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SSR MARKERS IN GENETIC DIVERSITY ASSESSMENT OF FIG Ficus carica L. POPULATIONS IN KURDISTAN REGION – IRAQ.

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ABSTRACT:
In the current study, simple sequence repeats (SSR) markers were used to assess the phylogenetic relationships and to investigate genetic polymorphism among 28 fig landraces in Kurdistan Region-Iraq. Fifteen SSR loci produced 73 alleles were produced across all studied genotypes. The observed heterozygosity (Ho) was (0.000) detected with all primers. The expected heterozygosity (He) was ranged from 0.000 to 0.875. The Polymorphic information content PIC was ranged from 0.000 to 0.843, and Fixation index values were ranged from +0.999 to +1.000. The SSR profiles produced were further used for assessing similarities (genetic distance) between the cultivars studied. Genetic distance calculation was achieved using computer software (NTSYS-PC). The genetic distances among the studied genotypes were ranged between (0.1029-0.9485). Genetic distances were supported by the developed dendrogram using UPGMA method. This dendrogram was split into two major groups, and each group was further divided into subgroups. The product of the general data and study of the clusters suggested that almost all the fig cultivars revealed significant genetic diversities. The microsatellite markers allowed clearly the differentiation between studied fig landraces and gave the reliability of these markers in fingerprinting of fig genotypes. It is worth to mention that the study findings will help the management of fig genotypes and might help the selection of landraces for future breeding program in this region.

KEYWORDS: Fig, Nucleic acids, SSR, Genetic diversity.

1. INTRODUCTION

Fig *Ficus carica* L. belongs to the family: *Moraceae*, the name, carica, is called after the location of Caria in Asia Minor, considered to be the birthplace of fig. (Neal, 1965; Dehgan, 1998). For a long time, *F. carica* has been grown in various places around the world for its fruit. In the exploration of sites dating back to at least 5,000 B.C, monuments of figs were found. Even fig trees are believed to have been the founder of Western Asia and human expansion into the Mediterranean (California Rare Fruit Growers, Inc. 1996). All plants in the genus are woody, from trees and shrubs to climbers (Neal, 1965). It is today an important world plant due to its dietary, medicinal and ornamental properties (Flaishman *et al.,* 2008). It has become a worldwide fruit of considerable importance; according to FAO estimates, the planet produces more than one million tons of figs each year (FAO, 2009). Fig is a healthy food rich in vitamin A and minerals that is commonly used in the food sector (Guasmi *et al.,* 2006), and this tree is historically considered a medicinal plant because it has many antibacterial, antiviral and antioxidant activities in its organic extracts (Trichopoulou *et al.,* 2006; Lansky *et al.,* 2008; Lazreg-Aref *et al.,* 2012; Ganopoulos *et al.,* 2015).

The traditional methods of research include morphological, agronomic components, conventional breeding methods and biochemical markers, such as cytology, isoenzymes (AL-Nema and AL-Mallah, 2020; Fornari *et al.,* 2001; Malvolti *et al.,* 2010). These approaches are vulnerable to environmental conditions, with a small number of markers, hence limiting work on fig diversity. Morphological classifications cause the genetic link between cultivars to be absent. As such, these phenotypic characteristics could differ over time and geographic regions and could be significantly influenced by the relationship between genotype and environment (Chatti *et al.,* 2010). Techniques with molecular markers like RFLP, ISSR, RAPD, and SSR have vastly enhanced knowledge on genome structure, organization, and evolution (Cervera *et al.,* 2000; Niu *et al.,* 2007; Li *et al.,* 2011). Most higher organism genomes contain three kinds of multiple copies of single repeat DNA sequences (satellite DNAs, minisatellites, and microsatellites). Microsatellites (Litt and Luty, 1989), also known as simple sequence repeats (SSRs; Tautz *et al.,* 1986). In some organisms

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microsatellite loci are more common than others and screening in some species is likely to produce some useful loci (Cooper, 1995). SSRs are favored markers in most areas of molecular genetics, because they are highly polymorphic even between closely related lines, requiring small amounts of DNA, can easily be configured for high-throughput screening, shared among laboratories and highly transferable among populations (Gupta *et al.,* 1999). SSRs are typically co-dominant markers, high polymorphism, simplicity of detection by PCR methods and are truly excellent for population genetic studies and mapping (Jarne and Lagoda, 1996; Goldstein and Schlotterer, 1999; Giraldo *et al.,* 2010). In Kurdistan Region of Iraq, fig plants are grown in rocky mountain slopes, valleys, hill sides and road sides throughout the Kurdistan region-Iraq, and replaced degraded Oak and Pine forests. Figs are also grown in dry vineyards and as house plants in irrigated orchards (Shahbaz, 2010). However, due to the difficulties in their genotype assessment using classical methods, many of fig populations in Kurdistan had very little attention by scientists. Moreover, it was not understood for many years whether they were native trees or new varieties brought to the region by the local people.

