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Research Article

Genetic diversity and phylogenetic analyses of Turkish sweet corn (*Zea mays* var. *saccharata*) varieties using ISSR markers and chloroplast *trnL-F* IGS region

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Abstract

Genetic diversity levels are critical for characterizing and utilizing germplasm collections and for making improvements related to elite germplasms. The current study investigated the genetic diversity level and phylogenetic relationships in ten Turkish sweet corn varieties (*Zea mays* var. *saccharata*) using 15 ISSR markers and *trn*L-F intergenic spacer regions, respectively. A total of 75 loci were identified, of which 57 (76%) were polymorphic. The highest polymorphism ratio (100%) was found using UBC811, UBC817, and UBC823 ISSR markers, while the lowest ratio (45.4%) was identified using UBC829. According to *trnL-F* intergenic spacer region analyses, nucleotide diversity was found as π: 0.030 for Nei and θ: 0.036 for Watterson, respectively. In *trnL-F* intergenic spacer regions, several polymorphic (variable) sites were identified 28 of which 57% (16/28) were parsimony informative sites and 399 sites were invariable (monomorphic). The phylogenetic analysis revealed that two major groups were observed named groups A and B and ten sweet corn genotypes clustered along with known maize genotypes in subgroup B2 with 98% bootstrap value. Consequently, the ISSR data obtained in this study revealed that Turkish sweet corn genotypes exhibit extensive genetic diversity, and the *trnL-F* intergenic spacer region was successfully utilized to differentiate between maize genotypes from various origins and whole plant taxa.

Keywords: cpDNA; maize; molecular marker; molecular breeding; phylogeny

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Introduction

Maize (*Zea mays* L.), commonly known as corn, is widely used as food for humans and forage for animals (Erenstein *et al*., 2022). It can be classified into normal, sweet, waxy, and popcorn types. Among these types, sweet corn (*Z. mays* var. *saccharata*) contains special and attractive characteristics, including high nutritional value, thin pericarp sweet taste, and endosperm with delicate texture (Niji, 2018; Yang *et al*., 2021). Maize was an important crop for Turkish agriculture until the 1970s and was cultivated on small scales for animal feed and human nutrition (Yılmaz *et al*., 2019). Today, it is mostly cultivated in the Black Sea Region (37%), followed by the Mediterranean (29%) and Marmara (16%) Regions. The largest portion of cultivated maize in Türkiye shows a hybrid nature, while traditional maize landraces are found on small scales in various parts of Türkiye, particularly in the Black Sea Region (Tasdan, 2005).

Among maize landraces, genetic diversity has been mainly investigated by using morphological and agronomic traits (Ilarslan *et al*., 2002; Mansilla *et al*., 2021; Munaiz *et al*., 2021; Mayer *et al*., 2022). Molecular markers are efficient tools in assessing the genetic diversity level of plant germplasm resources such as single nucleotide polymorphism (SNP), simple sequence repeats (SSR), random amplified polymorphic DNA (RAPD), sequence-related amplified polymorphism (SRAP), amplified fragment length polymorphism (AFLP), inter simple sequence repeat (ISSR) and inter-primer binding site (IPBS) (Filiz *et al*., 2015; Dumlupinar *et al*., 2016; Gungor *et al*., 2022; Hocaoglu-Ozyigit *et al*., 2022). Various studies were performed on Turkish maize germplasm such as fluorescently labeled SSR markers (Cömertpay *et al*., 2012), RAPD markers (Okumus, 2007), agronomical characteristics (Oner and Gulumser, 2014), enzyme polymorphism (Ilarslan *et al*., 2001), and *wip1* genes (Filiz *et al*., 2014). The chloroplast DNA (cpDNA) and sequences have been used extensively to express relationships at all taxonomic levels in plants (Shaw *et al.,* 2014). The *trnL*$^{(UAA)}$-*F*$^{(GAA)}$ intergenic spacer (IGS) sequence, which is a region between transfer RNA genes encoding for leucine and phenylalanine, has been commonly used for taxonomic and phylogenetic comparisons (Taberlet *et al*., 1991; Orton *et al*., 2017; Feng *et al*., 2022; Herman *et al*., 2023). Inter simple sequence repeat (ISSR) is a polymerase chain reaction PCR-based technique utilizing microsatellite sequences as primers in PCR to generate multi-locus markers (Pradeep *et al*., 2002; Gemmil and Grierson, 2021; Abouseada *et al.,* 2023).

