Saudi Journal of Biological Sciences 29 (2022) 3223–3231

Contents lists available at ScienceDirect

Saudi Journal of Biological Sciences

journal homepage: www.sciencedirect.com

Original article

ISSR and SCoT for evaluation of hereditary differences of 29 wild plants in Al Jubail Saudi Arabian

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ARTICLE INFO

Article history:
Received 15 September 2021
Revised 19 January 2022
Accepted 23 January 2022
Available online 29 January 2022

Keywords:
Wild plants
ISSR-PCR
SCoT-PCR
Polymorphism
Clustering
Al Jubail

ABSTRACT

This survey is concerned with the hereditary differences of 29 wild plants collected from fifteen different regions in Al Jubail, Saudi Arabia using two molecular marker systems, viz. inter simple sequence repeat (ISSR) and start codon targeted (SCoT) molecular markers. Ten ISSR and ten SCoT primers amplified a total of 142 and 163 bands with a 87% and 84% polymorphism, respectively. The average number of polymorphic bands for each pair of ISSR and SCoT primers combinations was 12.4 and 13.7, respectively. The highest genetic similarity for ISSR (0.97) and SCoT (0.90) were recognized between *Zygophyllum qatarense*-22 and *Juncus rigidus*-23, and between *Zygophyllum qatarense*-28 and *Zygophyllum qatarense*-29, whereas the lowest was (0.59) differentiated between *Zygophyllum qatarense*-6 and *Salsola imbricate*-18 for ISSR and between *Cyperus conglomeratus*-7 and *Halopeplis perfoliata*-14 for SCoT. This considers confirmed the value of molecular techniques such as ISSR and SCoT to assess the hereditary differences among the selected 29 weeds for hereditary preservation and plant enhancement.

1. Introduction

The hereditary differences among people or populaces can be decided by convening morphological and molecular markers. Phenotypic features have hindrances since they are influenced by natural variables and the formative organization of the plant. On the other hand, molecular markers tell us about differences at the DNA level and are independent of natural conditions. Molecular markers have demonstrated their benefit in areas such as scientific classification, physiology, embryology, hereditary qualities, etc (Domyati et al., 2011).

Molecular markers have been utilized within the development of molecular relation maps, hereditary differences investigations, cultivar identification, and molecular marker-assisted breeding (Kalia et al., 2011). Molecular markers, such as inter simple sequence repeat (ISSR) and start codon targeted (SCoT) have been connected for genetic diversity investigations for a few species of *Zygophyllaceae* (Morsy and El Sherbeny, 2015, Moawed and Ibrahim, 2016, Abd-Elgawad and Alotaibi, 2019). These molecular marker strategies are broadly utilized for hereditary differences examination, as they are basic and can deliver a gigantic number of DNA markers in any test. It is imperative to choose suitable marker strategies agreeing to the plant species, experiment hardware, and investigate financing.

ISSR is the subjective marker that ties a few genomic loci and replicates DNA parts in the introduction between two indistinguishable microsatellite locales (Zietkiewicz et al., 1994). ISSR is exceedingly polymorphic and is imperative in biodiversity, genome mapping, and developmental hereditary studies (Joshi and Dhawan, 2007). This PCR-based approach is utilized in totally different plant types and can resolve certain shortcomings in other marker approaches, such as the high costs of AFLP and the destitute reproducibility of RAPD (Reddy et al., 2002).

SCoT is an unused molecular instrument focusing on plant genes utilizing DNA markers planned based on the brief moderated districts flanking the ATG begin codon (Collard and Mackill, 2009). Since of the minimum recombination grades between its markers and the gene/trait, SCoT is straightforwardly utilized in planning marker-assisted breeding programs than RAPDs, ISSRs, and SSRs (Mulpuri et al., 2013). Other than that, it is basic, low-cost, and profoundly polymorphic that gives broad hereditary data utilizing

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Peer review under responsibility of King Saud University.

Production and hosting by Elsevier

https://doi.org/10.1016/j.sjbs.2022.01.053
1319-562X/

widespread primers in plants. Additionally, it gives reproducible prevailing and single primer amplification responses such as RAPD. These preferences were approved in numerous studies of hereditary differences in mango (Luo et al., 2010) and date palm (Adawy et al., 2014). SCoT have been proficiently utilized for DNA fingerprinting of *Tritordeum bergrothii* L. - *Poaceae* (Cabo et al., 2014). Additionally, the viability of exceedingly reproducible SCoT markers in getting the hereditary differences and relations were tested between Chinese *Elymus sibricus* L. - *Poaceae* accessions (Zhang et al., 2015). SCot markers were utilized to genetically characterize 14 cultivars of *T. aestivum* L. related to different Northern African countries (Mohamed et al., 2017). In any case, information on the hereditary differences and relation between *T. aestivum* L. cultivars localized in Asian nations is so limited but principal for upkeep and breeding programs that center on harboring of high quality and efficiency.

Madinat A1-Jubail Alsinaiya (MJS) is located in the eastern part of Saudi Arabia (Abdulrazzak and Khan, 1990; Al-A'ama and Nakhla, 1995). The components of the flora of Saudi Arabia are imperative for different biological systems and play a key part in keeping up the region's natural adjust and solidness. Vegetation of the Central and Eastern locales is by and large meager. Annual and perennial species constitute the vegetation cover ("Vegetation Saudi Arabia," n.d.).

The target of the current study is to display the genetic relationships between twenty-nine wild plants from different regions in Al Jubail, Saudi Arabia at the molecular scale using ISSR and the SCoT markers to evaluate the hereditary differences of the species.

