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RESEARCH ARTICLE

Assessment of genetic diversity and photosynthetic pigments among wild populations of Yellow Flag (*Iris pseudacorus*)

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ABSTRACT: Yellow flag (*Iris pseudacorus*) is a native plant with ornamental and medicinal properties in horticulture science. 16 ecotypes of *I. pseudacorus* species were collected and classified into three populations based on geographical location in the current study. The genetic diversity of *I. pseudacorus* was assayed using 16 ISSR markers. Photosynthetic pigments, including chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids, were measured by the spectrophotometry method. The primers generated 874 scalable bars ranging in size from 100-1200 bp. The polymorphism percentage of all primers was 100%. The primers ISSR_55 produced the most bands (234 bands in total), the highest marker index, and the highest amount of polymorphic information content (PIC). Primer ISSR-13 is in second place with a total PIC of 0.84. Also, the data obtained from the scoring tapes were analyzed by parsing the original coordinates. The analysis results showed that the first, second, and third components contained 29.88%, 21.24%, and 16.52% of the information, respectively. The results showed that genetic diversity within populations (97%) is more significant than diversity among populations (3%). The spectrophotometry results showed photosynthetic pigments obtained in the Q (Jouybar) location with the highest sunlight. Our results indicated that ISSR markers revealed the genetic relationships of Yellow flag samples for different agro-ecological adaptations. ISSR is a superb molecular tool to research the genetic variability of *I. pseudacorus*.

KEYWORDS: Chlorophyll, Flower, ISSR, Location, Marker.

INTRODUCTION

The diversity of attributes among members of a species is an intrinsic feature of biological involution. Most biological researches on plants diversity has focused on morphological traits and DNA markers. DNA finger-printing sample genome diversity is independent of environmental conditions and the developmental stage of the organism [24]. The ultimate genome diversity survey tool is the sequencing of a population's whole genome that reveals the potential of a population to express various phenotypic features [25].

Knowledge of the genetic diversity and intraspecific relationships within a collection of isolates is critical to understanding the structure of the population [38]. In the review of research, (ISSR) inter-simple sequence repeats have been successfully applied to plant diversity studies. These markers have high reproducibility, which reveals many information bands in a single amplification, thus being one of the most commonly used markers in intraspecific differentiation and highly effective for identifying genotypes of many species [40]. Among

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established molecular markers, inter-simple sequence repetition markers (RSSI) have been widely used to analyze genetic material [35]. The ISSR markers for abundance, multi-allelic behavior, high polymorphism, dominant inheritance, and excellent reproducibility are ideal for genetic diversity studies and marker-assisted selection in plant breeding [39]. These markers estimate the genetic relationship and variability, and the ISSR technique is successfully employed in various taxonomic and genetic diversity studies [10]. In the Yellow Flag study, ISSR markers are used for genetic diversity analysis because of their robustness, cost-effectiveness, higher reproducibility, and they are not being affected by environmental factors [25].

In the Iridaceae family, *Iris* L. is the most prominent and earliest Monocotyledon plant that was cultivated as garden flowers with various coloring and extreme diversity of characteristics. According to references, among more than 300 *Iris* species, 20 species have been reported in Iran. Chromosome number in *Iris* species is 2n=2x=18-48 that *Iris pseudacorus* L. is $2n = 34$ and have been considered by researchers as ornamental and medicinal plants [18, 15, 41]. The yellow flag is easily recognizable by its flowers because it is the only species of wild iris with yellow flowers and its underground rhizomes [12]. Irises have been medicinally used in Ancient folk medicine, also famous ornamental plants that have economic value in the perfume industry [23]. Also, numerous polyphenolic compounds with antioxidant, antimutagenic, and estrogenic activity are in the *Iris* species [37]. CO_2 fixation and the consequent production of carbohydrates and O_2 delivery, using an intermediary light energy [31].

