Phylogenetic Affinities of Wild and Cultivated Ornithogaloideae Based on ITS and \( trnL-F \) DNA Sequences by Extended Sampling from Iran

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ABSTRACT

The taxonomic classification of subfamily Ornithogaloideae has been a subject of considerable controversy in recent decades. \textit{Ornithogalum} is a relatively large genus in Ornithogaloideae including valuable ornamental and medicinal plants. These wild ornamentals, which are introduced into agriculture recently, are becoming increasingly popular as cut flowers, pot plants, and for gardening. This is the first molecular phylogenetic study that includes 10 of the 13 \textit{Ornithogalum} species native to Iran. The aims of the present study were to use ITS and \( trnL-F \) sequences to explore phylogenetic relationships and to evaluate genetic resources of Ornithogaloideae naturally occurring in Iran, with an increased sampling of species to be compared to previous phylogenetic studies. In the present study, the combined tree resulted in the best-resolved phylogenetic relationships at the generic level. The results of Maximum Likelihood and Bayesian analysis of molecular data were compared to those from hierarchical cluster analysis of morphological characters. Based on the results, all specimens collected in Iran across all previously recognized taxonomic genera in Ornithogaloideae were placed in \textit{Ornithogalum} \textit{sensu stricto} and \textit{Loncomelos}, which is in line with the morphological analysis. Divergent placements of multiple specimens of a single species in \textit{L. brachystachys}, \textit{O. orthophyllum}, and \textit{O. sintenisii} are attributed to the possibility of past hybridization events, although incomplete lineage sorting and ITS paralogy cannot be overlooked. Increased understanding of naturally occurring variation among wild \textit{Ornithogalum} populations of Iran and the phylogenetic relationships of wild and cultivated species of Ornithogaloideae could contribute to important opportunities to introduce new ornamentals and improve the agricultural performance of ornamental varieties.

Keywords: Molecular phylogenetics, Nuclear and Plastid DNA sequences, \textit{Ornithogalum}, \textit{Loncomelos}, \textit{Melomphis}, Ornamental plant.

INTRODUCTION

\textit{Ornithogalum} L. belongs to subfamily Ornithogaloideae of Hyacinthaceae, a family of about 700-900 species of bulbous plants mainly distributed through Africa, Europe, and southwest Asia, with one small genus found in South America (Oziroe\textsuperscript{e}) (APG II 2003). The taxonomic classification of this subfamily remains a subject for speculation in recent years (Martínez-Azorín \textit{et al.}, 2011). Manning \textit{et al.} (2009) extensively studied the possible classifications within this subfamily based on plastid molecular sequences, and finally proposed three tribes (\textit{Dipcadiaceae}, \textit{Ornithogaleae}, and \textit{Albuceae}), with only four genera, \textit{Albuca} L., \textit{Dipcadi} Medik., \textit{Ornithogalum} L. and \textit{Pseudogaltonia} Kuntze. They divided genus \textit{Ornithogalum} into four subgenera i.e. \textit{Galtonia} Decne., \textit{Aspasia} Salisb., \textit{Avonsera} Speta., and \textit{Ornithogalum}. Although

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Galtonia, Avonsera, and Aspasia were homogeneous in morphology, Ornithogalum (with seven sections) was extremely heterogeneous. Moreover, in order to make O. section Ornithogalum monophyletic, Manning et al. (2009) included Loncomelos Raf. [O. subgenus Beryllis (Salisb.) Baker] within this genus, therefore, constructing a morphologically heterogeneous aggregate which is difficult to define with regard to other sections. In the most recent classification on the basis of the phylogenetic analyses based on plastidial and nuclear DNA regions by Martínez-Azorín et al. (2011), 19 monophyletic genera are accepted within Ornithogaloideae: Albuca, Avonsera, Battandiera Maire., Cathissa Salisb., Coilonox Raf., Dipcadi, Eliokarmos Raf., Elsiea F.M.Leight., Ethesia Raf., Galtonia, Honorius Gray, Loncomelos, Melomphis Raf., Neopatersonia Schonland, Nicipe Raf., Ornithogalum, Pseudogaltonia, Stellarioides Medik., and Trimelopter Raf. In their study, the Loncomelos clade was sister to the monophyletic Ornithogalum s. str., which provides easy morphological circumscription for both groups. As pointed out by Müller Doblies and Müller Doblies (1996) dividing genus Ornithogalum based on the DNA molecular sequences seems to be by far the better taxonomic solution than including Albuca and other genera into Ornithogalum, which makes a huge taxonomic ‘dustbin’.