2. Material and methods

Twenty-nine plants were grown in fifteen known natural habitats in Al Jubail, Saudi Arabia was collected during February 2019. The geographical dispersion of collected accessions and their points of interest are accessible in (Table 1, Fig. 1) ("Google Maps," n.d.). The plant leaves were utilized as the source for DNA production.

Table 1
List of collection species grown in the studied area in Al Jubail Saudi Arabian and their position.

Site No.	Sample No.	Species	Family
1	1	*Zygophyllum qatarense*-1	*Zygophyllaceae*
	2	*Zygophyllum qatarense*-2	
2	3	*Cyperus conglomeratus*-3	*Cyperaceae*
	4	*Zygophyllum qatarense*-4	*Zygophyllaceae*
3	5	*Zygophyllum qatarense*-5	*Zygophyllaceae*
	6	*Zygophyllum qatarense*-6	
4	7	*Cyperus conglomeratus*-7	*Cyperaceae*
	8	*Zygophyllum qatarense*-8	*Zygophyllaceae*
5	9	*Zygophyllum qatarense*-9	*Zygophyllaceae*
	10	*Salsola imbricate*-10	*Amaranthaceae*
6	11	*Fagonia bruguieri*-11	*Zygophyllaceae*
	12	*Salsola imbricate*-12	*Amaranthaceae*
7	13	*Salsola imbricate*-13	*Amaranthaceae*
	14	*Halopeplis perfoliata*-14	
8	15	*Seidlitzia rosmarinus*-15	*Amaranthaceae*
	16	*Anabasis setifera*-16	
9	17	*Salsola imbricate*-17	*Amaranthaceae,*
	18	*Salsola imbricate*-18	
10	19	*Zygophyllum qatarense*-19	*Zygophyllaceae*
11	20	*Heliotropium bacciferum*-20	*Boraginaceae*
	21	*Zygophyllum qatarense*-21	*Zygophyllaceae*
12	22	*Zygophyllum qatarense*-22	*Zygophyllaceae*
	23	*Juncus rigidus*-23	*Juncaceae*
13	24	*Haloxylon salicornicum*-24	*Amaranthaceae*
	25	*Zygophyllum qatarense*-25	*Zygophyllaceae*
14	26	*Cyperus conglomeratus*-26	*Cyperaceae*
	27	*Calotropus procera*-27	*Asclepiadaceae*
15	28	*Zygophyllum qatarense*-28	*Zygophyllaceae*
	29	*Zygophyllum qatarense*-29	

Fig. 1. A map of the collection location in Al Jubail Saudi Arabian was created by using GPS data.

2.1. DNA Extraction

From each plant, the youthful were utilized for genomic DNA segregation; plant tissues were crushed with liquid nitrogen to a fine powder employing a mortar and pestle. Transfer the powder and liquid nitrogen to an appropriately sized tube and permit the liquid nitrogen to steam. Don't permit the test to defrost. The gotten homogenized powder of plant tissues was used for DNA production and purification using DNeasy 96 Plant Mini Kit (QIAGEN, Germany) according to the instructions of the manufacturer. Run 2 μl of the guardians DNA tests on 1% agarose gel in comparison to 10 μl of a DNA size marker (lambda DNA Hind III digest Phi X 174/HaeIII digest). To assess DNA concentration, contrast the level of fluorescence of the DNA test with the distinctive groups in the DNA size marker. The whole genomic DNA stock was put away at − 20 °C.

2.2. ISSR and SCoT-PCR enhancement

A set of ten ISSR and SCoT primers was utilized within the discovery of polymorphism Table 2, 3. The enhancement response was done in 25 μl response volume containing 12.5 μl Master Mix (Sigma), 2.5 μl primer (10pcmol), 3 μl template DNA (10 ng) and 7 μl dH_2O. PCR enhancement was prepared in a Perkin-Elmer/GeneAmp® PCR System 9700 (PE Applied Biosystems) modified to fulfill 40 cycles after an introductory denaturation cycle for 5 min at 94 °C. Each cycle is comprised of a denaturation stage at 94 °C for 1 min ISSR and 40 sec. SCoT-PCR, an annealing stage at 45 °C for 1 min ISSR and 50 °C for 50 sec. SCoT-PCR and a prolongation stage at 72 °C for 1.5 min ISSR-PCR and 60sec SCoT-PCR, respectively. The preliminary expansion section was expanded to 7 min at 72 °C within the last cycle. The enhancement items were settled by electrophoresis in a 1.5% agarose gel containing ethidium bromide (0.5ug/ml) in a 1X TBE buffer at 95 V. Thermo Scientific ™ ' Gene Ruler 1 kb DNA ladder was utilized as a molecular size level and the marker range was (250–10,000 bp). PCR items were seen on UV light and shot employing a Gel Documentation Framework (BIO-RAD 2000).

