Iran.

^c ENEA Casaccia, UTAGRI-ECO, via Anguillarese 301, 00123 Rome, Italy.

^d CABI Switzerland, Rue des Grillons 1, Delemont, Switzerland.

^e Department of Agronomy, Faculty of Agriculture, Ferdowsi University of Mashhad, P.O. Box 91775-1163, Mashhad, Iran.

^f Institute for Plant Protection and Environment, Banatska 33, 11080 Belgrade, Serbia.

^g BBCAonlus, Via Angelo Signorelli 105, 00123 Rome, Italy.

ABSTRACT

A new species of eriophyoid mite *Aceria alhagi* **n. sp.** inhabiting the weed *Alhagi maurorum* Medik., is described from the type locality in Iran, but it was also collected from Uzbekistan, Turkey and Armenia. This mite causes changes of the leaves and inflorescence. Infested plants develop cauliflower-like galls on the inflorescence and leaves deforming the reproductive structures and inhibiting seed production. The potential reduction in seed set suggests that this mite could constitute a potential biological control agent against this noxious weed. To investigate intraspecific variability between *A. alhagi* **n. sp.** populations from Iran, Turkey and Armenia, we analysed molecular sequences of the mitochondrial cytochrome oxidase subunit I (mtCOI). These results indicated that there are no significant intraspecific divergences among populations of *A. alhagi* **n. sp.** from the five different localities in three West Asia countries. This finding can be used in the future research of certain mite populations as biological control agent.

Keywords Eriophyidae, weed biological control, invasive weed, mtCOI, intraspecific variability, phytophagous mites

Zoobank <http://zoobank.org/0675CBF0-2A56-4F77-B1EC-7615D45983F0>

Introduction

The plant genus *Alhagi* belongs to the tribe Hedysareae of the Leguminosae together with another eight genera: *Corethroedendron*, *Ebens*, *Eversmannia*, *Greuteria*, *Hedysarum*, *Onobrychis*, *Sula* and *Taverniera* (Duan *et al.* 2015). According to the Plant List database (2016), *Alhagi* has 9 plant species. Our target species, *Alhagi maurorum* Medik., is a shrub commonly known as camelthorn, camelthorn-bush, Caspian manna, or Persian manna (CABI 2015). The

Received 07 February 2017
Accepted 27 September 2017
Published 22 February 2018

Corresponding author
Biljana Vidović:
magud@agrif.bg.ac.rs

Academic editor
Denise Navia

DOI
10.24349/acarologia/20184243

© Copyright
Vidović B. *et al.*

Distributed under
Creative Commons CC-BY 4.0

native range of this plant extends from Cyprus and Egypt in the West, to Mongolia and China in the East and South to India and Saudi Arabia (ILDIS 2002, Li *et al.* 2010). In its region of origin, camelthorn is used as a medicinal herb (Suthar *et al.* 2016). However no uses have been reported from the areas where it was introduced. Conversely in these areas it has become an invasive weed: in the USA it is listed as a noxious weed in seven states (USDA–NRCS 2002); Australia has declared it a state prohibited weed in Victoria (Munakamwe 2016) and in South Africa it is a declared Category 1 invasive species (AGIS–WIP 2006). No records of biological control agents are reported for this weed, although there is a potential in this field (Rassoul *et al.* 1988).

All Eriophyidae mites are phytophagous, many of them can reach pests status on crops, whereas many others are associated with weeds. Eriophyoid mites have high potential as classical biological control agents of weeds due to their strict host plant specificity (Lindquist *et al.* 1996, Smith *et al.* 2010).

According to the world catalogue (Amrine & Stasny 1994), Fauna Europaea (De Lillo 2004) and published records (Denizhan *et al.* 2007, Xue *et al.* 2012, Lotfollahi *et al.* 2014), six eriophyoid mites have been reported on Hedysareae hosts. These include, on Hedysareae type hosts, *Aculus hedysari* (Liro 1941) from *Hedysarum sibiricum* Ledeb. (junior synonym of *Hedysarum alpinum* L.); *Aculus longifilis* (Canestrini 1891) from *Onobrychis viciifolia* Scop.; *Aceria novellae* from *Hedysarum* sp. (Denizhan *et al.* 2007) and *Aculodes alhagi* Xue, Sadeghi & Hong from *A. maurorum* (Xue *et al.* 2012). The final two species, *Aceria medicaginis* (Keifer 1941) and *Aculops allotrichus* (Nalepa 1894) were recorded on *Hedysarum coronarium* L. and *A. maurorum* respectively as alternate hosts. Besides these six species one more was recorded as *nomen nudum*, i.e. *Aceria alhagi* from *A. maurorum* (Kamali 2011, Doryanizadeh *et al.* 2013).

Reliable identification is one of the key elements in the search for biological control agents of pests, including target weeds, in order to avoid unfavourable non-target effects. Phenotypic differences among eriophyoid mites belonging to the same genus associated with the closely related host plants are usually small. Intraspecific variability of morphological traits and the existence of cryptic species makes species determination difficult (Amrine *et al.* 1994, Skoracka *et al.* 2002, Navia *et al.* 2006). Recently, molecular analyses are widely accepted and applied as supplementary methods that help to avoid errors in systematics in such situations (Navajas & Navia 2010). The current study presents the morphological description of a new eriophyoid mite species, *A. alhagi* n. sp., found on *A. maurorum* as well as mt-COI nucleotide sequences of populations from different geographical areas.

