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RESEARCH PAPER

Morphological and molecular diversity of eggplant accessions (*Solanum melongena* L) using simple sequence repeats (SSR) markers

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Abstract

The evaluation of various desirable traits in eggplant genotypes has facilitated the efficient process of selecting and improving them. Morphological parameters have proven to be valuable in assessing the similarities or differences among different accessions, while molecular data have been used to support the conclusions drawn from the morphological analysis. This study was conducted to evaluate the performance of 42 eggplant genotypes collected from Malaysia, China, and Thailand. The characteristics under investigation were shown to be highly significant ($p < 0.01$) by analysis of variance (ANOVA). It was noted that the plants TV17 (5.59 kg) and MV18 (5.97 kg) produced large yields per plant. The SSR markers used exhibited moderate average values for the number of alleles (2.53). The major allele frequency displayed a high average value (0.53) and a moderate average number of effective alleles (2.31). Additionally, the observed Shannon's information index, expected heterozygosity, and PIC were high (0.84, 0.54, and 0.45, respectively). Using the unweighted pair-group approach with arithmetic averages based on similarity matrices (UPGMA) Dendrogram, 42 accessions were sorted into five primary groups based on similarities. The findings of this study indicate that the use of simple sequence repeat (SSR) markers can effectively estimate genetic diversity and analyze phylogenetic relationships. Moreover, these markers can assist eggplant breeders in selecting desirable quantitative traits within their breeding program.

Keywords

Eggplant, phenotyping, genotyping, SSR marker, molecular diversity

Introduction

Eggplant, scientifically known as *Solanum melongena* L., is a significant crop in the Solanaceae family. Commonly referred to as brinjal or aubergine, this vegetable holds significant agricultural importance in subtropical, tropical, and warm temperate regions (Sulaiman et al. 2020; Musa et al. 2021). The crop is considered valuable because of its exceptional antioxidant activity and nutritional content, as noted by Musa et al. (2021). Breeding efforts for this specific vegetable are relatively limited compared to other plants in the Solanaceae family, such as the potato and tomato, despite its economic potential and nutritional importance (Hurtado et al. 2012). The changing climate and rapid growth of the global population present significant challenges for the agricultural sector. Eggplants are cultivated using various methods around the world, leading to a wide range of physical charac-

teristics. This variability provides a valuable reservoir of potentially beneficial traits, allowing plant breeders and farmers to adapt the crop to diverse and evolving conditions. In general, morphological diversity is regarded as the initial stage in investigating genetic variation among cultivars of eggplant (Sulaiman et al. 2020). However, there are certain limitations when using morphological characters to distinguish between homozygous and heterozygous individuals. Furthermore, these individuals are unable to accurately assess the full spectrum of diversity in the germplasm because of the cumulative genetic influence that results in economically valuable characteristics (Jasim Aljumaili et al. 2018). Molecular markers are not influenced by the environment and can reveal genotypic differences at the DNA level. By understanding and assessing the range of genetic variations, breeders can make informed decisions about selecting suitable individuals to serve as parents for the next generation. This marks the initial stage in comprehending the diverse attributes and qualities of various eggplant cultivars. Through the analysis of the morphological characteristics of eggplants, researchers can gain insights into their genetic composition and potential diversities (Musa et al. 2020; Musa et al. 2023). To enhance genetic diversity in breeding programs, the use of DNA marker technology and molecular characterization is highly beneficial for selective breeding from diverse parental sources (Fu et al. 2006). Several molecular studies have indicated that eggplant cultivar groupings are genetically heterogeneous (Frary et al. 2011a; Cericola et al. 2013). SSR markers showed a significant genetic similarity among eggplant species (*Solanum viarum*, *Solanum melongena*, and *Solanum aethiopicum*) and were also found to be valuable for their potential use as markers in studying genetic variation (Adeniji and Aloyce 2012). The collection and genetic analysis of germplasm are essential for obtaining a genotype that can produce higher yields and other desirable traits. In order to meet the needs of a growing population, it is essential to enhance the productivity of eggplant crops. Malaysia is currently cultivating numerous genotypes with diverse traits and wide variability to achieve this goal. Certain potential genotypes have not yet been discovered due to their limited geographical range. A wide variety of morphological diversity and molecular markers have been extensively used in the study of eggplant accessions from various geographical locations. Assessing the diversity within different accessions of eggplant and studying the relationships between cultivated eggplant and their wild counterparts is important (Doyle and Doyle 1987; Prohens et al. 2005; Muñoz-Falcón et al. 2009; Tümbilen et al. 2011; Ge et al. 2013; Davidar et al. 2015; Mutegi et al. 2015). The management of germplasm collections, the preservation of eggplant genetic resources, and the execution of breeding projects have all benefited from the useful information these research have produced. Therefore, it is necessary to collect eggplant germplasm to select varieties that are suitable for the agro-ecological conditions of Malaysia. The present study was therefore conceptualized: (i) to evaluate genetic variation among 42 eggplant genotypes using agro-morphological traits under field conditions and (ii) to evaluate genetic diversity among collected materials using SSR markers as a preliminary step towards its improvement.