The issues related to genetic diversity bear vital importance, especially for the future of agricultural products (Hocaoglu-Ozyigit *et al*., 2022; Singh and Kaundal, 2023). Knowing the genetic diversity characteristics of sweet corn as an important crop and related with, revealing the lineage relationships of cultivated varieties of sweet corn are very important issues in terms of corn breeding practices. Related to the above-mentioned issue, our study's findings will contribute to understanding the genetic potential of the sweet corn gene pool in Türkiye and the use of the data as an application in the fields. Thus, this study aimed to investigate the genetic diversity characteristics of 10 Turkish sweet corn varieties using ISSR molecular markers and to reveal phylogenetic relationships among corn genotypes via using the *trnL-F* intergenic spacer (IGS) region.

Materials and Methods

Plant materials and growth conditions

The seeds of maize varieties ('Merit', 'Moreland', 'Argos', 'Vega', 'Caramelo', 'Tanem', 'Hazar', 'Baron', 'Overland', and 'Batem Tatlı') were collected from producers in Türkiye. Sampled maize varieties and the producers are shown in Table 1. The seeds were germinated at 4 °C for 2-4 days in dark conditions between moist filter papers in petri plates. After germination, seedlings were grown in a greenhouse at 25 °C and 70% relative humidity on an 8/16 day and night period for three weeks.

Table 1. Sampled maize varieties and the producers

No	Variety Name	Variety Owner
1	Argos	Semillas Fito
2	Overland	Syngenta
3	Moreland	Syngenta
4	Baron	MAY Seed
5	Tanem	MAY Seed
6	Caramelo	MAY Seed
7	Vega	MAY Seed
8	Merit	MAY Seed
9	Hazar	Biotek Seed
10	Batem Tatlı	West Mediterranean Agricultural Research Institute

DNA isolation

Total genomic DNA was extracted in 0.5 g of fresh plant leaf materials by using a standard cetyltrimethylammonium bromide (CTAB) protocol with minor modifications (Doyle, 1991). The DNA quality was measured by NanoDrop spectrophotometer (Shimadzu, Japan). The quality and integrity of the DNA were also analyzed by visualization on 1.0% 1X-TAE agarose gel. Finally, DNA stocks were diluted to 20 ng/µL for further molecular analyses.

ISSR-PCR and data analyses

For genetic diversity analyses, ten sweet corn varieties were studied using 15 universal ISSR markers (Nagaoka and Ogihara, 1997) (Table 2). The ISSR-PCR reaction mixture added up to a total volume of 25 µL, including 3.0 µL Taq buffer, 1.5 µL ISSR primer (10 mM), 3 µL $MgCl_2$, 16 µL molecular biology grade ultra-pure water, 1.0 µL dNTPs (25 mM), 1 U TaqDNA Polymerase, and 1.0 µL template DNA (50 ng/µL). The PCR reactions were performed in a thermal cycler (Aeris Thermal Cycler Model G96), with primer denaturation at 94 °C for 5 min followed by including 32-40 cycles of denaturation at 94 °C for 60 s, annealing at 36-55 °C (depending on primer) for 60 s, and extension at 72 °C for 60 s, followed by a final extension at 72 °C for 7 min. Amplified products were separated by electrophoresis in a 1% agarose gel with 1X TBE and digitally photographed under UV light with a 1000 bp DNA ladder marker (Thermo Scientific, USA).

The clear and scorable ISSR band profiles of the maize genotypes were converted into a numerical database. A binary matrix was obtained by scoring the presence (1) or absence (0) of each band in the agarose gels. The data were evaluated by PopGene version 1.32 (Yeh *et al.,* 1999) and MVSP 3.2 (multi-variate statistical package) (Kovach 2007). The genetic parameters, including effective alleles per locus (Ne) (Kimura and Chow, 2014), percentage of polymorphic loci (P), the mean number of observed alleles (Na), and Shannon's information index (I), and Nei's gene diversity (h) (Nei, 1973) were calculated by PopGene 1.32. A dendrogram was constructed by Euclidean's similarity coefficients using the UPGMA (unweight pair group method) method by MVSP 3.2.

