PHYTOLOGIA BALCANICA
vol. 32: 51-61 • Sofia • 2026
DOI 10.3897/phytolbalcan.32.e187443

Institute of Biodiversity and Ecosystem Research,
Bulgarian Academy of Sciences

Transferability and discriminating power of ISSR and SCoT markers for studying genetic diversity in *Dacryodes edulis* accessions from Nigeria

Temitope Omoniyi Oyebola[1], Adeniyi Akanni Jayeola[1], Kafilat Abiodun Odesola[1], Temitope Esther Shonde[3], Temitope Esther Owoeye[4]

1 *Department of Botany, University of Ibadan, Ibadan, Oyo State, Nigeria.*
2 *Department of Biological Sciences, Bells University of Technology, Sango Ota, Ogun state, Nigeria.*
3 *International Institute of Tropical Agriculture*
4 *National Biotechnology Research and Development Agency, Nigeria, email: temitoperosanwo@gmail.com (corresponding author)*

Received: July 01, 2025 | **Accepted:** October 29, 2025 | **Published:** February 3, 2026

Abstract

Dacryodes edulis is a culturally and economically important fruit tree native to Central and West Africa. Despite its benefits, its genetic diversity remains underexplored. This study has used Inter-Simple Sequence Repeat (ISSR) and Start Codon Targeted (SCoT) markers to assess the genetic diversity and relationships among 32 accessions collected from Nigeria. Genomic DNA was extracted using a modified CTAB protocol and amplified by 15 ISSR and 10 SCoT primers. The results highlight the effectiveness of these markers in elucidating genetic variation and phylogenetic relationships, thus providing a foundation for genetic resource management and conservation.

Keywords

Genetic diversity, DNA markers, polymorphic information content

Citation

Oyebola, T.O., Jayeola, A.A., Odesola, K.A., Shonde, T.E., Owoeye, T.E. 2026. Transferability and discriminating power of ISSR and SCoT markers for studying genetic diversity in Dacryodes edulis accessions from Nigeria. – Phytologia Balcanica, 32: 51-61. – ISSN 1310-7771 (print), 1314-0027 (online)

Introduction

Dacryodes edulis (G.Don) H.J Lam, commonly known as African Pear or Safou, is a fruit-bearing tree of the *Burseraceae* family, native to the humid tropical forests of Central and West Africa (Kadji & al. 2016; Makouate & Lekagne 2022). Valued for its nutritional and economic benefits, the species is rich in essential nutrients and stands as an important component in local diets (Oluwaniyi & al. 2017; Sika & al. 2021). Beyond its dietary relevance, its edible mucilage has emerging applications as a natural food additive with medicinal potential (Ajibesin 2011).

Despite its importance, *D. edulis* remains underutilised and under-characterised at the genetic level, especially in Nigeria. Morphological classification has been commonly employed in the earlier studies (Okafor 1983; Silou & al. 2002), but morphological traits can be influenced by environmental factors, which limit their reliability for identifying genetic variation. Molecular characterisation offers a robust alternative for understanding genetic diversity and population structure, with markers such as Simple Sequence Repeats, Random Amplified Polymorphic DNA, Amplified Fragment Length Polymorphism, and Single Nucleotide Polymorphisms, applied earlier in similar contexts (Olawuyi & Azeez 2019; Singh & al. 2020; Odesola & al. 2023; Olufemi & al. 2024). Earlier molecular studies on *Dacryodes edulis* have employed Simple Se-

This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

quence Repeat (SSR) markers to investigate genetic variation within the species (Makueti & al. 2015; Rimlinger & al. 2020). ISSR and SCoT markers are particularly useful due to their reproducibility, cost-effectiveness and capacity to detect high levels of polymorphism (Etminan & al. 2016; Luz & al. 2020). These markers have proven effective in characterising diversity in various plants, including *Moringa oleifera*, *Zea mays*, and *Lathyrus* species (Hassan & al. 2020; Osman & al. 2020; Soliman & al. 2021). This study explores the transferability and discriminating power of ISSR and SCoT markers in assessing genetic kinship among *D. edulis* accessions from Nigeria.

Material and methods

Plant material

Thirty-two accessions of *Dacryodes edulis* were collected from six states (Abia, Akwa Ibom, Cross River, Edo, Enugu, and Oyo) in Nigeria and appropriately coded (Table 1). Those regions in the south southern and southwestern parts of the country are known for the natural occurrence of the species. Geographic coordinates (longitude, and latitude) of each collection site were documented (Table 2). Mature fruits were harvested from healthy plants in each designated locality.

Planting and seedling maintenance

Seeds obtained from the fruits were sown individually in 7 kg pots filled with fertile soil at the Forestry Research Institute of Nigeria screen house. The experiment followed a randomised complete design with three replications. Pots were filled with soil and watered in the evening to soften it, and seeds were sown the next morning, covered with approximately ¼ inch (0.625 cm) of soil. Labels were used to indicate location numbers, state codes, and planting dates. The pots were arranged to ensure adequate sunlight and were watered once daily in the evening. Manual weeding was conducted regularly, and seedlings were thinned after four weeks to promote the growth of stronger plants.