Materials and methods

Planting materials and agronomic practices

The 42 eggplant accessions, which form three main populations from Malaysia (19 genotypes), China (6 genotypes), and Thailand (17 genotypes), were used for this study, as presented in Table 1 and Fig. 1. The accessions were assessed in an open field setting at Ladan 15, Universiti Putra Malaysia (UPM), Serdang, Selangor, Malaysia, between September 2018 and January 2019. The accessions were evaluated according to Musa et al. (2021) and plant maintenance including fertilizer application, pest and disease management, weed control were carried out as recommended by the Department of Agriculture, Malaysia (https://jpn.penang.gov.my/index.php/perkhidmatan/teknologi-tanaman/sayur-sayuran/78-terungsp-424).

Figure 1. Some of the eggplant genotypes used in this study.

Data collection

The eleven sets of growth, yield and yielding data were collected and measured under open field cropping conditions. They yield traits include fruit weight (FW), average fruit weight (AFW), fruit length in cm (FL), fruit width in mm (FD), fruit length/width (FL/W), number of fruits per plant (NF/P), and yield per plant (Y/P). While the growth parameters include number of branches per plant (NBPP), plant height (PH), first harvest (PH), and flowering days to 50% (D50%F). All data measurements and observations were conducted on the same day to minimize variations in the developmental stage of plant growth or environmental conditions.

Statistical analysis

Using SAS version 9.4 (SAS Institute Inc., Cary, NC, USA), all growth, yield, and yield-related data were subjected to analysis of variance (ANOVA), and means were separated using the least significant difference (LSD) at a 5% level of significance. For every attribute that was tested, the mean and standard deviation were also noted.

Table 1. Eggplant (Solanum melongena) accessions used in this study.

New codes	Original name	New codes	Original code
MV1	Mini eggplant (214)	CV3	China-3
MV2	Eggplant-Round Purple (311)	CV4	Mukta kashi
MV3	Green world (white eggplant 330)	CV5	Pahuja
MV4	AG seeds (F1 418 purple king)	CV6	Eggplant Bhagan
MV5	AG seeds (F1 428 Nyonya)	TV1	Long eggplant 02645/2551
MV6	Little Nyonya 313 F1 hybrid	TV2	Round eggplant 00558/2551
MV7	Super Naga 312 (F1 Hybrid)	TV3	Round eggplant 01451/2551
MV8	MTe 2 Eggplant (Terung Bulat)	TV4	Eggplant Long 01166/2551
MV9	HV-318 (F-2522)	TV5	Eggplant 1745/2550
MV10	Terong Baling (T E 204)	TV6	Eggplant 1253/2561
MV11	V-230 (Eggplant)	TV7	White east west seed
MV12	K-82 (Terung Mini)	TV8	Eggplant El rye
MV13	Eggplant (Terung Bulat)	TV9	Eggplant 01450/2551
MV14	White Crown	TV10	Metro seed round
MV15	White Princess	TV11	Eggplant parody
MV16	Gwauta	TV12	Eggplant 914/2558
MV17	Purple Dream (302)	TV13	Round Eggplant (Chao paya)
MV18	K-62 (Terung Panjang)	TV14	Round eggplant 01451/2551
MV19	K 94 (Terung Putih)	TV15	Round 01388/2552
CV1	Round eggplant 0138/2552	TV16	Round eggplant Metro seed
CV2	Eggplant Black Beauty	TV17	Eggplant 408/2556

Note: MV, Malaysian variety; CV, Chinese variety; TV, Thai variety.