Table 2. A detailed list of 15 ISSR markers used in this study, including primer name and code, their sequences, annealing temperatures, and the total number of bands and polymorphic bands. Y, R, and – show the C or T, A or G, and no bands, respectively

No.	Primed code	Primer sequence 5'-3'	Annealing temperature (°C)	Total number of bands	Number of polymorphic bands	Polymorphic bands (%)
1	UBC807	AGAGAGAGAGAGAGT	48 °C	10	7	70
2	UBC811	GAGAGAGAGAGAGAGAC	53 °C	7	7	100
3	UBC817	CACACACACACACACAA	50 °C	9	9	100
4	UBC818	CACACACACACACACAG	53 °C	_	_	_
5	UBC820	GTGTGTGTGTGTGTGTC	53 °C	_	_	_
6	UBC823	TCTCTCTCTCTCTCTCC	53 °C	7	7	100
7	UBC827	ACACACACACACACACG	53 °C	_	_	_
8	UBC825	AGAGAGAGAGAGAGAGYA	54 °C	6	4	66.7
9	UBC848	CACACACACACACACARG	56 °C	10	8	80
10	UBC849	GTGTGTGTGTGTGTGTYA	54 °C	_	_	_
11	UBC855	ACACACACACACACACYT	54 °C	_	_	_
12	UBC842	GAGAGAGAGAGAGAGAYG	56 °C	8	6	75
13	UBC875	CCCTCCCTCCCTCCCT	59 °C	_	_	_
14	UBC829	ACTGACTGACTGACTG	49 °C	11	5	45.4
15	UBC844	CTCTCTCTCTCTCTCTRC	56 °C	7	4	57.1
	Total			**75**	**57**	**76**

Sequencing and phylogenetic analyses

The *trnL-F* IGS region was amplified by using forward primer as 5'-AAAATCGTGAAGGTTCAAGTC-3' and reverse primer as 5'-GATTTGAACTGGTGACACGAG-3' (Sang *et al*., 1997). PCR reactions were performed for a cycle of 3 min at 94 °C, followed by 45 cycles of 1 min at 94 °C, 1 min at 52 °C, 1 min at 72 °C, and a final cycle of 7 min at 72 °C. Subsequently, PCR products were purified using a GeneJET Gel Extraction Kit (Thermo Scientific) and sequenced by the Iontek Sequencing Service (Türkiye). The sequence identity matrix was generated using Bioedit 7.2.5 (Hall *et al*., 1999). The *trnL-F* IGS region was analyzed with DnaSP 5.1 (Librado and Rosso, 2009), including estimates of genetic diversity, π (Nei, 1987) and θ (Watterson, 1975), and segregating (polymorphic) sites (S). To construct a joined phylogenetic tree, 31 *trnL-F* IGS sequences from 28 plant species were collected in the NCBI nucleotide database (https://www.ncbi.nlm.nih.gov) and accessions numbers were shown on the joined phylogenetic tree by using the MEGA X version (Kumar *et al.,* 2018). For phylogenetic analyses, the following parameters were adopted: maximum parsimony (MP) and maximum likelihood (ML) methods and the Tamura-Nei model, and 1000 replicates bootstrap value.

Results and Discussion

ISSR data analysis

ISSR markers have been extensively used to evaluate the extent of genetic diversity at inter- and intra-specific levels in a wide range of crop species (Pradeep *et al*., 2002; Uzun *et al*., 2011; Filiz *et al*., 2018). In this study, genetic diversity analyses were performed on ten Turkish sweet corn varieties using 15 ISSR primers, nine of which generated clear DNA bands (Table 2). The band profiles and polymorphism of the UBC807 primer are shown in Figure 1. The ISSR-PCR analysis indicated that nine ISSR primers showed 75 distinct bands and 57 of these were polymorphic (76%) (Table 2). In ISSR analysis, the total number of bands was found between 6 and 11, while the number of polymorphic bands ranged from 4 to 9. The highest level of

polymorphism (100%) was found with primers UBC811, UBC817, and UBC823 while the lowest polymorphism (45.4%) was observed with primer UBC829. Also, the percentage of polymorphic loci (P%), observed number of alleles (Na), effective number of alleles (Ne), Nei's gene diversity (h), and Shannon's information index (I) were found as 76%, 1.76, 1.45, 0.26, and 0.39, respectively. The values are shown in Table 3.