Several species of Ornithogaloideae such as Eliokarmos thyrsoides (Jacq.) Raf. and E. dubius (Houtt.) Mart.-Azorín, M.B.Crespo & Juan have been developed as cut flowers (Luria et al., 2000) and pot plants (Anderson 2006). Also, Ornithogalum Umbellatum L., Loncomelos pyramidale (L.) Raf. and Honorius nutans (L.) Gray. are used in gardens and Melomphis arabica (L.) Raf. and Galtonia saundersiae (Baker) Mart.-Azorín, M. B. Crespo & Juan as cut flowers (Plančič et al., 2015). On the other hand, many plants from this subfamily have been used for various medicinal purposes, while several species are implicated in livestock poisoning (Watt and Breyer-Brandwijk 1932, Botha et al., 2000). For example, O. cuspidatum Bertol. is used in Iranian traditional medicine to treat respiratory and inflammatory diseases (Samavati et al., 2010). Furthermore, it has been used as an anti-

irritant and relaxant and as a food additive (Nazifi et al., 2010). Recently, some studies suggested Ornithogaloideae species contain compounds that exhibit cytotoxic properties against a variety of malignant tumor cells (Asadi et al., 2014). Despite this potential importance, the genetic resources available within this subfamily are still largely unexploited (Anderson, 2006).

Iran is recognized as one of the 34 hotspots of biodiversity in the world (http://www.biodiversityhotspots.org/xp/Hotspots). It is also a country with high diversity of bulbous plants. More than 200 species of bulbous plants from different families grow in Iran (Farahmand and Nazari, 2015), including 15 species of Ornithogalum (Rechinger, 1995; Maroufi, 2010; Heidaryan, 2011; Bidarlord and Gahremaninejad, 2016). Baker (1872) traditionally placed these species in 3 subgenera: O. subgen. Beryllis (Salisb) Baker (= Loncomelos), O. subgen. Ornithogalum (Syn.: Subgen Heliocharnos Baker) (= Ornithogalum s. str.), and O. subgen. Caruelia (Parl) Baker (= Melomphis p. p.) (Rechinger, 1995).

Although there are several published studies about the phylogenetic and morphological characterization of Ornithogaloideae around the world, to date there are no published studies of phylogenetic affinities for Ornithogaloideae species native to Iran. Placing Iranian species in a phylogenetic context should improve our understanding of the extent and distribution of their biodiversity, which, in turn, should have important implications for germplasm selection in breeding programs aimed at development of these species as ornamental and medicinal plants.

In the present study, we aimed to use nuclear (ITS) DNA and plastid (trnL–F) sequences to: (a) Explore phylogenetic relationship of the cultivated and wild Ornithogaloideae species, with increased sampling of species native to Iran compared to previous studies; (b) Evaluate generic and infrageneric taxonomy of 3 genera of Ornithogaloideae from Iran; and (c) Evaluate genetic resources of this genus in Iran in order to provide important information for plant breeders interested in generating new Ornithogaloideae cultivars for medicinal and ornamental purposes.
MATERIALS AND METHODS

Plant Material

Young leaves of 50 specimens representing 10 species of *Ornithogalum*, *Loncomelos* and *Melomphis* were collected through 50 localities in Iran (Table 1). The samples were labeled and immediately placed in liquid nitrogen. The coordinates of the readings were determined by the Global Positioning System (GPS). The map for geographical distribution of collected samples was generated from GPS data using ArcGIS Desktop (ESRI, Inc.) (Figure 1a-b). Samples were stored at -80°C till DNA extraction. DNA was extracted using the DNeasy Plant Mini Kit (Qiagen, USA) according to the manufacturer’s recommendations. The identification of taxa was made by an expert botanist [Mozafarian (PhD), Research Institute of Forests and Rangelands, Tehran, Iran] and deposited in the herbarium of Iranian Biological Research Center. Voucher numbers are shown in Table S2.

Morphological Characters

All plants chosen for DNA extraction were morphologically described and 26 morphological characters were used for a hierarchical cluster analysis. Of these, 11 were continuous (including plant, scape and inflorescence length; leaves and flower number; leaves, perigone and bulb length and width) while the remaining 15 were discrete (Table 2). The datasets were subjected to a hierarchical cluster analysis using Ward’s method and squared Euclidean distances (Version 9.3.1; SAS Institute Inc, Cary, NC).