Genomic DNA extraction and PCR analysis

A modified cetyl trimethylammonium bromide (CTAB) technique was used to extract genomic DNA from early leaves (3 to 4 weeks old) of the 42 genotypes of eggplant (Doyle and Doyle 1987). From the sequence data that was available in the published literature (Khapte et al. 2018; Pandiyarajet al. 2019), exactly 17 SSR markers were chosen. The details of the 17 polymorphic primers and their sequences are presented in Table 2. PCR was performed in a total volume of 16 µL containing 40 ng template DNA, 0.8 µM concentration of each primer (forward and reverse), 8 µL master mix (2×Power Taq PCR MasterMix), 3.2 µL DNA and 3.2 µL nuclease-free water. PCR amplification for background markers was conducted according Khapte et al. (2018) with slight modification.

Molecular data analysis and cluster analysis

The polymorphism information content (PIC) value for each SSR locus was computed using the formula PIC = 1-Σpi^2, where pi is the frequency of the i^{th} allele in the set of 42 eggplant genotypes studied (Weir BS 1990). The POPGENE 1.31 program by Yeh et al. (1999) was used to calculate the observed number of alleles, effective number of alleles (Ne), He, Nei's expected heterozygosity (Nei's), and Shannon's information index (I). In all eggplant genotypes investigated, amplified fragments were evaluated for the presence (1) or lack (0) of the corresponding bands. Based on the binary data, cluster analysis was performed using NTSYS-PC version 2.1 and the unweighted pair group method with arithmetic averages (UPGMA). The results are presented as a dendrogram using the Rohlf (2000) approach.

Results and discussion

Growth and yield characterization

Statistical analysis revealed a highly significant ($p \leq 0.01$) difference for the traits under study (Table 3). The mean performance for the morphological and yielding

Table 2. Primer sequences of seventeen SSR markers.

Primers	Forward sequence	Reverse sequence
emf01K16	ATTTGGACAAGAACAAGGATGGCT	GTTTCACTCACAATTCGAGACACTCGGT
emb01D10	AAGAATCGGTCCTCTTTGCATTGT	TGCTTTTCACCTCTCCGCTATCTC
emh21J12	ACAGAACAATTCACCAGCAGTCAA	GTTTAGGAACAGGGAAAATCGTATCGGT
SSR–46	AATAAAGTTATGCCACAGGGC	CACCCTTCACCACCAACAAT
emh02E08	AGGCGTTCAGCAGAGAAGAAATTA	GTTTGCTTCCTTAAGTGGCATCTGAAA
emh11I06	ATTTCAAACCGTTCCTCTGCTCTT	GTTTGCACAATCATCAAGGCTCCTCTTT
eme05B09	ATGAAAACTCCACTCTACTCTACTCCAC	GTTTGCTAACGTACGCCTCAATTGCTCT
SSR40	TGCAGGTATGTCTCACACCA	TTGCAAGAACACCTCCCTTT
emk04N11	ATCTCCCCCTCAACTTTGAACAAT	GTTTGTGTGATATAGCCCAACAATTCAC
emf01E10	ACATATCCAACTGACCTCGGAAGA	GTTTAACCGCTTTGTCCCCAAATACAG
emf21K08	ATCAATGACACCCAAAACCCATTT	GTTTGAAAACCCAATACAAATCCGA
eme05B10	ATGAAAACTCCACTCTACTCTACTCCAC	GTTTGCTAACGTACGCCTCAATTGCTCT
emk03O04	ATGATTTGGGCAGCCACTTTTGTA	GTTTGGAACCAACTAAACTTAGGGCA
emb01C12	AAAAAGCTCTGCCCAAACAAGC	GACTTTCCTCACTAATTCACAACCA
emh11B18	ATCAAAACCAACCTCCAGTTCTCG	GTTTCAAATCGCAGAGTTCATCCTTCCT
emh11B19	ATCAAAACCAACCTCCAGTTCTCG	GTTTCAAATCGCAGAGTTCATCCTTCCT
SSR125	CCTAAAGAAGATAGGAAGAAATGCC	TCTCTCCTACTGAAACAACCAA

Table 3. Analysis of variance for growth and yielding traits of 42 eggplant genotypes.