Therefore, the objectives of this study were: establishment of genetic relationships between fig populations in Iraq, Kurdistan region and detection of polymorphism among the individuals and populations by applying SSR markers.

2. MATERIALS AND METHODS

2.1 Sample collection

Samples (fresh leaves) from 28 fig cultivars were collected from different districts in the Kurdistan Region – Iraq. These samples were obtained from the Ministry of Agriculture fields in Duhok, Akre, Erbil and Sulaimani cities. The cultivars of Fig selected for this study were [Duhok 1-7] Shingaly, Benatty, Ketek, Hijazi, Ahee Bag, Rebwary Rash, Rebwary Zar. [Akre 8-14] Rash Khal, Hejeer Ban, Soor Khal, Ahee Bag payazi, Tafseek Sor, Tafseek Zar, Ahee Bag Havenee. [Sulaimani 15-21] Zarda Roon, Shela, Kola, Nejefee, Gala Zard, Henjeer Rash, Henjeer Boondoar. [Erbil 22-28] Hejeer Rash, Rash Khomali, Tafseek, Rehan Zard, Rehan Rash, Sumaq Kholy Zard, Hejeer zard.

2.2 DNA Extraction

Genomic DNA was derived from healthy, fresh tissue according to (Weigand *et al.,* 1993), in which 3 g tissues were ground to fine powder with liquid nitrogen 40 ml for each fig genotype. The fine powder has been dissolved in a preheated environment (60 C^{o}) 2x CTAB extraction buffer (2gm CTAB (cetyl trimethyl ammonium bromide), 28 ml of 5 M NaCl, 10ml of 1M Tris-HCl, 4 ml of 0.5 M EDTA, the volume was adjust to 100 ml by distilled water), and incubated at 60°C in a water bath with shaking for 30 min. Extracted the mixture with an equal amount of choloroform / isoamyl alcohol (24:1, v/v) (Maniatis *et al.,* 2001). The mixture was then centrifuged at 4000 rpm for 30 min. The aqueous phase was moved to a fresh tube and precipitated by 8 ml cold isopropanol volume. Precipitated DNA were then dissolved in 500µl Tris EDTA TE-buffer (1 ml of 1M tris-HCl (PH8.0) 0.2µl of 0.5M EDTA.

2.3 PCR Amplification of SSR- primers

Overall 15 SSR primers previously produced by Zavodna *et al.,* (2005) and Vignes *et al.,* (2006) were used for PCR amplifications. Master reactions were performed by mixing 12.5µl of master mix, 1 µl from each forward and reverse primer (6 pmol/µl) and 2µl of (25-50ng) genomic DNA. Deionized distilled water made up the volume up to 25µl. Finally, the PCR reactions were placed in to a thermo cycler for amplification (Applied Biosystems-2720). The PCR cycle parameters were as follows; initial denaturation at 94°C/45s for 1 cycle, denaturation at 94°C/45s, annealing 50°C - 56°C/45s, extension at 72°C/2-3min for 30 cycles and final extension at 72°C /10 min for 1 cycle. Electrophoresis on agarose gel 2 % verified the PCR products; 100bp ladder was used to check sample size, stained with ethidium bromide, and UV trans illuminator was used to visualize fragment bands.

2.4 Data scorning and analysis

On the basis of the gel electrophoresis results, DNA fragments were scored in binary data as present (1) or absent (0). The fragments were arranged based on their allele sizes and the genetic diversity was analyzed on the basis of these scores. To check the ability of the markers chosen to differentiate between the germplasm accessions examined and to assess genetic diversity, various parameters were calculated. The software POPGENE 4.2 (Rousset, 2008), was used to calculate the observed heterozygosity (Ho) and expected heterozygosity (He). Polymorphic information content (PIC), Fixation index genetic distances and phylogenetic tree.