Sequence Generation

The *trnL* intron and *trnL–F* spacer (the *trnL–F* region; hereafter *trnL–F*) were amplified as a single fragment using primers c and f (Taberlet *et al*., 1991). ITS was amplified using ITS6 and ITS9 primers (Potter *et al*., 2007). A total volume of 50 µL was used in the PCR amplification process as follows: 2 µL dNTP, 5 µL 10X PCR buffer (Qiagen, USA), 1 µL (10 µM) of forward and reverse primers (each), 1 µL of MgCl₂ (25 mM), 0.5 µL of Taq DNA Polymerase, 38.5 µL deionized water and 1 µL of DNA template plus 1 µL DMSO for ITS amplification. PCR amplifications were performed with an initial 5 min at 95 °C, followed by 35 cycles of 1 minute at 95°C, 1 minute at 50°C, 1 minute at 72°C, followed by a final 7 minutes at 72°C. PCR products were subjected to gel electrophoresis and were cleaned up using a QIAquick Gel Extraction Kit (Qiagen, USA). Purified PCR products were directly sequenced in both forward and reverse directions, using the corresponding primers. The sequencing process was performed using ABI 3730 Capillary Electrophoresis Genetic Analyzers. Sequencher 5.4 (Gene Codes Corporation, Ann Arbor, MI, USA) was used to assemble complementary strands. The sequences’ identities were confirmed by comparison with various published sequences.
**Figure 1.** Geographical distribution of collected samples (a) and hierarchical cluster analysis of morphological characters (b) using Ward’s method.
Table 2. Discrete morphological characters included in the analysis of genus *Ornithogalum* in Iran.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Descriptor state</th>
<th>Characters</th>
<th>Descriptor state</th>
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<tbody>
<tr>
<td>1. Leaves color</td>
<td>Chartreuse</td>
<td>9. Petal stripe color</td>
<td>Without strip</td>
</tr>
<tr>
<td></td>
<td>Electric lime</td>
<td></td>
<td>Dandelion</td>
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<td></td>
<td>Bright green</td>
<td></td>
<td>Dark yellow</td>
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<td></td>
<td>Bitter lemon</td>
<td></td>
<td>Fluorescent yellow</td>
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<td></td>
<td>Green</td>
<td></td>
<td>Green</td>
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<tr>
<td></td>
<td>Dark olive green</td>
<td></td>
<td>Deep green</td>
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<tr>
<td></td>
<td>Deep green</td>
<td></td>
<td></td>
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<tr>
<td>10. Petal stripe width</td>
<td>Without strip</td>
<td></td>
<td>Narrow</td>
</tr>
<tr>
<td></td>
<td>Narrow</td>
<td></td>
<td>Semi_wide</td>
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<tr>
<td></td>
<td>Semi_wide</td>
<td></td>
<td>Wide</td>
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<tr>
<td>2. Leaves tip shape</td>
<td>Semi_lanceolate</td>
<td></td>
<td>Wider</td>
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<tr>
<td></td>
<td>lanceolate</td>
<td></td>
<td></td>
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<tr>
<td>3. Leaves position</td>
<td>Erect</td>
<td>11. Ovary color</td>
<td>Dandelion</td>
</tr>
<tr>
<td></td>
<td>Non erect</td>
<td></td>
<td>Dark yellow</td>
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<tr>
<td>4. Margin of leaves</td>
<td>Non_wavy</td>
<td></td>
<td>Brown</td>
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<tr>
<td></td>
<td>Slightly wavy</td>
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<td></td>
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<tr>
<td></td>
<td>Wavy</td>
<td></td>
<td></td>
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<tr>
<td>5. Leaves shape</td>
<td>Wide linear</td>
<td>12. Anther color</td>
<td>Creamy</td>
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<tr>
<td></td>
<td>Semi_wide linear</td>
<td></td>
<td>Yellow</td>
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<tr>
<td></td>
<td>Linear</td>
<td></td>
<td>Deep lemon</td>
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<tr>
<td></td>
<td>Narrowly linear</td>
<td></td>
<td>Dark yellow</td>
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<tr>
<td></td>
<td>Very narrowly linear</td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>Equal</td>
<td></td>
<td>Eggshell</td>
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<td></td>
<td>Yes</td>
<td></td>
<td>Canary</td>
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<td></td>
<td></td>
<td></td>
<td>Corn</td>
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<td></td>
<td></td>
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<td>Citrine</td>
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<tr>
<td>7. Inflorescence compaction</td>
<td>Non_compact</td>
<td>14. Scale style</td>
<td>Semi_contiguous</td>
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<tr>
<td></td>
<td>Compact</td>
<td></td>
<td>Semi_free</td>
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<tr>
<td></td>
<td>Compressed and</td>
<td></td>
<td>Free</td>
</tr>
<tr>
<td></td>
<td>compact</td>
<td></td>
<td></td>
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<tr>
<td>8. Perianth color</td>
<td>Snow</td>
<td>15. Erect scape</td>
<td>Yes</td>
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<td></td>
<td>Conditioner</td>
<td></td>
<td>No</td>
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<tr>
<td></td>
<td>Milk</td>
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<td></td>
<td>Cream</td>
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<td></td>
<td>Blond</td>
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available in GenBank. Consensus sequences for each specimen were deposited in GenBank; accession numbers are listed in supplementary data (Table S2).

**Phylogenetic Reconstruction**

*Bowiea volubilis* Harv. ex Hook. f. was selected as the out-group based on Martínez-Azorín et al. (2011). The Ornithogaloideae was used as a query to search the non-redundant (nr) dataset of GenBank in order to obtain additional ingroup sequences (Searched on 1st of May, 2017) (Table S2). The majority of available *trnL–F* sequences in Genbank were short (300-500 bp); in order to avoid large proportions of missing data, we did not include the sequences under 908 bases in length in our *trnL–F* and combined data analyses.

In combination with sequences generated by this study, 112 sequences from 93 taxa for ITS, and 70 sequences from 44 taxa for *trnL–F* were included in the following analyses. The collected sequences were first aligned using MUSCLE (Edgar, 2004) through MEGA7 (Kumar et al., 2016) followed by manual adjustments. Aligned sequences were then analyzed using jModeltest 2.
v2.1.7 (Darriba et al., 2012) to estimate the best substitution model based on AIC, cAIC, and BIC. The estimated model was then passed on to RAxML v8.2.8 (Stamatakis, 2014) under default algorithm (Option: -f d) to generate a maximum likelihood tree. Model parameters and equilibrium base frequencies were estimated by RAxML. Four parallel searches were conducted in order to avoid selecting a tree lodged on a local optimum. Bootstrap values were calculated from 100 replicates, and corresponding coefficients were indicated above each branch.