SOV	df	D50%F	FH	NB	PH	FL	FD
Rep	2	0.929ns	7.452*	2.560*	67.980*	1.664ns	2.450*
Genotypes	41	65.531**	67.094**	11.432**	178.612**	99.685**	120.854**
Error	82	0.790	1.160	0.334	18.938	1.165	0.692
SOV	df	FL/D	AFW	FW	NF	Y/p	
Rep	2	0.005ns	1356.716ns	0.257ns	0.568ns	0.014ns	
Genotypes	41	0.435**	9773.90**	41523.90**	96.251**	4.148**	
Error	82	0.006	0.459	0.516	0.400	0.010	

Note: * Significant at 5%, ** highly significant at 1%, ns = not significant at p > 5%, SOV, source of variation; df, degree of freedom; D50F, days to 50% flowering; FH, first harvest; NB, number of branches; PH, plant height; FL, fruit length; FD, fruit width; FL/D, fruit length/width ratio, AFW, average fruit weight, FW, fruit weight; NF, number of fruits; Y/p, yield per plant.

traits are presented in Tables 4, 5. The number of days to attain 50% flowering ranged from 57.33 to 77.67 days, as MV12 and MV19 (57.33 days) had the shortest days to attain 50% flowering, whereas the longest days to 50% flowering (77.67 days) were recorded in MV11, which were not statistically different from MV8 and MV11 (77.33 days). In terms of first harvest, the highest number of days (90 days) was recorded in MV11, whereas MV13 and MV19 produce fruits earlier at 69.67 days. In this study, the number of branches was observed among the varieties in which TV13 recorded the highest (10.22), whereas TV2 and TV3 had the lowest (2.67 and 2.55 respectively). The tallest plant in this trial was observed in TV15 (99.55 cm), whereas the shortest plant was observed in TV17 (59.33 cm). The significant variation in vegetative growth among different types of eggplant showed that there is potential for improving these types in terms of all the characteristics that contribute to the reproductive phase of the plant. The wide range of vegetative growth among the different types of eggplant indicates that there is a promising opportunity to enhance the studied types in all aspects that ultimately support and prepare the plant for reproduction. The presence of a genetic composition combined with the influence of the environment was observed as a possible explanation for this(Sulaiman et al. 2020; Chukwu et al. 2022). The values for fruit diameter ranged from 36.57 cm to 10.00 cm. The TV17 genotype had the highest value, whereas MV9 had the lowest value. In the case of fruit length, the values were between 31.50 and 10.70. The longest fruit (31.50 cm) was from TV2 which is not statistically different from TV12 (30.63 cm), whereas the shorted fruit (10.70) was from MV9 which is not statistically different from TV14 (10.53 cm). The fruit length/diameter ratio ranged from 2.29 to 0.48 cm, and the highest (2.29 cm) was observed in MCV11 followed by TV12 (1.82 cm), whereas the lowest fruit length/diameter (0.48 cm) was recorded in TV17, which was statistically similar to TCV16 (0.50 cm). In terms of fruit weight, the weightiest fruit (303.83 g) was recorded in TV17, whereas TV8 produced fruits with the lowest weight (17.23 g). Significant differences were recorded for average fruit weight. MV18 (269.38 g) produced the weightiest fruits, followed by TV17 (249.00 g), whereas TV8 produced lighter fruits (86.03 g). Significant differences were observed among the varieties in terms of the number of fruits per plant, with values ranging from 41.83 to 20.53 fruits. The highest number of fruits in the individual plant was recorded in TV2 (41.83), which was statistically similar to TV12 (40.63 cm), while the lowest value for this trait was recorded in MV9 (20.37), which was statistically similar to TV14 (20.53 cm). Highly significant yield plant was recorded in MV18 (5.97 kg), followed by TV17 (5.49 kg), whereas TV8 recorded the lowest yield (0.98 kg). Overall, there was a notable variation in yield characteristics among all genotypes, indicating their strong diversity. This discrepancy can be attributed to the distinct origins of each genotype, leading to variation within the population (Musa et al. 2020). Several studies have also been conducted on the variation in characteristics among different types of eggplant. The results of these studies align with the findings of Caguiat and Hautea (2014), which further support the claim made by Naujeer (2009) that increasing yield and improving fruit quality are the primary goals of eggplant breeding programs.

Co-dominant gene characterization

The seventeen SSR markers used demonstrated successful amplification (Table 6). However, all primers were polymorphic and amplified between two and four alleles, resulting in a total of 43 alleles across all markers. This equated to an average of 2.53 alleles per SSR marker. The most common allele had an average frequency of 0.53, ranging from 0.33 to 0.83. The average number of effective alleles (Ne) was 2.31, which was slightly lower than the total number of alleles (Na) at 2.53. The range for Ne was 1.36 to 3.79. The SSR marker is valuable for assessing genetic variation in eggplant. In this study, the average PIC value was 0.45, ranging from 0.29 to 0.68. This value was higher than the average PIC value of 0.401 reported by Vilanova et al. (2012), but lower than the value of 0.83 reported by Datta et al. (2021). A PIC value above 0.5 suggest locus with high levels of polymorphism. The classification of a PIC value into low polymorphic, moderate polymorphic, and high polymorphic loci has been established by several studies (Nunome et al. 2009; Kalia et al. 2011; Ge et al. 2013; Gramazio et al. 2019).