3. RESULTS AND DISCUSSION

A total of 15 loci (primers) provided reproducible results from repeated preliminary experiments used for genetic diversity detection between 28 fig cultivars in Kurdistan Reign-Iraq including four populations (Duhok, Akre, Sulaimani and Erbil). The findings are listed in (Table 1). Data total of 73 alleles were produced across all studied genotypes using all the SSR primers. Number of alleles varied between (1-9) with an average of (4.886) allele's per locus. The data also showed that all tested primers produced polymorphic banding patterns, whereas only one locus (MFC2) showed monomorphic banding patterns. The highest number of alleles was 9 detected at FinsI12FAM-L, while in FinsN1HEX-L the numbers of alleles were 8, whereas in (FinsK9HEX-L, FinsQ5FAM-L and MFC3) the numbers of bands were 6. In (FinsM5HEX-L, FinsJ10NED-L, FinsA1NED-L, MFC5 and MFC7) the numbers of bands were 5, but in (FinsQ6HEX-l, FinsP8NED-L, FinsH5HEX-L and MFC4) the numbers of bands were 3. While the lowest number of alleles was 1, which was found with primer (MFC2). The number of alleles got in this study was less than that pointed out by Achtak *et al.,* (2009) that used SSR as reliable way for Fig cultivar identification.

Table 1. Average statistical outcome for all primers used in this study according to POPGENE and Cerves software for data analysis.

Primers	**Sequence(5' – 3')**	**No of alleles**	**Ho**	**He**	**PIC**	**PID**	**Size of alleles bp**	**F(Null)**
FinsK9HEX-L	F ACGCACTTAACCCTTTCAG R TTCGAGTCAACGAAACAAA	6	0.000	0.705	0.657	0.102	135-175	+1.000
FinsQ5FAM-L	F CATGTCAGGAGGTGTCTAGG R CTCCAAATGGGTATGTCAAG	6	0.000	0.730	0.685	0.112	150-185	+1.000
FinsQ6HEX-l	F TTCTCCAATTAAACCTCCAA R CATGAAATCACCTTACTCAT	3	0.000	0.662	0.577	0.196	110-115	+1.000
FinsI12FAM-L	F AGGTGGAATGAGGAGAGAGT R AAACATCCTTTCTGGACTTG	9	0.000	0.865	0.832	0.041	150-190	+1.000
FinsM5HEX-L	F ATGAATGGTGAAATCCTGAA R CATGGCCTCAACTTAGAAAC	5	0.000	0.652	0.596	0.174	180-205	+1.000
FinsP8NED-L	F TGAAGAAAACGGAGCTTG R CTAAATCTGACGGTTCAAAA	3	0.000	0.584	0.491	0.264	160-170	+0.999
FinsJ10NED-L	F GAACCTTCAACCTCAATCAA R CTCCCCTTTCCTAGTCCTTA	5	0.000	0.756	0.699	0.110	150-175	+1.000
FinsH5HEX-L	F GACCGTATAGATGATTTGGG R CATCCTGTGAACGACACTT	3	0.000	0.569	0.481	0.272	260-280	+0.998
FinsA1NED-L	F AATCCCCGTACTTCACTTG R AGAACTTATTGCACGGACAG	5	0.000	0.808	0.760	0.076	280-300	+1.000
FinsN1HEX-L	F AGGGCTGAGATAGGTTGATT R TAAGTTGGTGTGTGGCATC	8	0.000	0.875	0.843	0.036	165-200	+1.000
MFC2	F GCTTCCGATGCTGCTCTTA R TCGGAGACTTTTGTTCAAT	1	0.000	0.000	0.000	1.000	190	NS
MFC3	F GATATTTTCATGTTTAGTTTG R GAGGATAGACCAACAACAAC	6	0.000	0.818	0.775	0.067	140-170	+1.000
MFC4	F CCAAACTTTTAGATACAACTT R TTTCTCAACATATTAACAGG	3	0.000	0.522	0.450	0.300	240-255	+0.996
MFC5	F ACCAATCCAAATAATAATCC R ACACGCTTACTAGAATTACC	5	0.000	0.792	0.742	0.085	130-150	+1.000
MFC7	F CACAATCAAAATAGTTACCG R AGCGAAGACAGTTACAAAGC	5	0.000	0.751	0.693	0.114	180-200	+1.000
Average		4.866	0.000	0.672	0.618	0.196		