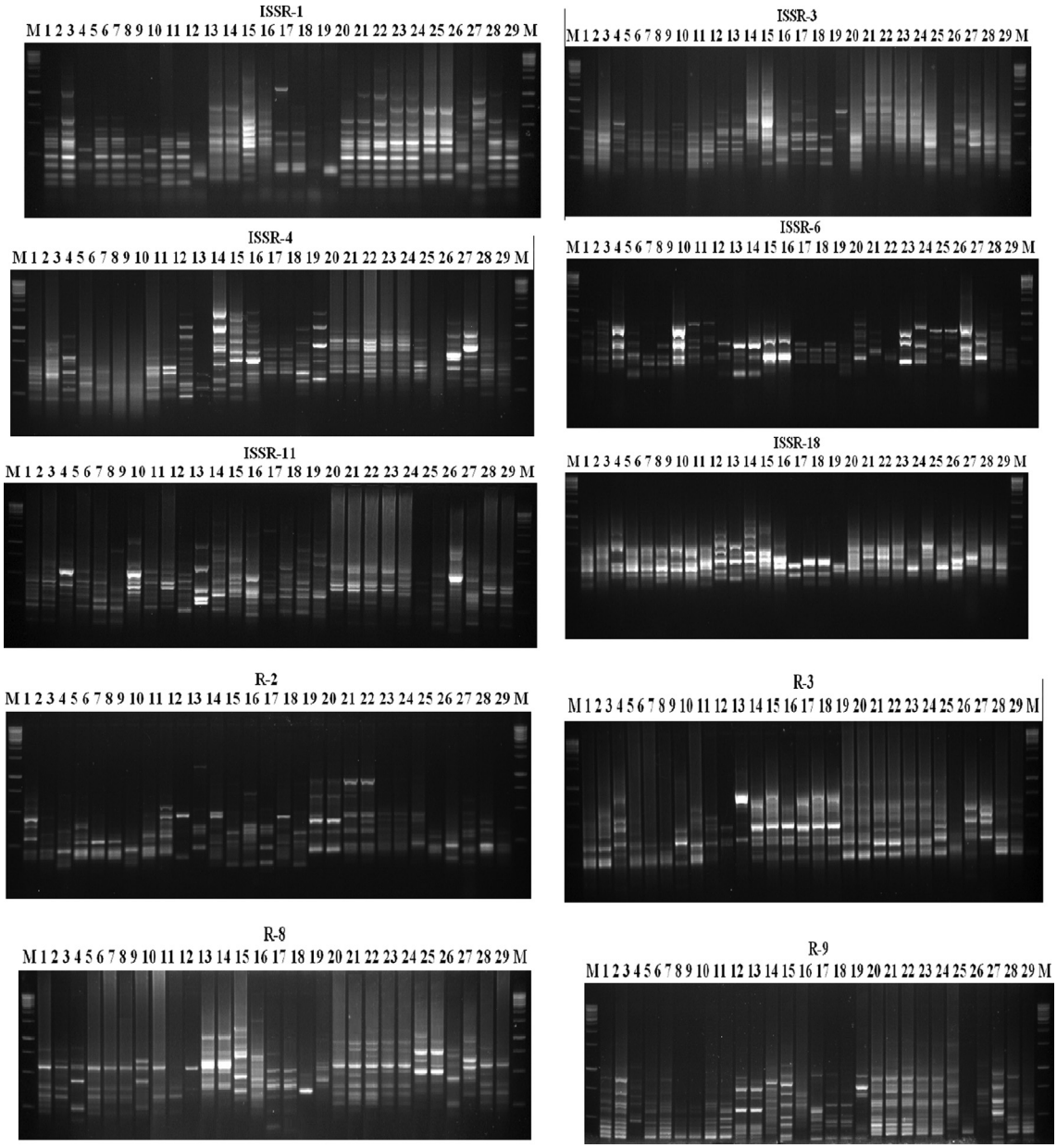

Fig. 2. ISSR profiles of 29 genotypes were by using ten primers. M: 1 kb DNA marker. Numbers refer to species codes (see Table 1).

2.3. Data investigation

The banding designs produced by ISSR and SCoT markers examinations were contrasted to decide the hereditary relation of the samples under study. Clear and particular enhancement items were scored as '1′ for nearness and '0′ for the nonattendance of groups. Groups of the same compactness were scored as indistinguishable. The genetic similarity coefficient (GS) between two genotypes was assessed agreeing to the Dice coefficient Sneath and Sokal (1973).

Dice equation: GSij = 2a/(2a + b + c)

Where GSij is the degree of hereditary closeness between individuals i and j, a is the number of groups shared by i and j, b is the number of groups present in i and truant in j, and c is the number of groups show in j and lost in i.

The framework of similarity was gotten by clustering agreeing to the Unweighted Pair-Group Strategy utilizing Arithmetic Average (UPGMA) Sneath and Sokal (1973). The polymorphism rate was assessed by dividing the number of polymorphic groups by the whole number of groups. An examination of the molecular variance was performed utilizing PAST, ver. 3.22 software (Hammer et al., 2001) to compare genetic and geographic separations. To demonstrate hereditary connections between all tests, the hereditary separate framework was submitted to cluster examination investigation was done (Havill et al., 2007; Muthusamy et al., 2008). The PCA is connected to relegate the variables to genes based on their genetic relationships between all tests. The multivariate investigation was done by building a Heatmap network utilizing the program (Metsalu and Vilo, 2015).

3. Results

3.1. Polymorphism examination recognized by ISSR markers

To explore the similarity and relationship among the twenty-nine genotypes, 10 ISSR primers were used (Fig. 2). A total of 142

Table 2
Ten ISSR (a) and ten SCoT (b) primer sequences used in this study, the total (T), monomorphic (M), polymorphic (P), percentage of polymorphic (%P), mean of band frequency (F), and unique bands (U).