Materials and methods

Plant samples of *Alhagi maurorum* Medik. (Leguminosae) were collected from Iran, Uzbekistan, Turkey and Armenia during 2012, 2013 and 2015 and examined at the laboratory under a dissection stereomicroscope. Since this mite species was recorded first in Iran (Kamali 2011), we decided to use this material as the type material for morphological description and measurements. Mite specimens from samples representing certain populations were used for morphological and molecular analyses and fixed in 75% and 96% ethanol respectively.

Morphological analysis

Mites were extracted from the plants using a fine pin with the aid of direct examination under a dissection stereomicroscope and/or using extraction methods described by de Lillo (2001) and Monfreda *et al.* (2007). The mites were mounted in Keifer's F medium (Amrine & Manson 1996) and then examined using a Leica DMLS research microscope with phase-contrast. The morphology and nomenclature follows Lindquist (1996) and genus classification is based on Amrine *et al.* (2003). Measurements and illustrations were made according to Amrine & Manson (1996) and de Lillo *et al.* (2010). Morphometry was performed using the software

package IM 1000 (Leica, Wetzlar, Germany) and for drawings a camera lucida was used. All measurements are given in micrometers (μm) and, unless stated otherwise, are the lengths of the structures. Morphometric data of *A. medicaginis* which were used for comparison with *A. alhagi* n. sp., were obtained from the literature (Keifer 1941). Plant names are in accordance with The Plant List (2016) on-line database.

The holotype and the paratype slides are deposited in the collections of the Acarology Laboratory, Department of Entomology and Agricultural Zoology, Faculty of Agriculture, University of Belgrade, Serbia; one paratype slide is deposited in the Department of Plant Protection, Razavi Agricultural and Natural Resources Research Centre, Mashhad, Iran.

Scanning electron micrographs (SEM) were taken according to Alberti & Nuzzaci (1996). Live mites were collected individually using a fine pin from fresh plant material under a stereomicroscope. For sample preparation before being placed on the SEM holder, mites were sputter-coated with gold for 100 s under 30 mA ion current.

The samples were then studied in the vacuum chamber of a JEOL Scanning Electron Microscope (SEM, JEOL-JSM6390) at the Laboratory of Electron Microscopy, Faculty of Agriculture, University of Belgrade, Serbia.

Molecular analysis

Material collected for molecular analysis included samples of populations from Iran, Turkey and Armenia (Table 1). Prior to molecular analysis, mite specimens were preserved in 96% ethanol and stored at 4°C until DNA extraction. Total DNA was extracted from a pool of 15–20 whole specimens using QIAGEN DNeasy® Blood & Tissue Kit (QIAGEN, Hilden, Germany), according to the manufacturer's instructions. The barcoding region of the mitochondrial cytochrome oxidase subunit I gene was amplified by polymerase chain reaction (PCR) using a forward primer LCO1490 (Folmer *et al.* 1994), and reverse primer HCOd (Chetverikov *et al.* 2015). Polymerase chain reactions (PCR) were conducted using High Yield Reaction Buffer A with Mg (1x), 2.5 mM MgCl_2 , 0.6 mM of each dNTP, 0.5 μM of each primer and 1 U of KAPA TaqDNA polymerase (Kapa Biosystems, London, UK) in a 25 μL final volume. PCR was carried out in a Master cycler ep gradient S thermal cycler (Eppendorf, Hamburg, Germany) applying the following steps: 95°C for 5 min (initial denaturation), 35 cycles at 94°C for 1 min, 1 min at 54°C (annealing), 1 min 30 s at 72°C, with a final extension at 72 °C for 7 min. PCR amplicons were purified using the QIAquick PCR purification Kit (QIAGEN) according to the manufacturer's instructions, and sequenced on automated equipment by Macrogen (Seoul, South Korea) with the same primer pairs as in the initial PCR procedure. The sequences were manually edited using FinchTVv.1.4.0 (www.geospiza.com), and aligned by CLUSTAL W integrated in MEGA5 software (Tamura *et al.* 2011). Uncorrected pairwise genetic distances were used to calculate the average genetic distance between *A. alhagi* n. sp. populations associated with *A. maurorum* collected from different localities (Table 1).

Results

Taxonomy

Family: Eriophyidae Nalepa, 1898

Aceria alhagi n.sp. Vidović et Kamali, 2016 (Figures 1-2)

Zoobank: [B78B39BC-C1E7-44F2-9C4E-9AE24D293F5C](https://zoobank.org/B78B39BC-C1E7-44F2-9C4E-9AE24D293F5C)

Female (n = 10) — holotype and 9 paratypes. Body vermiform, 178 (174 – 225), 55 (45 – 55) wide, white.

Gnathosoma — 24 (19 – 24) projecting obliquely downward, dorsal pedipalpal genual setae (d) 5 (5 – 7) unbranched, cheliceral stylets 14 (12 – 17).

Table 1 Collection data for *Aceria alhagi* n. sp. inhabiting *Alhagi maurorum* populations.

	Country	Locality, – date	GPS coordinates	Name of collector	Accession numbers COI
1	Iran	Shirvan, -- June 2015	37°24'28"N; 57°59'12"E	Cristofaro M.	MF150169
2	Iran	Honameh, -- July 2014	37°31'12"N; 58°01'42"E	Cristofaro M.	MF150170
3	Turkey	Sarayhan, -- November 2013	38°33'25"N; 33°53'32"E	Cristofaro M.	MF150171
4	Turkey	Cavusin, -- June 2015	38°41'10"N; 34°52'01"E	Cristofaro M.	MF150172
5	Armenia	Vedi, -- July 2015	39°58'05"N; 44°52'23"E	Cristofaro M.	MF150173

Prodorsal shield — 26 (24 – 27) including frontal lobe, 35 (30 – 38) wide, semi-elliptical, basally-flexible frontal lobe, over gnathosomal base. Shield pattern almost smooth, without median line, with two short admedian lines and shorter submedian lines I and II; scapular setae *sc* dorsal tubercles on rear shield margin, 19 (17 – 20) apart, scapular setae *sc* 34 (28 – 37), directed posteriorly.