Table 4. Mean performance of growth and yielding traits of 42 eggplant genotypes.

Genotypes	D50%F	FH	NB	PH	FD	FL
MCV1	67.33fghi	79.33ghij	8.57defg	69.48l-p	15.98opq	19.50kl
MCV2	64.00 lm	76.33lm	7.55hijk	77.947d-j	16.17nop	15.10qr
MCV3	69.33d	81.67e	6.78kl	75.89e-m	29.91cd	19.53kl
MCV4	73.67bc	85.67d	5.67 m	75.00e-n	14.73q	13.60rs
MCV5	74.00b	86.67 cd	7.56hijk	86.66b	17.83jkm	21.03k
MCV6	64.00lm	76.33 lm	7.64ghijk	73.72f-n	15.17pq	17.30nop
MCV7	67.33fghi	79.67fghij	7.67ghijk	84.33bcd	19.30hij	28.20cde
MCV8	77.33a	89.33ab3	6.33ml	71.78i-o	28.73d	16.73opq
MCV9	65.33jkl	78.00jkl	7.67ghijk	79.33c-g	10.00u	10.70u
MCV10	67.33fghi	79.67fghij	6.78kl	76.89e-k	17.04lmno	26.90def
MCV11	77.67a	90.00a	5.67 m	77.11e-k	12.97rs	29.60bc
MCV12	64.00 lm	76.33 lm	9.67ab	70.34k-p	25.47e	19.03lmn
MCV13	57.33q	69.67o	9.33abcd	66.44o-r	10.67tu	11.93stu
MCV14	69.33d	81.33ef	7.78fghij	71.56j-o	25.27e	18.70lmn
MCV15	64.33klm	76.33lm	4.11o	71.56j-o	13.20r	15.77pq
MCV16	68.67def	81.00efg	6.33ml	81.33b-e	18.35jkl	22.90j
MCV17	66.33hij	78.67hij	4.67no	72.56g-o	17.47lmn	23.47ij
MCV18	59.67p	72.00n	3.78op	68.72n-q	19.73ghi	17.60mno
MCV19	57.33q	69.67o	2.89qp	75.89e-m	25.47e	23.20ij
CCV1	66.67ghij	80.00efghi	7.56hijk	73.67f-n	17.37lmn	24.50hij
CCV2	66.67ghij	79.33ghij	8.47defgh	79.00d-h	20.52fgh	28.63cd
CCV3	67.33fghi	79.67fghij	6.00ml	86.22bc	19.73ghi	25.50fgh
CCV4	69.00de	81.67e	5.44mn	76.44e-l	30.91bc	18.55lmn
CCV5	67.67efgh	80.00efghi	8.11fghi	78.78d-i	30.94bc	20.03kl
CCV6	65.67jk	78.00jkl	6.33ml	79.67b-f	18.13jklm	26.51efg
TCV1	72.33c	85.67d	6.00ml	77.11e-l	24.83e	19.57kl
TCV2	64.33klm	76.67klm	2.67q	60.78rs	19.13ijk	31.50a
TCV3	68.67def	81.00efg	2.55q	61.95qrs	18.10jklm	17.63mno
TCV4	67.33fghi	79.67fghij	9.33a-d	68.89m-q	19.17ijk	19.10 lm
TCV5	63.67mn	76.33lm	8.66c-f	79.22c-g	18.37jkl	24.83ghi
TCV6	68.00defg	80.33efgh	5.99ml	78.22d-j	11.81st	12.50st
TCV7	63.33mn	75.67m	9.22bcde	73.56f-n	16.98mno	17.73mno
TCV8	65.67jk	78.00jkl	9.55abc	73.55f-n	18.87ijk	17.70mno
TCV9	67.67efgh	80.00efghi	7.78ghij	63.78p-s	11.83st	11.80tu
TCV10	62.33no	75.67 m	5.78 m	72.00h-o	16.47nop	26.37 fg
TCV11	73.67bc	85.67d	7.33ijk	68.00n-q	21.77f	12.70st
TCV12	66.67ghij	79.00hij	8.67cdef	86.67b	16.80mno	30.63ab
TCV13	66.00ij	78.33ijk	10.22a	78.11d-j	20.69fg	17.37m-p
TCV14	61.00op	72.67n	8.33efgh	70.44k-p	11.07tu	10.53u
TCV15	59.67p	71.33no	8.00fghi	99.55a	10.93tu	11.63tu
TCV16	74.67b	87.67bc	6.89jkl	64.45p-s	31.31b	15.50q
TCV17	65.67jk	78.00jkl	4.22o	59.33s	36.57a	17.60mno
Mean	66.86	79.24	6.89	74.66	19.74	19.42
SEM	0.42	0.43	0.18	0.76	0.52	0.56
LSD (p = 0.05)	1.44	1.75	0.94	7.07	1.75	1.35

