Rostaniha 21(2): 174-184 (2020)-Research Article

DOI: 10.22092/BOTANY.2020.343028.1200

Systematics of *Alhagi*: molecular phylogeny and morphology revisited

Received: 19.07.2020 / Accepted: 13.10.2020

Arezoo Amirkhosravi: PhD Student, Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran

Younes Asri : Research Associate Prof., Research Institute of Forests and Rangelands, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran (asri@rifr-ac.ir)

Mostafa Assadi: Research Prof., Research Institute of Forests and Rangelands, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran

Iraj Mehregan: Associate Prof., Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran

Abstract

Alhagi is a small genus of desert or semi-desert shrubs with about six species widely distributed throughout northern Africa, eastern Mediterranean, the Middle East to the Central Asia, and small parts of India and China. Despite previous molecular and morphological studies on the genus, the taxonomy of *Alhagi* has been remained controversial. In order to delimit natural groups as well as to clarify interspecific relationships of *Alhagi* species distributed in Iran, 45 ingroup taxa representing 30 accessions of the genus *Alhagi* and 15 species from the sister genera, as well as two species, namely, *Astragalus arthuri* and *Colutea persica* as outgroups were selected. The nuclear ribosomal DNA internal transcribed spacer was employed for phylogenetic reconstructions. Phylogenetic analyses were performed using maximum parsimony, maximum likelihood and Bayesian inference. The obtained results recovered *Alhagi* accessions as a well-supported monophyletic group. All three traditionally recognized species in Iran split into two distinct morphologically well-supported lineages similar to splits graph. The results showed that, *Alhagi maurorum* and *A. graecorum* are recognized as two distinct species distributed in two phytogeographical regions of Irano-Turanian and Saharo-Sindian. As a complementary taxonomic treatment, the diagnostic key and description of the species are also provided herewith.

Keywords: Alhagi graecorum, A. maurorum, Fabaceae, phylogenetic relationships, taxonomy

سیستماتیک جنس خارشتر: بررسی مجدد فیلوژنی مولکولی و ریختشناسی* دریافت: ۱۳۹۹/۰۴/۲۹ / پذیرش: ۱۳۹۹/۰۲/۲ آرزو امیرخسروی: دانشجوی دکتری، گروه زیستشناسی، واحد علوم و تحقیقات، دانشگاه آزاد اسلامی، تهران، ایران یونس عصری⊠: دانشیار پژوهش، مؤسسه تحقیقات جنگلها و مراتع کشور، سازمان تحقیقات، آموزش و ترویج کشاورزی، تهران، ایران (asri@rifr-ac.ir) مصطفی اسدی: استاد پژوهش، مؤسسه تحقیقات جنگلها و مراتع کشور، سازمان تحقیقات، آموزش و ترویج کشاورزی، تهران، ایران

ایرج مهرگان: دانشیار گروه زیستشناسی، واحد علوم و تحقیقات، دانشگاه آزاد اسلامی، تهران، ایران

خلاصه

خارشتر (Alhagi) جنسی کوچک از تیره باقلاییان شامل شش گیاه بوتهای بیابانی و نیمه بیابانی میباشد که به طور گستردهای در سراسر شمال آفریقا، شرق مدیترانه و از خاورمیانه به سمت آسیای مرکزی و بخشهای کوچکی از هند و چین پـراکنش یافتـه است. بـهرغـم مطالعـات ریختشناختی و مولکولی گذشته روی این جنس، مباحث مربوط به تاکسونومی آن به صورت بحث برانگیـز بـاقی مانـده است. در راسـتای تعیـین گروههای طبیعی و روشن شدن روابط بین گونههای پراکنش یافته در ایران، در این مطالعه، ۴۵ آرایه به عنوان درون گروه شامل ۳۰ نمونه از جنس خارشتر و ۱۵ گونه از جنسهای خویشاوند به عنوان درون گروه و دو گونه به اسامی Astragalus arthur و Astragalus به عنوان بـرونگـروه انتخاب شدند. از توالیهای ریبوزومی هستهای ناحیه فاصلهگذار رونویسیشونده داخلی برای مطالعات فیلوژنی استفاده شـد. آنالیزهـای فیلـوژنی بـ استفاده از روشهای بیشینه صرفهجویی، بیشینه درستنمایی و Bayesia انجام شد. نتایج حاصل نشان داد که اعضای جنس مذکور، در یک گـروه تک تبار با حمایت خوب قرار گرفتهاند، به طوری که سه گونه شناخته شده در مفهوم Rechinger برای ایـران، بـه دو دومـان مجـزا بـا حمایـت و ویژگیهای متمایز ریختشناختی تقسیم شدهاند که مشابه با نتایج حاصل از Rechinger است. طبق یا در مار محرا بـ و میت مینان دو که اعضای جنس مدی بیشینه درستنمایی و مناخته شده در مفهوم Rechinger بـرای ایـران، بـه دو دودمـان مجـزا بـا حمایـت و ویژگیهای متمایز ریختشناختی تقسیم شدهاند که مشابه با نتایج حاصل از Pality است. طبق نتایج به دست آمـده، سراکنش یافتـهانـ همچنین، پس از بررسی کامل تاکسونومیکی، کلید شناسایی و شرح این گونهها ارایه گردید.