The Bayesian analysis was conducted with MrBayes 3.1.2 (Huelsenbeck and Ronquist, 2005). The Markov Chain Monte Carlo chains were run for 20x10^{6} for ITS and 10x10^{6} generations for trnL–F and combined trees and setting the ‘burnin’ at 50,000 for ITS and 25,000 for trnL–F and combined trees. We used the Markov Chain Monte Carlo method within a Bayesian framework to estimate the posterior probabilities of the phylogenetic trees (Larget and Simon, 1999) using the 50% majority rule.

RESULTS

Morphological Characters

On the basis of the morphological analysis, including 26 characters, the species of Loncomelos [= O. subgen. Beryllis (Salisb) Baker] and Melomphis [= O. subgen. Caruelia (Parl) Baker] were grouped together in one clade. Melomphis persica (Hausskn. ex Bormm.) Mart.-Azorín, M. B. Crespo & Juan, the sole member of Melomphis (= O. subgenus Caruelia) included in our study, was placed as sister to Loncomelos kurdicum Bormm. Ornithogalum s. str. [= O. subgen. Ornithogalum (Syn.: Subgen Heliocharmos Baker)] was placed as sister to Loncomelos and Melomphis. In the morphological character tree, multiple individuals of a single species clustered together.

3.2. Phylogenetic Relationships amongst Ornithogaloidae Species Based on DNA Sequences

Despite difficulties in amplification and sequencing, PCR amplicons were successfully obtained for all the samples, and for most examined taxa yielded data useful for phylogenetic evaluation. Six of these sequences when aligned to others were missing a part of the 5.8S rDNA region; thus, we determined these as pseudogenes (Hříbová et al., 2011). After the exclusion of these pseudogene sequences, 26 sequences for ITS and 33 sequences for trnL–F regions remained from the original 50 genotypes.

For ITS, the resulting alignment contained 691 positions (with 448 variable and 316 parsimony-informative sites). For trnL–F, the resulting alignment contained 1,089 positions (with 169 variable and 97 parsimony-informative sites). For the combined analysis, the resulting alignment contained 1682 positions (with 481 variable and 267 parsimony-informative sites). Moreover, jModeltest2 (Darriba et al., 2012) found GTR+I+G for ITS, GTR+G for trnL–F and GTR+G for combined tree to be the best model based on AIC, cAIC, and BIC. In Maximum Likelihood analysis, RAxML with estimated parameters (α= 1.450162 and l= 0.272202 for ITS, α= 0.309291 for trnL–F and α= 0.299892 for combined tree) generated the most likely phylogeny with the likelihood score of -6203.766527 for ITS, -3006.911030 for trnL–F and -8064.615813 for combined tree. In all three of our trees, all of the Iranian native species appeared in a single large clade. In the ITS and combined trees, the clade was strongly supported (1.00 PP; 100% BS), while in the trnL–F tree, the clade was weakly supported (69 PP; 50% BS) (Figures 2, 3, and 4).

ITS tree

The ITS tree includes two main clades. The first one comprises Ornithogalum, Honorius, Loncomelos, Cathissa, Melomphis, Nicipe and Elsiea (Clade A), which includes two main sub-clades. The first sub-clade contains Ornithogalum and Honorius and the second one includes Loncomelos plus 3 specimens of M. persica. The Iranian species are nested in clade A within genera Ornithogalum, Honorius and Loncomelos. The genus Nicipe forms a monophyletic clade sister to the clade comprising Ornithogalum, Honorius and Loncomelos. The species of Cathissa, Melomphis and Elsiea do not form monophyletic clades.
Figure 2. Bayesian inference analysis obtained from ITS sequences in the phylogenetic analysis of Ornithogaloideae. Sequences specified with bold words are generated by this study. The new proposed generic circumscription of the present study for Iranian species is shown on the right side. Posterior probabilities and bootstrap percentages are shown next to nodes. The generic treatment by Martínez-Azorín et al. (2011) is followed for the studied samples.
Figure 3. Bayesian inference analysis obtained from trnL-F sequences in the phylogenetic analysis of Ornithogoaloideae. Sequences specified with bold words are generated by this study. The new proposed generic circumscription of the present study for Iranian species is shown on the right side. Posterior probabilities and bootstrap percentages are shown next to nodes. The mentioned genera in this tree are accepted by Martínez-Azorín, Crespo et al. (2011). The species not studied by Martínez-Azorín et al. (2011) are shown in checkered.
Figure 4. Bayesian inference analysis obtained from the combination of ITS and \( trnL-F \) sequences in the phylogenetic analysis of Ornithogaloideae. Sequences specified with bold words are generated by this study. The new proposed generic circumscription of the present study for Iranian species is shown on the right side. Posterior probabilities and bootstrap percentages are shown next to nodes. The mentioned genera in this tree are accepted by Martínez-Azorín et al. (2011).
The first sub-clade in clade A includes *Ornithogalum* and *Honorius*. In this sub-clade, *O. sintenisii* specimens do not form a monophyletic group and are placed in three different sub-clusters; one includes 3 specimens and the other one includes *O. sintenisii*1. The sequence of the specimen obtained from GenBank, which was also collected in Iran (Martínez-Azorín et al., 2011), and the specimens collected in this study are resolved into two distant clades. The four specimens of *O. orthophyllum* Ten. collected in Iran form a sub-cluster and are placed distant from the specimen obtained from GenBank, which is based on a collection from Italy (Martínez-Azorín et al., 2011). *O. neurostegium* Boiss. & C. I. Blanche ex Boiss. is placed as sister to the rest of species in *Ornithogalum*. Two specimens of *O. cuspidatum* formed a sub-cluster sister to *O. oligophyllum* E. D. Clarke. (Figure 2).