No.	Primer code	Primer nucleotide sequence (5′→3′)	T	M	P	%P	U	F
a) ISSR primers								
1	ISSR-1	AGAGAGAGAGAGAGAGYC	18	1	17	94	2	0.48
2	ISSR- 3	ACACACACACACACACYT	14	2	12	86	0	0.57
3	ISSR −4	ACACACACACACACACYG	16	2	14	88	0	0.48
4	ISSR- 6	CGCGATAGATAGATAGATA	9	2	7	78	0	0.56
5	ISSR- 11	ACACACACACACACACYA	16	2	14	88	1	0.48
6	ISSR- 18	ATACACACACACACACAT	12	2	10	83	1	0.50
7	R-2	CACACACACACACACARG	13	2	11	85	1	0.43
8	R-3	AGAGAGAGAGAGYC	11	2	9	82	0	0.59
9	R-8	CTCTCTCTCTCTCTCTT	16	2	14	88	2	0.48
10	R-9	ACACACACACACACACG	17	1	16	94	1	0.46
		Total	142	18	124		8	5
		Average	14.2	1.8	12.4	87	0.8	0.5
b) SCoT primers								
1	SCoT-1	ACGACATGGCGACCACGC	17	2	15	88	1	0.51
2	SCoT-2	ACCATGGCTACCACCGGC	16	2	14	88	2	0.51
3	SCoT-4	ACCATGGCTACCACCGCA	13	1	12	92	0	0.52
4	SCoT-5	CAATGGCTACCACTAGCG	20	3	17	85	1	0.50
5	SCoT-6	CAATGGCTACCACTACAG	19	2	17	90	0	0.40
6	SCoT-7	ACAATGGCTACCACTGAC	15	2	13	87	0	0.46
7	SCoT-9	ACAATGGCTACCACTGCC	16	4	12	75	0	0.59
8	SCoT-11	ACAATGGCTACCACTACC	15	3	12	80	1	0.54
9	SCoT-12	CAACAATGGCTACCACCG	17	4	13	77	0	0.51
10	SCoT-16	CCATGGCTACCACCGGCA	15	3	12	80	0	0.51
		Total	163	26	137		5	5
		Average	16.3	2.6	13.7	84	0.5	0.5

A: Adenine, T: Thymine, G: Guanine, C: Cytosine, Y: (C or T).

bands were amplified, with an average of 14.2 bands/ primer (Table 2; a). The lowest number of bands (9) was created by the ISSR-6, whereas the highest number of bands (18) was uncovered by the ISSR-1. There are a total of 18 monomorphic bands, with an average of 1.8 bands/ primer. The average of the total number of polymorphic bands (124) was 12.4 bands/ primer. The lowest number of polymorphic bands (7) was created by the ISSR-6, while the highest number of polymorphic bands (15) was revealed by the ISSR-1 and R-9. The percentage of polymorphism was extended from 78% (ISSR-6) to 94% (ISSR-1 and R-9). The average level of polymorphism was assessed as 87%. The frequency extended from 0.43 to 0.59 for the R-2 and R-3; respectively.

3.1.1. Genetic similarity and cluster analysis based on ISSR marker

To show the hereditary likeness and clustering structure among the twenty-nine genotypes of ISSR markers depended on the UPGMA and Dice coefficient were used (Fig. 3; a). The hereditary likeness was assessed between 0.97 and 0.59, revealing a high level of closeness. The primary high genetic similarity (0.97) was recognized between *Z. qatarense*-22 and *J.* rigidus-23, whereas the lowest was (0.59) differentiated between *Z. qatarense*-6 and *S. imbricate*-18. The dendrogram appeared in two main clusters; *C. conglomeratus*-3 and *C. conglomeratus*-7 was isolated from the other species as the primary main cluster. While the second main cluster was recognized as two sub-clusters, the primary sub-cluster was separated into one cluster of *S. rosmarinus*-15 and *A. setifera*-16, and three isolated branches of *S. imbricate*-17, *S. imbricate*-18, and *H.* perfoliata-14. The second sub-cluster was differentiated into 7 clusters of *S. imbricate*-10 and *F. bruguieri*-11, *Z. qatarense*-28 and *Z. qatarense*-29, *Z. qatarense*-22 and *J. rigidus*-23, *H. bacciferum*-20 and *Z. qatarense*-21, *S. imbricate*-12 and *S. imbricate*-13, *Z. qatarense*-1 and *Z. qatarense*-9, *Z. qatarense*-4 and *Z. qatarense*-5. While *Z. qatarense*-2, *Z. qatarense*-6, *Z. qatarense*-8, *Z. qatarense*-19, *Z. qatarense*-25, *H. salicornicum*-24, *C. conglomeratus*-26 and *C. procera*-27 were recognized as 8 isolated branches.

To appear the hereditary relationship among the twenty-nine genotypes, the principal coordinate analysis (PCA) and Heat Map (heatmap) were coordinated based on Dice's similarity matrix (Fig. 3; b and c). The multivariate technique was used to bolster the gathering comes since the bunch examination has shown a higher determination for closely related populations. The first PCA has clarified around 14.2% of all-out genotypes, whereas the second PCA settled 11.3% of all-out genotypes. The structure assessed by the PCA was in concurrence with the bunching examination.

3.2. Polymorphism investigation identified by SCoT markers

In this ponder, ten SCoT primers were used for the investigation of 29 genotypes delivered intensification items and all were brought about in polymorphic unique mark designs (Table 2; b). A total of 163 DNA fragments were obtained from ten primers, with an average of 16.3 bands per primer (Fig. 4). Only 137 of the 163 amplified parts were polymorphic, with an average of 13.7 polymorphic bands/ primer. This represented a level of polymorphism of 84% from these ten primers. The number of monomorphic bands reached 26 with an average of 2.6 bands/ primer. Primer SCoT-6 was the foremost polymorphic band, where 17 polymorphic enhancement items were identified. The most reduced number of intensified polymorphic parts (12) was identified by primer SCoT-4, SCoT-9, SCoT-11, and SCoT-16. The polymorphism percentage extended from 75% (SCoT-9) to 92% (SCoT-4). The frequency ranged from 0.40 to 0.59 for the SCoT-6 and SCoT-9; individually.