Table 1. List of *Dacryodes edulis* accessions used in this study

S/NO	Accession names	State of collection	S/NO	Accession names	State of collection
1	EN1	Enugu	17	CRS17	Cross River
2	EN2	Enugu	18	AK18	Akwa Ibom
3	EN3	Enugu	19	AK19	Akwa Ibom
4	EN4	Enugu	20	AK20	Akwa Ibom
5	EN5	Enugu	21	AK21	Akwa Ibom
6	EN6	Enugu	22	AK22	Akwa Ibom
7	EN7	Enugu	23	AK23	Akwa Ibom
8	EN8	Enugu	24	UM24	Abia
9	EN9	Enugu	25	UM25	Abia
10	EN10	Enugu	26	UM26	Abia
11	CRS11	Cross River	27	UM27	Abia
12	CRS12	Cross River	28	IB28	Oyo
13	CRS13	Cross River	29	IB29	Oyo
14	CRS14	Cross River	30	IB30	Oyo
15	CRS15	Cross River	31	ED31	Edo
16	CRS16	Cross River	32	ED32	Edo

Table 2. Geographical data of the collection sites

S/N	Collection state	Natural vegetation	Latitude	Longitude
1	Abia	Rain forest	5°27′0.12′′N	7°52′6.20′E
2	Akwa Ibom	High forest	4°59′22.75′′N	7°54′38.80′′E
3	Cross River	Rain forest	4°56′27.28′′N	8°24′16.11′′E
4	Edo	High forest	6º18′45.80″N	5º14′10.50″E
5	Enugu	Rain forest	6º49′39.60″N	7º23′30.15″E
6	Oyo	Rain forest	7º13′10.00″N	3º53′34.00″E

Source: Sowunmi and Akintola, (2010); climate-data (2018)

Genomic DNA extraction

Genomic DNA was isolated from fresh leaf tissues of the thirty-two *Dacryodes edulis* accessions using a modified CTAB protocol based on Saghai-Maroof's (1984) method. The modification incorporated 20% SDS as a detergent and 1% PVP. Fresh leaf samples (500 mg) were ground with 400 µl of extraction buffer (1M Tris-HCl pH 8, 0.5M EDTA, 5M NaCl, 1% PVP, 20% SDS, β-mercaptoethanol) to create a homogeneous mixture. That mixture was incubated at 65°C for 25 minutes, then cooled for 5 minutes. After cooling, 200 µl of 5M potassium acetate was added to neutralize SDS and halt lysis, followed by a 20-minute incubation on ice. Subsequently, 350 µl of chloroform isoamylalcohol (24:1) was added, and the mixture was centrifuged at 4000g for 10 minutes. The supernatant was then precipitated with 400 µl of ice-cold isopropanol and incubated at -20°C for 10 minutes. After centrifuging at 4000g for 20 minutes, the supernatant was discarded leaving the DNA pellets at the bottom of the tube. The DNA pellets were washed twice with 300 µl of 70% ethanol, air-dried, and resuspended in 50 µl of sterile distilled water for storage at -20°C.

DNA quantification and qualification

DNA concentration was estimated using 1% agarose gel containing 8% ethidium bromide solution. The concentration and quality of the DNA were further quantified using a nanodrop spectrophotometer (N.D.1000) at an absorbance ratio of 260/280 nm. The quantification procedure involved blanking the nanodrop with 2 µL of sterile H_2O, then measuring the DNA concentration by loading 2 µL of DNA sample into the spectrophotometer. Optimal purity was indicated by a ratio between 1.6 and 1.8 ng/µL protein contamination, and a ratio above 2.0 ng/µL indicates RNA contamination. A working solution with a concentration of 20 ng/µL was prepared from the stock DNA solutions for further use.

ISSRs and SCoT marker analysis

For genetic analysis, 25 polymorphic primers were employed to screen the genomic DNA of 32 *Dacryodes edulis* accessions (Table 3). Fifteen ISSR primers were selected for initial amplification. Each 25 µl reaction contained 2.5 µl of PCR buffer, 2.5 mM dNTPs, 50 mM $MgCl_2$, 0.1 unit of Taq polymerase, 1 µl of DMSO, 13.4 µl of PCR-grade water, 1 µl of each primer, and 3 µl of DNA. The amplification process was carried out using an Applied Biosystem Thermal Cycler with the following program: initial denaturation at 95°C for 2 minutes; two cycles of 30 seconds at 95°C, 1 minute at 37°C, and 2 minutes at 72°C; followed by two cycles of 30 seconds at 95°C, 1 minute at 35°C, and 2 minutes at 72°C; then 41 cycles of 30 seconds at 94°C, 1 minute at 35°C, and 2 minutes at 72°C; concluding with a final extension at 72°C for 5 minutes, and then cooling to 4°C.