Chlorophylls a and b and these pigments mainly capture light in the antenna complex via photosystem II, consequent electron transport [30]. Other pigments, including carotenoids, also present in plants are considered accessory components in the photosynthetic complex by providing photoprotection and stability of proteins present in the photosystem [33]. The efficiency of the pigment system depends on the conformity between its structure and function and environmental conditions (first of all, illumination) [11]. Latitudinal changes in the rate of solar radiation must affect the pigment system of the leaves, whose efficiency directly influences the photosynthetic productivity of plants [27]. Chlorophyll metabolism is affected by plant developmental stage, light and hormone levels, and other factors [36]. At the same time, the data about changes in the plant pigment complex along the global latitudinal gradients are not numerous. The majority of known works deal with the content of plant pigments under extreme environmental conditions [27]. Some medical studies suggest that there are positive effects of secondary compounds of these plants in the treatment of cancers or antibacterial and viral infections [16]. Due to the unique features and economic matter of this rich ornamental plant like; the ability to cultivate in ornamental gardens, supply as a cut flower, phytoremediation, valuable in secondary metabolites, and also the indefinite of its genetic diversity in Iran, it seems to be important to necessary to evaluate its genetic diversity and photosynthetic pigments from existing ecotypes. So current study is the first attempt to determine the genetic diversity of native Yellow Flag ecotypes of northern Iran using ISSR molecular markers.

MATERIALS AND METHODS

Plant material

According to the field and botanical studies, populations of Yellow flag plants have been identified, and rhizomes samples were collected from 16 sites selected for sample collecting. The ecotype samples were divided based on geographical location in 3 different natural places in the north of Iran (Supplementary File 1, Fig. 1). Each ecotype's location latitude, longitude, and altitude were carefully determined and recorded (Supplementary File1, Table 1). In July (After the flowering season), rhizome samples having a diameter of 4-6 cm were collected and labeled carefully. Rhizomes were divided into equal parts and planted in medium pots with clay + peat + sand. Operations of planting and maintenance of young leaves from the rhizome until emergence were done regularly.

Assessment of photosynthetic pigments

In this section, photosynthetic pigments, including chlorophyll a, b, total, and carotenoids, are evaluated [2]. In this method, first, 0.5 g of fresh tissue is crushed and poured into a test tube, then 10 ccs of pure methyl sulfoxide (DMSO) is added. It is then placed in an oven at 70° C for three hours until the pigments are extracted and the leaves are entirely colorless. Strain the samples with Whatman filter paper, take one ml of it, and make a volume of 5 ml. We read its absorption at 663, 645, 480, and 510 nm. Finally, we calculate the number of photosynthetic pigments from the following formulas in milligrams per gram of fresh weight:

$$Chla = \frac{(12.7 * OD\ 663) - (2.69 * OD\ 645) * \text{Volume} * \text{Dilution rate}}{1000 * \text{Sample weight}}$$

$$Chlb = \frac{(22.7 * OD\ 645) - (4.68 * OD\ 663) * \text{Volume} * \text{Dilution rate}}{1000 * \text{Sample weight}}$$

$$Total\ Chl = \frac{(20.2 * OD\ 645) - (8.02 * OD\ 663) * \text{Volume} * \text{Dilution rate}}{1000 * \text{Sample weight}}$$

$$Carotenoid = \frac{(7.6 * OD\ 480) - (1.49 * OD\ 510) * \text{Volume} * \text{Dilution rate}}{1000 * \text{Sample weight}}$$

ISSR analysis

Young leaves samples were powdered in liquid nitrogen in the DNA extraction method and stored in a freezer at -80 °C. DNA extraction was performed by the modified CTAB method [26]. The quality and quantity of DNA extracted were measured by electrophoresis based on sybergold, agarose gel, and spectrophotometer, respectively. PCR was done in a final volume of 10 µl containing 5 µl of 2X MasterMix (Ampliqon), 1 µl of primer (10 µM), 3 µl H2O and 1 µl DNA (10 ng). The following temperature profile was used for amplification: 94 °C for 2 min, 35 cycles of 94 °C for 30″, (49.9-52.4°C According to Annealing temp for each primer) for 1″, 72 °C for 1 min and 30 seconds, ending with 72 °C for 20 min. In the following 5 µl of PCR products were loaded on 1% agarose gel, run in 1X TAE buffer, stained with sybergold, and photographed under UV light to control the qualified fragments and success of the amplification. PCR products were labeled with SybrGold fluorescent dye (Invitrogen, Canada) and were loaded on 5% polyacrylamide gels in GS2000 (Corbette Australia). Electrophoresis was performed at 1200-volt constant power in TBE (1X) buffer as a running buffer, and stopped depending on the real-time dimension of the digital picture and expected product size of each primer set. Molecular sizes of the amplified fragments were estimated using a 100-bp ladder. Digitally captured picture subjected to future analysis. All genotypes were scored using the eye to attribute the exact size of the allele if obscure. The presence and absence of alleles related to ISSR markers were 1 and 0, respectively [8].