Legs — with all usual segments and setae present. Leg I 29 (25 – 32), femur 7 (6 – 9), genu 6 (5 – 7), tibia 7 (5 – 7), tarsus 8 (6 – 8), tarsal solenidion (ω) 8 (8 – 9) distally rounded, tarsal empodium (*em*) simple, 5 (5 – 7), 6-rayed; basiventral femoral setae (*bv*) 16 (12 – 16), antaxial genual setae (*l''*) 21 (20 – 25), paraxial tibial setae (*l'*) 8 (6 – 8) (5 – 7), paraxial fastigial tarsal setae (*ft'*) 13 (11 – 14), antaxial fastigial tarsal setae (*ft''*) 24 (21 – 28). Leg II 26 (25 – 29), femur 6 (6 – 9), genu 5 (4 – 6), tibia 5 (4 – 6), tarsus 8 (6 – 8), tarsal solenidion (ω) 8 (6 – 9) distally rounded, tarsal empodium (*em*) simple, 6 (4 – 6), 6-rayed; basiventral femoral setae (*bv*) 13 (12 – 16), antaxial genual setae (*l''*) 11 (10 – 14), paraxial fastigial tarsal setae (*ft'*) 6 (5 – 7), antaxial fastigial tarsal setae (*ft''*) 24 (20 – 28).

Coxigenital area — coxisternal plates granulated; anterolateral setae on coxisternum I (*lb*) 10 (9 – 13), 7 (7 – 8) apart; proximal setae on coxisternum I (*la*) 23 (21 – 26), 5 (4 – 6) apart; proximal setae on coxisternum II (*2a*) 35 (33 – 46), 18 (17 – 18) apart. Prosternal apodeme 5 (5 – 7).

Opisthosoma — with subequal annuli, 67 (66 – 76) dorsal and 74 (67 – 74) narrow ventral annuli (counted from first annulus after coxae II), 5 (4 – 6) coxigenital annuli. Microtubercles elliptical on dorsal annuli and circular on ventral annuli. Setae *c2* 28 (24 – 28) on ventral annulus 12 (9 – 12), 46 (38 – 47) apart; setae *d* 77 (65 – 80) on ventral annulus 26 (22 – 26), 35 (31 – 37) apart; setae *e* 17 (14 – 18) on ventral annulus 41 (36 – 41), 18 (15 – 19) apart; setae *f* 27 (24 – 27) on ventral annulus 68 (61 – 68), 19 (15 – 20) apart. Last 5 ventral annuli with numerous elongated linear microtubercles. Setae *h2* 122 (110 – 144), setae *h1* 6 (4–6).

Genital coverflap 12 (9 – 12), 20 (17 – 20) wide, with 16 (15 – 17) longitudinal striae; proximal setae on coxisternum III (*3a*) 34 (30 – 36), 13 (12 – 14) apart. Internal genitalia—Anterior, transversal apodeme trapezoidal, longitudinal bridge relatively long, the post spermathecal part of the longitudinal bridge is reduced; spermathecal tubes directed latero-posterad, spermathecae egg-shaped, globose.

MALE (n=3) — Similar to female, body vermiform, 168 – 176, 48 – 49 wide, white. Gnathosoma — 21 – 24 down curved, cheliceral stylets 14 – 15. Prodorsal shield — 25 – 27, 37 – 40 wide. Prodorsal shield tubercles on the rear shield margin 18 – 20 apart, scapular setae *sc* 29 – 33, projecting posteriorly. Shield design similar to female. Leg I 24 – 30, femur 8 – 9, genu 5 – 6, tibia 5 – 6, tarsus 7, tarsal solenidion (ω) 6 – 7, tarsal empodium (*em*) 4 – 5, and 6 rayed; basiventral femoral setae (*bv*) 12 – 16, antaxial genual setae (*l''*) 23, paraxial tibial setae