واژههای کلیدی: باقلاییان، تاکسونومی، روابط فیلوژنتیکی، Alhagi graecorum مالمون مالمون مالم

*مستخرج از رساله دكتري نگارنده نخست به راهنمايي دكتر يونس عصري و دكتر مصطفي اسدي ارايه شده به واحد علوم و تحقيقات دانشگاه آزاد اسلامي

Introduction

The Alhagi Gagnebin (Fabaceae, genus Hedysareae) consists of six species growing as shrubs or subshrubs (Hassler 2019) distributed throughout northern Africa, the eastern Mediterranean and the Middle East, eastwards to western China (Chamberlain 1970, Townsend 1974, Meikle 1977, Yakovlev 1979, Rechinger 1984, Lock & Simpson 1991, Awmack & Lock 2002, Langran & Larsen 2010). Potential vegetation for this genus is largely desert and semi-desert areas with salty or gravely soils (Rechinger 1984, Zahran & Willis 1992). The species of Alhagi have economic relevance both as weeds and in medicine as herbals (Townsend 1974). The genus is characterized by spiny branches, glabrous and simple leaves, articulatemoniliform and indehiscent legumes with 1-9 seeds (Rechinger 1984, Awmack & Lock 2002).

The considerable morphological similarities and broad geographical distribution among Alhagi species have complicated the identification and delimitation of species, as this status is appeared in several synonyms and several nomenclatural problems (Yakovelov 1979, Rechinger 1984, Awmack & Lock 2002, Sheidai et al. 2001). Fedtschenko (1972) and Rechinger (1984) recognized five species (A. canescens (Regel.) Shap. ex Keller & Shap., A. kirghisorum Schrewnk, A. persarum Boiss. and Buhse, A. pseudalhagi (M.Bieb.) Desv., and A. mannifera Desv.) in the area covered by the corresponding flora, whereas the majority of other floras (e.g. Townsend 1974, Meikle 1977) recognized two widespread species of Alhagi in the western part of the range of the genus, A. graecorum Boiss. and A. maurorum Medik. Moreover, only one species with three subspecies have been recognized by Yakovlev (1979): A. maurorum subsp. kirghisorum (Schrenk) Yakovlev, A. maurorum subsp. canescens (Regel) Yakovlev, and A. maurorum subsp. maurorum, the last subspecies being divided in two varieties, viz. var. maurorum and var. turcomanica Yakovlev.

Hair characteristics in genus *Alhagi*, like majority of the other members of *Fabaceae* (Zarre 2003,

Ghahremaninejad 2004), have taxonomic importance. Also, based on the hairiness of the ovary and pod, Awmack & Lock (2002), reduced two species recognized by Meikle (1977) to the subspecies level. Accordingly, *A. mannifera* Desv. has been synonymized with *A. maurorum* Medik. subsp. graecorum (Boiss.) Awmack & Lock, and *A. persarum* Boiss. & Buhse with *A. pseudalhagi* (M.Bieb.) Desv. were treated as new combinations under *A. maurorum* Medik. subsp. *maurorum*.

Despite recent phylogentic attempts to address the relationships across tribe Hedysareae (Ahangarian et al. 2007, Amirahmadi et al. 2014, Duan et al. 2015), some ambiguities in the phylogeny and taxonomy of Alhagi remained. According to the most recent molecular phylogenetic studies (Amirahmadi et al. 2014, Duan et al. 2015), the monophly of this genus is confirmed and the analyzed species of Alhagi formed a well-supported clade as the first diverging lineage of the tribe Hedysareae. The main problem in taxonomy of Alhagi is the delimitation of the species, which is addressed in the present study. We employed a comprehensive dataset of nuclear ribosomal DNA internal transcribed spacer (nrDNA ITS) from several accessions representing different taxa and different geographical areas in Iran to assess the phylogenetic relationships among members of Alhagi and to delimit Alhagi species. In addition, we used morphological characters to discriminate the taxa of this genus present in Iran.

Materials and Methods

- Field survey and herbarium studies

In order to prepare a diagnostic key for members of *Alhagi*, a total of 110 individuals from 22 populations were collected and examined in Iran. Voucher specimens are deposited at Islamic Azad University Herbarium (IAUH). For phylogenetic study, the 45 ingroups represent 30 accessions of the genus *Alhagi* (three species), and 15 species of the sister genera *Caragana*, *Chesneya*, *Ebenus*, *Gueldenstaedtia*, *Halimodendron*, *Hedysarum*, *Onobrychis*, and *Taverniera*. Two other species, viz. Astragalus arthuri and Colutea persica were selected as outgroups according to previous molecular studies (Amirahmadi *et al.* 2014, Duan *et al.* 2015, Liu *et al.* 2017). Twenty two nrDNA ITS sequences of *Alhagi* are newly generated in this study and the remaining sequences were downloaded from GenBank. Voucher specimens and GenBank accession numbers of the analyzed sequences are listed in table 1.

Table 1. Localities and vouchers of Alhagi species and the related genera used in the current study