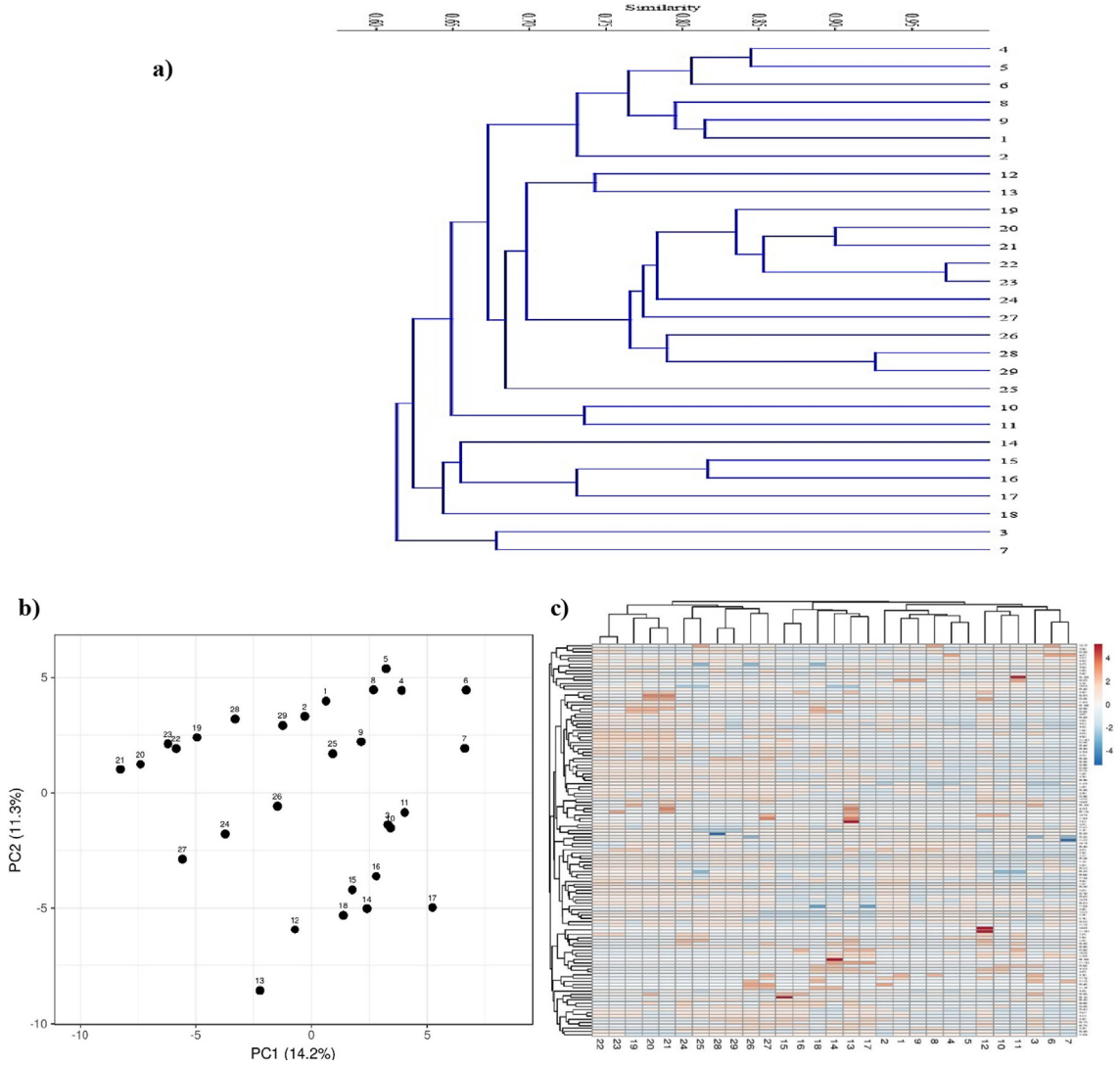

Fig. 3. The hereditary differences of 29 genotypes based on ISSR polymorphism illustrating by a) cluster tree, b) principal component analysis (PCA), and c) multivariate heatmap. Numbers refer to species codes (see Table 1).

3.2.1. Genetic similarity and cluster analysis based on SCoT marker

The hereditary likeness and clustering structure of SCoT markers information were among the twenty-nine genotypes based on the UPGMA and Dice coefficient (Fig. 5; a). The genetic closeness was evaluated between 0.90 and 0.59, revealing a high level of similitude. The most elevated hereditary closeness was (0.90) identified between *Z. qatarense*-28 and *Z. qatarense*-29, whereas the least was (0.59) distinguished between *C. conglomeratus*-7 and *H. perfoliata*-14. The dendrogram appeared two primary clusters; the primary fundamental cluster has partitioned into 7 clusters of *Z. qatarense*-8 and *Z. qatarense*-9, *Z. qatarense*-1 and *Z. qatarense*-6, *Z. qatarense*-4 and *Z. qatarense*-5, *Z. qatarense*-28 and *Z. qatarense*-29, *Z. qatarense*-22 and *J. rigidus*-23, *Z. qatarense*-19 and *H.bacciferum*-20, *F. bruguieri*-11 and *S. imbricate*-12. While *C. conglomeratus*-7, *C. conglomeratus*-26, *H. salicornicum*-24, *C. procera*-27, *Z. qatarense*-2, *Z. qatarense*-21 and *Z. qatarense*-25 were distinct as 7 isolated branches. The moment primary cluster was distinct into 4 separated branches of *H. perfoliata*-14, *S. rosmarinus*-5, *S. imbricate*-10, and *S. imbricate*-18. While *S. imbricate*-17 and *A. setifera*-16, and *C. conglomeratus*-3 and *S. imbricate*-13 were clustered together.