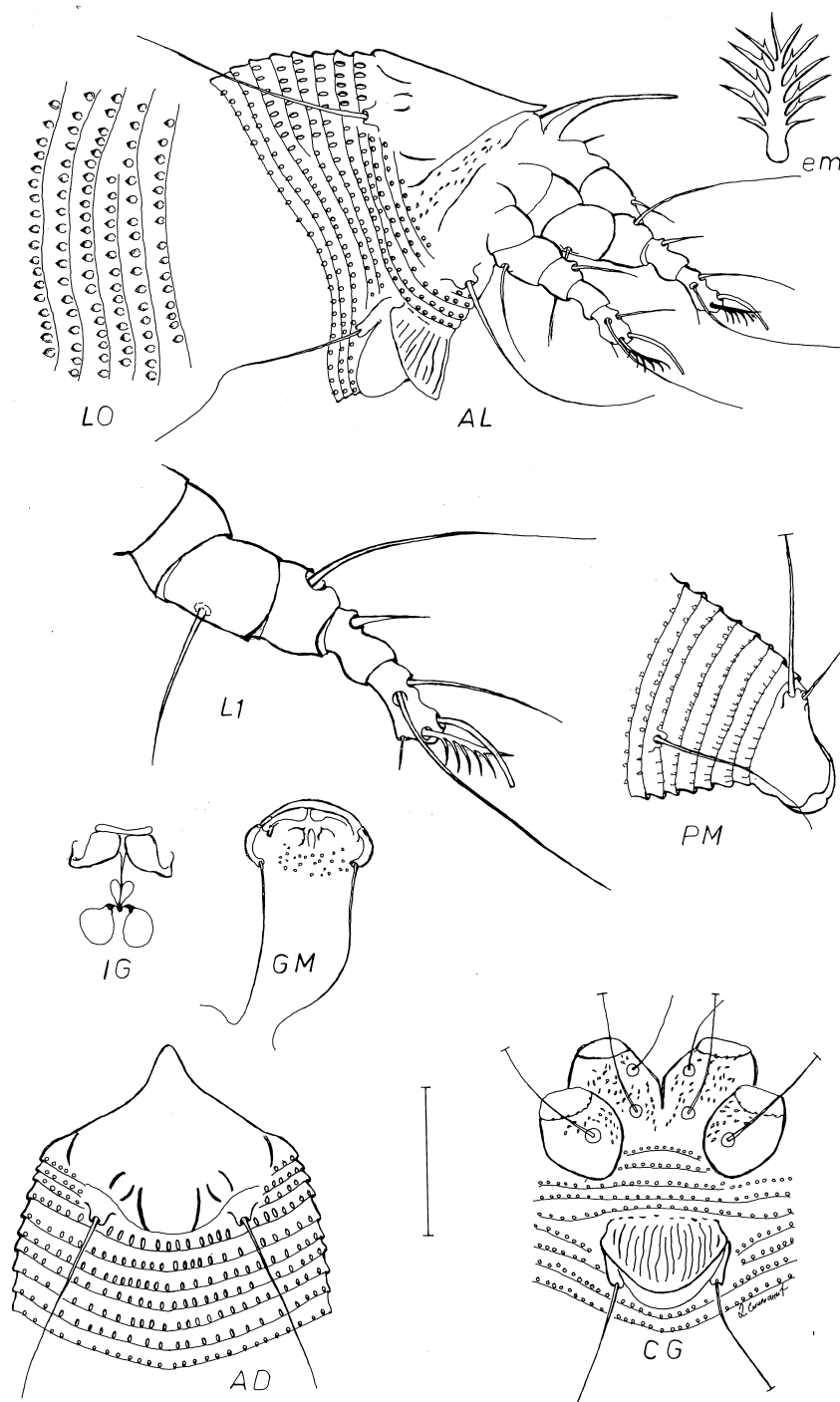


Figure 1 *Aceria alhagi* n.sp.: AD – Antero-dorsal mite; AL – Antero-lateral view of mite; CG – Coxigenital region of female; em – Empodium; GM – Genital region of male; IG – Internal female genitalia; L1 – Leg I of female; LO – Lateral opisthosoma; PM – Postero-lateral mite. Scale bar: 20µm for AD, AL, CG, GM, IG, LO, PM; 10µm for L1; 5µm for em.