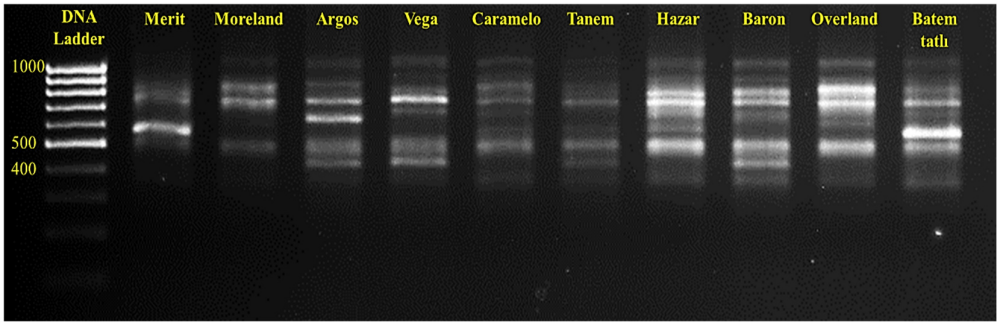

Figure 1. ISSR-PCR amplification profiles of ten maize genotypes with UBC807 primer. The yellow label above each well shows the variety name (1000 bp standard marker)

Table 3. Summary of genetic variation statistics for all loci by using diploid ISSR data

	Polymorphic locus number	PPL (%)	na	ne	h	I
Average	57	76	1.7600	1.4472	0.2626	0.3946

PPL: Percentage of polymorphic loci, na: number of observed alleles
ne: number of effective allele (Kimura & Crow 1964)
h: Nei's gene diversity (Nei 1973)
I: Shannon Information Index (Lewontin 1972)

According to genetic analyses based on ISSR data, two major groups were identified and named groups A and B in the dendrogram (Figure 2). Intriguingly, the Hazar variety was isolated from other genotypes and found alone in group A. In contrast, the other maize genotypes were grouped in the B1 subgroup ('Batem Tatlı', 'Baron', 'Tanem', and 'Caramelo') and the B2 subgroup ('Vega', 'Argos', 'Overland', 'Moreland', and 'Merit'). While the lowest genetic distance was found at 3.606 between the 'Baron' and 'Tanem' varieties in subgroup B1, the highest genetic distance was found as 5.158 between the 'Hazar' variety and group B1. Based on cluster analysis, varieties from different sources clustered together, suggesting that these genotypes may have been derived from identical or similar ancestors by maize breeding programs in Türkiye.

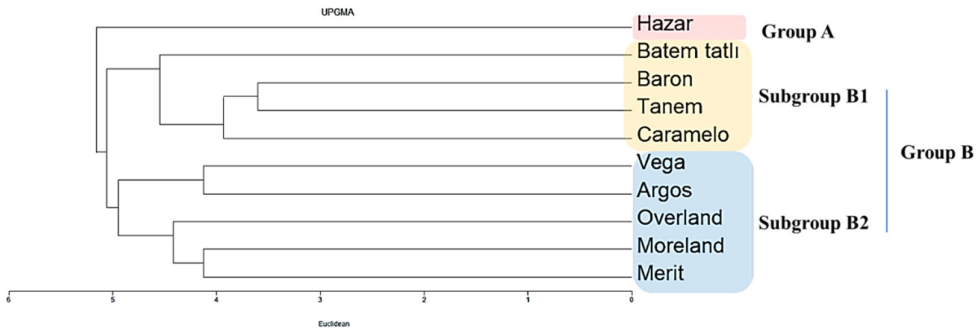

Figure 2. The dendrogram of genetic relationships among ten Turkish sweet corn varieties based on 57 ISSR loci using the UPGMA clustering method. The tree was constructed based on Euclidean's similarity coefficients by using MVSP 3.2 and the x-axis shows dissimilarity values

