Karyological Studies of _Fritillaria_ (Liliaceae) Species from Iran

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Summary Five species (13 ecotypes) belonging to three subgenera of ornamental-medicinal Iranian _Fritillaria_ were karyotypically studied, using a standard squash technique. All species were diploid (2n=2x=24) having mean chromosome lengths of 15.8±15.2–16.7 µm. Their satellites varied in number (1–3 pairs) and in size (1.2–2.6 µm), mostly being located on long arms. Four chromosome types (‘m’, ‘sm’, ‘st’, ‘T’) formed 10 different karyotype formulas: ‘T’ type chromosome is reported for the first time in most species (with the exception of S4, _Fritillaria. reuteri_ Boissi). ANOVA confirmed significant intra- and inter-specific chromosomal variation across the Iranian _Fritillaria_ species. Twelve different methods were used to assess the degree of karyotype asymmetry. Among those, one qualitative parameter (Stebbins classification) and eight quantitative (CV, TL, DI, A₁, A₂, AI, AsK, MCA, CVCA) parameters verified that S2 (_F. gibbosa_ Boiss.) and S5 (_F. zagrica_ Stapf.) species represented the most asymmetrical and symmetrical karyotypes, respectively.

Key words _Fritillaria_, Cytogenetics, New chromosome type, Karyotype, Iran.

The name _Fritillaria_ is likely based on the word "fritullus" which means a cup in Latin (Ulug et al. 2010). _Fritillaria_ was one of the earliest horticultural products in Europe, and was described by Linnaeus (Linnaeus 1753). Iran supports a great range of unique plants and habitats, and it is one of the main diversity centers of _Fritillaria_ in the world (Rix 1977). There are 14 species of local importance (De Hertogh and Le Nard 1993). An additional 18 species of _Fritillaria_ and _Rhinopetalum_ have been recorded, seven of which (_F. zagrica_ L., _F. ariana_ Losinsk. & Vved., _F. kotschyan_ Herb., _F. straussii_ Bomm., _F. oliveri_ Baker, and _F. raddeana_ Regel.) are endemic to Iran (Mozaffarian 1992, Khani 2005). Overall, _Fritillaria_, a genus of about 100 species of bulbous plants within the family Liliaceae, comprises perennial temperate herbs that grow on mountain slopes and in sub-alpine meadows, typically located on open, stony and moist hillsides of the Northern Hemisphere (Maharjan et al. 2012). The reclassideration of the genus _Fritillaria_, according to Rix (2001), divided this genus into eight subgenera: _Davidi_ Rix, _Japonica_ Rix, _Liliorhiza_ Bentli. & Hook, _Fritillaria_ L., _Petitun_ L. Baker, _Rhinopetalum_ Fisch. ex Alexander, the monotypic _Theresia_ Koch and _Korolkowsia_ Regel (Rix 2001, Rønsted et al. 2005, Leitch et al. 2007, Ambrozova et al. 2011), two sections, and 165 taxa (Rix 2001). All Iranian species belong to four subgenera: _Fritillaria_., _Theresia_., _Petitun_ and _Rhinopetalum_. The _Petitun_ subgenus comprises two well-known species, _F. imperialis_ L. and _F. raddeana_ Regel. The _Fritillaria_ subgenus is morphologically classified into six complexes: the _F. crassifolia_ Boiss. & Noe, _F. kotschyan_ ssp. Herbert, _F. graeca_ Boiss. & Spruner, _F. meleagris_ L., _F. cirrhosa_ D-Don and _F. cuncasica_ Adams. groups. Jafari et al. (2014) reported chromosomal and karyotypical parameters and their association with either the evolutionary or intra/inter-specific variation through five species (_F. persica_., _F. kotschiana_., _F. imperialis_ Lutea Maxima, _F. crassifolia_., _F. straussii_) belonging to three subgenera (_Theresia_, _Fritillaria_, _Petitun_) of Iranian _Fritillaria_. In this study, twelve different methods were used to assess the degree of karyotype asymmetry. Among those, one qualitative (Stebbins classification) and seven quantitative (TP, CV, DI, AsK, A₁, AI, AsK) parameters verified that _F. kotschiana_ and _F. straussii_ species are recognized as having the most asymmetrical and symmetrical karyotypes, respectively.