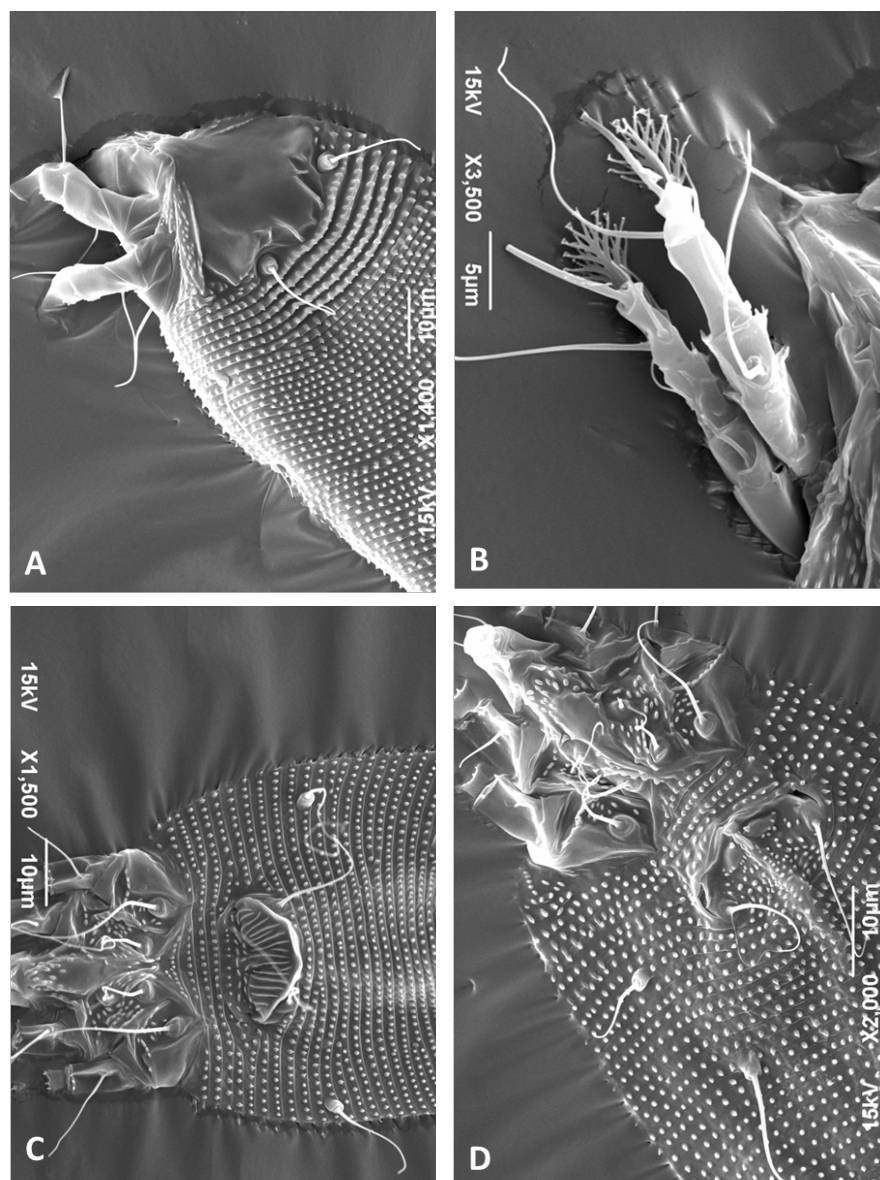


Figure 2 SEM images of *Aceria alhagi* n. sp.: A – prodorsal shield; B – tarsal empodia on legs I and II; C – ventral view of coxigenital area of female; D – ventral view of coxigenital area of male.

(*l'*) 5, paraxial fastigial tarsal setae (*ft'*) 9 – 13, antaxial fastigial tarsal setae (*ft''*) 22 – 28. Leg II 22 – 26, femur 6 – 7, genu 4, tibia 5, tarsus 6 – 7, tarsal solenidion (*ω*) 8 – 9, tarsal empodium (*em*) 4 – 5; basiventral femoral setae (*bv*) 10 – 14, antaxial genual setae (*l''*) 11 – 12, paraxial fastigial tarsal setae (*ft'*) 5 – 7, antaxial fastigial tarsal setae (*ft''*) 22 – 24. Coxigenital area — coxisternal plates granulate; sternal line 6 – 7; anterolateral setae on coxisternum I (*lb*) 8 – 9, 7 apart; proximal setae on coxisternum I (*la*) 25 – 27, 4 – 7 apart; proximal setae on coxisternum II (*2a*) 32 – 41, 16 – 17 apart. Genitalia 17 – 18 wide; proximal setae on coxisternum III (*3a*) 27 – 30, 12 – 14 apart. Opisthosoma — with subequal annuli: 58 – 61 dorsal and 63 – 72 ventral annuli; 5 – 6 coxigenital annuli. Setae *c2* 22 – 27, 40 – 44 apart, on annulus 11; setae *d* 62 – 81, 32 – 34 apart, on annulus 18 – 19; setae *e* 13 – 15, 15 – 17 apart, on annulus 30 – 33; setae *f* 22 – 28, 16 – 17 apart, on annulus 54 – 55; setae *h* 297 – 126, 6 – 8 apart, setae *hl* 5 – 6, 5 – 6 apart.



Figure 3 *Alhagi maurorum*, plant with typical *Aceria alhagi* n. sp. symptoms where the shoot tips and reproductive structures are replaced by cauliflower-like galls (by Dr. Hashem Kamali and Dr. Massimo Cristofaro)

Nymph and Larva — Not found

Host plant — *Alhagi maurorum* Medik (Fabaceae) commonly known as camelthorn, camelthorn-bush, Caspian manna, and Persian manna plant.

Relation to the host plant — This mite caused changes of the leaves and inflorescence. The edge of the leaves become twisted and the inflorescence do not develop fully, with deformation of the reproductive structures. The flowers are replaced by cauliflower-like galls (Figure 3).

Type Material — Holotype: female, Shirvan, Iran (37°24'28"N; 57°59'12"E), 27 June 2015. coll. Cristofaro M. Paratypes: 20 females, 4 males, same data.

Additional studied material — Mashad, Iran (37°30'81"N; 58°01'18"E), 12 September 2012, 30 slides; Honameh, Iran (37°31'12"N; 58°01'42"E), 12 July 2014, 10 slides; Ohalik, Uzbekistan (39°32'01"N; 66°53'43"E), 18 August 2013, 25 slides; Bukhara, Uzbekistan (39°46'37"N; 64°24'02"E) 21 August 2013, 30 slides; Sarayhan, Turkey (38°33'25"N; 33°53'32"E), 10 November 2013, 30 slides; Cavusin, Turkey (38°41'10"N; 34°52'01"E) 20 June 2015, 8 slides; Vedi, Armenia (39°58'05"N; 44°52'23"E) 07 July 2015, 7 slides; coll. Cristofaro M. All slides are deposited in the Department of Entomology and Agricultural Zoology, Faculty of Agriculture, University of Belgrade, Serbia.

Etymology — The species designations *alhagi* is from the genus name of the host plant.

GenBank accession numbers — The domain mtCOI was successfully amplified and sequenced. The sequence of this region in *A. alhagi* n. sp. is available from GenBank under accession number MF150169 – MF150173.

Differential diagnosis and remarks — Until now, only one eriophyoid mite was described

Table 2 Comparison of available key morphological characters between females of *Aceria alhagi* **n. sp.** and *Aceria medicaginis* (Keifer, 1941). The characters that are different between the two species are highlighted in bold.