To show the genetic relationship among the twenty-nine genotypes, the principal coordinate analysis (PCA) and Heat Map (heatmap) were directed based on Dice's similarity matrix (Fig. 5; b and c). The multivariate strategy was used to back the grouping results since the bunch investigation has appeared higher resolution for closely related populations. The primary PCA has clarified approximately 13.1% of all-out genotypes, while the moment PCA settled 9.3% of all-out genotypes. The structure assessed by the PCA was in concurrence with the bunching analysis.

4. Discussion

4.1. Hereditary connections as uncovered by ISSR markers

In this consider, hereditary differing qualities have been evaluated utilizing 142 markers produced by 10 ISSR primers; with an average of 87% polymorphism ranges between 78% for ISSR-6 and 94% for two primers (ISSR-1 and R-9). These results agreed with Luo (Luo et al., 2010) reported that the tall rate of polymorphism recognized within the show consider by ISSR markers is

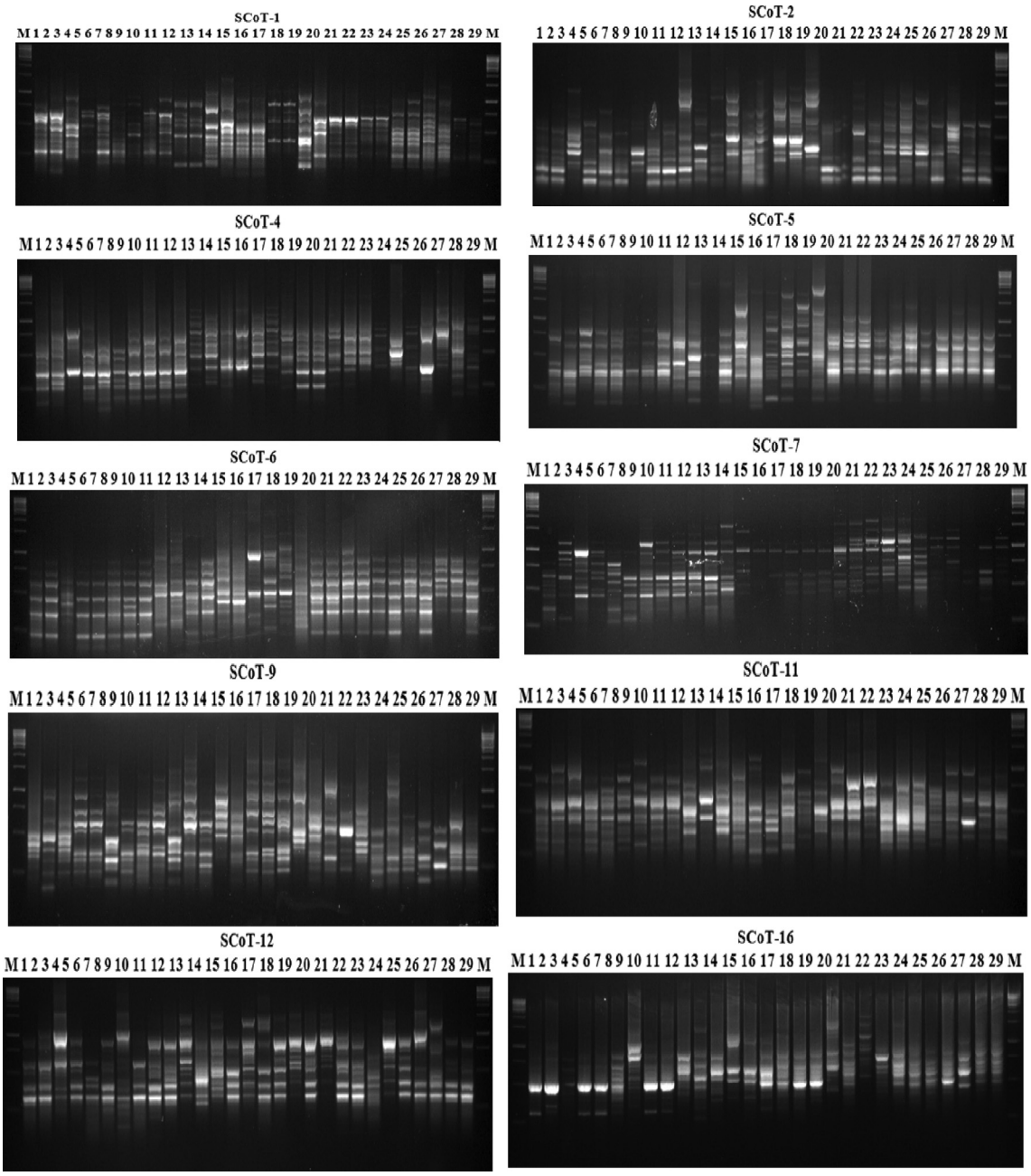

Fig. 4. SCoT profiles of 29 genotypes were by using ten primers. M: 1 kb DNA marker. Numbers refer to species codes (see Table 1).

random markers that tie a few genomic loci and reproduce DNA fragments in introduction between two indistinguishable microsatellite districts. ISSR is profoundly polymorphic and is imperative in biodiversity, genome mapping, and developmental genetics studies (Adawy et al., 2014). The ISSR is anticipated to be connected to utilitarian genes and comparing characteristics (Xiong et al., 2011); other than these markers are multilocus, which are accommodating in getting high hereditary polymorphism. The value of hereditary differences parameters uncovered by ISSR markers were utilized to calculate the hereditary differing qualities of 29 genotypes shown that the two species of *C. conglomeratus*-3 and *C. conglomeratus*-7 are separated from other species.