Taxon	Locality, source and voucher	GenBank accession No.
Alhagi graecorum Boiss.	Iran: Hormozgan province, Amirkhosravi 15103 (IAUH)	*
A. graecorum Boiss.	Iran: Ilam province, Amirkhosravi 15117 (IAUH)	*
A. graecorum Boiss.	Iran: Kohgiluyeh & Boyer-Ahmad province, Amirkhosravi 15107 (IAUH)	*
A. graecorum Boiss.	Iran: Bushehr province, Amirkhosravi 15121 (IAUH)	*
A. graecorum Boiss.	Saudi Arabia	KF805117 ^a
A. maurorum Medik.	Iran: Tehran province, Amirkhosravi 15100 (IAUH)	*
A. maurorum Medik.	Iran: Kerman province, Amirkhosravi 15101 (IAUH)	*
A. maurorum Medik.	Iran: Fars province, Amirkhosravi 15104 (IAUH)	*
A. maurorum Medik.	Iran: Khorasan (N) province, Amirkhosravi 15105 (IAUH)	*
A. maurorum Medik.	Iran: Kermanshah province, Amirkhosravi 15106 (IAUH)	*
A. maurorum Medik.	Iran: Hamadan province, Amirkhosravi 15108 (IAUH)	*
A. maurorum Medik.	Iran: Khorasan (S) province, Amirkhosravi 15109 (IAUH)	*
A. maurorum Medik.	Iran: Khorasan (RZ) province, Amirkhosravi 15110 (IAUH)	*
A. maurorum Medik.	Iran: Khorasan (RZ) province, Amirkhosravi 15111 (IAUH)	*
A. maurorum Medik.	Iran: Khorasan (RZ) province, Amirkhosravi 15112 (IAUH)	*
A. maurorum Medik.	Iran: Kurdistan province, Amirkhosravi 15113 (IAUH)	*
A. maurorum Medik.	Iran: Yazd province, Amirkhosravi 15114 (IAUH)	*
A. maurorum Medik.	Iran: Isfahan province, Amirkhosravi 15115 (IAUH)	*
A. maurorum Medik.	Iran: Sistan & Baluchistan province, Amirkhosravi 15116	*
	(IAUH)	
A. maurorum Medik.	Iran: Golestan province, Amirkhosravi 15118 (IAUH)	*
A. maurorum Medik.	Iran: Azarbayejan (W) province, Amirkhosravi 15119 (IAUH)	*
A. maurorum Medik.	Iran: Khorasan (S) province, Amirkhosravi 15120 (IAUH)	*
A. maurorum Medik.	Iran: Khuzestan province, Amirkhosravi 15123 (IAUH)	*
A. maurorum Medik.	Iran: Kazempour Osaloo 2008-2 (TMUH)	AB854477 ^a
A. maurorum Medik.	Iran: Kazempour Osaloo 2007-1 (TMUH)	AB374181ª
A. maurorum Medik.	China: Shihezi, Xinjiang	KJ486540 ^a
A. maurorum Medik.	*	GQ246125 ^a
A. maurorum Medik.	Iran: Kazempour Osaloo 2008-1 (TMUH)	AB854476 ^a
A. sparsifolia Shap.	*	KX942204 ^a
A. sparsifolia Shap.	* China: S.M.Duan TLF001 (TURP)	KP338103 ^a
Astragalus arthuri Jones.	USA: Wojciechowski 509	AF121739 ^a
Caragana arborescens Lam.	*	DQ311963ª
Chesneya astragalina Jaub. & Spach	Iran: Assadi & Maassoumi 55503 (TARI)	AB051906 ^a
Colutea persica Boiss.	Iran: Foroughi 17434 (TARI)	AB051907 ^a
Ebenus stellata Boiss.	Iran: Ahangarian & Kazempour Osaloo 2006-1 (TMUH)	AB329691 ^a
Gueldenstaedtia verna (Georgi) Boriss.	USSR: Ulanova & Bassargin 39025 (MSB)	AB854489 ^a
Halimodendron halodendron (Pall.) Voss	Iran: Maassoumi et al. 86046 (TARI)	AB329693ª
Hedysarum boreale Nutt.	*	KY366158 ^a
H. damghanicum Rech.f.	Iran: Kazempour Osaloo et al. 2009-2 (TMUH)	AB854493 ^a
H. hedysaroides (L.) Schinz & Thell.	Russia: Zaslavskaja 6184 (TARI)	AB854495 ^a
Onobrychis afghanica Sirj. & Rech.f.	Afghanistan: Podlech 15931 (MSB)	AB854501 ^a
O. atropatana Boiss.	Turkey: Nydegger 28212 (MSB)	AB854503 ^a
<i>O. montana</i> DC.	*	KF015324 ^a
O. ptolemaica DC.	Iran: Salehi & Zahrabi 395 (KNRCH)	AB854507 ^a
O. transcaucasica Grossh.	*	HM542539 ^a
O. viciifolia Scop.	Spain: Podlech 6892 (MSB)	AB854512 ^a
Taverniera spartea DC.	Iran: Mozaffarian 49325 (TARI)	AB329707 ^a

(*) Data not available in GenBank; (*) Sequences from GenBank; Abbreviations used: IAUH, Islamic Azad University Herbarium, Tehran, Iran; TARI, Herbarium of the Research Institute of Forests and Rangelands, Tehran, Iran; TMUH, Tarbiat Modares University Herbarium, Tehran, Iran; MSB, Herbarium of Ludwig-Maximilians-Universitat, Munchen, Germany; KNRCH, Khuzestan Natural Resource Research Center Herbarium of Khuzestan, Ahwaz, Iran; TURP, Turpan Eremophytes Botanical Garden, China.

- DNA extraction, amplification, and sequencing

Total genomic DNA was extracted from silica gel-dried leaf material with the Dneasy plant mini kit (Qiagen, Inc., Germany). The nrDNA ITS region was amplified using the primers AB101F and AB102R (Douzery *et al.* 1999).

The PCR amplification was carried out in the volume of 20 μ l, containing 8 μ l deionized water, 10 μ l of the 2 × Taq DNA polymerase master mix Red (Amplicon) 0.5 μ l of each primer (10 pmol/ μ l), and 1 μ l of template DNA. PCR cycles consisted of predenaturation at 94 °C for 3 min followed by 28–35 cycles, each consisting of denaturation at 94 °C for 1 min, annealing at 55 °C for 1 min and elongation at 72 °C for 1 min followed by a final elongation step of 7 min at 72 °C. The quality of the PCR products was checked by electrophoresis on a 1% (w/v) agarose gel (using 1 × TBE as the gel buffer) stained with ethidium bromide. PCR products along with the primers used for amplification were sent for Sanger sequencing at StaSEQ (Mainz, Germany).