Data processing and analysis

For the final analysis, it (Table of 1 and 0) became a matrix using NTedit software. Using NTSYSpc software, Simple Matching (SM) and Dice were calculated with UPGMA, similarity coefficients Jaccard, Single (Slink) and Complete (Clink) algorithms, and the dendrogram of each matrix was plotted by the mentioned methods to select the best clustering method and similarity coefficient, quantitative correlation coefficient was used. GenALEX software was used to take the original coordinate analysis and molecular analysis of variance test. Pop Gene software was used to analyze parameters related to total alleles of populations, including the number of determination of polymorphic information content, effective alleles, polymorphism rate, Shannon information, index allelic frequency, F-test, and genetic similarity between populations.

To determine the similarity of the 16 studied cluster, analysis was carried out [13, 14]. In cluster analysis, various methods were used to classify samples using similarity or distance matrices: 1- Jacquard similarity coefficient. 2- Simple simulation coefficient. 3- Dice's similarity coefficient. In this research, genotypes were classified and were drawn as a tree diagram using SAS.V.9.0 and SPSS.V.16 software. Factor analysis was carried out by the principal components method and maximum likelihood, and for better interpretation, factors were rotated by the Varimax method. In this study [13, 14], SAS.9.0 software was used to factor analysis and calculate principal component analysis.

Decomposition into main coordinates

In this analysis, the number of principal variables of functions can be defined, called principal coordinates (PCO).

Polymorphic Information Content (PIC)

The larger the statistic, the higher the number of alleles and the higher the frequency of polymorphisms for the locus in the study population and the positive response of different genotypes to the primer. In calculating PIC, the number of alleles of a gene locus and their relative frequency in the available samples are considered and are more affected by alleles with higher frequency. PIC= 2Σpi(1-Pi)

RESULTS

Ten of 14 ISSR primers including (ISSR-12, ISSR-13, ISSR-14, ISSR-15, ISSR-16, ISSR-21, ISSR-53, ISSR-54, ISSR-55, ISSR-58) used could produce reproducible bands. The primers generated a total of 874 scalable bars ranging in size from 100-1200 bp (Table 1).

The polymorphism percentage of all primers was 100%. The primer ISSR_55 produced the most bands (234 bands in total) (Fig. 1). Also, the highest marker index was related to the ISSR_55 primer, and the highest amount of polymorphic information content (PIC) was related to primer ISSR_55. Primer ISSR-13 is in second place with a total PIC of 0.84.

In the classification of populations based on geographical location information, three groups were identified: population one (A, B, C), population two (E, F, G, H, I, J, K, L, M), and population three (N, O, P, Q) (Table 2).

According to Table 2 (genetic diversity among different populations based on geographical location), the values of genetic diversity like the percentage of polymorphic

Table 1. Characteristics of 14 microsatellite loci.

Primer Name	Primer sequence	motif	Annealing temp	PIC	MI	Observed domain of alleles
ISSR-12	AGAGAGAGAGAGAGAGT	$(AG)_8T$	49.9	0.73	7.4825	100-1100
ISSR-13	AGAGAGAGAGAGAGAGG	$(AG)_8G$	52.4	0.84	26.6112	100-600
ISSR-14	GAGAGAGAGAGAGAGAT	$(GA)_8T$	49.9	0.6	3.876	100-600
ISSR-15	GAGAGAGAGAGAGAGAC	$(GA)_8C$	52.4	0.79	6.4148	100-500
ISSR-16	GAGAGAGAGAGAGAGAA	$(GA)_8A$	49.9	0.7	9.177	100-1100
ISSR-17	CTCTCTCTCTCTCTCTA	$(CT)_8A$	49.9	-	-	-
ISSR-18	CTCTCTCTCTCTCTCTG	$(CT)_8G$	52.4	-	-	-
ISSR-21	CACACACACACACACAG	$(CA)_8G$	52.4	0.72	7.4304	100-950
ISSR-22	GTGTGTGTGTGTGTGTA	$(GT)_8A$	49.9	-	-	-
ISSR-53	AGAGAGAGAGAGAGAGC	$(AG)_8C$	52.4	0.71	39.8736	100-1100
ISSR-54	AGAGAGAGAGAGAGAGA	$(AG)_8A$	49.9	0.82	45.51	100-1200
ISSR-55	GAGAGAGAGAGAGAGAG	$(GA)_8G$	52.4	0.94	109.98	100-1100
ISSR-58	ACACACACACACACACG	$(AC)_8G$	52.4	0.71	16.8625	100-1000
ISSR-59	TGTGTGTGTGTGTGTGG	$(TG)_8G$	52.4	-	-	-

Table 2. Genetic diversity indices in *I. pseudacorus* populations.