Morphometric characters	<i>Aceria alhagi</i> n. sp.	<i>Aceria medicaginis</i>
Length of body	178 (174 – 225)	150 – 180
Width of body	55 (45 – 55)	40 – 50
Length of gnathosoma	24 (19 – 24)	23
Length of prodorsal shield	26 (24 – 27)	30
Width of prodorsal shield	35 (30 – 38)	35 – 40
Length of setae <i>sc</i>	34 (28 – 37)	24
Tubercles of <i>sc</i> apart	19 (17 – 20)	27
Length of leg I	29 (25 – 32)	32
Length of tibia I	7 (5 – 7)	7,5
Length of tarsus I	8 (6 – 8)	8
Length of empodium I <i>em</i>	5 (5 – 7)	8
Number of rays on tarsal empodium	6	5
Length of leg II	26 (25 – 29)	28,5
Length of tibia II	5 (4 – 6)	5,5
Length of tarsus II	8 (6 – 8)	6,5
Length of empodium II <i>em</i>	6 (4 – 6)	8,5
Length of female genitalia	12 (9 – 12)	15
Width of female genitalia	20 (17 – 20)	21
Number of ridges	16 (15 – 17)	10 – 12
Length of setae <i>3a</i>	34 (30 – 36)	16
Length of setae <i>c2</i>	28 (24 – 28)	46
On annulus no:	12 (9 – 12)	7
Length of setae <i>d</i>	77 (65 – 80)	63
On annulus no:	26 (22 – 26)	19
Length of setae <i>e</i>	17 (14 – 18)	23,5
On annulus no:	41 (34 – 41)	36
Length of setae <i>f</i>	27 (24 – 27)	27
Number of complete annuli	67 – 76	60

from *A. maurorum*, *Aculodes alhagis* Xue, Sadeghi and Hong, 2012. No *Aceria* spp. have been previously described from this host plant, and only two on the same tribe (Hedysareae), namely *A. medicaginis*, associated with *H. coroniarum* as an alternate host, and *A. novella* (Denizhan *et al.* 2007) on the *Hedysarum* sp..

A. alhagi **n. sp.** is close to *A. medicaginis*, but it can be distinguished by the following characters: number of rays on the tarsal empodium (*A. alhagi* **n. sp.** = 6; *A. medicaginis* = 5); number of striae on the female genital coverflap (*A. alhagi* **n. sp.** with 15 – 17; *A. medicaginis* with 10 – 12); prodorsal shield design (*A. alhagi* **n. sp.** with almost smooth prodorsal shield, with short admedian and submedian lines on the rear margin of the shield, while *A. medicaginis* with completely smooth prodorsal shield without any lines). The differing morphometric characters between *A. alhagi* **n. sp.** and *A. medicaginis* are presented in Table 2.

Molecular Analyses

The final alignment included the whole mt-COI barcoding region. No insertions or deletions were found between the sequences. In total, 4/658 (0.6%) nucleotides were polymorphic, of which two were parsimony informative. Base pair frequencies show that the region is AT-rich (A: 0.228, C: 0.153-0.160, G: 0.157-0.158, T: 0.456-0.460). The translation of the nucleotide

Table 3 Uncorrected p-distance among *Aceria alhagi* n. sp. populations of *Alhagi maurorum* from different localities.

Population- Locality	1	2	3	4	5
1 Iran-Shirvan					
2 Iran-Honameh	0.005				
3 Turkey-Sarayhan	0.000	0.005			
4 Turkey-Cavusin	0.002	0.006	0.002		
5 Armenia-Vedi	0.003	0.002	0.003	0.005	0.000

Population numbers refer to populations collected from locations as listed in Table 1.

sequence resulted in a 219 amino acid positions, of which one was variable. The average mean divergence over all the sequence pairs was 0.3% and ranged from 0% to 0.6% (Table 3). Similar level of divergence was obtained within six populations of *Aceria tulipae* (Keifer), range 0.0 – 0.5% (Kiedrowicz *et al.*, 2017), as well as within *Phytoptus avellanae* (Nal.) range 0.0 – 0.4% (Cvrković *et al.*, 2016). In *Tegolophus celtis* Guo, Li, Wong, Xue & Hong, 2015, divergence within the same gene, among protogyne and deutogyne females was 0% to 0.9% (Guo *et al.* 2015), while intraspecific nucleotide sequence divergence within each host strain of *Abacarus hystris* ranged from 0.2% – 13.9% (Skoracka & Dabert 2010).

Results obtained in this study indicate that there are no significant intraspecific divergences among populations of *A. alhagi* n. sp. from the five different localities in western Asia.

Four different haplotypes were obtained for populations of *A. alhagi* n. sp. collected on *A. maurorum* from different geographic localities, and the sequences are available from GenBank under accession numbers MF150169 – MF150173.

Discussion

Alhagi maurorum is considered a weed of significance in many regions of the world where it has been introduced (AGIS–WIP 2006, Munakamwe 2016; USDA–NRCS 2002) and potential control options need to be considered. Biological control offers a safe and sustainable method, which can be used to control a weeds density and reduce spread (McFadyen 1998). The main mode of spread of camelthorn is through seed dispersal, where each self-fertile plant can produce up to 6000 seeds (Ambasht 1963). The eriophyoid, *A. alhagi* n. sp. has been observed causing serious damage on the reproductive output of *A. maurorum* in western Asia (five regions of the current study). The inflorescences of the infested plants are replaced by cauliflower-like galls and seed production is massively reduced. Although *A. alhagi* n. sp. is unlikely to reduce densities of the weed in the short term, a reduction in seed set of plants in the introduced range would limit the long distance dispersal of this weed through various abiotic (wind and water) (Ambasht 1963) and biotic (cattle, sheep, horses) (Kerr *et al.* 1965) factors.

The finding from this study allows us to conclude that only one species of *Aceria* is present on *A. maurorum*, with no doubt about its taxonomic status, *A. alhagi* n. sp.. This is an important finding for the development of a biological control programme since eriophyoid mites are usually highly host specific and are gaining popularity in classical weed biological control (Lindquist *et al.* 1996, Smith *et al.* 2010). Future classical biological control studies targeting the reduction in reproductive output of *A. maurorum* should consider *A. alhagi* n. sp. a potential biological control agent with a high impact on inflorescence production, ultimately reducing seed set.