The closeness is additionally clear between the diverse species of the same accession to each other and the same species of the diverse accessions with a few likenesses between a few species. This closeness was shown specific between *Z. qatarense*-22 and *J. rigidus*-23; *Z. qatarense*-28 and *Z. qatarense*-29; *H. bacciferum*-20 and *Z. qatarense*-21 in cluster analysis, *C. conglomeratus*-3 and *S. imbricate*-10, and between *Z. qatarense*-22 and *J. rigidus*-23, as shown in PCA analysis, and between *Z. qatarense*-22 and *J. rigidus*-23; *H. bacciferum*-20 and *Z. qatarense*-21 in heatmap analysis. The separation of the inspected species of distinctive accessions may be caused by different biological conditions, which might contribute to expanding the hereditary variety between species. These results agreed with several results recorded that, ISSR polymorphism in *C. procera* showed a hereditary variety of 18 individual genotypes gathered from six diverse regions over Egypt (El-Bakry et al., 2014), among tumbleweed (*Salsola*) species (Ayres et al., 2009), and *Salsola* species gathered from 53 destinations in California (Welles and Ellstrand, 2016), ISSR were utilized to assess the hereditary differences among 85 plant tests from 17 populations of *S. rosmarinus* in a few locales of Iran (Sedighi et al., 2021),

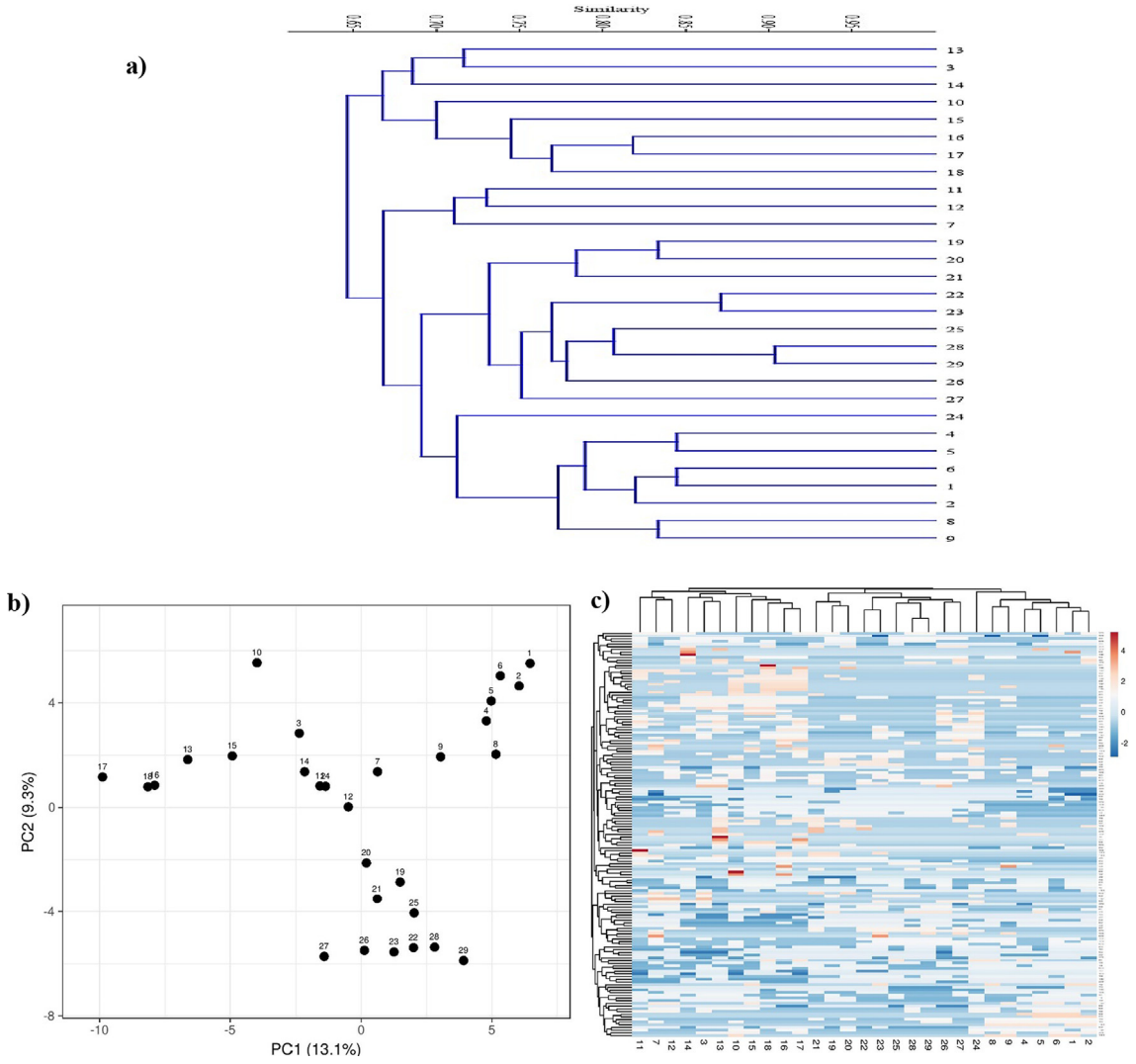

Fig. 5. The hereditary differences of 29 genotypes based on SCoT polymorphism illustrating by a) cluster tree, b) principal component analysis (PCA), and c) multivariate heatmap. Numbers refer to species codes (see Table 1).