Note: D50F, days to 50% flowering; FH, first harvest; NB, number of branches; PH, plant height; FL, fruit length; FD, fruit width.

In this study, the average PIC value was determined to be 0.45, indicating a moderate level of polymorphism in the loci. It is worth noting that the measurement of genetic diversity in eggplants varies across different literature sources. The expected gene heterozygosity (He) for each pair of primers ranged from 0.28 to 0.74, with an average value of 0.54. This study is comparable to the findings of Hurtado et al. (2012), who conducted a study on genetic diversity in Sri Lankan accessions and reported a high diversity value of He = 0.54. Similarly, our research revealed values of Shannon 's information index ranging from 0.45 to 1.36, with an average of 0.84. This finding aligns with the results reported by Datta et al. (2021), who also observed a Shannon's index value of 0.85. However, our result was higher than the value reported by Ge et al. (2013), where the Shannon index value was 0.570. These variations in diversity measures may be attributed to differences in the materials studied, analytical approaches employed, and types of markers used (This et al. 2004).

Table 5. Mean performance of yield and yielding traits of 42 eggplant genotypes.

Genotypes	FL/D	FW (g)	AFW (g)	FN	Y/P (kg)
MCV1	1.22hij	148.51fgh	130.32kl	29.60ijk	2.38mnopq
MCV2	0.94p-s	44.61rs	106.49opqr	27.93klmn	1.58tuvw
MCV3	0.65vw	112.58kl	184.11defg	29.53ijk	3.96cde
MCV4	0.92qrs	97.37ml	173.70fgh	23.60p	2.92ijkl
MCV5	1.18h-l	139.78ghi	136.04kjl	31.03hi	2.66lmn
MCV6	1.14i-m	62.41pq	120.75l-p	27.30mn	1.92qrst
MCV7	1.46de	279.52b	162.30hi	38.20b	4.29bc
MCV8	0.58wx	151.64efg	179.41efgh	26.73no	3.46efgh
MCV9	1.07k-o	155.29efg	192.05cde	20.37r	2.89ijkl
MCV10	1.58cd	196.15c	136.54jkl	36.90bc	3.19hijk
MCV11	2.29a	43.02rst	110.23nopq	38.60b	2.31nopqr
MCV12	0.75uv	40.21rstu	110.01nopq	28.70jklm	1.72stu
MCV13	1.12j-n	94.02mn	167.02igh	27.37mn	2.57lmno
MCV14	0.74uv	132.29hij	164.89hi	28.37jklmn	3.26ghij
MCV15	1.20h-k	40.83rstu	127.86klmn	25.43o	1.97pqrst
MCV16	1.25ghi	123.88ijk	133.11kl	32.90g	2.73klmn
MCV17	1.35efg	153.61efg	123.33lmno	33.47fg	2.45lmnop
MCV18	0.89rst	163.83def	269.38a	27.27mn	5.97a
MCV19	0.91rst	173.82d	165.75hi	32.53gh	3.77def
CCV1	1.42ef	53.83pqrs	110.97m-q	34.17efg	2.08opqrs
CCV2	1.39ef	19.73w	98.37qrs	38.30b	1.85rst
CCV3	1.29fgh	112.85kl	171.05f-i	35.50cde	4.30bc
CCV4	0.60xw	154.03efg	172.62f-i	28.88jklm	3.53defgh
CCV5	0.64vw	166.39de	176.21efgh	30.03ij	3.79def
CCV6	1.46de	66.30op	154.33ij	36.18 cd	3.77def
TCV1	0.79tu	164.20def	201.50 cd	29.57ijk	4.47b
TCV2	1.64c	120.77jk	129.88kl	41.83a	3.34fghi
TCV3	0.98o-r	27.68tuvw	107.14opqr	27.63lmn	1.58stuv
TCV4	1.00o-r	25.20uvw	94.36qrs	29.10jkl	1.29uvwx
TCV5	1.35efg	121.27jk	134.27kl	34.83def	2.93ijkl
TCV6	1.06l-p	79.47no	206.76c	22.50pq	3.52efgh
TCV7	1.04m-q	22.42vw	90.45rs	27.73lmn	1.12vwx
TCV8	0.94p-s	17.23w	86.03s	27.37mn	0.98x
TCV9	1.00n-r	37.75stuv	127.21klmn	21.80qr	1.68stu
TCV10	1.60c	152.24efg	129.16klm	35.70cde	2.83jklm
TCV11	0.58wx	49.61qrs	135.47kl	23.03pq	1.97pqrst
TCV12	1.82b	178.71d	142.02jk	40.63a	3.74defg
TCV13	0.84stu	54.89pqr	198.09cd	21.93pqr	4.03bcd
TCV14	0.95o-s	18.06w	102.49pqrs	20.53r	1.08wx
TCV15	1.07l-o	18.23w	101.21qrs	21.63qr	1.10vwx
TCV16	0.50x	201.37c	185.45def	25.50o	3.45fgh
TCV17	0.48x	303.83a	249.00b	27.60lmn	5.49a
Mean	1.09	120.49	154.91	29.71	2.85
SEM	0.03	10.40	5.04	0.50	0.10
LSD (p = 0.05)	0.13	1.17	1.10	1.03	0.20