The identification of extensive variation provides the genus _Fritillaria_ with agronomic and economic importance (Metin et al. 2013). Members of this genus in particular are the source of components having medicinal properties, and these are finding increased medical applications (Rønsted et al. 2005, Maharjan et al. 2012). Comparative karyotype analysis of related species has been used to describe patterns and directions of chromosomal evolution through a group, and to estimate the evolutionary role that such karyotype changes may have played (Peruzzi et al. 2009). The chromosomes of Liliaceae have long attracted attention, given their diversity in number, size, and structure (Peruzzi et al. 2009). Chromosome numbers have been reported for more than 50 species of _Fritillaria_. Most species have a basic chromosome num-

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The sampled species belong to three subgenera of Liliaceae, Rhinopetalum and Petillium. The first step of this program involved sampling 13 ecotypes of related species including: Fritillaria imperialis, F. persica L., F. raddeana, and F. reuteri Boissier. This involved over 15000 km of exploratory trips in Iran in Spring, 2011 (Table 1 and Fig. 1). The exploratory trips were arranged according to the logical climatic pattern of different zones of Iran, from the warmest climates to the coolest. The main aim of this research was to study chromosomal parameters and their association with the evolution and intra/inter-specific variations through five species of Iranian Fritillaria.

Materials and methods

After thorough washing with distilled water, the roots were transferred to 70% (v/v) aqueous ethanol, and stored in a refrigerator until used. Hydrolysis was carried out with 1 M HCl overnight at 4°C (Karimzadeh et al. 2010, 2011, Ebadi-Almas et al. 2012, Shariat et al. 2013, Jafari et al. 2014, Abedi et al. 2015). After thorough washing with distilled water, the roots were fixed in Carnoy’s fixative (glacial acetic acid: ethanol; 1:3 v/v) overnight at 4°C (Karimzadeh et al. 2010, 2011, Ebadi-Almas et al. 2012, Shariat et al. 2013, Jafari et al. 2014, Abedi et al. 2015). The stained root tips were washed three times with distilled water (each 5 min) at RT. In order to achieve best separation of the chromosomes at metaphase, roots were placed in KCl (0.1 M, 0.56% (w/w)) for 60 min at RT. They were subsequently fixed in Carnoy’s fixative (glacial acetic acid: ethanol; 1:3 v/v) overnight at 4°C (Karimzadeh et al. 2010, 2011, Ebadi-Almas et al. 2012, Shariat et al. 2013, Jafari et al. 2014, Abedi et al. 2015). The stained root tips were afterwards squashed in a droplet of 45% (v/v) acetic acid. The cover slips were then removed after quick freezing the slides on dry ice (Rechinger 1990). At least five well-spread metaphase plates from different individuals were observed.

Table 1. Locations of the collected exotic and endemic Fritillaria spp.