Population	na	ne	h	I	Number of polymorphic places	polymorphic places%
Population 1	1.70±0.45	1.47±0.45	0.27±0.19	0.40±0.27	110	70.06%
Population 2	1.95±0.25	1.42±0.27	0.27±0.13	0.43±0.17	150	95.54%
Population 3	1.68±0.46	1.35±0.32	0.22±0.17	0.34±0.25	107	68.15%
Total	2.00±0.00	1.46±0.24	0.29±0.11	0.46±0.13	157	100%

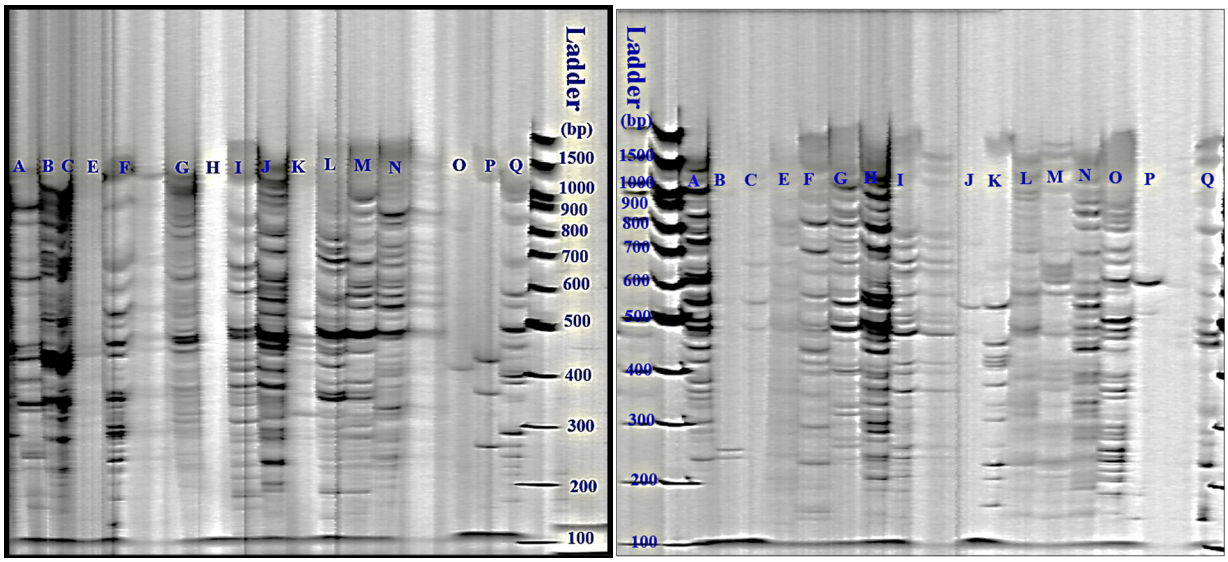

Figure 1. The bands produced by SSR primer ISSR_55 and ISSR_54 (respectively) fluorescently visualized in GS2000.

genetic location and Shannon index within populations and between populations showed that the parameters of gene position (150), polymorphism percentage 95.54% and the number of observed alleles (1.95± 0.25) were higher in the population 2 than in the other populations.

Table 3. Number of F gene loci of *I. pseudacorus* populations.

Nm	Gst	Hs	Ht
2.49	0.166	0.25±0.00	0.30±0.01

Table 4. Table of similarity (above diameter) and genetic distance (below diameter) of the nei calculated for populations based on the geographical location of the ISSR marker.

Populations	1	2	3
1	***	0.8918	0.8382
2	0.1145	***	0.9591
3	0.1765	0.0417	***

Table 5. Percentage of changes described in the first three axes in PCoA analysis.

Axis	1	2	3
Relative variance (%)	29.88	21.24	16.52
Cumulative variance (%)	29.88	51.11	67.63

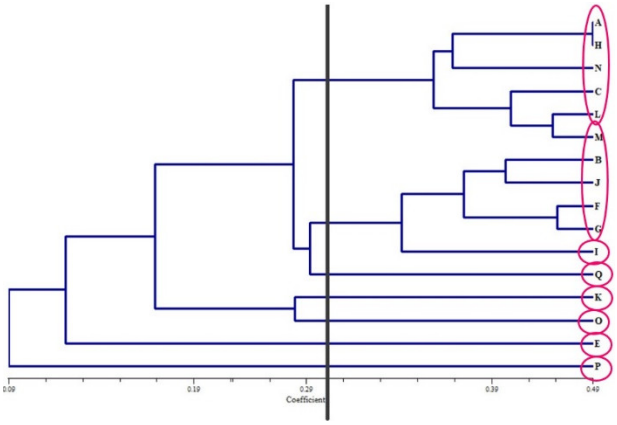

Figure 2. UPGMA dendrogram based on Jaccard's similarity coefficient among Iris ecotypes.