Carvalho *et al.* (2002) reported that a total of 153 DNA fragments were identified and 116 (75.8%) were found to be polymorphic in 81 accessions of maize. In another study, 15 ISSR primers produced 266 bands, out of which 228 (88.9%) were polymorphic in fifty accessions of maize from different origins (do Amaral Júnior *et al*., 2011). In inbred maize (*Zea mays* L.) genotypes, a high level of polymorphism was determined as 69% among studied genotypes by 25 ISSR primers (Idris *et al*., 2012). Tiarovská *et al.,* (2013) reported that a total of 22 band levels were detected of which 16 (72.73%) were polymorphic in ten maize inbred lines. Muhammad *et al.* (2017) reported that a total of 190 different alleles were amplified by using 20 ISSR primers with an average of 9.5 ISSR alleles per locus in 21 maize genotypes with different origins. Also, polymorphic alleles were found between 4 and 17. Genetic relationship and variability of maize cultivars bred in the Rajouri region of Pir Panjal Himalaya, India, were evaluated using ISSR and morphological markers. According to the results, a total of 108 loci were generated with 6.35 loci per primer and it is observed that 83 of them were polymorphic with a ratio of 75.2% by using 17 ISSR markers. The Shannon information index and Nei's genetic diversity values were calculated in the range of 0.056-0.176 and 0.037-1.121, respectively. The authors stated that the observed high level of genetic diversity can be utilized in Indian breeding programs (Dar *et al.,* 2018). The genetic polymorphism of 38 dark maize varieties from Azerbaijan were investigated using 6 selected ISSR markers. According to the results, the polymorphism ratio was calculated as 94.6% with an average PIC value of 0.35. The genetic diversity index of Nei was calculated as 0.92 (Valiyeva *et al.,* 2019). For breeding new varieties, the genetic diversity of 100 Iranian maize lines was evaluated by using 16 ISSR markers. The markers amplified 81 loci 78 of which showed polymorphism with a ratio of 95.12%. The PIC value ranged from 0.65 to 0.93 with a mean of 0.77. The authors concluded that the ISSR markers were a useful tool for the genetic fingerprinting of maize genotypes (Azar *et al.,* 2019). To analyze the genetic diversity of a global maize collection, Soliman *et al.* (2021) used 15 ISSR markers on 40 maize cultivars collected around the world. According to the results, 180 loci were obtained, of which 161 were polymorphic (89.59%). These results suggest that the level of genetic diversity in Turkish sweet corn maize genotypes is similar to previous findings, and our studied Turkish sweet corn varieties exhibit extensive genetic diversity.

Variations in chloroplast trnL-F IGS regions

About 36 coding and noncoding regions of the plastid genome have been sequenced to infer phylogenetic relationships among the different lineages of land plants. The *trnL-F* IGS region with the *trnL*^{UAA} intron and *trnL-F* intergenic spacer is often used as molecular markers in plant genetic research (Taberlet *et al.,* 1991; Hao *et al.,* 2009; Hocaoglu-Ozyigit *et al.,* 2022; Herman *et al.,* 2023). A total of 10 *trnL-F* IGS regions in Turkish sweet corn varieties were amplified and accession numbers are shown in Table 4. The length of all *trnL-F* IGS regions was found to be 428 bp and GC contents (%) were found between 31.54 and 33.18. In addition, the sequence identity values among sweet corn genotypes were identified between 95% and 99%. While the highest sequence identity was found between 'Moreland' and 'Argos' varieties with 99%, the lowest sequence identity was found at 95% between 'Tanem' and 'Hazar' and 'Tanem' and 'Overland' varieties, respectively.

Table 4. The sequence features and NCBI accession numbers of *trnL-F* IGS regions in ten Turkish sweet corn varieties

No.	Genotype name	Length (bp)	GC content (%)	NCBI accession number
1	Merit	428	33.18	MF509755
2	Moreland	428	32.94	MF509756
3	Argos	428	32.24	MF509757
4	Vega	428	31.78	MF509758
5	Caramelo	428	32.94	MF509759
6	Tanem	428	31.78	MF509760
7	Hazar	428	32.71	MF509761
8	Baron	428	31.54	MF509762
9	Overland	428	32.71	MF509763
10	Batem Tatlı	428	32.00	MF509764

In sequence analysis of *trnL-F* IGS regions (Figure 3), the number of polymorphic (variable) sites was identified as 28, of which 57% (16/28) were parsimony informative sites and 399 sites were invariable (monomorphic). The nucleotide diversity was identified as π: 0.030 and θ: 0.036, respectively and 360 nucleotides in length conserved cpDNA region were detected between 54 and 414 positions. Thus, it can be suggested that *trnL-F* IGS regions were well conserved in Turkish sweet corn varieties.