<table>
<thead>
<tr>
<th>Family &amp; genera names</th>
<th>Subgenera</th>
<th>Species name</th>
<th>Ecotypes codes</th>
<th>Local collection locations</th>
<th>Exotic/Endemic</th>
<th>Latitude (N)</th>
<th>Longitude (E)</th>
<th>Altitude (m)</th>
<th>Mean temp (°C)</th>
<th>Mean rainfall (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Liliaceae—Fritillaria</td>
<td>Petillium</td>
<td>F. imperialis</td>
<td>S1-E1*</td>
<td>Aligudarz, Lorestan, Iran</td>
<td>Exotic</td>
<td>33°08’</td>
<td>49°25’</td>
<td>2734</td>
<td>11.0</td>
<td>409</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. imperialis</td>
<td>S1-E2</td>
<td>Aligudarz, Lorestan, Iran</td>
<td>Exotic</td>
<td>33°08’</td>
<td>49°27’</td>
<td>2497</td>
<td>11.0</td>
<td>409</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. imperialis</td>
<td>S1-E3</td>
<td>Marivan, Kordestan, Iran</td>
<td>Exotic</td>
<td>35°18’</td>
<td>46°11’</td>
<td>1978</td>
<td>14.7</td>
<td>831</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. imperialis</td>
<td>S1-E4</td>
<td>Sarmil, Kermanshah, Iran</td>
<td>Exotic</td>
<td>34°19’</td>
<td>46°07’</td>
<td>1663</td>
<td>15.4</td>
<td>484</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. imperialis</td>
<td>S1-E5</td>
<td>Khonsar, Isfahan, Iran</td>
<td>Exotic</td>
<td>33°09’</td>
<td>50°24’</td>
<td>2743</td>
<td>19.5</td>
<td>264</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. imperialis</td>
<td>S1-E6</td>
<td>Malayer, Hamedan, Iran</td>
<td>Exotic</td>
<td>34°17’</td>
<td>48°51’</td>
<td>1778</td>
<td>11.3</td>
<td>290</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. imperialis</td>
<td>S1-E7</td>
<td>Khoshcheylaq, Golestan, Iran</td>
<td>Exotic</td>
<td>36°50’</td>
<td>55°22’</td>
<td>1573</td>
<td>17.8</td>
<td>515</td>
</tr>
<tr>
<td>Rhinopetalum</td>
<td>F. gibbosa</td>
<td>S2-E1</td>
<td>Maimai, Sennan, Iran</td>
<td>Exotic</td>
<td>36°22’</td>
<td>55°47’</td>
<td>1300</td>
<td>17.4</td>
<td>152</td>
<td></td>
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<td>Petillium</td>
<td>F. raddeana</td>
<td>S3-E1</td>
<td>Aladagh, Golestan, Iran</td>
<td>Exotic</td>
<td>37°21’</td>
<td>57°07’</td>
<td>2410</td>
<td>17.8</td>
<td>515</td>
<td></td>
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<td></td>
<td>F. raddeana</td>
<td>S3-E2</td>
<td>Cheshmeh Khan, Golestan, Iran</td>
<td>Endemic</td>
<td>37°20’</td>
<td>56°02’</td>
<td>1307</td>
<td>17.8</td>
<td>515</td>
</tr>
<tr>
<td>Fritillaria</td>
<td>F. reuteri</td>
<td>S4-E1</td>
<td>Sabze Kooh, Shahrekord, Iran</td>
<td>Exotic</td>
<td>31°45’</td>
<td>30°59’</td>
<td>2698</td>
<td>19.4</td>
<td>328</td>
<td></td>
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<td></td>
<td></td>
<td>F. zagrica</td>
<td>S5-E1</td>
<td>Sanandaj, Kordestan, Iran</td>
<td>Endemic</td>
<td>35°16’</td>
<td>47°07’</td>
<td>1818</td>
<td>14.7</td>
<td>389</td>
</tr>
<tr>
<td></td>
<td></td>
<td>F. zagrica</td>
<td>S5-E2</td>
<td>Khonsar, Isfahan, Iran</td>
<td>Endemic</td>
<td>33°09’</td>
<td>50°23’</td>
<td>2818</td>
<td>19.5</td>
<td>264</td>
</tr>
</tbody>
</table>

* S: species, E: ecotype
analyzed per ecotype. The best metaphase spreads were recorded photographically, using a DP12 digital camera (Olympus Optical Co., Ltd., Tokyo, Japan) mounted on the BX50 Olympus microscope (Olympus Optical Co., Ltd., Tokyo, Japan). The morphologies of the chromosomes was described using the nomenclature proposed by (Le-van et al. 1964).