Whereas it was greater than those obtained by Ikegami *et al.,* (2009) and Chatti *et al.,* (2010). The total number of alleles obtained in this study was partially lower than that mentioned by Perez-JiMénez *et al.,* (2012). The high number of alleles might be due to increasing of heterozygosity levels in modern cultivars during selection program (Khadari *et al.,* 2004), however, type and number of genotypes should be taken into consideration in any comparison. The observed heterozygosity (Ho) was (0.000) detected with all primers. Additionally, the expected heterozygosity (He) ranged from 0.000 (MFC2) to 0.875 (FinsN1HEX-L). Higher values of expected heterozygosity were reported by Ikegami *et al.,* (2009). In contrast, lower values were obtained by Khadari *et al.,* (2004) and Perez-JiMénez *et al.,* (2012). Furthermore, the mean of expected heterozygosity obtained in this study was higher than observed heterozygosity. This might be attributed to the much more diverse genetic background within these genotypes (Liang *et al.,* 2015). Gene diversity was a parameter which assumed as the fundamental genetic variability of a species or a population which act as a tool for stability of natural communities or ecosystem as well as increase productivity and invasion resistance (Urrestarazu *et al.,* 2012; Takahashi *et al.,* 2018). The PIC value was between 0.000 and 0.843, with an average of (0.618).The highest polymorphic information content was 0.843 obtained with FinsN1HEX-L locus while the lowest information content was 0.000 found at MFC2 locus. The highest PIC was lower than PIC obtained by Baraket *et al.,* (2011) and Saddoud *et al.,* (2011). Additionally, 14 SSR primers had PIC values greater than 0.5. PIC value depicts the richness of the SSR markers and their capability in detection of variability among genotypes depending on their genetic relationships (Kumari *et al.,* 2018). The PIC values in the current study might indicate that these loci have a high polymorphism and could be exploited in genetic diversity analysis. Botstein *et al* (1980) described any locus that has a PIC ≥ 0.5 as highly polymorphic. In this study only one primer (MFC2) was not met with this criterion. Contrastingly, PIC values less than 0.5 indicate low polymorphism of the locus (Botstein *et al.,* 1980), because for previous primer (MFC2) with all samples product the same sized allele 190pb, product (monomorphic allele). That means there is no polymorphisms appear between genotypes by using this primer.

Fixation index values obtained in this study ranged between +0.999 (FinsK9HEX-L, FinsP8NED-L, FinsH5HEX-L and MFC4) and +1.000 (FinsH5HEX-L, FinsQ6HEX-l, FinsI12FAM-L, FinsM5HEX-L, FinsJ10NED-L, FinsA1NED-L, FinsN1HEX-L, MFC3, MFC5 and MFC7). While F(Mull) for locus MFC2 ND. The positive fixation index present with 14 SSR markers, the positive F value indicated an excess of observed homozygotes while the negative F value depicted an excess of observed heterozygotes (Ganopoulos *et al.,* 2015). Differences between studies might be differences in the type of genotypes, number of SSR loci used in each research as well as the differences in genetic diversity present within genotypes (Kumari *et al.,* 2018).

The SSR profiles produced were further used for the evaluation of similarities (genetic distance) between the cultivars studied. The genetic distance calculation was performed using computer software (NTSYS-PC., version 1.8). The results were showed in Table 2; genetic distances ranged 0.1029-0.9485. The lowest genetic distance was (0.1029) found between Hejeer Ban and Gala Zard cultivars, this was indicated their close relatedness, they were genetically similar, have similar alleles and share the same common ancestor (Esselman *et al.,* 2000). Thus, these genotypes might have some common morphological features like leaf shape, fruit shape and fruit color. The highest genetic distance was (0.9485) registered between Shingaly and Ahee Bag Havenee, Ahee Bag and Tafseek Sor, Rebwary Rash and Tafseek Sor, Rash Khal and Tafseek Zar, Tafseek Zar and Shela, and Ahee Bag Havenee with Zarda Roon, this was indicated, they were less similarity and have different alleles. Genetic distance information was useful for evaluation of the diversity at genetic level among genotypes which could aid and simplify the selection process in breeding program, preservation and introducing of new accessions before elimination of the redundant genotypes (Govindaraij *et al.,* 2015).