Similarly, ten SCoT primers were selected for another set of amplifications, also with a final volume of 25 µl per reaction. Each reaction contained 2.5 µl of PCR buffer, 2.5 mM dNTPs, 50 mM $MgCl_2$, 0.1 unit of Taq polymerase, 1 µl of DMSO, 13.4 µl of PCR-grade water, 1 µl of each primer, and 3 µl of DNA. The PCR program for SCoT primers included initial denaturation at 94°C for 3 minutes, followed by 10 cycles of 30 seconds at 94°C, 1 minute at 55°C, and 1 minute at 72°C. This was followed by 30 cycles of 30 seconds at 94°C, 1 minute at 45°C, and 1 minute at 72°C, with a final extension at 72°C for 7 minutes.

Polyacrylamide gel electrophoresis

The PCR product was further run on PAGE to have a better separation of fragments, 6% polyacrylamide gel was prepared containing 7.5 mL of Acrylamide/Bis 19:1 40% (Ambion, Woodward Austin), TX was added to 2.5 mL of 5× TBE buffer and 40 mL of distilled water to give a total volume of 50 mL. Five hundred microlitres (500 µL) of 10% ammonium persulfate (Sigma, Saint Louis, MO, USA) and 50 µL of N, N, N, N′-tetramethylethylenediamine (Sigma, Saint Louis, MO, USA) were added to the mixture to complete the gel preparation before the acrylamide polymerised. Once the molten gel was cast and solidified, PCR products were electrophoresed for 1 hr 30 minutes at 80 V and stained with ethidium bromide solution for 5 minutes. The gels were observed under UV transillumination (Aplegen imager).

Molecular data analysis

The ISSR and SCoT profiles for identical molecular weight fragments from each individual accession were rated as presence (1) or absence (0) in the data matrix. Using Jaccards' similarity coefficient, the data received from scoring the bands was put through a genetic similarity matrix (Jaccard, 1908). The NTSYS-pc software version 2.02 (Rohlf, 2000) was applied for cluster analysis, utilising the unweighted pair-group method with arithmetic averages (UGPMA) to find phylogenetic relationships. Polymorphic information content (PIC) was calculated by the formula:

PIC = 1- ∑pi2.

Where pi is the frequency of the ith allele

Results

Representative amplification profiles generated using two primers, ISSR primer UBC-888 and SCoT primer SCoT-2, have demonstrated clear polymorphic banding patterns across the 32 *Dacryodes edulis* accessions (Fig. 1 & 2). Both sets of DNA primers (15 ISSR and 10 SCoT) produced distinct and polymorphic bands in the genotype.

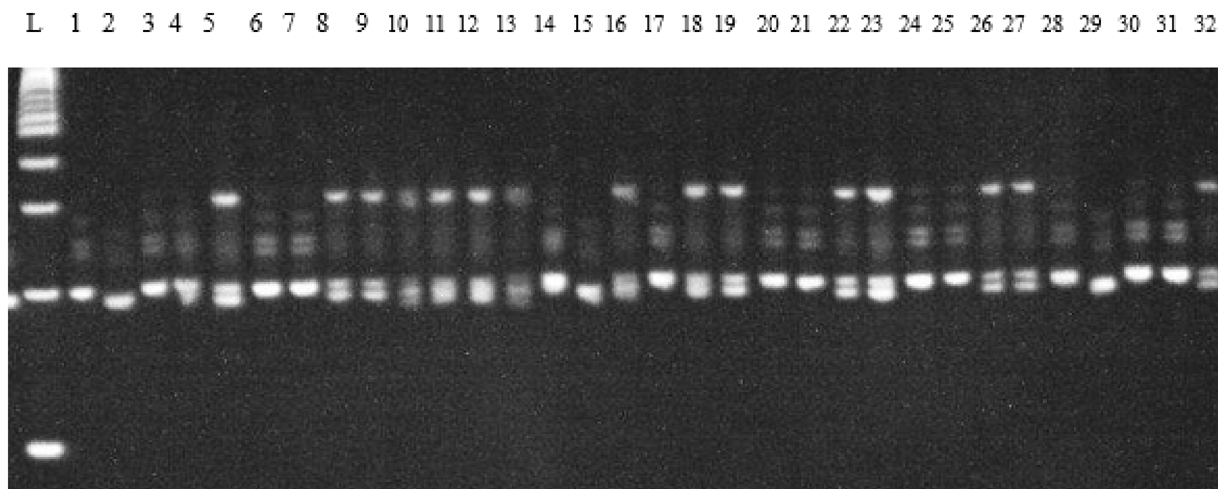
ISSR markers

Fifteen ISSR primers amplified clear and reproducible DNA fragments across the 32 *Dacryodes edulis* accessions.