The second sub-clade in clade A includes *Loncomelos* plus 3 specimens of *Melomphis persica*. Seven specimens of *L. brachystachys* are also placed in this sub-clade, but in different sub-clusters; three specimens of *L. brachystachys* including 2, 5, and 7, formed one sub-cluster, and three other specimens of *L. brachystachys* including 8, 3, and 10, formed another sub-cluster. *L. brachystachys*12 plus *O. orthophyllum*.5 are placed on a well-supported sub-cluster (1.00 PP; 98% BP) which is sister to *L. bungei* Boiss.1. All 3 specimens of *M. persica* formed a small well-supported (1.00 PP; 100% BP) sub-cluster (Figure 2) which is sister to *L. arcuatum* Steven. (85 PP; 67% BP). Finally, *L. kurdicum* is sister to all of these taxa (67 PP; 98% BP).

Clade B includes *Albuca*, *Coilonox*, *Stellarioides*, *Trimelopter*, *Dipcadi*, *Battandiera*, *Neopatersonia*, *Eliokarmos*, *Galtonia*, *Ethesia* and *Avonsera*. This clade is further divided into two main sub-clades. The first one comprises genera *Albuca* plus *Coilonox*, which are sisters to *Stellarioides*, and finally *Trimelopter* falls as sister to this clade. Also, *Dipcadi* and *Battandiera* form sister clades and *Neopatersonia* falls as sister to the latter. The second sub-clade includes *Eliokarmos* as monophyletic. *Galtonia* and *Ethesia* are sister to *Eliokarmos*.

**trnL–F Tree**

In the *trnL–F* tree one main clade can be distinguished and successively sister groups appear in that large clade. According to our results, the *trnL–F* analysis reveals a large clade (0.69 PP; 50% BS) for the Iranian native species included in this study. The *trnL–F* tree follows the ITS tree arrangement where *Ornithogalum*, *Honorius* and *Loncomelos* are placed in one clade. In this tree, *Ornithogalum* and *Loncomelos* cannot be identified as monophyletic. Also, in this tree, different specimens of each species do not form monophyletic groups. All members of *Ornithogalum* s. str., except *O. oligophyllum*.1 and *O. orthophyllum*.5, grouped in one clade. The specimens of *L. brachystachys* are placed in different sister clades as are 3 specimens of *M. persica*. The other sister clade shows a close relationship between *L. kurdicum* and *L. arcuatum* which form a well-supported cluster (1.00 PP; 100% BS). Furthermore, the *trnL–F* tree reveals the same relationship as ITS tree between *L. brachystachys*.12 and *O. orthophyllum*.5 specimens (1.00 PP; 99% BS). Different specimens of *O. sintenisii* form a monophyletic group (95 PP; 78% BS) and different specimens of *O. cuspidatum* are placed in sister clades. *Eliokarmos* is recovered as monophyletic (1.00 PP; 100% BS) and sister to the rest of genera in the main clade. The other genera are placed as sister clades to this main clade.

**Combined Tree**

The combined tree, including 59 taxa, reveals that the specimens included in this study are clearly divided into 2 main clades. The first main clade in the combined tree, Clade A, includes *Ornithogalum*, *Honorius*, *Loncomelos*, *Cathissa*, *Melomphis*, *Nicipe*, *Eliokarmos*, *Ethesia* and *Galtonia*. There is a well-supported main sub-clade (1.0 PP; 100% BP) comprising *Ornithogalum*, *Honorius* and *Loncomelos*. In this clade, these three genera are divided in two main sub-clades which include all Iranian species. The second sub-clade in clade A includes *Eliokarmos*, *Ethesia* and *Galtonia*. Clade B, the
second main clade, comprises Collonox, Albuca, Stellarioideae and Dipcadi.

Within clade A, specimens of M. persica form a moderately supported sub-cluster (97 PP, 73% BP) which is found as sister to O. orthophyllum. Loncomelos brachytachys.12 and O. orthophyllum.5 are found in the same position as in the trnL–F and ITS trees within a well-supported sub-cluster (1.0 PP; 100% BP). The phylogenetic relationships among the rest of the species and specimens in the combined tree are generally similar to those in the ITS tree (Figure 2).