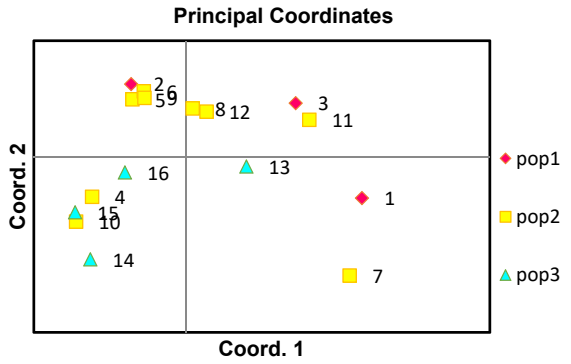

Figure 3. Principal component analysis (PCA) based on ISSR polymorphism.

According to Table 2 (genetic diversity among different populations based on geographical location), the values of genetic diversity like the percentage of polymorphic genetic location and Shannon index within populations and between populations showed that the parameters of gene position (150), polymorphism percentage 95.54% and the number of observed alleles (1.95± 0.25) were higher in the population 2 than in the other populations. While the number of effective alleles with 1.48±0.45 in the first population was higher than the second population (1.42±0.27) and the third population (1.35±0.32). Nei gene diversity in the first population (0.27± 0.19), the second population (0.27 ± 0.13), the third population (0.22± 0.17) and the Shannon index was in the first population (0.40± 0.27), the second population (0.43± 0.17) in the third population (0.34± 0.25) (Table 2).

Evaluation of the genetic structure of the populations showed that the GST means in the total population was 0.166, total genetic diversity (Ht) (0.30± 0.01), and genetic diversity within the populations (Hs) (0.25 ±0.00) were estimated. The Ht positive value in the whole population indicates the balance in the population. Gene flux in the whole population was estimated to be 2.49 (Table 3).

The study of genetic similarity between different populations showed that the highest genetic similarity was calculated between the second and third populations (with a value of 0.95). Also, the highest genetic distance was related to the second population with the first (with a value of 0.11) (Table 4).

Grouping the studied populations using cluster analysis

Cluster analysis was performed for 3 populations using simple similarity coefficients, Jacquard and Dice and three UPGMA clustering algorithms, nearest neighbor (SLINK) and farthest neighbor (CLINK), and finally by. calculating the coefficient coefficient of Jaccard and UPGMA algorithm (Due to having the highest value of r = 89%) was used to group 16 ecotypes and dendrograms were drawn (Fig. 2). Cluster analysis grouped the 3 studied populations into 8 clusters, of which 6 groups were single members

According to the resulting dendrogram, genotypes are divided into 8 main groups (the first group includes A, H, N, C, and L, the second group contains 5 ecotypes including M, B, J, F, and G, the third to eighth groups in

Table 6. Molecular ANOVA for genetic differences between populations based on geographical location for ISSR marker.

Source of variations	df	SS	MS	Est. var	%Diversity	φpt
Among populations.	2	73.410	36.705	0.95	3%	0.029*
Within populations	13	419.278	32.252	32.252	97%	
Total	15	492.688		33.202	100%	