Nine chromosomal parameters were either measured or calculated, including long (L) and short (S) arms, total chromosome length (TL) and volume (TCV), arm ratio (AR), r-value, relative length of chromosome (RL), chromosome form percentage (F%) and centromeric index (CI). Their formulas are as follows:

\[ TL = L + S \]

Arm ratio (AR) = \( \frac{L}{S} \)

r-value = \( \frac{S}{L} \)

\[ RL\% = \frac{TL \times 100}{TL} \]

F\% = \( \frac{S \times 100}{TL} \)

CI = \( \frac{S}{TL} \)

Twelve different methods were used to assess the degree of karyotype asymmetry, comprising the dispersion index (DI; Lavania and Srivastava 1999), the total form percentage (TF\%); Huziwa 1962), the total chromatin length (X) and the coefficient of variation of total chromosome length (TL; Paszko 2006), the mean centromeric asymmetry (M\%CA; Peruzzi and Eroglu 2013), the coefficient of variation of centromeric index (CV\%CI; Paszko 2006), the degree of karyotype asymmetry (A; Watanabe et al. 1999), the Asymmetry index (AI; Paszko 2006), the index of karyotype symmetry (Syi) and the index of chromosome size resemblance (Rec; Greilhuber and Speta 1978), the centromeric gradient (CG\%; Lavania and Srivastava 1999), the percentage karyotype asymmetry index (AsK\%; Arano 1963), the Romero-Zarco (1986) method, and Stebbins’ classification (1971). Their formulas are as follows:

\[ DI = \frac{S_{CI} \times CV_{TL} - 100}{100} = \frac{CG\% \times CV\%}{100} \]

\[ TF\% = \frac{\sum S}{\sum TL \times 100} \]

\[ X = 2 \times \sum TL \]

\[ A = \frac{\sum_{i=1}^{n} \frac{Li - Si}{Li + Si}}{n} \times 100 \]

\[ AI = \frac{CV_{CI} \times CV_{CI}}{100} \]

\[ Rec = \frac{\sum_{i=1}^{n} \frac{CIi}{LC}}{n} \times 100 \]

\[ Syi = \frac{X_{S}}{X_{L}} \]

\[ AsK\% = \frac{\sum L}{\sum TL \times 100} \]

\[ CG\% = \frac{\sum L}{X_{L} \times 100} = 100 \]

In order to examine differences between species (interspecific variation) and differences between ecotypes within the same species (intraspecific variation), a nested design was performed with 5 replications of metaphase cells. The resultant chromosomal data were first tested for normality, followed by the Bartletts and Levene’s tests for the homogeneity of variances, using Minitab 16 statistical software and then they were analyzed. The LSD test was carried out for mean comparisons of ecotypes within species, using Minitab 16 statistical software. Principal component analysis (PCA) was carried out to differentiate the studied species based on chromosomal parameters (Jolliffe 1986).

Results

All five species (13 ecotypes) were diploid (2n=2x=24). The karyotypes of the somatic complement and the idiograms of haploid complement of the studied Fritillaria species are given in Figs. 2 and 3, respectively. The ANOVA of chromosomal parameters was performed to assess inter- and intraspecific chromosomal variations. Hence, in term of interspecific variation, ANOVA indicated significant differences for four chromosomal parameters, including AR, r-value (p<0.05), F% and CI (p<0.01), but in term of intraspecific variation, only TCV was highly significant (p<0.001; Table 2).
At the level of subgenera, ANOVA verified significant differences for the all chromosomal parameters (data not shown).