- Alignment and phylogenetic analyses

The single marker data set was aligned using the web-based version of MUSCLE (Edgar 2004) under default parameters followed by manual adjustment. Indels were treated as missing data in all analyses.

Phylogenetic analyses were performed using maximum parsimony (MP) and Bayesian inference (BI). Parsimony analyses were conducted using PAUP* 4.0b10 (Swofford 2002). The heuristic search option was employed for each data set, using tree bisectionreconnection (TBR) branch swapping, 100 random sequence addition sequence replicates and no maximum tree limit. Branch support was assessed via the nonparametric bootstrap, MPB, (Felsenstein 1985) using 1,000 bootstrap replicates each with simple sequence addition. For likelihood analysis, the best models of sequence evolution were selected using MrModeltest 2.3 (Nylander, 2004) based on the Akaike information criterion (AIC) (Posada & Buckley 2004). This program identified GTR+G for nrDNA ITS. Maximum likelihood

(ML) analyses were performed using RAxMLGUI Ver. 1.5 (Silvestro & Michalak 2012). Nonparametric bootstrap values (MLB) were calculated in RAxMLGUI based on 1,000 bootstrap replicates with one search replicate per bootstrap replicate. The program MrBayes 3.2.4 (Ronquist et al. 2012) was used for the Bayesian phylogenetic analyses. Posteriors on the model parameters were estimated from the data, using the default priors and running the MCMC chains for 10 million generations. MrBayes performed two simultaneous analyses starting from different random trees (Nruns = 2) each with four Markov chains (i.e., one cold and three heated) and parameters sampled every 1000 generations. The first 25% trees were discarded as the burn-in. The remaining trees were then used to build a 50% majority rule consensus tree accompanied with posterior probability (PP) values. Tree visualization was carried out using TreeView version 1.6.6 (Page 2001). Mean pairwise sequence divergence and calulating variable sits were done in MEGA Ver. 6 (Tamura et al., 2013).

Phylogenetic networks: Neighbor-Net (NN), a distance-based network construction method, allows for graphical representation of conflicting phylogenetic signals and interpretation of evolutionary histories which are not tree-like (Bryant & Moulton 2004). NN splits graphs have been used with varying success to detect reticulate history (Carine *et al.* 2007, Frajman & Oxelman 2007, Grimm & Denk 2008, Weiss-Schneeweiss *et al.* 2008, Ramdhani *et al.* 2010, Schulte *et al.* 2010). Splits graphs were constructed using the NN algorithm with uncorrected p-distances in SplitsTree Ver. 4.14.4 (Huson 1998).

Results

Visual inspection of all clades and sister group relationships revealed no major differences among tree topologies obtained from MP and BI, respectively. Therefore, we will focus on the better resolved BI trees. The aligned nrDNA ITS data set contained 669 characters of which 300 were variable and 229 parsimony informative. Mean pairwise sequence divergence among nrDNA ITS haplotypes was 0.106. The number of variable sits within *Alhagi* sequences was 52. Heuristic search yeilded 10000 most parsimonious trees (length=624 steps, CI=0.683, RI=0.893). In the obtained cladogram (Fig. 1), the accessions representing the genus *Alhagi* were inferred as monophyletic (PP=1.00, MPB=100, MLB=100) and found to be composed of two well-supported clades. One clade (PP=1.00, MPB=100, MLB=99) included most

representatives of *Alhagi* split into several subclades, and the other clade contained the remining *Alhagi* accessions in one well-supported clade (PP=1.00, MPB=100, MLB=96). Similar to the Bayesian consensus tree (Fig. 1), the splits graph revealed two main groups (Fig. 2). Mean pairwise sequence divergence among these two main groups was 0.048. The number of variable sites in the larger and smaller clades contained twenty and six, respectively.



Fig. 1. Fifty percent majority rule consensus tree resulting from Bayesian inference of nrDNA ITS dataset of *Alhagi* and its related genera. Numbers above branches are posterior probability and parsimony bootstrap values, those below branches likelihood bootstrap values. Values <50% are not shown.



Fig. 2. Splits graph for nr DNA ITS data set of Alhagi and its related genera.

Discussion

The remarkable morphological similarities among the proposed species of Alhagi (Fabaceae, Hedysareae) have leaded to some complexities in the taxonomy and delimitation of the species of the genus (Chamberlain 1970, Townsend 1974, Meikle 1977, Yakovelov 1979, Rechinger 1984, Awmack & Lock 2002). The circumscription of Alhagi species has undergone several changes in the past (Rechinger 1984, Yakovlev 1979, Awmack & Lock 2002, Sheidai et al. 2001). Regarding potential vegetation of this genus on desert and semidesert areas and salty or rocky soils, Iran is taken into account as one of intermediate distribution corridors of the genus consisting of three species sensu Rechinger (1984). In this survey, to test the hypotheses on circumscription and relationships among Alhagi spp., and to redefine and to establish a taxonomic treatment, a comprehensive taxon sampling from all habitats and geographical regions of Iran along with special focus on type localities were conducted. The current molecular phylogeny based on nrDNA ITS sequences provides a relatively well-supported scenario of relationships within Alhagi. In agreement with recent molecular studies, the genus was retrieved as a monophyletic group as the first diverging lineage of the tribe Hedysareae (Ahangarian