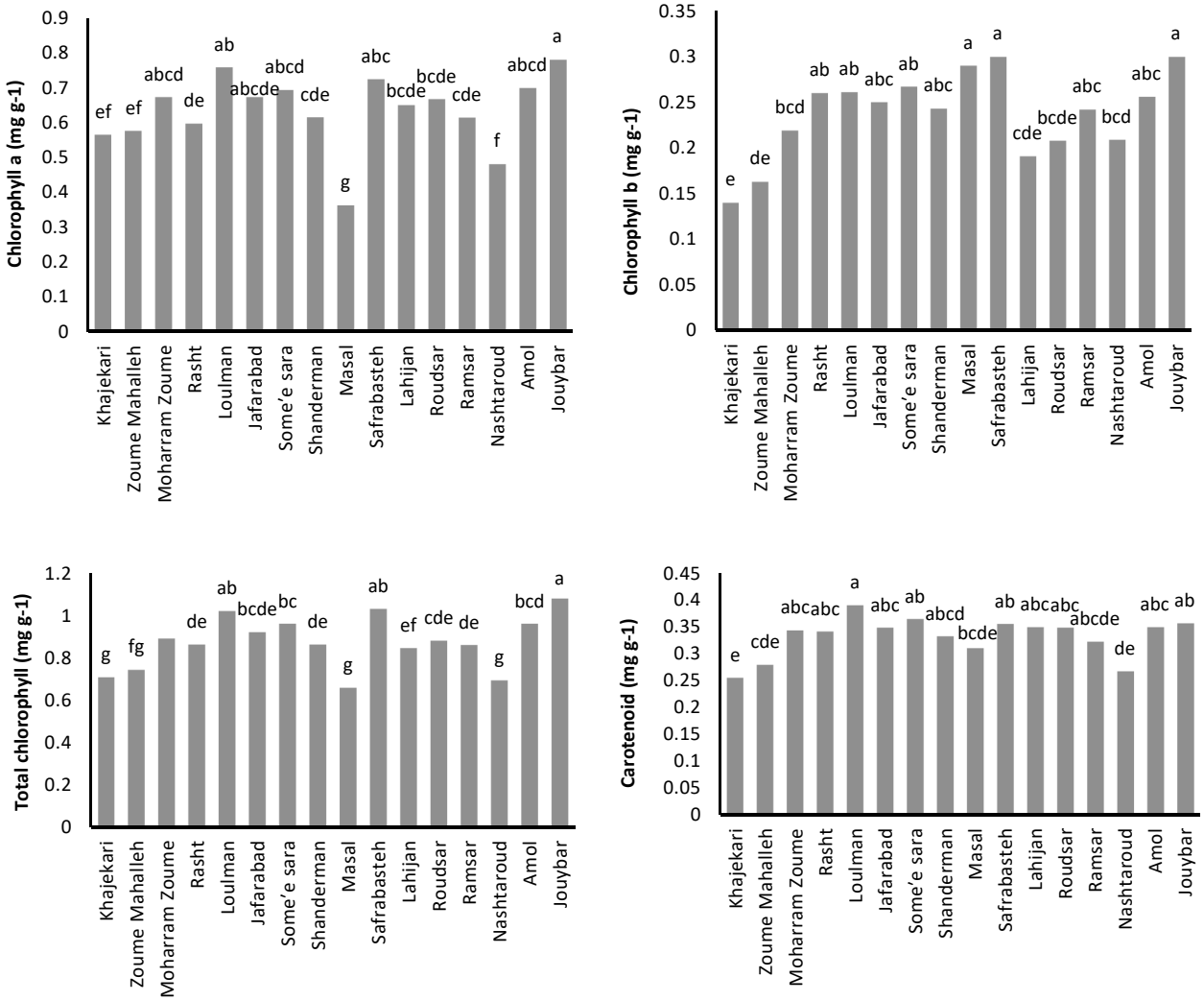

Figure 4. Photosynthetic pigments in *Iris pseudacorus* ecotypes.

separate groups) they got. As seen from the dendrogram, the ecotypes classified into one group had many genetic similarities.

To further analyze the information obtained from the ISSR marker, the data obtained from the scoring tapes were analyzed by parsing the original coordinates (Fig. 3). The analysis results showed that the first, second, and third components contained 29.8 %, 21.24%, and 16.52% of the information, respectively (Table 5).

In the decomposition into main coordinates, the molecular variance analysis of the studied populations showed that according to PhiPT statistics, there was a significant difference among the groups at the level of 5% (Fig. 3). The results showed that genetic diversity within populations (97%) is more significant than diversity between populations (3%) (Table 6).

The data obtained from photosynthetic pigment graphs include chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids showed in Fig. 4. Chlorophyll a (0.781 mg g^{-1}), chlorophyll b (0.300 mg g^{-1}), and total chlorophyll (1.08 mg g^{-1}) had the highest levels in ecotype Q (Jouybar). The lowest levels were obtained in chlorophyll a in ecotype J (0.363 mg g^{-1}), chlorophyll b in ecotype A (0.40 mg g^{-1}), and total chlorophyll in ecotype j (0.658 mg g^{-1}). Among the samples, the highest amount of carotenoids was obtained in ecotype F (0.390 mg g^{-1})

and the lowest amount was obtained in ecotype A (0.255 mg g^{-1}) (Fig. 4).

DISCUSSION

A dendrogram was changed into built based on Nei's genetic distance among populations with the UPGMA technique [22]. A PCO becomes achieved at the identity matrix to have a higher-dimensional representation of the population connection. The populations were divided into eight major groups, which reflect roughly the geographic distribution. Genetic transfer between geographical distances of populations is not possible. The miniature genetics style among the populations is perhaps because of being the equal authentic species.