DISCUSSION

The New Proposed Generic Circumscription for Iranian Species within Ornithogaloideae:

As traditionally treated by Baker (1872), this subfamily is considered as one genus and consists of 9 subgenera, 3 of which occur in Iran: O. subgen. Beryllis (Salisb) Baker, O. subgen. Ornithogalum (Syn.: subgen Heliocharmos Baker), and O. subgen. Caruelia (Parl) Baker (Rechinger, 1995). According to the most recent classification (Martínez-Azorín et al., 2011), 19 monophyletic genera are accepted within subfamily Ornithogaloideae. These 19 genera are well characterized morphologically, and are circumscribed in such a way that allows easy definition and makes easier subsequent attribution of a taxon to a given genus. In the new arrangement, Martínez-Azorín et al. (2011) treated the species traditionally included in O. subgenus Beryllis in 4 different genera including Loncomelos, Nicipe, Stellarioideae, and Trimelopter, the species traditionally included in O. subgenus Ornithogalum in genus Ornithogalum and the species traditionally included in O. subgenus Caruelia in genera Melomphis and Eliokarmos.

The species traditionally classified by Baker (1872) in O. subgenus Ornithogalum and O. subgenus Beryllis include Eurasian and North African species. In our morphological analysis, each of these subgenera formed a monophyletic group. As Martínez-Azorín et al. (2011) noted, these two subgenera are clearly differentiated by the morphology of inflorescences, capsules, and seeds as Ornithogalum and Loncomelos, respectively. Furthermore, O. subgenus Caruelia, represented by M. persica in this study, formed a small cluster and was placed in a nested position within Loncomelos.

The nested position of Honorius within Ornithogalum (1.0 PP; 94% BS) and also the sister relationship of these two genera with Loncomelos clade (1 PP; 98% BS) in our ITS tree (Figure 2) is similar to that in the ITS tree reported by Martínez-Azorín et al., (2011). In our ITS tree, all sampled taxa of Ornithogalum from Iran fell in the clades corresponding to Ornithogalum s. str. and Honorius, which together formed a strongly supported clade (1.0 PP; 94% BS). Furthermore, the Iranian Loncomelos species were placed in a clade, similar to the results of Martínez-Azorín et al. (2011). Melomphis persica appeared as an independent clade and nested within Loncomelos in our ITS tree. In contrast, the trnL–F tree generated in this study revealed the nested position of Ornithogalum within Loncomelos with a sister relationship to Honorius (0.62 PP; 50% BS) (Figure 3) and justified segregation of the latter genus from Ornithogalum. The phylogenetic study by Manning et al. (2009) revealed the same relationship. Like ITS tree, the trnL–F tree included M. persica in Loncomelos. The combined tree (Figure 4) justified segregation of Ornithogalum, Loncomelos and Honorius and placed them in three different clades. In our combined tree, M. persica again was placed within the Loncomelos clade. Melomphis persica is clearly differentiated from Loncomelos by the morphology of the inflorescences, tepals and gynoecium, which are more similar to M. arabica; on the other hand, it is similar to Loncomelos in some morphological characters like plant height, leaf number, leaf length, flower number, perigone length and width, and bulb length, width, and color. The phylogenetic placement of M. persica and its morphological characters could reflect a possible hybrid origin from a cross between M. arabica and some eastern Loncomelos species. However, a wider sampling of related taxa is needed to improve our knowledge of phylogenetic relationships within these genera. The topology of our combined tree is similar to that obtained by Martínez-Azorín et al. (2011).
Our results support the classification of all Iranian species of Ornithogaloideae in *Ornithogalum s. str.* and Loncomelos. The ITS, trnL–F and combined trees reveal that Iranian species were placed in clades corresponding to *Ornithogalum*, Loncomelos, and Honorius clades and clearly are divided into 2 main clades in the ITS and combined trees (Figures 2 and 4) which is in line with the morphological analysis (Figure 1). Genus Honorius, represented by *H. nutans*, segregated in different ways from these two genera in different trees. In the trnL–F and combined trees Loncomelos clade did not form a monophyletic group where *O. oligophyllum* was placed within this genus. This conflict suggests the possibility of past hybridization events in *O. oligophyllum*. However, further studies are needed to confirm its final position. Despite this misplacing, which may reflect hybridization event in this species, we consider the combined tree as the most informative phylogenetic tree in this study (Figure 4) and it justifies segregation of *Ornithogalum*, Loncomelos and Honorius. Furthermore, combination of ITS and trnL–F sequences resulted in a phylogenetic tree that supports the monophyly of genera previously described on the basis of molecular data and morphological characters as shown by Martínez-Azorín et al. (2011). Honorius, Ornithogalum, Loncomelos, Melomphis, Nicipe, Eliokarmos, Ethesia, Galtonia, Coilonox, Albucia, Stellariooides, Dipcadi are segregated as proper genera on the basis of last classification by Martínez-Azorín et al. (2011). The phylogenetic relationships of genus Cathissa are not fully resolved in this tree, maybe because of the lack of trnL–F sequences in this tree for the related taxa and genera. The most important cultivated horticultural species include *E. thyrsoides*, *E. dubius*, *O. umbellatum*, *H. nutans*, *M. arabica* and *G. saundersiae*. Similar to the most recent study by Martínez-Azorín et al. (2011), our phylogenetic tree based on ITS tree placed Melomphis, Ornithogalum, Honorius in the first main clade (clade A) and Eliokarmos and Galtonia in the second main clade (clade B). Also, our combined tree derived from ITS and trnL–F sequences is similar to the combined tree derived from ITS, trnL–F, matK and rbcL sequences in Martínez-Azorín et al. (2011) study, both of which placed all five of these genera in clade A.