Comparing species with each other, the mean total chromosome length ($TL$) was determined as 15.8 $\mu m$, with a range varying from 15.2 $\mu m$ (S3) to 16.7 $\mu m$ (S5); these differences were not significant. The mean $TCV$ was 109.8 $\mu m^3$, ranging from 88.4 $\mu m^3$ (S3) to 132.3 $\mu m^3$ (S5). The mean $CI$ of the complement varied from 18 (S2, S3) to 21 (S1). Using Levan et al. (1964) chromosome nomenclature, four chromosome types, types $l^mz$ (centromere at the median region), $l^{sm}z$ (centromere at the submedian region), $l^{st}z$ (centromere at the subterminal region), and $l^Tz$ (centromere at the terminal point), formed ten distinctive karyotypes (Table 3). The $l^Tz$ chromosome type is being reported for the first time in most species (excluding S4). Comparing ecotypes within species, in the S1 species (seven ecotypes), the mean $TCV$ was 100.4 $\mu m^3$, ranging from 82.9 $\mu m^3$ (S1-E3) to 104.7 $\mu m^3$ (S1-E2; 26.3% increase; $p<0.001$). In the S3 species (two ecotypes), the mean $TCV$ was 128.2 $\mu m^3$, varying from 99.1 $\mu m^3$ (S3-E1) to 157.3 $\mu m^3$ (S3-E2; 58.7% increase; $p<0.001$). In the S5 species (two ecotypes), the mean $TCV$ was 117.7 $\mu m^3$, ranging from 78.3 $\mu m^3$ (S5-E2) to 148.1 $\mu m^3$ (S5-E1; 89.1% increase; $p<0.001$). The satellites varied in number (1–3 pairs) and in size (1.2–2.6 $\mu m$), typically being located on the long arms. The karyotypes of all five species (13 ecotypes) were classified as the 3B type of Stebbins (1971) classification. According to various indices of karyotype symmetry, the studied *Fritillaria* species showed different behavior within these groups. For example, the highest value of $TF\%$ was detected in S1 (23.2; the most symmetric; Table 3), whereas the lowest was in S2 (19.4; the most asymmetric). The highest and the lowest values $CV\%$ were identified in S4 (23.8%; the most asymmetric) and S5 (19.3%; the most symmetric), respectively. Similar to the result of $CV\%$, the highest value of $DP\%$ was detected in S4 (5.0%; the most asymmetric) while S5 showed the lowest (4.0%; the most symmetric). $AI$ varied from 0.6 (S1) to 0.64 (S2). The highest value of $M_{CA}$ was identified in S2 (63.9%) while S1 demonstrated the lowest value (56.1%). The mean $CV_{CI}$ was determined as 44.7 $\mu m^3$, varying from 38.5 $\mu m^3$ (S3) to 55.2 $\mu m^3$ (S2). The highest and the lowest values of $CG\%$ were distinguished in S1 (23.2%) and S2 (19.4%), respectively. The highest value of $A$ was identified in S2 (0.64) while S1 gave the lowest value (0.56). The highest and the lowest values of $Syi$ were found in S1 (29.6) and S2 (24.1), respectively. The highest value of $Rec$ was recognized in S5 (73.0%) while S2 showed the lowest (66.3%). The highest value of $AsK\%$ was identified in S2 (80.6%) while S1 demonstrated the lowest value (77.2%). To determine the total variation in species and parameters, PCA was performed, showing that the first three principal components account for the 99% of the cumulative variation. The first two components were projected in a two-dimensional graphic format (Fig. 4).

Moreover, cluster analysis was performed (using the matrix of karyotype similarities, UPGMA, Cophenet correlation $r=0.92$, data not shown), confirming the results obtained from the PCAs three main groups (S1 & S2, S3 & S4, S5; Fig. 4).