Geographical and hydrological conditions can explain high PIC in the current study on ecotypes [17]. A high level of PIC clarifies the accepTable results obtained in this study to identify populations with the ISSR technique.*Iris pseudacorus* plants occur in radially spreading clones, which become fragmented as they develop [34]. Clonal plant populations rarely contain only one genet, and numerous studies have reported high levels of genetic diversity within the populations of clonal species [17]. *Iris pseudacorus* plants occur in radially spreading clones, which become fragmented as they develop [34]. The study of geographical diversity in wild plants with genetic markers has shown that most have high genetic diversity within populations and little difference [3].

In the field, working and visiting the habitats, differences in climatic conditions have been seen. As shown in Table 1, latitude and longitude, altitude, temperature, rainfall, humidity, and sunshine have been varied in location. So that rainfall in Shanderman location, latitude, sundial, and temperature in Jouybar, humidity in Rasht was the highest in the other locations. The least amount of rain and longitude in the Amol location has been shown. In the mentioned locations, single-member groups were obtained, and geographical and climatic factors were probably able to create different groups of the same species. Environmental factors can have long-lasting effects on gene expression and chromatin. Apart from natural processes, including vernalization, it remains largely unknown how the environment triggers alterations in the epigenetic [5].

Perhaps the climate and geographical conditions can be explained as an important cause for occurred difference, so it is possible that the long-distance caused the genetic drift of this population that cause to different groups from studied ecotypes [20]. Geographical distance and gene flow between wild plant populations define the genetic distance. High gene flow in species can cause the short genetic distance of populations and scattered genetic diversity within populations. In the species mentioned, if abnormal factors such as habitat degradation due to overgrazing and other factors interrupt the gene flow between habitats, the distance of the discontinued populations will increase, and due to increased homogeneity and differentiation between populations, Genetic erosion will occur [9]. Science on the genetic variety of the selected uniques is of final importance since it contributes to the information on the species and allows the selection of genotypes to be included in future maintenance and breeding programs. Thus, the most divergent and similar genotypes can be selected according to the research interest. The conservation of this level of genetic diversity should allow this species to maintain its potency to adapt to new environmental changes. Ultimately, the excellent homogeneity of the diversity indices suggests that the species has sufficient capacity to oppose the natural loss of genetic diversity by drift [21].

High intra-population diversity prevented the entire inter-population diversity incidence [19]. In the plant diversity study by molecular markers, a small part of the genome is considered that the gene locus may not be detected gene diversity and groups in the genetic division are classified in same groups that are separated in the phenotypic grouping. In general, the environment, genotype, and the interaction of these main factors have affected the phenotypic attributes. So, different results are constructed from the same genotype in different environments under other conditions. According to this theory, it cannot be expected that the effect of genetic diversity that is only affected by genotype is the same as the result of phenotypical traits that the environment has influenced. The gene expressions have been changed by conditions [29]. In the end, by using ISSR marker structures, the intra-populace range became accomplished extra than inter-populace diversity. ISSR is a superb molecular device to research the genetic variability of *Iris pseudacorus*.

Although plant growth results from regular and complete physiological processes and inhibition by environmental factors cannot be attributed to a specific physiological function, the predominant physiological phenomenon is photosynthesis [32]. According to meteorological data, the geographical location of the stream has a higher

average temperature and sunny hours than other ecotypes (Table 1). Increased radiation during the plant growing season increases the production of photosynthetic materials and improves the growth of different parts of the plant [43]. Increasing the light intensity from 100 to 450 µmol / m2 in Panax has increased the chlorophyll content from 484 to 515 $mg.m^{-2}$ [4].

Various results of chlorophyll changes have been observed in the study of sources, and it can be said that the response of different plants to changes in light intensity is relatively diverse. Increasing the amount of chlorophyll due to the plant's desire to enrich the absorption system to produce more photosynthetic materials and high levels of chlorophyll can be used as an indicator in selecting cultivars for efficient photosynthesis in less light conditions [7]. Light controls the growth and development of plants through photosynthesis, primarily through the absorption of carbon dioxide. The light intensity affecting photosynthesis varies depending on time and place in each habitat, although they increase their adaptation to different light intensities [42].