The data obtained in this study were further analyzed to determine the genetic relationship among fig cultivars for the resultant dendrogram supported these genetic distances shown in Figure 1. This dendrogram may be split into two main groups each one split further into sub groups. The classification of genotypes in different clusters typically relies on their geographical distribution and their evolutionary paths. In addition, such classification and phylogeny, which rely entirely on the genetic history of the genotypes via stable genetic markers, are crucial for the elimination of blind selection for the purpose of breeding program and/or type preservation (Gregory, 2008). The first main group divided into two sub-groups, and each sub-group divide into several one. The first sub group included C1 Shingaly and C2 Benatty, whereas C17 Kola lined up alone. Then C26 Rehan Rash also lined up alone with the sub-group C27 Sumaq Kholy Zard C28 Hejeer zard. The other sub-group contains C12 Tafseek Sor which also lined up alone with the sub-group C13 Tafseek Zar and C14 Ahee Bag Havenee; the last sub-group includes C15 Zarda Roon and C16 Shela.

The second main group divided into two sub-groups and further divided into seven sub-groups. Sub-group one includes C3 Ketek & C4 Hijazi. Sub-group two divided into more sub-groups which include C18 Nejefee, C19 Gala Zard and C20 Henjeer Rash in one group, C24 Tafseek & C25 Rehan Zard in one group, then C21 Henjeer Boondoar, C22 Hejeer Rash and C23 Rash Khomali in one line.

The second sub-group also divided into two sub-groups, the first one includes C5 which lined up alone, and then C6 and C7, also C8 lined up alone. C9 & C10 grouped together, finally C11 also lined up alone.

Table 2. Genetic distance value based on SSR data among selected samples for this study.

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14
C1	0.0000													
C2	0.7621	0.0000												
C3	0.1321	0.7621	0.0000											
C4	0.1321	0.7621	0.6899	0.0000										
C5	0.1609	0.9162	0.7621	0.7621	0.0000									
C6	0.1098	0.9162	0.1609	0.1609	0.4054	0.0000								
C7	0.1321	0.1098	0.2014	0.2014	0.6286	0.2231	0.0000							
C8	0.2014	0.1321	0.1609	0.1609	0.1098	0.6286	0.5108	0.0000						
C9	0.1980	0.1064	0.1287	0.1287	0.1064	0.1064	0.7276	0.4763	0.0000					
C10	0.1321	0.1098	0.1321	0.1098	0.9162	0.9162	0.9162	0.9162	0.3709	0.0000				
C11	0.9162	0.9162	0.1098	0.1321	0.1098	0.1321	0.1321	0.1321	0.7276	0.4054	0.0000			
C12	0.1130	0.1130	0.1130	0.1354	0.9485	0.9485	0.1354	0.1130	0.1319	0.1354	0.6608	0.0000		
C13	0.1130	0.1354	0.1641	0.1641	0.1130	0.1130	0.1130	0.9485	0.1096	0.1641	0.1354	0.4700	0.0000	
C14	0.9485	0.1641	0.1354	0.1354	0.1641	0.6410	0.1354	0.1130	0.1319	0.2047	0.1641	0.6931	0.2076	0.0000
C15	0.7621	0.1321	0.1609	0.1609	0.1609	0.1609	0.2014	0.1321	0.1574	0.9162	0.9162	0.6608	0.7944	0.9485
C16	0.9162	0.1609	0.1609	0.1609	0.2014	0.2014	0.2708	0.1321	0.1574	0.1321	0.1321	0.7944	0.9485	0.1130
C17	0.7621	0.1098	0.1098	0.1098	0.1609	0.1321	0.1609	0.2014	0.1287	0.9162	0.9162	0.1641	0.1641	0.1641
C18	0.1321	0.6286	0.9162	0.1098	0.1098	0.1098	0.1321	0.1609	0.8817	0.1098	0.9162	0.1130	0.2047	0.2047
C19	0.1287	0.8817	0.1064	0.8817	0.8817	0.7276	0.8817	0.1287	0.1029	0.1064	0.1574	0.1607	0.2012	0.1607
C20	0.1321	0.1098	0.9162	0.9162	0.6286	0.9162	0.1098	0.1321	0.1287	0.1609	0.1609	0.1641	0.2047	0.1641
C21	0.1609	0.1321	0.9162	0.9162	0.9162	0.1321	0.7621	0.7621	0.7276	0.1098	0.1098	0.1641	0.1354	0.1641
C22	0.1321	0.1098	0.9162	0.9162	0.1098	0.1609	0.9162	0.9162	0.8817	0.1321	0.1321	0.2047	0.1641	0.1641
C23	0.1321	0.1098	0.7621	0.7621	0.9162	0.1321	0.1098	0.1321	0.8817	0.1321	0.1609	0.1641	0.1354	0.1641
C24	0.2014	0.1098	0.7621	0.7621	0.9162	0.1098	0.9162	0.7621	0.1064	0.1609	0.1609	0.1354	0.1354	0.1130
C25	0.1609	0.1098	0.1098	0.9162	0.9162	0.9162	0.7621	0.9162	0.1064	0.1098	0.2014	0.1641	0.1130	0.1130
C26	0.1321	0.1609	0.1321	0.1609	0.1321	0.1609	0.1609	0.1609	0.1287	0.1098	0.1321	0.2047	0.2740	0.2740
C27	0.7621	0.1321	0.1321	0.1321	0.1321	0.2014	0.2014	0.1609	0.1287	0.1321	0.9162	0.1641	0.1641	0.1641
C28	0.7621	0.1098	0.1321	0.1321	0.1321	0.2014	0.2014	0.2014	0.1574	0.1098	0.7621	0.1354	0.1130	0.1354