Acknowledgements

We are grateful to Mrs. Dragica Smiljanić for the technical illustrations and to Mrs. Francesca Di Cristina for her technical assistance in field collections. The study was partly supported by the Serbian Ministry of Science and Environment Protection (Grant III 43001).

References

- AGIS–WIP 2006. Weeds and Invasive Plants of South Africa, version 2.0. June 2006. Available from: <http://www.agis.agric.za/wip>
- Alberti G., Nuzzaci G. 1996. SEM and TEM Techniques. In: Lindquist E.E., Sabelis M. W., Bruin J. (Eds). Eriophyoid mites — their biology, natural enemies and control. Amsterdam: Elsevier. pp. 399–410. doi:10.1016/S1572-4379(96)80025-X
- Ambasht R.S. 1963. Ecological studies of *Alhagi camelorum* Fisch. Tropical Ecology, 4: 72–82.
- Amrine J.W.Jr., Stasny T.A.H. 1994. Catalog of the Eriophyoidea (Acarina: Prostigmata) of the World. Indira Publishing House, West Bloomfield, Michigan, USA, 804 pp.
- Amrine J.W.Jr., Stasny T.A.H., Flechtmann, C.H.W. 2003. Revised Keys to the World Genera of the Eriophyoidea (Acari: Prostigmata). Indira Publishing House, Michigan, West Bloomfield, USA, 244 pp.
- Amrine J.W.Jr., Manson D.C.M. 1996. Preparation, mounting and descriptive study of eriophyoid mites. In: Lindquist E.E., Sabelis M.W., Bruin, J. (Eds). Eriophyoid Mites: Their Biology, Natural Enemies and Control. Elsevier Science Publ., Amsterdam, pp. 383–396. doi:10.1016/S1572-4379(96)80023-6
- Amrine J.W.Jr., Duncan G.H., Jones A.T., Gordon S.C., Roberts I.M. 1994. Cecidophyopsis mites (Acari: Eriophyidae) on Ribes spp. (Grossulariaceae). Int. J. Acarol., 20: 139–168 doi:10.1080/01647959408684014
- CABI 2015. Invasive Species Compendium. Wallingford, UK. CAB International. Available from: www.cabi.org/isc.
- Canestrini G. 1891. Sopra due nuove specie di Phytoptus. Attidella Societa Veneto-Trentina di Scienzanaturali Padova, 12(2): 379–381.
- Chetverikov P.E., Cvrković T., Makunin A., Sukhareva S., Vidović B., Petanović R. 2015. Basal divergence of Eriophyoidea (Acariformes, Eupodina) inferred from combined partial COI and 28S gene sequences and CLSM genital anatomy. Exp. Appl. Acarol., 67(2): 219–245. doi:10.1007/s10493-015-9945-9
- Cvrković T., Chetverikov P., Vidović B., Petanović R. 2016. Cryptic speciation within *Phytoptus avellanae* s.l. (Eriophyoidea: Phytoptidae) revealed by molecular data and observations on molting “*Tegonotus*-like” nymphs. Exp. Appl. Acarol., 68(1): 83–96. doi:10.1007/s10493-015-9981-5
- De Lillo E. 2001. A modified method for eriophyoid mite extraction (Acari: Eriophyoidea). Int. J. Acarol., 27: 67–70. doi:10.1080/01647950108684228
- De Lillo E. 2004. Fauna Europaea: Eriophyidae. In: Magowski W., de Jong Y. (Eds.), Fauna Europaea: Acari: Acariformes. Fauna Europaea version 2.5. Available from <http://www.faunaeur.org> (accessed 21 December 2016)
- De Lillo E., Craemer C., Amrine J.W.Jr., Nuzzaci G. 2010. Recommended procedures and techniques formorphological studies of Eriophyoidea (Acari: Prostigmata). Exp. Appl. Acarol., 51(1–3): 283–307. doi:10.1007/s10493-009-9311-x
- Denizhan E., Monfreda R., Cobanoglu S., De Lillo E. 2007. Studies on the eriophyoid mites (Acari: Eriophyoidea) of Turkey: Three new species associated with Fabaceae. Int. J. Acarol., 33(1): 21–27. doi:10.1080/01647950708684496
- Doryanizadeh N., Akrami M.A., Kamali H. 2013. Eriophyoidea (Acari: Trombidiformes; Prostigmata) fauna of Shiraz County, Iran. Persian Journal of Acarology, 2(2): 331–334.
- Duan L., Wen J., Yang X., Liu P.L., Arslan E., Ertugrul K., Chang Z.Y. 2015. Phylogeny of *Hedysarum* and tribe Hedysareae (Leguminosae: Papilionoideae) inferred from sequence data of ITS, *matK*, *trnL-F* and *psbA-trnH*. Taxon, 64(1): 49–64. doi:10.12705/64.26
- Folmer O., Black M., Hoeh W., Lutz R., Vrijenhoek R. 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. Mol. Mar. Biol. Biotechnol., 3: 294–299.
- Guo J.F., Li H.S., Wang B., Xue X.F., Hong X.Y. 2015. DNA barcoding reveals the protogyne and deutogyne of *Tegolophus celtis* sp. nov. (Acari: Eriophyidae). Exp. Appl. Acarol., 67: 393–410.
- ILDIS 2002. International Legume Database and Information Service. University of Southampton, UK. Available from: <http://www.ildis.org/database/>.
- Kamali H. 2011. Current knowledge on Eriophyoidea (Acari: Prostigmata) as biological control agent of weeds in Iran. Abstract and Proceeding Book of the First Persian Congress of Acarology, 22–23 December 2011, Kerman, Iran, p. 72.
- Keifer H.H. 1941. Eriophyid Studies 11. Bull. Cal. Dept. Agric., 30: 206, pl. 161.
- Kerr H.D., Robocker W.C., Muzic T.J. 1965. Characteristics and control of camelthorn. Weeds, 13: 156–163. doi:10.2307/4041160
- Kiedrowic A., Rector B., Lommen S., Kuczyński L., Szydło W., Skoracka A. 2017. Population growth rate of dry bulb mite, *Aceria tulipae* (Acariformes: Eriophyidae), on agriculturally important plants and implications for its taxonomic status. Exp. Appl. Acarol., 73(1): 1–10. doi:10.1007/s10493-017-0173-3
- Li N., Zhang G., Xiong Y., Makhabel B., Li X., Jia X. 2010. New isoflavonolignan with quinone reductase inducing activity from *Alhagipseudalhagi* (M.B.). Fitoterapia, 81(8): 1058–61.