Carotenoids can capture high-energy short-wavelengths, convert single oxygen to ternary, and play an antioxidant role by capturing the oxygen radicals produced [6]. Numerous factors can affect the quantity and quality of carotenoids, including climatic factors. Carotenoids can increase plants' antioxidant capacity and support photosynthesis by increasing the antioxidant capacity of cells and the production of new proteins [1]. Light is one of the most important factors affecting plant growth that involves changes in radiation, growth, morphology, anatomy, and various aspects of cell physiology and biochemistry [43]. Since the lowest sundial is recorded in Ecotype A, it is probably possible to justify the reduction of carotenoids in this ecotype. In contrast, not enough ATP is produced under low radiation conditions to stabilize carbon and carbohydrate biosynthesis, which leads to reduced plant growth [28].

CONCLUSION

For the first time, the genetic diversity of different *Iris pseudacorus* populations was analyzed using ISSR molecular markers. The current study reveals that ISSR is the informative marker for characterizing *I. pseudacorus* diversity at the DNA level. The results showed the relatively high efficiency of ISSR markers in identifying various individuals from different *I. pseudacorus* populations. The informative primers identified in our studies could be helpful in genetic analysis of *I. pseudacorus* germplasm, breeding management, and utilization. The current study results also suggested the great value of the *I. pseudacorus* species for use in pharmacognosy industries. Genetic variations among genotypes could be helpful in selecting parents to be crossed for generating appropriate populations intended for both breeding purposes and genome mapping. Further studies for sequencing the ISSR fragments may help the understanding of several genes regulation. The complementation of the ISSR technique by metabolic profiles for breeding, medical and conservation purposes in the Yellow flag is recommended. Furthermore, it is helpful to conduct comparative studies with different marker systems. Photosynthetic pigments showed different results in other locations. In addition to genetics, the environment can also influence phenotypic traits. Therefore, photosynthetic pigments had the highest temperature and light in the Jouybar location.

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ارزیابی تنوع ژنتیکی و رنگیزه‌های فتوسنتزی در جمعیت‌های وحشی زنبق مردابی (*Iris pseudacorus*)

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چکیده

زنبق مردابی (*Iris pseudacorus*) گیاهی بومی با خواص زینتی و دارویی در علم باغبانی است. در مطالعه حاضر ۱۶ اکوتیپ از گونه زنبق مردابی جمع آوری و بر اساس موقعیت جغرافیایی در سه جمعیت طبقه‌بندی شد. تنوع ژنتیکی زنبق مردابی با استفاده از ۱۶ نشانگر ISSR مورد سنجش قرار گرفت. رنگیزه‌های فتوسنتزی شامل کلروفیل a، کلروفیل b، کلروفیل کل و کاروتنوئیدها نیز با روش اسپکتروفتومتری اندازه‌گیری شدند. آغازگرها ۸۷۴ نوار قابل امتیازدهی در اندازه های ۱۰۰-۱۲۰۰ جفت باز تولید کردند. درصد چندشکلی تمامی آغازگرها ۱۰۰ درصد بود. نشانگر ISSR_55 دارای بیشترین باند (در مجموع ۲۳۴ باند)، بیشترین شاخص نشانگر و بیشترین مقدار محتوای اطلاعات چندشکلی (PIC) بود. نشانگر ISSR-13 با مجموع اطلاعات چندشکلی (PIC) ۰/۸۴ در جایگاه دوم قرار دارد. همچنین داده‌های به دست آمده از نوارهای امتیازدهی با تجزیه مختصات اصلی مورد تجزیه و تحلیل قرار گرفت. نتایج تجزیه و تحلیل نشان داد که مولفه های اول، دوم و سوم به ترتیب شامل ۲۹/۸۸ درصد، ۲۱/۲۴ درصد و ۱۶/۵۲ درصد اطلاعات بودند. نتایج نشان داد که تنوع ژنتیکی درون جمعیت‌ها (۹۷ درصد) از تنوع بین جمعیت‌ها (۳ درصد) معنی دارتر است. نتایج اسپکتروفتومتری نشان داد که بیشترین رنگیزه‌های فتوسنتزی در محل Q (جویبار) با بیشترین نور خورشید به دست آمده است. نشانگرهای ISSR روابط ژنتیکی نمونه‌های زنبق مردابی را برای سازگاری‌های مختلف زراعی- اکولوژیکی به خوبی نشان داد. بنابراین نشانگرهای ISSR یک ابزار مولکولی عالی برای تحقیق در مورد تنوع ژنتیکی زنبق مردابی می‌باشد.

کلمات کلیدی: کلروفیل، گل، ISSR، مکان جغرافیایی، نشانگر.