Table 3. Primer names and sequences for amplification of the 32 accessions of *Dacryodes edulis*.

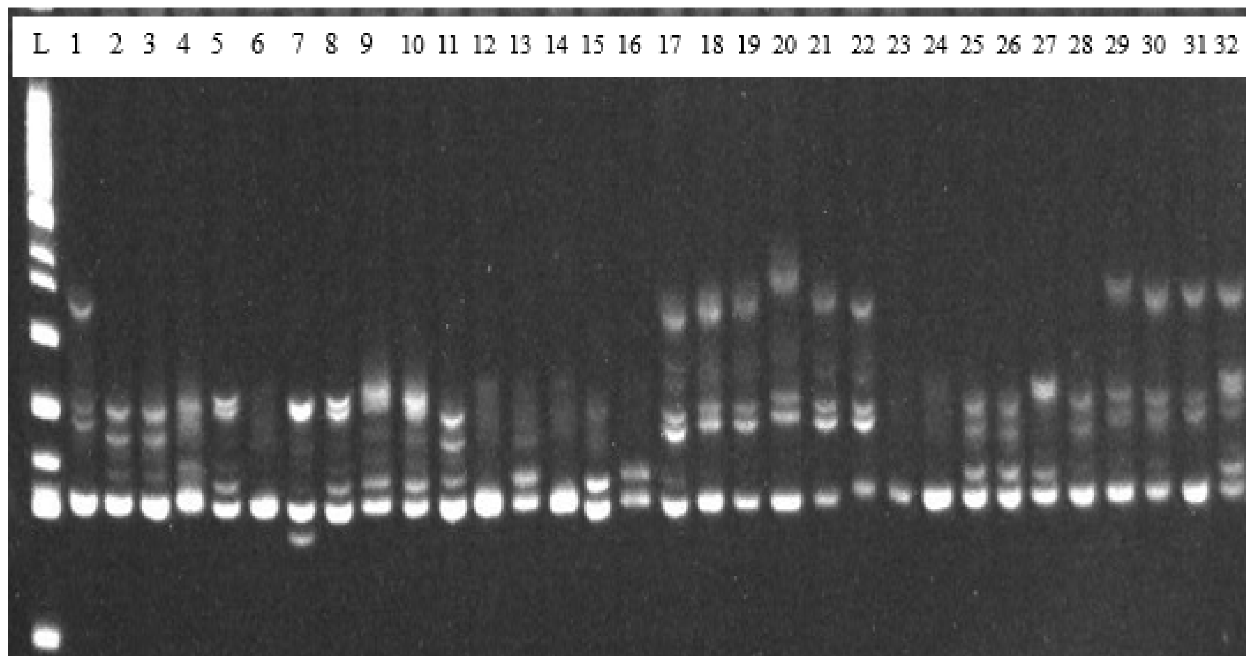
S/NO	Primer ID	Primer sequence
Inter simple sequence repeat		
1	UBC-808	AGAGAGAGAGAGAGAGC
2	UBC-811	GAGAGAGAGAGAGAGAC
3	UBC-824	TCT CTC TCT CTC TCT CG
4	UBC-825	ACACACACACACACACT
5	UBC-880	GGAGAGGAGGAGAGGAGA
6	UBC-840	GAG AGA GAG AGA GAG A (CT) A
7	UBC-888	(GCT) (AGT) (GCT) CAC ACA CAC ACA CA
8	UBC-841	GAG AGA GAG AGA GAG A (CT) C
9	UBC-843	CTC TCT CTC TCT CTC T (AG) A
10	UBC-846	CAC ACA CAC ACA CAC A (AG) T
11	UBC-849	GTG TGT GTG TGT GTG TYA
12	UBC-850	GTG TGT GTG TGT GTG TYC
13	UBC-851	GTG TGT GTG TGT GTG TYG
14	UBC-869	GTT GTT GTT GTT GTT GTT
15	UBC-866	CTC CTC CTC CTC CTC CTC
SCoT primers		
1	SCoT 1	CAACAATGGCTACCACCA
2	SCoT 2	CAACAATGGCTACCACCC
3	SCoT 3	CAACAATGGCTACCACCG
4	SCoT 16	ACCATGGCTACCACCGAC
5	SCoT 18	ACCATGGCTACCACCGCC
6	SCoT 22	AACCATGGCTACCACCAC
7	SCoT 28	CCATGGCTACCACCGCCA
8	SCoT 33	CCATGGCTACCACCGCAG
9	SCoT 35	CATGGCTACCACCGGCCC
10	SCoT 36	GCAACAATGGCTACCACC

Fig. 1. ISSR-PCR amplification products of the 32 *Dacryodes edulis* accessions generated by marker UBC-888.



Note: L -DNA ladder.

Fig. 2. SCoT-PCR amplification products of the 32 *Dacryodes edulis* accessions generated by marker SCoT-2.



Note: L -DNA ladder.