**Fig. 1.** Geographic distribution of sampled *Fritillaria* on the map of Iran using ArcGIS.
Discussion

All five *Fritillaria* species (13 ecotypes) of Iran were diploid (2n=2x=24). This is in agreement with previous studies (Fedorov 1969, Marchant and Macfarlane 1980, Khaniki 2002a). According to previous reports (Zhang et al. 1992, Wang et al. 2006, Gao et al. 2009), the genus *Fritillaria* has more obvious secondary constrictions (dips) in comparison with those reported for other species within the Liliaceae. These dips were positioned on the long arms of *Fritillaria* chromosomes, and were stable through the population. On the chromosomes of some of the species, 1–3 pairs of satellites were detected, the majority of which were located on the long arms. Furthermore, this finding is in agreement with that obtained by Khaniki (2002a). On the other hand, in the case of *F. zagrica*, up to four B chromosomes have been reported (Khaniki 2002b) whereas, in the current study, no B chromosomes were seen for the *Fritillaria* species that were studied. Different chromosome types have been reported in *Fritillaria*. For example, Peruzzi et al. (2009) reported four chromosome types in 27 different species of *Fritillaria*, including "m", "sm", "st" and "t", with the "st" and "sm" types appearing at the highest and the lowest frequencies, respectively. In the present study, four chromosome types ("m", "sm", "st" and "T") were identified in five different species of *Fritillaria*, with the "st" and "T" types at the highest and the lowest frequencies, respectively; the "T" chromosome type is being reported for the first time in most Iranian *Fritillaria* species (except for ecotypes of the S4 species). The existence of "T" chromosome type in these species probably indicates their high degree of evolution in comparison to other species in the present study and to those reported by Peruzzi et al. (2009) and Jafari et al. (2014). In the Peruzzi et al. (2009) report, which included 61 accessions and 27 distinct species, the average TL was 12.8 µm (ranging 8.6–18.8 µm), which was 3%
less than that in the present study. In other words, the chromosomes of Iranian *Fritillaria* are 3% longer than those reported by Peruzzi et al. (2009). As a whole, in the present study, remarkable interspecific variations were clearly identified for four chromosomal parameters (AR, r-value, F%, CI) and to a lesser extent, intraspecific variation was observed for TCV. Such variation in TCV within species can be attributed to environmental changes (Swanson et al. 1981).

Karyotypic asymmetry was evaluated based on differences identified using either a qualitative classification method or quantitative indices. Thus, according to Stebbins (1971), karyotypes of different species of Iranian *Fritillaria* studied in the present report were

![Fig. 3. Haploid chromosomes idiograms of five species (13 ecotypes) Iranian *Fritillaria* (2n=2x=24).](image-url)
located in group 3B, which is classified as a relatively asymmetric, or more developed, karyotype. In other reports (Khaniki 2002a, b, c), karyotypes of *F. reuteri* and *F. imperialis* were not located in 3B but, similar to our results, those of *F. raddeana* and *F. zagrica* were. In the study of Gao *et al.* (2009) on two different species of *Fritillaria* (*F. cirrhosa, F. unibracteata*), the symmetric groups of Stebbins (3A, 2B and 3B) were reported, even

Table 3. Mean chromosomal and karyotypic parameters of *Fritillaria* spp.

<table>
<thead>
<tr>
<th>Parameters</th>
<th>ST1</th>
<th>S2</th>
<th>S3</th>
<th>S4</th>
<th>S5</th>
<th>Species range</th>
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<tr>
<td>S (µm)</td>
<td>3.48</td>
<td>3.14</td>
<td>2.95</td>
<td>3.28</td>
<td>3.50</td>
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<td>L (µm)</td>
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<td>13.04</td>
<td>12.23</td>
<td>12.40</td>
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<td>TL (µm)</td>
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<td>15.69</td>
<td>16.69</td>
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<td>AR</td>
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<td>6.18</td>
<td>5.52</td>
<td>5.05</td>
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<td>r-value</td>
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<td>0.25</td>
<td>0.26</td>
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<td>T%</td>
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<td>1.62</td>
<td>1.75</td>
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<td>TCV (µm³)</td>
<td>105.55</td>
<td>104.71</td>
<td>88.44</td>
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<td>132.27</td>
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<td>0.18</td>
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<td>TF%</td>
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<td>19.44</td>
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<td>X (µm)</td>
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<td>364.61</td>
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<td>23.82</td>
<td>19.25</td>
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<td>4.16</td>
<td>4.99</td>
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<td>A1</td>
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<td>0.21</td>
<td>0.24</td>
<td>0.19</td>
<td>S5 S2, S4</td>
</tr>
<tr>
<td>AI</td>
<td>9.22</td>
<td>13.05</td>
<td>8.20</td>
<td>9.87</td>
<td>9.04</td>
<td>S3 S2</td>
</tr>
<tr>
<td>AsK%</td>
<td>77.22</td>
<td>80.56</td>
<td>80.50</td>
<td>79.04</td>
<td>79.00</td>
<td>S1 S2, S3</td>
</tr>
<tr>
<td>Rec</td>
<td>68.93</td>
<td>66.31</td>
<td>69.32</td>
<td>66.66</td>
<td>73.03</td>
<td>S2 S5</td>
</tr>
<tr>
<td>Syi</td>
<td>29.57</td>
<td>24.13</td>
<td>24.24</td>
<td>26.51</td>
<td>26.58</td>
<td>S2 S1</td>
</tr>
<tr>
<td>A</td>
<td>0.56</td>
<td>0.64</td>
<td>0.62</td>
<td>0.61</td>
<td>0.61</td>
<td>S1 S2</td>
</tr>
<tr>
<td>MCA</td>
<td>56.06</td>
<td>63.92</td>
<td>62.48</td>
<td>61.28</td>
<td>60.84</td>
<td>S1 S2, S3</td>
</tr>
<tr>
<td>CG%</td>
<td>23.24</td>
<td>19.44</td>
<td>19.46</td>
<td>20.95</td>
<td>20.97</td>
<td>S2 S1</td>
</tr>
<tr>
<td>CV Cl</td>
<td>41.78</td>
<td>55.20</td>
<td>38.51</td>
<td>41.42</td>
<td>46.61</td>
<td>S3 S2</td>
</tr>
</tbody>
</table>