et al. 2007, Amirahmadi et al. 2014, Duan et al. 2015, Liu et al. 2017). Possessing spiny branches, glabrous, simple leaves, articulate and moniliform, indehiscent pods with 1-9 seeds are synapomorphic traits for diagnosing this genus from the other genera of Hedysareae (Rechinger 1984). However, the current study indicated that, morphological similarities cause some difficulties in diagnosing Alhagi species. This status is confirmed by previous morphological studies resulting in several synonymies (Yakovelov 1979, Rechinger 1984, Awmack & Lock 2002, Sheidai et al. 2001). Similar to the other Alhagi species, these taxonomic changes can be observed in the three recognized species of Iran sensu Rechinger (1984), viz. A. mannifera, A. persarum, and A. pseudalhagi. Following the botanical nomenclature priority rules (Article 11. 1-10, in Turland et al. 2018) the accepted name for A. mannifera is A. graecorum, since the characters used by both Boissier (1872) and Keller & Shaparenko (1933) to separate A. graecorum from A. mannifera had been proved to be unreliable (Chamberlain 1970). Based on a cytological and morphometric study, Sheidai et al. (2001) considered A. persarum as a synonymy of A. pseudalhagi and Iran housing only two species, i.e. A. graecorum and A. pseudalhagi. However, in the western part of distribution of Alhagi, Awmack & Lock (2002) recognized a single variable species A. maurorum, A. pseudalhagi, and A. persarum were considered as synonyms of A. maurorum subsp. Maurorum, and A. graecorum as A. maurorum subsp. graecorum. In agreement with the previous morphological and cytological studies (Sheidai et al. 2001, Awmack & Lock 2002), the extensive morphological similarities between A. persarum and A. pseudalhagi was confirmed by the current molecular and morphological study, as the collected specimens from the localities reported by Rechinger (1984) for these two species did not indicate distinct molecular and morphological separation.

In agreement with the previous study (Amirahmadi et al. 2014), our analyses with the comprehensive taxon sampling from Iran indicated that, Alhagi accessions are divided into two well-supported clades which are geographically and morphologically distinct. The larger clade, distributed in the eastern part of the range of the genus, is confined to Irano-Turanian floristic region. As Alhagi pseudoalhagi, A. persarum, A. sparsifolia, and A. maurorum with remarkable morphological similarities joined together to form this larger clade. This clade is clearly distinct from the smaller clade with several morphological features such as the height and color of plant, the absence/presence hairs on stem, calyx, pod and ovary, the number of flowers on the axis of inflorescence. The smaller clade distributed in the western and south western of Iran related to SaharaSindian region. Therefore, sufficient genetic and morphological differences confirmed these two clades as clearly distinct species. With regarding to the botanical nomenclature priority rules, the members of the larger and smaller clades are belonging to the species "*A. maurorum*" and "*A. graecorum*", respectively.

Based on the hairiness of the ovary and pod, Awmack & Lock (2002) with comprehensive taxon sampling treated these two last species as a single variable species with two subspecies. Likewise, Mabberly (2017) introduced *Alhagi* as a monospecific genus, with *A. maurorum* as the only species. However, the present molecular and morphological evidence supported by adequate nucleotide difference in nrDNA ITS maker, the convincing number of diagnosed characters, and distinct biogeographic distribution patterns suggest recognizing two species of *Alhagi* in Iran, viz. *A. graecorum* and *A. maurorum*.

Taxonomic treatment

- Alhagi Gagnebin

Based on the molecular and morphological results of this study, it is quite clear that, there are only two distinct species in Iran. The two species differ morphologically and occur in different phytogeographical regions, i.e. Irano-Turanian and Saharo-Sindian. Comparing the results of this study with that of Awmack & Lock (2002), a key to these species is presented below.

Key to the species

1. Alhagi graecorum Boiss., Diagn. P1. Orient. Nov. ser.1 (9): 144 (1849); Fl. Orient. 2: 559 (1872); Townsend, Fl. of Iraq 3: 499, P1. 96, Figs 1–10 (1974) Syn.: Hedysarum alhagi L., Spec. Plant. 745 (1753) p.p.; A. mannifera Desv., J. Bot. Agric. 1: 120, t. 4, Fig. 4 (1813) nom. nud.; A. maurorum sensu DC., Prodr. 2: 352 (1825), sensu Boiss., Fl. Orient. 2: 558 (1872) et sensu Rech. f., Ark. Bot. ser. 2, 1: 426 (1950), non Medik.; Alhagi maurorum Medik. subsp. graecorum (Boiss.) Awmack & Lock, Kew Bull. 57(2) 441 (2002).

Plant dwarf perennial subshrub, up to 40 cm (-60 with green habit, erect to ascending or cm), subspreading, shortly pubescent or hirsute; branches strong, condensed, 8-20 cm long, spines strong, with quadrant-section, up to c. 4.5 cm long and up to c. 2.2 mm in diameter, each tipped c. 2.5-6 mm in length, spines of the lateral stems slender than main stem; leaves simple, relatively hairy, rectangular to obovate, about 2–6 times shorter than spines, obtuse, petioles very short 0.5-1 mm, hairy; inflorescence racemose, axillary, axis spine-tipped, 1-3-flowered (-1-5), peduncles 1-2 mm long, hairy; bracts very minute 0.2-0.6 mm; calyx 2-4 mm long, appressed hairy, the teeth conspicuous, about one-third to one-quarter the length of the tube, with acute sinuses, 0.37-0.95 mm; corolla red to purplish; standard 5-9 mm, obovate, with a short claw; keel slightly shorter or subequal to the standard, slightly falcately oblong, with rounded apex; wings shorter or subequal to keel, oblong. Ovary linear, sericeous. Pods linear, moniliform, hairy, 1-5 on an axis ending to spine, irregularly constricted between the seeds, often variousely twisted or falcate, $10-21 \times 1-4$ mm, stipe hairy with 1-3 mm long; seeds c 1-4 mm, subspherical to rhomboid, brown, smooth.