Table 4. Characteristics of 15 ISSR markers used to assess genetic diversity of *Dacryodes edulis* accessions.

Marker	MAF	NPF	GD	PIC
UBC-808	0.28	13	0.86	0.84
UBC-811	0.31	9	0.82	0.80
UBC-824	0.44	7	0.73	0.70
UBC-825	0.28	13	0.86	0.85
UBC-840	0.13	23	0.94	0.94
UBC-841	0.41	6	0.70	0.65
UBC-843	0.66	6	0.54	0.51
UBC-846	0.25	15	0.88	0.87
UBC-849	0.25	10	0.85	0.84
UBC-850	0.47	5	0.65	0.59
UBC-851	0.19	13	0.89	0.88
UBC-866	0.41	7	0.75	0.72
UBC-869	0.22	13	0.88	0.87
UBC-880	0.19	13	0.87	0.86
UBC-888	0.75	4	0.41	0.37
Mean	**0.35**	**10.47**	**0.77**	0.75

Legend: MAF-major allele frequency, NPF- number of polymorphic fragments, GD-gene diversity, PIC- Polymorphic information content

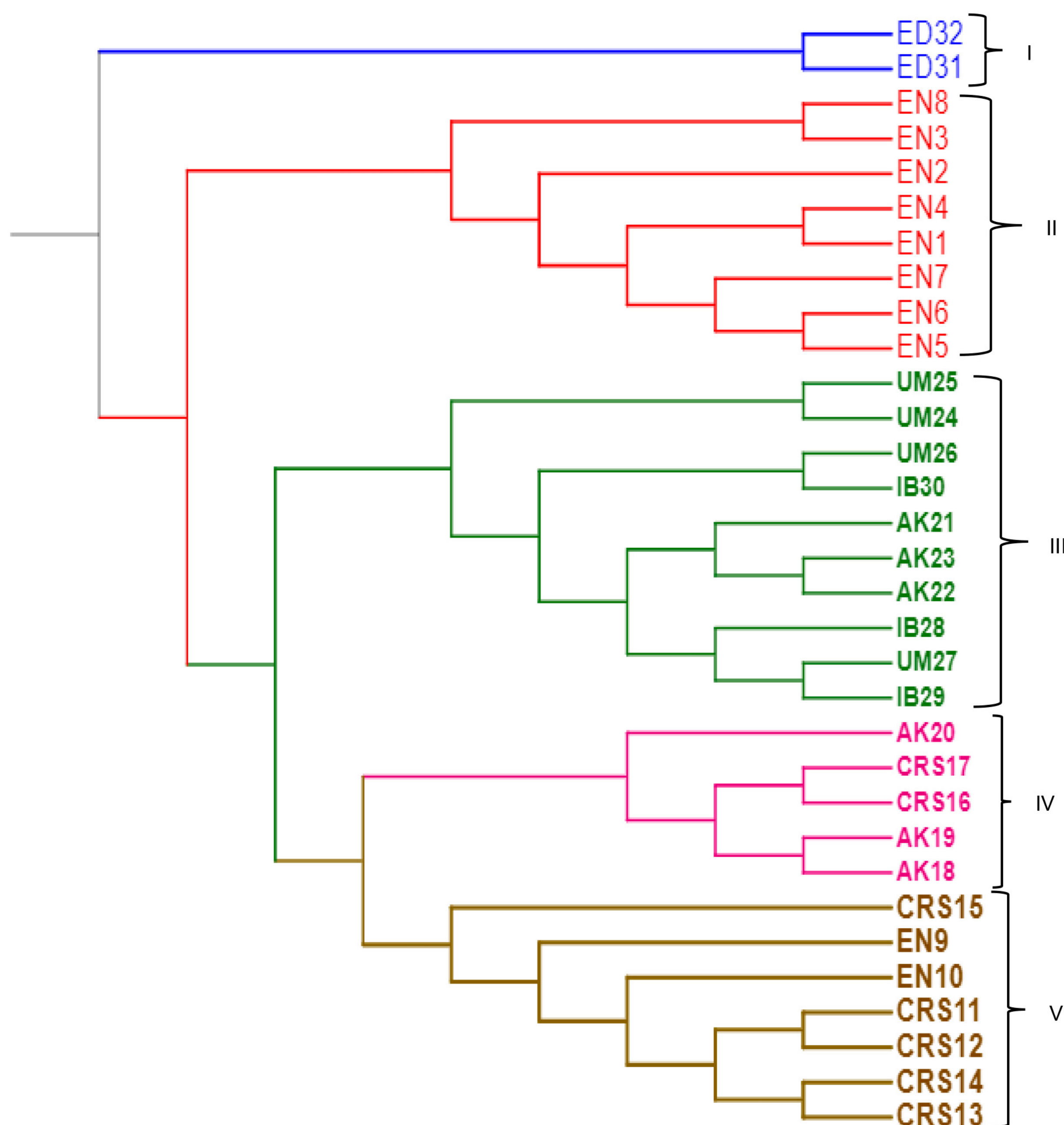


Fig. 3. Hierarchical cluster analysis of the 32 accessions of *D. edulis* based on ISSR markers.