	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28
C15	0.0000													
C16	0.2231	0.0000												
C17	0.1321	0.1098	0.0000											
C18	0.2014	0.2014	0.7621	0.0000										
C19	0.1980	0.1980	0.1287	0.4763	0.0000									
C20	0.2014	0.2014	0.1609	0.6286	0.1886	0.0000								
C21	0.2708	0.2708	0.1321	0.7621	0.1064	0.7621	0.0000							
C22	0.2708	0.2708	0.1321	0.6286	0.8817	0.6286	0.6899	0.0000						
C23	0.2708	0.2708	0.1321	0.6286	0.8817	0.7621	0.2231	0.1431	0.0000					
C24	0.2014	0.2014	0.1098	0.6286	0.5941	0.6286	0.6286	0.6286	0.6286	0.0000				
C25	0.1609	0.1321	0.7621	0.7621	0.7276	0.1098	0.9162	0.9162	0.9162	0.5108	0.0000			
C26	0.1321	0.9162	0.1098	0.9162	0.1574	0.2014	0.1609	0.1609	0.1609	0.1321	0.7621	0.0000		
C27	0.9162	0.9162	0.1098	0.1321	0.1980	0.2014	0.1609	0.1609	0.1609	0.1609	0.1321	0.4054	0.0000	
C28	0.5108	0.7621	0.1321	0.1609	0.1980	0.2014	0.1609	0.1609	0.1609	0.1609	0.1321	0.6286	0.2231	0.0000

[Duhok 1-7] C1=Shingaly, C2=Benatty, C3=Ketek, C4=Hijazi, C5=Ahee Bag, C6=Rebwary Rash, C7=Rebwary Zar. [Akre 8-14] C8=Rash Khal, C9=Hejeer Ban, C10=Soor Khal, C11=Ahee Bag payazi, C12=Tafseek Sor, C13=Tafseek Zar, C14=Ahee Bag Havenee. [Sulaimani 15-21] C15=Zarda Roon, C16=Shela, C17=Kola, C18=Nejefee, C19=Gala Zard, C20=Henjeer Rash, C21= Henjeer Boondoar. [Erbil 22-28] C22=Hejeer Rash, C23=Rash Khomali, C24=Tafseek, C25=Rehan Zard, C26=Rehan Rash, C27=Sumaq Kholy Zard, C28=Hejeer zard.

These results can benefit the field of improvement of fig genotype (plant breeding) by making cross between fig genotypes that have great genetic distances or they are genetically far from each other in order to increase genetic diversity (Zhang *et al.,* 1995). The results obtained by Teoman *et al.,* (2017) showed that fig genotypes collected from the same area were not grouped into a category that suggested that the fig genotypes did not cluster on the basis of their collection sites. This phenomenon was found also in the present study were some of Kurdistan figs collected from the same location were clustered together in a group, inversely some of Kurdistan figs collected from the same location was not clustered together in a group and there was variation among fig genotypes in this region. The study found that there was a high genetic variance between fig genotypes by SSR markers to differentiate between fig genotypes assessed, also the study demonstrated that SSR markers is one of the suitable for genetic analysis in figs.