H. digynum in several locales of Saudi Arabia (Wahabi and Bukhari, 2014), *C. esculentus* L. in Turfgrass (Li, 2019), *C. procera* from distinctive phytogeographical districts of Egypt (El-Bakry et al., 2014), the chosen medicinal plants such as *Zygophyllum* (Domyati et al., 2011), and hereditary changeability inside and among eight extant populations of *T. mongolica* Maxim. (Ge et al., 2003). The hereditary differing qualities of the four mean taxa of *Brassica* genus were examined by utilizing ISSR (Yaman et al., 2020). The high hereditary differing qualities in *K. galanga* were due to the different natural conditions found in its wide dissemination zone in Indonesia (Subositi et al., 2020). These come about affirmed the significance of ISSR investigation to characterize a few species with the occurrence of particular markers and create enlightening groups that recognized the past taxa.

4.2. Hereditary connections as uncovered by SCoT markers

In the current study, hereditary differences have been surveyed using 163 markers created by 10 SCoT primers; with 84% the mean percentage of polymorphic ranges between 75% for SCoT-9 and 92% for SCoT-4. The high percentage of polymorphism recognized inside the show consider by SCoT may indicate interest with the moderated flanking brief locale of the ATG or begin codon in plant genes (Collard and Mackill, 2009). These findings were agreed with among annual *Cicer* species ranged from 86.6 % to 100 % with an average polymorphism of 97 % using SCoT markers (Amirmoradi et al., 2012).

The esteem of hereditary differing qualities parameters uncovered by SCoT markers was utilized to calculate the genetic varying qualities of 29 genotypes. The convergence was shown between some species as indicated between *Z. qatarense*-28 and *Z. qatarense*-29; *Z. qatarense*-22 and *J. rigidus*-23 in clustering analysis; *F. bruguieri*-11 and *H. salicornicum*-24, and between *A. setifera*-16 and *S. imbricate*-18 in PCA analysis; between *Z. qatarense*-28 and *Z. qatarense*-29, and *Z. qatarense*-25, *Z. qatarense*-22 and *J. rigidus*-23 in heatmap analysis. The separation of the inspected species of unmistakable increases may be caused by diverse biological conditions, which might contribute to expanding the hereditary variety between species, which might contribute to growing the innate assortment between species. These results were agreed with other reports which used SCoT markers in estimating the genetic relationships, as in *Tritordeum bergrothii* L. - *Poaceae* (Cabo et al., 2014), Saudi Arabian date palm cultivars (Al-Qurainy et al., 2015), between Chinese *Elymus sibricus* L. - *Poaceae* accessions (Zhang et al., 2015), between 14 cultivars of *T. aestivum* L. related to different Northern African countries (Mohamed et al., 2017), and among indigenous EPNs belonging to *H. indica* species (Abd El Azim and Khashaba, 2021). Hereditary

characterizations of the halophyte *Suaeda maritima* in Thailand given by SCoT profiles (Rittirongsakul et al., 2020), and cultivar characters based on hereditary solidness with SCoT molecular marker in modern new Polish lines of *Chenopodium quinoa* Willd (Lema-Rumińska et al., 2018). Comparable discoveries were gotten with few molecular examinations of *Zygophyllaceae* (Hammad and Qari, 2010; Moawed and Ibrahim, 2016; Sheahan and Chase, 2000). Comparable come about were gotten in which SCoT primers appeared particular unmistakable bands permitting the separation of appointed summer squash landraces (Xanthopoulou et al., 2015). The hereditary variety in ten individual *M. oleifera* plants was separated from the individual plants of moringa by utilizing ten primers of ISSR and SCoT markers (Hassan et al., 2020). This appeared the proficiency of ISSR and SCoT markers, demonstrating that the exceedingly reproducible ISSR and SCoT markers were proficient in surveying the relations among the examined taxa of family *Zygophyllaceae, Cyperaceae, Amaranthaceae, Boraginaceae, Juncaceae, Asclepiadaceae.*

5. Conclusions

In this consider, the utilize of ten ISSR combined with SCoT markers revealed hereditary contrasts among 29 genotypes grown in 15 accessions of Al Jubail, giving a hypothetical premise for equitably assessing the hereditary differing qualities of diverse species and broadening the hereditary premise of Saudi Arabia. *C. conglomeratus*-3 and *C. conglomeratus*-7 was separated by ISSR from other species, ISSR primers were able to uncover inconstancy between the examined taxa and succeeded to deliver particular markers that made a difference in species recognizable proof. The highest hereditary similarity was identified between *Z. qatarense*-22 and *J. rigidus*-23 for ISSR and between *Z. qatarense*-28 and *Z. qatarense*-29 for SCoT. The closeness is clear between the diverse species of the same accession to each other. The lowest hereditary similarity was identified between *Z. qatarense*-6 and *S. imbricate*-18 for ISSR and between *C. conglomeratus*-7 and *H. perfoliata*-14 for SCoT. The separation of the inspected species of distinctive accessions may be caused by different biological conditions, which might contribute to expanding the hereditary variety between species. The hereditary differing qualities watched shows that there's incredible potential for hereditary enhancement of wild plants for future preservation methodologies and for utilizing this hereditary differing quality in genetic improvement and breeding programs.

Funding

This research project was funded by Deanship of Scientific Research, Princess Nourah bint Abdulrahman University, through the **Program of Research Project Funding After Publication, grant No (41- PRFA-P-28)**.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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