A total of 157 fragments were obtained, with the number of polymorphic loci per primer ranging from 4 (UBC-888) to 23 (UBC-840) (Table 4). The mean number of polymorphic loci per primer was 10.47. The amplified products ranged in size from 100 to 3000 bp. Polymorphic information content (PIC) values varied from 0.37 (UBC888) to 0.94 (UBC840), with an average value of 0.75. Gene diversity similarly ranged from 0.41 to 0.94 for UBC888 and UBC840 respectively, with a mean value of 0.77.

The hierarchical cluster analysis based on the ISSR markers grouped the 32 accessions into five main clusters (Fig. 3). The first cluster consisted of two genotypes from Edo State. The second cluster comprised eight accessions (EN1 to EN8), all from Enugu, which formed a distinct subgroup. The third encompassed accessions from multiple states including IB28-IB30, AK21-AK23 and UM24-UM27, forming an intermediate group. The fourth cluster included genotypes from Akwa Ibom (AK18-20) and Cross River (CRS16-CRS17). The last cluster grouped five genotypes from Cross River (CRS11-CRS15) with two from Enugu (EN9 and EN10).

2.2. SCoT markers

SCoT primers amplified a lesser amount of scorable PCR products, generating a total of 59 polymorphic fragments across all accessions (Table 5). The number of amplified fragments varied from 2 (SCoT3) to 13 (SCoT16), with an average of 5.9 fragments per primer. Gene diversity of SCoT ranged from 0.12 (SCoT3) to 0.87 (SCoT16), with an average of 0.55. The size of fragments produced by SCoT-PCR varied from 180 to 3000 bp. The average value of polymorphic information content in the set of used SCoT primers was 0.51. The highest value of PIC (0.86) was detected with the SCoT16 primer. On the other hand, SCoT3 showed the lowest value of PIC (0.11).

Cluster analysis based on the SCoT data have separated the accessions into seven groups (Fig. 4). Some clusters contained accessions from the same state such as Enugu and Cross River, while others showed mixed genotypes from different locations (e.g., Ibadan, Umuahia, and Akwa Ibom). The "royal blue cluster" stands as the first cluster having two accessions EN7 and EN2, while the second cluster had accessions from three geographically separated locations, two from Edo (ED31, ED32), two from Ibadan (IB29, IB30) and three from Enugu (EN8, EN4, EN1). The third group has been comprised of EN9 and CR12 accessions. The fourth, included UM25 as a single divergent genotype, likewise UM24 stood as an outlier. The sixth cluster grouped accessions from multiple localities, including Umuahia (UM26, UM27), Akwa Ibom (AK18, AK19) and Ibadan (IB28). The last cluster comprised the accessions EN6, AK23, AK21, EN5, AK22, CRS16, EN3, AK20, CRS17, CRS14 - another distinct group with internal similarities. This clustering reveals a varying degree of genetic kinship among accessions across different geographic origins.

Comparative analysis of ISSR and SCoT markers

The comparative summary of marker efficiency is presented in Table 6. The ISSR primers amplified a larger number of fragments (157) than the SCoT primers (59), producing an average of 10.47 and 5.90 polymorphic fragments per primer, respectively. The mean gene diversity (GD = 0.77) and polymorphic information content (PIC = 0.75) obtained for the ISSR markers were higher than those of the SCoT markers (GD = 0.55; PIC = 0.51), indicating that ISSRs were more informative and had stronger discriminatory power. In contrast, the mean major allele frequency (MAF = 0.59) of SCoT markers was higher than that of ISSRs (MAF = 0.35), reflecting a more conserved nature of the genomic regions targeted by SCoT primers. Together, both marker systems provided complementary insights, with ISSRs capturing broader genome-wide variation and SCoTs detecting polymorphisms associated with functional, gene-rich regions.

Combined ISSR and SCoT markers analysis

A combined analysis of the molecular data of the two-marker set used for constructing the dendrogram has further revealed a hierarchical cluster analysis that grouped the *Dacryodes edulis* accessions into five main clusters (Fig. 5). Merged molecular data yielded clearer resolution and demonstrated clear genetic differentiation between populations, with ED samples forming the most distant group. The EN samples split into two separate clusters II and V. The combined dataset produced a more refined and consistent clustering of the accessions, in line with their geographical distribution. Cluster I contained all Edo accessions, while cluster II grouped all Enugu accessions together, except for EN9 and EN10. Cluster III comprised

Table 5. Characteristics of the 10 SCoT markers used to assess genetic diversity of *Dacryodes edulis* accessions.