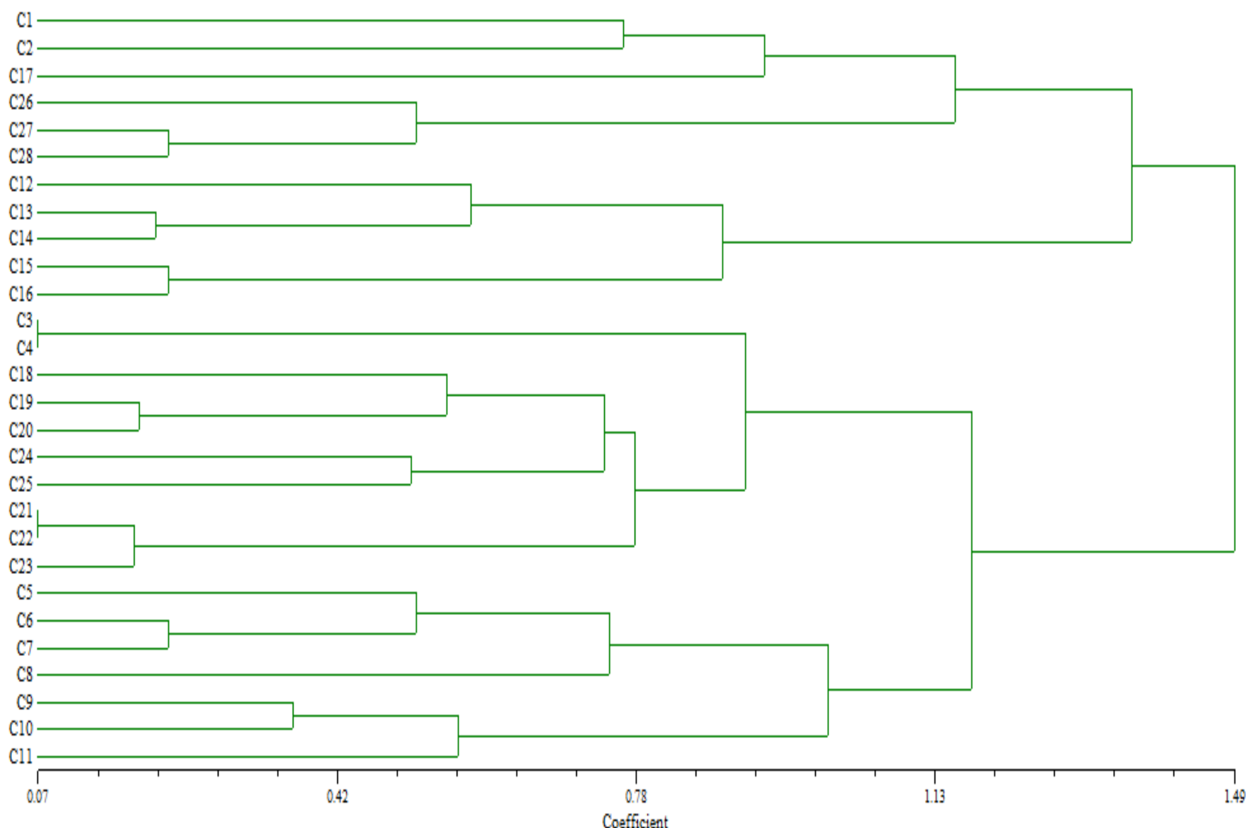

Figure 1. Dendrogram based on the genetic distance study of 28 fig genotypes, resulting from microsatellites. Cluster analysis was performed using the UPGMA algorithm.

[Duhok 1-7] C1=Shingaly, C2=Benatty, C3=Ketek, C4=Hijazi, C5=Ahee Bag, C6=Rebwary Rash, C7=Rebwary Zar. [Akre 8-14] C8=Rash Khal, C9=Hejeer Ban, C10=Soor Khal, C11=Ahee Bag payazi, C12=Tafseek Sor, C13=Tafseek Zar, C14=Ahee Bag Havenee. [Sulaimani 15-21] C15=Zarda Roon, C16=Shela, C17=Kola, C18=Nejefee, C19=Gala Zard, C20=Henjeer Rash, C21= Henjeer Boondoar. [Erbil 22-28] C22=Hejeer Rash, C23=Rash Khomali, C24=Tafseek, C25=Rehan Zard, C26=Rehan Rash, C27=Sumaq Kholy Zard, C28=Hejeer zard.

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