*KF2: Stebbins classification (1971), KF: Karyotype formula*
though Paszko (2006) describes Stebbins’ classification (1971) as a qualitative method, and therefore less powerful and flexible in terms of the types of conclusions it can provide. Thus, more quantitative indices need to be considered to archive greater measurement correctness. For example, in the current study, in case of TF%, all of the species were asymmetric, having the mean value of 20.8%, ranging from 19.4% (S2) to 23.2% (S1), which is 0.2% more than the average (21%) reported by Peruzzi et al. (2009). The gradual changes in the amounts of TF% are probably due to chromosomal abnormalities. The morphological changes in the appearance of chromosomes might be a consequence of chromosome duplication or translocation (Das et al. 1998). Peruzzi et al. (2009) reported the average of DF% as 4.6%, while this parameter in our study was more or less the same (4.5%, ranging from 4% in S5 to 5% in S4). In our present study, the CV% across the species was 21.8%, ranging from 19.3% (S5, the most symmetric) to 23.8% (S4, the most asymmetric). Peruzzi et al. (2009) reported the CVc1 as 62.6, while that in our study was 44.7 (ranging from 38.5 in S3 to 55.2 in S2), about 29% less. In the case of AE in the current study, it was 9.9, ranging from 8.2 (S3) to 13.05 (S2) which is 4% less than that (13.8) achieved by (Peruzzi et al. 2009). Our results for the CVT1, A1, A2 and Ask% parameters are in agreement with those reported by Peruzzi et al. (2009), whereas Gao et al. (2009) reported 10% fewer for the Ask% index. According to our understanding, there is no complete karyotype analysis on Iranian Fritillaria species within the literature. In the present report, the five species (13 ecotypes of Iranian Fritillaria) were diploid (2n=2x=24), having satellites mostly on their long arms. Four chromosome types (‘m’, ‘sm’, ‘st’, ‘T’) were identified; the latter is being reported for the first time. Iranian Fritillaria species show low degree of karyotypic symmetry, probably indicating their high degree of evolution in comparison to other species. The present study verifies more diversity between Fritillaria species rather than within ecotypes of the same species.

As a conclusion, according to our knowledge, there is no complete karyotype analysis on Iranian Fritillaria species in the literature. In the present report, the studied five species (13 ecotypes) of Iranian Fritillaria were diploid (2n=2x=24), having satellites mostly on their long arms. Four chromosome types (‘m’, ‘sm’, ‘st’, ‘T’) were identified; the latter is being reported for the first time. Hence, Iranian Fritillaria species show low degree of karyotypic symmetry, probably indicating their deeper evolution in comparison to other species. The present study verifies more diversity between Fritillaria species rather than ecotypes within species.

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References