Marker	MAF	NPF	GD	PIC
SCoT 1	0.28	9	0.82	0.79
SCoT 2	0.69	6	0.50	0.48
SCoT 3	0.94	2	0.12	0.11
SCoT 16	0.28	13	0.87	0.86
SCoT 18	0.81	3	0.32	0.30
SCoT 22	0.59	4	0.57	0.51
SCoT 28	0.41	12	0.78	0.76
SCoT 33	0.72	4	0.43	0.38
SCoT 35	0.56	4	0.59	0.52
SCoT 36	0.63	2	0.47	0.36
Mean	0.59	5.9	0.55	0.51

Legend: MAF-major allele frequency, NPF- number of polymorphic fragments, GD-gene diversity, PIC- Polymorphic information content

Fig. 4. Hierarchical cluster analysis of the 32 accessions of *D. edulis* based on SCoT markers.

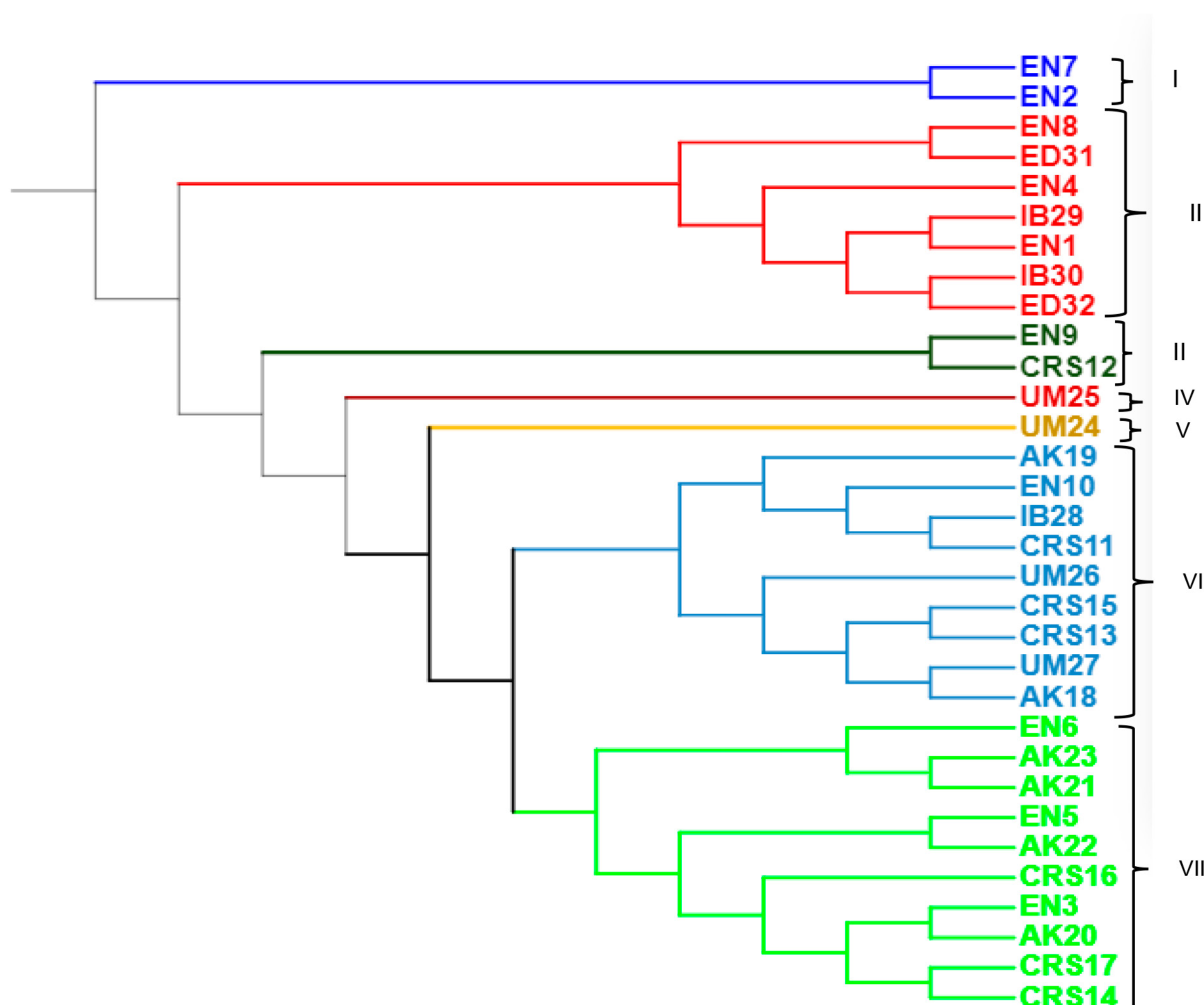


Table 6. Comparison of the efficiency of ISSR and SCoT markers for genetic diversity assessment in *Dacryodes edulis* accessions