Distribution and habitat: Algeria, Bahrain, Chad, Cyprus, E. Aegean Is, Egypt, Greece, Iran, Iraq, Jordan, Kuwait, Lebanon, Libya, Niger, Paleastine, Saudi Arabia, Sinai, Sudan, Syria, and Turkey (Hassler 2019). Most often on often edges of ditches and saline places at low elevation, mostly 100–500 m.

Selected specimens: Iran: Hormozgan province, Hajiabad, 5 km from Hajiabad to Baghat, 1109 m, 55°56.28 E, 28°22.56 N, Amirkhosravi IAUH-15103; Kohgilouyeh & Boyer-Ahmad province, Dogonbadan, 5 km from Dogonbadan to Talkhabshirin, 718.2 m, 50°47.37 E, 30°21.31 N, Amirkhosravi IAUH-15107; Ilam province, Dehloran, Bishehzar, 339.5 m, 46°56.36 E, 32°48.23 N, Amirkhosravi IAUH-15117; Khuzestan province, Shoshtar, 2 km from Shoshtar Sardaran, 36.5 m, 48°50.58 E, 32°1.21 N, to Amirkhosravi IAUH-15123; Bushehr province, Bandar-Dayyer, 2 km from Bandar-Dayyer to Bardestan, 10.7 m, 51°53.34 E, 27°50.3 N, Amirkhosravi IAUH-15121.

2. A. maurorum Medik., Vorles. Churpf. Phys.-Oecon. Ges. 2: 397 (1787)

Syn.: Hedysarum alhagi L., Spec. Plant. 745 (1753) p.p.;
H. pseudoalhagi M. Bieb., Fl. Taur.-Cauc. 2: 174 (1808);
Alhagi pseudoalhagi (M.Bieb.) Desv, Journ. Bot. 3: 120 (1813); A. persarum Boiss. & Buhse, Nouv. M6m. Soc.
Imp. Naturalistes Moscou 12: 76 (1860); A. camelorum
Fisch., Cat. Jard. Gorenki, ed. 2: 72 (1812); Boiss., Fl.
Orient. 2: 559 (1872); A. sparsifolia Shap. ex Keller et
Shap. in Sovjetskaja Bot. 3–4 (1933) 167, pro var.

Plant erect, glabrous or subglabrous, spiny perennial shrub, mostly 75-150 cm, with blue-green habit; stems relatively strongly branching; spines sparsely branched with circle-section, erect-ascending to subcurved with broad angle, up to c. 5 cm long and up to c. 2.8 mm in diameter, each tipped c. 2-9 mm in length, spines of the lateral stems slender than main stem; leaves simple, rectangular to obovate, 8-22 mm long, 2-8 mm wide, obtuse or slightly acute, in both surfaces glabrous or more or less sparingly hairy, petioles short 1-2.5 mm; racemes 1-8-flowered, the axis spine like, peduncles 1.5-2 mm long; bracts minute 0.2-0.8 mm; calyx 1.5-5 mm, glabrous, the teeth almost obsolete, smaller than the tube, 0.18-2.47 mm, with obtuse sinuses; corolla red to purplish; standard 7-10.5 mm, obovate, abruptly narrowed to a short claw; keel slightly shorter or subequal to the standard, slightly falcate-oblong, with rounded apex; wings shorter or subequal to keel, oblong. Ovary linear, glabrous. Pods linear, moniliform, glabrous, 1–9 on an axis ending to spine, regularly and strongly constricted between the seeds, $8-35 \times 1-4$ mm, stipe glabrous with 1–3 mm long; seeds c 1–4 mm, subspherical to rhomboid, brown, smooth.

Distribution and habitat: Afghanistan, Armenia, Azerbaijan, Bahrain, China, Cyprus, E. Aegean Is, India, Iran, Iraq, Jordan, Kazakhstan, Kirgizstan, Lebanon, Paleastine, Pakistan, Russia, South Africa, Syria, Tadzhikistan, Turkey, Turkmenistan, and Uzbekistan (Hassler 2019). Most often on sand dunes, saline areas, field margins and as a weed in agricultural crops, mostly at 700–2300 m elevation.

Selected specimens: Iran: Tehran province, Varamin, 2 km from Varamin to Pishva, 923.1 m, 51°38.2 E, 35°19.59 N, Amirkhosravi IAUH-15100; Kerman province, Baft, Asiajofteh, 2304.7 m, 56°33.00 E, 29°14.58 N. Amirkhosravi IAUH-15101; Fars province, Polfasa, 1 km from Pol-e Fasa to Shiraz, 1475.2 m, 52°37.21 E, 29°31.16 N, Amirkhosravi IAUH-15104; Khorassan (N) province, Ashkhaneh, 1 km from Ashkhaneh to Mehmanak, 764.1 m, 56°54.39 E, 37°32.42 N, Amirkhosravi IAUH-15105; Kermanshah province, Biston, 15 km from Biston to Kermanshah, 1408.8 m, 47°14.11 E, 34°21.1 N, Amirkhosravi IAUH-15106; Hamedan province, Lalehjin, Dinarabad, 1713.2 m, 48°28.55 E, 34°58.18 N, Amirkhosravi IAUH-15108; Khorassan