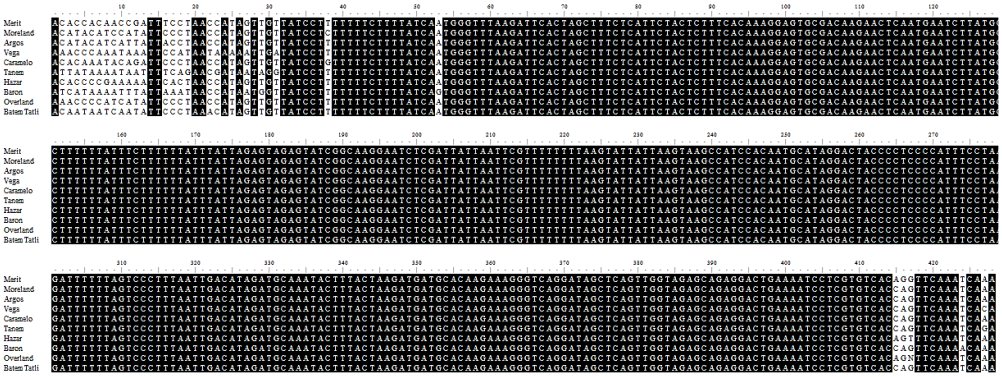

Figure 3. Sequence alignment of *trnL-F* intergenic spacer from ten Turkish sweet corn varieties using BioEdit software. Sequences were aligned by ClustalW and identical residues were shaded as black

Phylogenetic analyses

Chloroplast DNA (cpDNA) is an important genetic resource and is commonly used in studies related to variations between populations, species, genera and sometimes even higher taxonomic levels (Brinegar, 2009; Orton *et al.,* 2017; Hocaoglu-Ozyigit *et al.,* 2022). Firstly, the phylogenetic tree of ten sweet corn varieties based on *trnL-F* IGS sequences was constructed by MEGA X using the ML method for 1000 bootstraps (Figure 4). The phylogenetic tree showed two main clades named group A and B and group A further separated into two subgroups, which were designated as subgroups A1 and A2. The 'Vega', 'Tanem', and 'Baron' varieties in group B were isolated from other maize genotypes and this clade showed the highest bootstrap value (76%). ISSR data supported the phylogenetic data that 'Tanem' and 'Baron' clustered together in the dendrogram (Figure 2). Genome instability is one of the major forces for evolution. Minor or local changes related to inaccurate DNA replication, DNA repair, or recombination can cause mutations, in other words, genetic variation (Aguilera *et al.,* 2008; Hu *et al.,* 2016). The larger group A showed lower bootstrap values ranging from 44% to 73%, suggesting that genetic variations (found as π: 0.030 and θ: 0.036) may cause these differences in their *trnL-F* IGS regions. According to the MP tree, the same cluster topologies such as subgroup A1 ('Hazar', 'Overland', and 'Merit') and A2 ('Vega', 'Tanem', and 'Baron') were identified (Figure 5). In the MP

tree, group B showed a mixed structure and 'Batem Tatlı' was particularly separated from other maize genotypes. Finally, the same conserved clusters were identified in both ML and MP phylogenetic trees, suggesting that the *trnL-F* IGS region can be a strong and distinguishable molecular tool in understanding the phylogenetic relationships of Turkish sweet corn varieties.