Note: FL/D; fruit length/width ratio; AFW, average fruit weight; FW, fruit weight; number of fruits; Y/P; yield per plant.

Cluster analysis using SSR markers

The seventeen SSR markers were selected based on the Euclidean distances between the 42 eggplant genotypes to create a UPGMA dendrogram, as shown in Table 7 and Fig. 2. The dendrogram classified 42 eggplant genotypes into five main groups with a similarity coefficient of 4.24, which was the best fit for convenient discussion, implying that eggplant genotypes have a high level of variation. Group I had the largest number and consisted of 46 genotypes. Malaysian varieties had the largest number (MV1, MV5, MV14, MV15, MC16, MV18 and MV19), followed by Thailand varieties (TV5, TV2, TV6, TV12 and TV13), while Chines varieties had four varieties (CV2, CV3, CV5 and CV6). Group II consisted of five genotypes: four from Malaysia (MV2, MV4, MV9 and MV14) and one from Thailand (TV11). Group III had the second largest number and consisted of 10 genotypes. Thailand varieties had the largest number with seven genotypes (TV1, TV4, TV8, TV10, TV15, TV16 and TV17), followed by Chinese varieties (CV1 and CV4), while

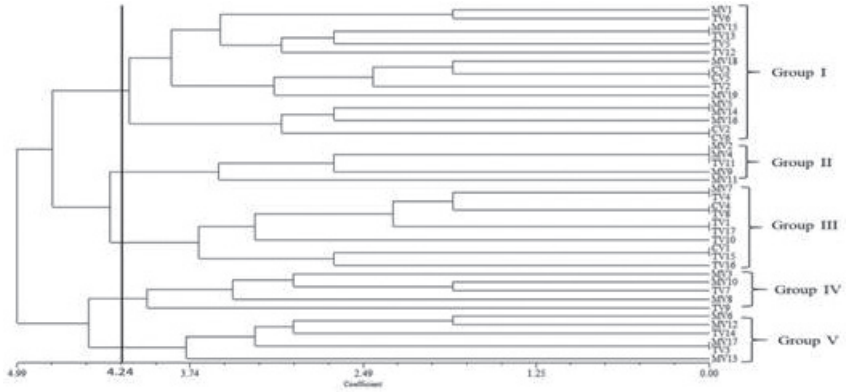

Figure 2. The genetic relationship among the 42 eggplant accessions based on seventeen SSR markers was determined using the unweighted pair group method with arithmetic mean (UPGMA) at a 4.24 similarity coefficient using SAHN clustering on the UPGMA method.

Table 6. Prominent features of microsatellite loci analysis.