**Relationships at the Species Level for Iranian Species**

Divergent placement of multiple specimens of a single species is found in *L. brachystachys*, *O. orthophyllum* and *O. sintenisii*. In the ITS tree, seven specimens of *L. brachystachys* were placed in three different sub-clusters. In this regard, the bio-geographical distribution of each group has a peculiar pattern. Specimens from northwestern Iran (*L. brachystachys*, 2, 5, 7) formed the first sub-cluster and specimens from southwestern Iran formed the second sub-cluster (*L. brachystachys*, 8, 3, 10). The third sub-cluster included *L. brachystachys* 12 and *O. orthophyllum*.5. Based on morphological data, the first and second sub-clusters grouped together but are morphologically diagnosable by scape length, which is longer in *L. brachystachys*.2, 5, 7. Karyotypic differences among the species and ecotypes of *Ornithogalum* have been observed (Anderson, 2006). Five cytotypes were documented among *L. brachystachys* specimens collected in five different locations of Iran, with the chromosome numbers 2n=12, 2n=16, 2n=22, 2n=24 and 2n=30 (Heidaryan, 2011). However, we do not have the cytotypes for the specimens we sampled.

Within *Ornithogalum*, considerable divergence of specimens of a single species was found for *O. sintenisii*. The specimens of this species were placed in quite different positions; 4 specimens which are collected for this study were placed in the same sub-clade of clade A in the ITS tree but in different positions. *O. sintenisii* 4, *O. sintenisii* 6 and *O. sintenisii* 11 formed one sub-cluster distant from *O. sintenisii* 1. However, this relationship reflects the clear morphological divergence in morphology. In the morphological analysis, different specimens of *O. sintenisii* were placed in two sister clades. *O. sintenisii* 1 was placed in a clade sister to *O. sintenisii* 4, *O. sintenisii* 6 and *O. sintenisii* 11 clade (Figure 1). *O. sintenisii* 1 is defined morphologically by smaller plant size and more numerous flowers in comparison with *O. sintenisii* 4, *O. sintenisii* 6 and *O. sintenisii* 11. The specimen obtained from GenBank, which was also collected in Iran (Martínez-Azorín et al., 2011), was placed far from these 4 specimens. Potential conflict may arise within a single dataset as a result of
extended paralogy (Catalán et al., 2004). Pseudogene copies of ITS sequences, accumulating quite a few mutations in *O. sintenisii*, and misidentification of the specimen used from the GenBank are all valid on theoretical grounds to cause divergent placements of the *O. sintenisii* sequences. Thus, this divergence remains a subject for speculation and requires more studies.

In the ITS tree, the four specimens of *O. orthophyllum* collected in Iran formed a sub-cluster and were placed distant from the specimen obtained from GenBank, which is based on a collection from Italy (Martínez-Azorín et al., 2011). *O. orthophyllum* is a poorly-known floristic species and was treated in different ways as a synonym for other species or defined as other species (Herrmann, 2002). This is a native species to Italy and at the latest checklist of the vascular flora native to Italy it is recognized a different species from the previous statements (Bartolucci et al., 2018). Unfortunately, we did not have access to *trnL*–*F* sequences of the specimen collected in Italy. Further studies are required to distinguish final position of these specimens. In both the ITS and *trnL*–*F* trees as well as the combined tree, *L. brachystachys* 12 and *O. orthophyllum*.5 formed a well-supported sub-clade and were placed in the same position in the *Loncomelos* clade, apart from the remaining specimens of related species. Morphological clustering does not explain the close relationship between these 2 specimens in the phylogenetic trees based on sequence data. In morphological clustering, *L. brachystachys*.12 falls as sister to the rest of *L. brachystachys* specimens and *O. orthophyllum*.5 falls as sister to the rest of *O. orthophyllum* specimens (Figure 1). On the other hand, both of these specimens are characterized by their pale color in comparison with the rest of related specimens. Their special color in morphological characters could provide evidence to consider them as natural mutants. The conflict between morphological and genetic results for these two specimens may be due to interspecific hybridization, which is reported in this genus (van Raamsdonk, 1985; Griesbach et al., 1993; Joung and Roh, 2004). We have compared ITS and *trnL*–*F* trees to identify topological incongruences that may indicate hybridization events involved in the origin of *L. brachystachys*.12 and *O. orthophyllum*.5. If they were hybrids between *L. brachystachys* and *O. orthophyllum* species, we would expect phylogenetic trees based on their cpDNA sequences to place them in a clade with their maternal parent, while trees based on nuclear ITS sequences might place both species in a clade with the paternal parent. Thus, if they are hybrids, the maternal parent must be a third species, presumably one not sampled in this study. A final possibility would be to consider each of them as a new species. However, before taking such a step, further investigations are required to understand their identities.