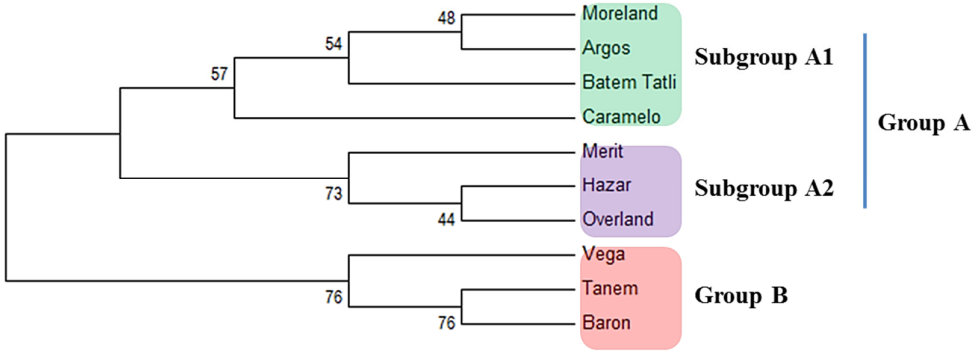

Figure 4. Phylogenetic tree of *trnL-F* IGS regions from ten sweet corn genotypes. The phylogenetic tree was constructed by MEGA X software with the maximum likelihood (ML) method for 1000 bootstrap replicates

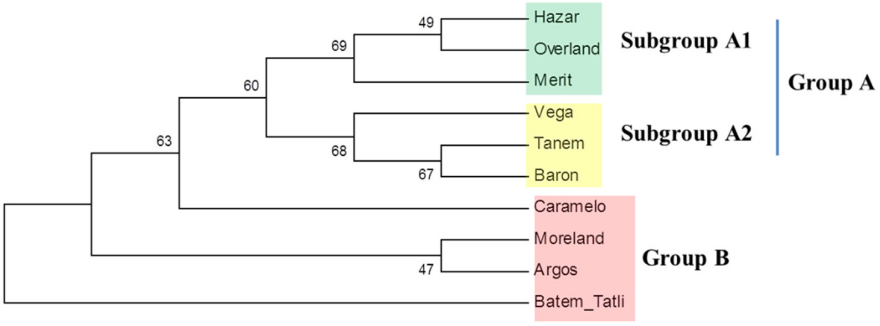

Figure 5. Phylogenetic tree of *trnL-F* IGS regions from ten sweet corn genotypes. The phylogenetic tree was generated using MEGA X software with the maximum parsimony (MP) method for 1000 bootstrap replicates

To infer phylogenetic relationships among plant taxa, 31 *trnL-F* IGS sequences from 28 plant taxa were used, and a joined phylogenetic tree was generated by the maximum likelihood (ML) method for 1000 replicates bootstrap (Figure 6). The two major groups named groups A and B were identified and group B was further divided into two subgroups B1 and B2. Group A consisted of only dicot species, while subgroups B1 and B2 included only polycots and monocots, respectively. Based on general tree topology, it can be proposed that the *trnL-F* IGS region is an efficient tool in terms of separating plant groups. When compared to major groups A and B, group B (polycots and monocots) separated as group A (dicots) with the highest bootstrap value (100%), suggesting that the *trnL-F* IGS region may be a more powerful tool for polycots and monocots. Turkish sweet corn varieties were grouped in group B2 together with known maize genotypes (bootstrap value as 79%). In addition, *Hordeum* and *Festuca* genotypes joined this cluster with a 64% bootstrap value. Markedly, the monocot cluster showed a high bootstrap value of 98% in the joined tree. As a result, it can be suggested that the *trnL-F* IGS region is an efficient tool for understanding phylogenetic relationships for maize genotypes and even higher plant taxa.