SSR Locus	Na	F	Ne	I	He	PIC
emf01K16	2	0.57	1.96	0.68	0.50	0.37
emb01D10	2	0.76	1.57	0.55	0.37	0.36
emh21J12	2	0.52	2.00	0.69	0.50	0.37
SSR–46	2	0.57	1.96	0.68	0.50	0.37
emh02E08	2	0.55	1.98	0.69	0.50	0.37
emh11I06	2	0.52	2.00	0.69	0.50	0.37
eme05B09	2	0.50	2.00	0.69	0.50	0.38
emb01C12	4	0.36	3.63	1.33	0.73	0.29
eme05B10	3	0.41	2.91	1.08	0.66	0.37
emh11B18	3	0.43	2.77	1.05	0.65	0.40
emh11B19	3	0.43	2.80	1.06	0.65	0.58
SSR40	2	0.83	1.36	0.45	0.28	0.58
SSR125	2	0.60	1.93	0.68	0.49	0.68
emf21K08	3	0.34	2.97	1.09	0.67	0.64
emk03O04	4	0.33	3.79	1.36	0.74	0.56
emk04N11	2	0.52	2.00	0.69	0.50	0.57
emf01E10	3	0.75	1.68	0.73	0.41	0.37
Average	2.53	0.53	2.31	0.84	0.54	0.45

Na, number of alleles; F, major allele frequency; Ne, number of effective alleles; I, Shannon's information index; He, expected heterozygosity; PIC, polymorphic information content.

Table 7. Relationship among the 42 eggplant genotypes based on seventeen SSR markers using SAHN clustering using the UPGMA method.

Cluster	No of Accessions	Accessions	Origin
I	16	CV2, CV3, CV5, CV6, MV1, MV5, MV14, MV15, MC16, MV18, MV19, TV5, TV2, TV6, TV12 and TV13	China (4) Malaysia (7) Thailand (5)
II	5	MV2, MV4, MV9, MC14, and TV11	Malaysia (4) Thailand (1)
III	10	CV1, CV4, MV7, TV1, TV4, TV8, TV10, TV15, TV16 and TV17	China (2) Malaysia (1) Thailand (7)
IV	5	MV3, MV8, MV9, MV10, TV7	Malaysia (4) Thailand (1)
V	6	MV6, MV12, MV13, MV17, TV3, and TV14	Malaysia (4) Thailand (2)

Malaysia had one variety (MV7). Another group (Group IV) includes four Malaysian varieties (MV3, MV8, MV9 and MV10) and one Thailand variety (TV7). Meanwhile, cluster V had six genotypes, viz are MV6, MV12, MV13, and MV17 from Malaysia and TV3 and TV14 from Thailand. Several studies have employed SSR markers to investigate the genetic diversity of eggplant. Nunome et al. (2003), Stagel et al. (2008), Demir et al. (2010), and Datta et al. (2021) have reported on this topic. These studies used accessions from various countries, either a shared ancestry or similar morphological traits among these accessions. In contrast, the accessions exhibited significant spatial separation, implying variations in agronomical characteristics or diverse origins. The presence of accessions from distinct clusters and different geographic sources genetic exchange among plant breeders located in various regions. The dissimilarities observed among the accessions may be attributed to prolonged exposure to distinct environmental conditions (Datta et al. 2021).

Conclusion

The genetic structure of fruit yield is determined by the overall performance of various yield components that interact with each other. The 42 eggplant genotypes exhibited variation in terms of their physical and genetic diversity. The presence of genetic variation suggests that they may have originated from different sources, which explains the differences in their traits. This research provides information about the genetic variation of a specific group of eggplants, which can be valuable for future studies. The use of SSR markers is important in understanding the genetic connections among different eggplant genotypes from Malaysia, China and Thailand.

Author contributions

Conceptualization, I.M. (Ibrahim Musa) and M.R.Y. (Mohd Rafii Yusop); methodology, I.M. (Ibrahim Musa) and M.R.Y. (Mohd Rafii Yusop); software, I.M. (Ibrahim

Musa), S.C.C. (Samuel Chibuike Chukwu); validation, U.M. (Usman Magaji); formal analysis, I.M. (Ibrahim Musa), M.R.Y. (Mohd Rafii Yusop), U.M. (Usman Magaji) and I.M. (Isma'ila Muhammad); investigation, I.M. (Ibrahim Musa) and B.Y.R. (Bashir Yusuf Rini); resources, I.M. (Ibrahim Musa) and M.R.Y. (Mohd Rafii Yusop); data curation, I.M. (Ibrahim Musa) and A.S.K. (Audu Sanusi Kiri); writing—original draft preparation, I.M. (Ibrahim Musa); writing—review and editing, A.F.A. (Arolu Fatai Ayanda) and I.M. (Ibrahim Musa); All authors have read and agreed to the published version of the manuscript.

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