References

- Ahangarian, S., Kazempour Osaloo, Sh. & Maassoumi, A.A. 2007. Molecular phylogeny of the tribe Hedysareae with special reference to *Onobrychis* (Fabaceae) as inferred from nrDNA ITS sequences. The Iranian Journal of Botany 13(2): 64–74.
- Amirahmadi, A., Kazempour Osaloo, Sh., Moein, F., Kaveh, A. & Maassoumi, A.A. 2014. Molecular systematics of the tribe Hedysareae (Fabaceae) based on nrDNA ITS and plastid *trn*L-F and *mat*K

(S) province, Boshroeeyeh, 40 km from Ferdos to Devhook, 1254.1 m, 57°11.27 E, 33°53.13 N, Amirkhosravi IAUH-15109; Khorassan (RZ) province, Chenaran, Radkan, 1180.3 m, 59°5.3 E, 36°38.57 N, Amirkhosravi IAUH-15110; Khorasan (RZ) province, Torbat Heydarieh, Robat Sang, 1710.4 m, 47°14.11 E, 34°21.1 N, Amirkhosravi IAUH-15111; Khorasan (S) province, Bajestan, 2 km from Bajestan to Gonabad, 1322.9 m, 58°10.23 E, 34°29.25 N, Amirkhosravi IAUH-15112; Kurdistan province, Bijar, 20 km from Bihar to Ghajoor, 1714 m, 47°46.42 E, 35°53.45 N, Amirkhosravi IAUH-15113; Yazd province, Taft, Cham, 1436.6 m, 54°15.29 E, 31°47.3 N, Amirkhosravi IAUH-15114; Esfahan province, Kashan, Taherabad, 984.5 m, 51°20.5 E, 34°1.54 N, Amirkhosravi IAUH-15115; Sistan & Baluchistan province, Saravan, 5 km from Saravan to Hooshak, 1275 m, 62°31.51 E, 27°17.21 N, Amirkhosravi IAUH-15116; Golestan province, Gonbade Kavous, Alghajar, 123.7 m, 55°20.25 E, 37°12.4 N, Amirkhosravi IAUH-15118; Azarbayejan (W) province, Urmia, 20 km from Urmia to Sero, 1349.7 m, 45°2.32 E, 37°35.27 N, Amirkhosravi IAUH-15119; Khorasan (S) province, Nehbandan, 10 km from Nehbandan to Sefidabeh, 1088.4 m, 59°49.36 E, 31°27.8 N, Amirkhosravi IAUH-15120.

Acknowledgment

The authors wish to thank to the anonymous reviewers for valuable comments on earlier draft.

sequences. Plant Systematics and Evolution 300(4): 729–747.

- Awmack, C. & Lock, J. 2002. The genus Alhagi (Leguminosae: Papilionoideae) in the Middle East. Kew Bulletin 57(2): 435–443.
- Boissier, E. 1872. Alhagi. Pp. 588–589. In: Flora Orientalis, Vol. 2. Genevae, Basilae and Lugundi.
- Bryant, D. & Moulton, V. 2004. Neighbor-Net: An agglomerative method for the construction of phylogenetic networks. Molecular Biology and Evolution 21(2): 255–265.

- Carine, M.A., Robba, L., Little, R., Russel, S. & Guerra, A.S. 2007. Molecular and morphological evidence for hybridization between endemic Canary Island *Convolvulus*. Botanical Journal of the Linnean Society 154(2): 187–204.
- Chamberlain, D.F. 1970. Alhagi. Pp. 596–597. In: Davis, P.H. (ed.), Flora of Turkey and the East Aegean Island, Vol. 3. Edinburgh University Press, Edinburg.
- Douzery, E., Pridgeon, A., Kores, P., Linder, H.P., Kurzweil, H. & Chase, M. 1999. Molecular phylogenetics of Disease (Orchidaceae): a contribution from nuclear ribosomal ITS sequences. American Journal of Botany 86(6): 887–899.
- Cunningham, C.W. 1997. Can three incongruence tests predict when data should be combined? Molecular Biology and Evolution 14(7): 733–740.
- Duan, L.J., Wen, J.N., Yang, X., Liu, P.L., Arslan, E.,
 Ertu rul, K. & Chang, Z.Y. 2015. Phylogeny of *Hedysarum* and tribe Hedysareae (Leguminosae: Papilionoideae) inferred from sequence data of ITS, *mat*K, *trn*L-F and *psb*A-*trn*H. Taxon 64(1): 49–64.
- Edgar, R.C. 2004. Muscle: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research 32(5): 1792–1797.
- Farris, J.S., Källersjö, M., Kluge, A.G. & Bult, C. 1994. Testing significance of incongruence. Cladistics 10(3): 315–319.
- Fedtschenko, B.A. 1972. *Hedysarum* L. (Leguminosae).
 Pp. 199–243. *In*: Komarov, V.L., Shishkin, B.K.
 & Bobrov, E.G. (eds), Flora of the USSR, Vol.
 13. Israel Program for Scientific Translation, Jerusalem.
- Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39(4): 783–791.
- Frajman, B. & Oxelman, B. 2007. Reticulate phylogenetics and phytogeographical structure of *Heliosperma* (Sileneae, Caryophyllaceae) inferred

from chloroplast and nuclear DNA sequences. Molecular Phylogenetics and Evolution 43(1): 140–155.