- Lindquist E.E. 1996. External anatomy and notation of structures. In: Lindquist E.E., Sabelis M.W., Bruin J. (Eds). *Eriophyoid Mites: Their Biology, Natural Enemies and Control*. Elsevier Science Publ., Amsterdam, The Netherlands, pp. 3-31. doi:10.1016/S1572-4379(96)80003-0
- Lindquist E.E., Sabelis M.W., Bruin J. 1996. Eriophyoid mites their biology, natural enemies and control. *Elsevier World Crop Pests* 6, 790 pp
- Liro J.I. 1941. Über neue und seltene Eriophyiden (Acarina). *Ann. Bot. Soc. Zool. Bot. Fenn. Vanamo*, 8: 1-54.
- Lotfollahi P., Haddad K., Nejad I., De Lillo E. 2014. Eight new records for the Eriophyid (Trombidiformes Eriophyoidea Eriophyidae) mite fauna of Iran. *Redia* XCVII, 51-61.
- Monfreda R., Nuzzaci G., De Lillo E. 2007. Detection, extraction, and collection of Eriophyoid mites. *Zootaxa*, 1662: 35-43.
- Munakamwe Z. 2016. Tackling camelthorn (*Alhagimaurorum* Medik.) in Victoria, Australia. *Plant Protection Quarterly*, 31(2): 44-45.
- McFadyen, R.E.C. 1998. Biological control of weeds. *Annual review of entomology*, 43(1): 369-393. doi:10.1146/annurev.ento.43.1.369
- Nalepa A. 1894. Beiträge zur Kenntnis der Phyllocoptiden. *Nova Acta Leop.-Carol. Akad.*, 61(4): 289-324.
- Nalepa A. 1898. Zur Kenntniss der Gattung Trimerus Nal. *Zoologische Jahrbuecher*, 11(5): 405-411.
- Navajas M., Navia D. 2010. DNA-based methods for eriophyoid mite studies: review, critical aspects, prospects and challenges. *Exp. Appl. Acarol.*, 51: 257-271. doi:10.1007/s10493-009-9301-z
- Navia D., Moraes G.J., Querino R.B. 2006. Geographic variation in the coconut mite, *Aceria guerreronis* Keifer (Acari: Eriophyidae): a geometric morphometric analysis. *Int. J. Acarol.*, 32(3): 301-314. doi:10.1080/01647950608684473
- Rassoul A., Dawah H.A., Othman N.Y. 1988. Camel thorn seed insects and their presence on leguminous plants in Iraq. *J. Biol. Sci. Research*, 19: 853-862.
- Smith L., De Lillo E., Amrine J.W.Jr. 2010. Effectiveness of eriophyid mites for biological control of weedy plants and challenges for future research. *Exp. Appl. Acarol.*, 51: 115-149. doi:10.1007/s10493-009-9299-2
- Skoracka A., Dabert M. 2010. The cereal rust mite *Abacarus hystrix* (Acari Eriophyoidea) is a complex of species: evidences from mitochondrial and nuclear DNA sequences. *Bulletin Entomological Research*, 100: 263-272 doi:10.1017/S0007485309990216
- Skoracka A., Kuczynski L., Magowski W.L. 2002. Morphological variation in different host populations of *Abacarus hystrix* (Acari: Prostigmata: Eriophyoidea). *Exp. Appl. Acarol.*, 26(3-4): 187-193 doi:10.1023/A:1021144729837
- Suthar P., Mathur K., Goyal M., Yadav S.K. 2016. Traditional uses, phytochemistry, pharmacological properties of plant *Alhagimaurorum* (Medik.). A review world journal of pharmacy and pharmaceutical sciences, 5(4): 682-692. doi:10.20959/wjpps20164-6421
- Tamura K., Peterson D., Peterson N., Stecher G., Nei M., Kumar S. 2011. MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance and maximum parsimony methods. *Mol. Biol. Evol.*, 28: 2731-2739. doi:10.1093/molbev/msr121
- The Plant List database. A working list of all plant species 2016. Available from <http://www.theplantlist.org> (accessed 21 December 2016).
- USDA-NRCS 2002. The Plant Databases, version 3.5. National Plant Data Center, Baton Rouge, USA. Available from: <http://plants.usda.gov>
- Xue X.F., Sadeghi H., Hong X.Y. 2012. Four new eriophyoid mite species (Acari: Eriophyoidea: Eriophyidae) from Iran. *Zootaxa*, 3544: 28-40.