However, conflict between the *trnL*–*F*, ITS and combined trees in the placement of the different specimens of each species may reflect the possibility of past hybridization events (Catalán et al., 2004), although incomplete lineage sorting and ITS paralogy cannot be overlooked (Catalán et al., 2004). Also, pseudogene copies of ITS sequences and chromosome duplication events may have an impact on the nuclear ITS sequences used in the phylogenetic reconstruction leading to the divergent placements of different members of the species observed here (Marinho et al., 2014). A final possible explanation would be the misidentification of the specimens used to generate the sequences we obtained from Genbank or collected samples for this study.

**Distribution of Wild and Cultivated Species of Ornithogaloideae**

*Ornithogaloideae* are distributed in Africa, Asia-Temperate (which includes Iran), and Europe (Eastern, Middle Northern, Southeastern, Southwestern). The natural habitats of the wild species of *Ornithogalum* and *Loncomelos* range from dry semi-desert areas to marshy wetlands and riverbanks, to mountaintops (Anderson, 2006). Species of these genera have also been introduced and naturalized in Africa (northwest coast of Africa), Asia-Tropical, Europe (Eastern and Northern), Australia (South Australia, Western Australia), and North America (Manning et al., 2003; Manning et al., 2009; eMonocot, 2017; Royal Botanic Gardens, 2017; The Global Biodiversity Information Facility, 2017). Our results followed those of Martínez-
Azorín et al. (2011), where the first main clade in ITS and combined trees includes all north African and Eurasian taxa of Ornithogalum, Honorius, Loncomelos, Melomphis and Cathissa plus the eastern and southern African species that correspond to Elsia and Nicipes. The second main clade comprises Albuca, Coilonox, Stellarioides, Trimelopter, Dipcadi, Battandiera, Neopatersonia, Eliokarmos, Galtonia, Ethesia and Avonsera, which mainly occur in Africa.

CONCLUSIONS

This is the first phylogenetic study employing nuclear ITS and plastid trnL–F sequences to examine the phylogenetic diversity of several Ornithogaloideae species collected from a broad range of climatic conditions of Iran with the goals of improving our understanding of relationships among these species within Ornithogaloideae, and comparing molecular diversity of these populations in Iran. Following the concept of Martínez-Azorín et al. (2011) classification, we put the species of O. subgenus Ornithogalum collected in Iran in Ornithogalum and the species of O. subgenus Beryllis collected in Iran in Loncomelos on the basis of phylogenetic and morphological evidence. Additionally, the inclusion of the only member of Melomphis included in this study, M. persica, within genus Loncomelos in the morphological clustering and trees based on phylogenetic analysis of molecular data requires a wider sampling of related taxa to improve the status of our knowledge of phylogenetic relationships among these genera. Better understanding of the complex phylogenetic relationships that exist within Ornithogaloideae species contributes important information about their evolutionary history and helps to improve our knowledge for developing effective conservation, utilization, and management practices. Improved understanding of naturally occurring variation among wild Ornithogalum populations of Iran and the phylogenetic relationships among wild and cultivated species, as revealed in this study, could provide important opportunities to introduce new ornamental plants or improve the agricultural performance of modern ornamental varieties. Also, these results offer the opportunity to guide future breeding initiatives involving Ornithogalum.

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مطالعه رویابط فیلوژنی گونه‌های وحشی و اهلی زیرخانواده Ornithogaloideae با توسعه نمونه‌برداری از ایران

چکیده

طیب‌نامی زیرخانواده Ornithogaloideae در طی دهه‌های اخیر به مساله مهمی در علم تاکسوومی می‌شود. تبدیل شده است و به گونه‌های Ornithogalum بسیار وسیع شده‌اند. با این حال، علت بهبود تعداد گیاهان زیرخانواده در ایران، به‌همراه گیاهان زیرخانواده در سطح جهانی نیز به‌طور مشابه با گیاهان زیرخانواده در ایران در مطالعات اولیه این تغییرات از نظر حاصل از آنالیز اطلاعات فیلوژنیکی جهت مطالعه گونه‌های این زیرخانواده انجام می‌شود.

خوش‌بیای ویژگی‌های ریختی مورد مقایسه قرار گرفت. بر اساس نتایج حاصل از مطالعه حاضر، همه زنوتیب‌های جمع‌آوری شده از ایران، در میان آخرين جنس‌های معروف شده در زیرخانواده Loncomelos و Ornithogalum در جنس Ornithogaloideae طبقه‌بندی شدند؛ این طبقه‌بندی با نتایج حاصل از آنالیز‌های ریختی هم‌رستان می‌باشد. در اکتش زنوتیب‌های مختلف یک گونه O. sintenisii در درخت فیلوزنیک در گونه‌های مشاهده شد؛ که ممکن است به علت رخ دادن دورگ در گیری، تفرق ناقص آل‌ها و زن‌ها پارالوگ ITS باشد. تنواع طبیعی موجود میان جمعیت‌های مختلف این گیاه در ایران، و روابط فیلوزنیک میان گونه‌های وحشی و کشت شده می‌تواند فرصت مهمی جهت معرفی گیاهان زیتونی جدید به صحت گیاهان زیتونی و یا به‌هود صفات باغبانی ارقام تجاری موجود باشد.