- Ghahremaninejad, F. 2004. Value of trichome characteristics for separating of bifurcating *Astragalus* (Fabaceae) on sectional level. Turkish Journal of Botany 28(1/2): 241–245.
- Grimm, G.W. & Denk, T. 2008. ITS evolution in *Platanus* (Platanaceae): Homoeologues, pseudogenes and ancient hybridization. Annals of Botany 101(3): 403–419.
- Hassler, M. 2019. World Plants: Synonymic Checklists of the Vascular Plants of the World (version Nov. 2018). *In*: Roskov, Y., Ower, G., Orrell, T., Nicolson, D., Bailly, N., Kirk, P.M., Bourgoin, T., DeWalt, R.E., Decock, W., Nieukerken, E., Zarucchi, J. & Penev, L. (eds). Species 2000 & ITIS Catalogue of Life, 25th Mar. 2019. Digital resource from: www.catalogueoflife.org/col. Species 2000: Naturalis, Leiden, Netherlands.
- Huson, D.H. 1998. SplitsTree: A program for analysing and visualizing evolutionary data. Bioinformatics 14(1): 68–73.
- Keller, B.A. & Shaparenko, K.K. 1933. Materials for a systematic and ecological monograph of *Alhagi* Tourn. ex Adans. Sovetsk Botanika 3–4: 150–185 (In Russian).
- Langran, X. & Larsen, K. 2010. Alhagi. Pp. 526–527. In: Wu, Z.Y., Raven, P.H. & Hong, D.Y. (eds), Flora of China, Vol. 10 (Fabaceae). Science Press, Beijing, and Missouri Botanical Garden Press, St. Louis.
- Liu, P.-L., Wen, J., Duan, L., Arslan, E., Ertu rul, K. & Chang, Z.-Y. 2017. *Hedysarum* L. (Fabaceae: Hedysareae) is not monophyletic-Evidence from phylogenetic analyses based on five nuclear and five plastid sequences. PLoS ONE 12(1): e0170596.
- Lock, J.M. & Simpson, K. 1991. Legume of the West Asia: a check-list. Royal Botanic Gardens, Kew, London, 274 pp.

- Mabberly, D.J. 2017. Mabberly's Plant-book: A Portable Dictionary of Plants, Their Classification and Uses. 4th edition. Cambridge University Press, Cambridge.
- Meikle, R.D. 1977. Flora of Cyprus, Vol. 1. Bentham-Moxon Trust, Royal Botanic Gardens, Kew, London, 832 pp.
- Nylander, J.A.A. 2004. MrModeltest version 2. Program Distributed by the Author. Evolutionary Biology Center, Uppsala University, Uppsala.
- Page, D.M. 2001. Treeview (Win32) version 1.6.6. Available from: https://treeview.software.informer.com/1.6.
- Posada, D. & Buckley, T.R. 2004. Model selection and model averaging in phylogenetics: advantages of akaike information criterion and Bayesian approaches over likelihood ratio tests. Systematic Biology 53(5): 793–808.
- Ramdhani, S., Cowling, R.M. & Barker, N.P. 2010. Phylogeography of *Schotia* (Fabaceae): Recent evolutionary processes in an ancient thicket biome lineage. International Journal of Plant Sciences 171(6): 626–640.
- Rechinger, K.H. 1984. Alhagi. Pp. 470–475. In: Rechinger K.H. (ed.), Flora Iranica: Papilionaceae II, No. 157. Akademische Druck- und Verlagsanstalt, Graz.
- Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Hohna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. 2012.
 MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542.
- Schulte, K., Silvestro, D., Kiehlmann, E., Vesely, S., Novoa, P. & Zizka, G. 2010. Detection of recent hybridization between sympatric Chilean *Puya* species (Bromeliaceae) using AFLP markers and reconstruction of complex relationships. Molecular Phylogenetics and Evolution 57(3): 1105–1119.
- Sheidai, M., Yazdanbakhsh, Z., Assadi, M. & Moussavi, M. 2001. Cytology and morphometry study of

Alhagi (Leguminosae) species in Iran. Nordic Journal of Botany 21(1): 83–91.

- Swofford, D.L. 2002. PAUP*: Phylogenetic Analysis Using Parsimony (*and Other Methods), 4.0b4a. Sinauer Associates, Sunderland, Massachusetts.
- Tamura, K., Stecher, G., Peterson, D., Filipski, A., Kumar, S. 2013. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725–2729.
- Townsend, C.C. 1974. Alhagi. Pp. 494–503. In: Townsend, C.C. & Guest, E. (eds), Flora of Iraq, Vol. 3. Ministry of Agriculture of the Republic of Iraq, Baghdad.
- Turland, N.J., Wiersema, J.H., Barrie, F.R., Greuter, W., Hawksworth, D.L., Herendeen, P.S., Knapp, S., Kusber, W.-H., Li, D.-Z., Marhold, K., May, T.W., McNeill, J., Monro, A.M., Prado, J., Price, M.J. & Smith, G.F. (eds). 2018. International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code) adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017. Regnum Vegetabile 159. Glashütten: Koeltz Botanical Books. https://doi.org/10.12705/Code.2018.
- Weiss-Schneeweiss, H., Tremetsberger, K., Schneeweiss, G.M., Parker, J.S. & Stuessy, T.F. 2008. Karyotype diversification and evolution in diploid and polyploid South American *Hypochaeris* (Asteraceae) inferred from rDNA localization and genetic fingerprint data. Annals of Botany 101(7): 909–918.
- Yakovelov, G.P. 1979. Notes on the taxonomy of the genus *Alhagi* Gagneb (Fabaceae). Botanicheskii Zhurnal 64: 1794–1799.
- Zahran, M. & Willis, A. 1992. The vegetation of Egypt. Springer, Netherlands, 424 pp.
- Zarre, S. 2003. Hair micromorphology and its phylogenetic application in thorny speices of *Astragalus* (Fabaceae). Botanical Journal of Linnean Society 143: 323–330.