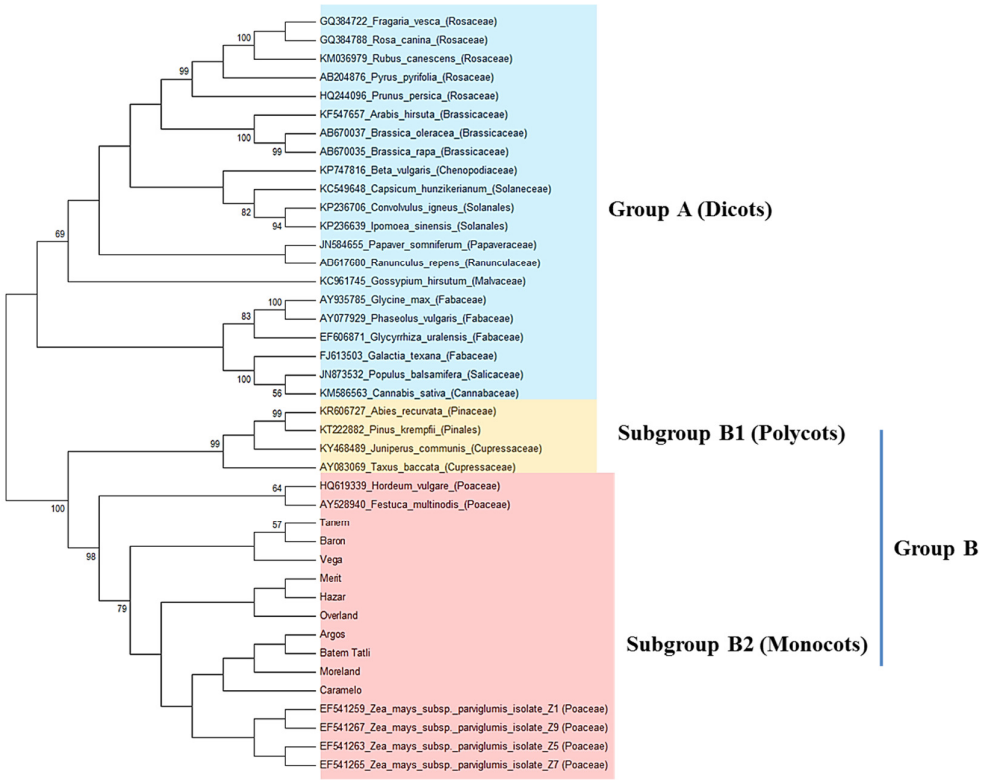

Figure 6. Phylogenetic distribution of identified and collected maize *trnL*-F IGS by MEGA X software. Phylogeny was constructed with the maximum likelihood (ML) method for 1000 bootstrap replicates using a total of 31 *trnL-F* sequences from 28 different plant species

There are some studies conducted to reveal *trnL-F* IGS based phylogenetic relationships of agriculturally important plant species such as banana (*Musa* sp.)(Retnoningsih *et al*., 2014), grape (*Vitis vinifera*) (Fidan *et al*., 2018), olive (*Olea europaea*) (Kaya *et al*., 2018), rice (*Oryza sativa)* (Filiz *et al*., 2018), lemon (*Citrus* sp.) (Sevindik and Yalcin, 2018), mango (*Magnifera* sp.) (Juliantari *et al*., 2018), pomegranate (*Punica granatum*) (Pakyürek *et al*., 2019), apple (*Malus* sp.) (Sevindik *et al*., 2019), mulberry accessions (*Morus* sp.) (Xuan *et al*., 2019), pistachio and pea (*Pistachio vera* and *Pisum sativum*) (Sen *et al*., 2020) cotton (*Gossypium hirsutum*) (Hocaoglu-Ozyigit *et al*., 2022), *Citrus ichangensis* (Kim *et al*., 2021), coffee (*Coffea arabica*) (Mishra *et al*., 2022) and pear (*Pyrus communis*) (Sevindik *et al*., 2023). Phylogenetic analyses revealed that based on using *trnL-F* IGS, *Zea mays* var. *saccharata* was found to be involved in the phylogenetic tree together with other corn varieties as well as the members of the monocot group Poaceae. Subsequently, polycot and dicot plants were found to be the closest groups to this group, respectively.

Conclusions

In this study, the analyses were performed to understand the genetic diversity and phylogenetic relationships among Turkish sweet corn varieties by using ISSR and *trnL-F* IGS sequence data. The ISSR marker method was used as an efficient tool for the evaluation of the genetic diversity characteristics of corn genotypes. Also, 'Baron', 'Tanem', and 'Caramelo' varieties belonged to one group (as subgroup B1), while 'Overland' and 'Moreland' varieties belonged to another group (as subgroup B2). The other varieties were included or excluded from these two groups. It can be concluded that during the breeding process, common

ancestors having the desired characteristics were utilized, with the exception of the "Hazar" variety, which may have come from different genetic sources. In phylogenetic analyses, *trnL-F* IGS sequences were successfully used to discriminate the maize genotypes from different origins as well as in whole plant taxa. The data obtained from this study could make contributions to Turkish corn breeding programs, particularly for sweet corn in the future.

Authors' Contributions

Data curation, formal analysis, methodology, project administration, and supervision EF and IIO; resources and writing - review, HG; software, validation, visualization, and writing - original draft MEU and NO.

All authors read and approved the final manuscript.

Ethical approval (for researches involving animals or humans)

Not applicable.

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Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

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