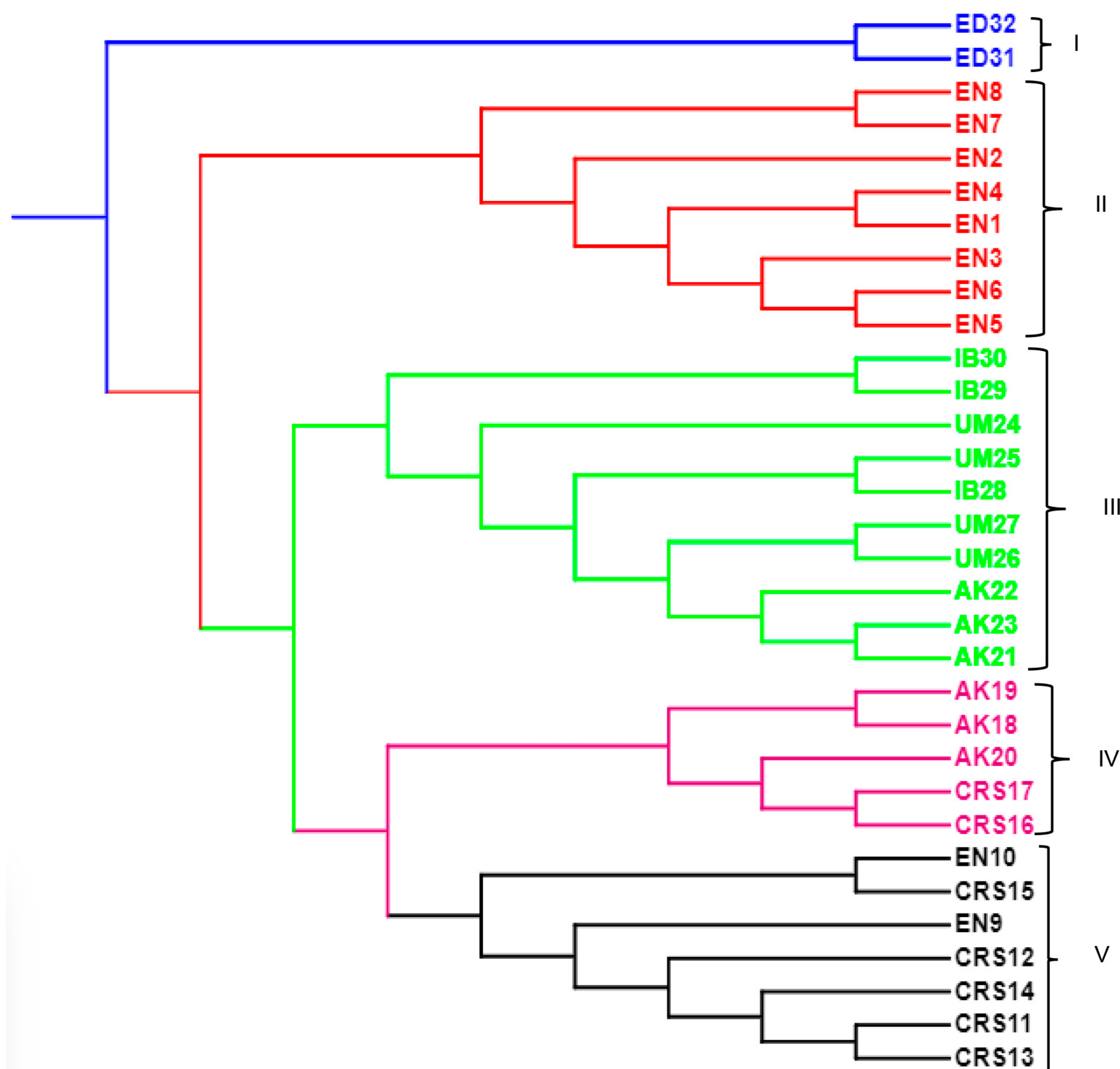
Type of marker	ISSR	SCOT
Number of analysed genotypes	32	32
Number of primers	15	10
Average number of polymorphic fragments per primer	10.47	5.90
Mean major allele frequency	0.35	0.59
Mean gene diversity	0.77	0.55
Mean polymorphic information content	0.75	0.51

a combination of Umuahia and Ibadan accessions highlighting strong genetic similarities, while Akwa Ibom accessions were positioned between Clusters III and IV. Thus, Akwa Ibom accessions appeared as a distinct but transitional group, sharing traits with neighbouring clusters. They showed proximity to Umuahia and Ibadan in Cluster III and to Cross River in Cluster IV. Most Cross River accessions have been grouped within the fifth cluster, along with two extra accessions from Enugu.

Discussion

The molecular analyses using ISSR and SCoT markers have revealed clear and reproducible banding patterns across all *Dacryodes edulis* accessions (Figs 1-2), confirming that both marker systems were reliable and informative for assessing genetic diversity. As shown in Tables 4 and 5, all primers amplified polymorphic loci, although the degree of informativeness varied. ISSR primers gen-

Fig. 5. Hierarchical cluster analysis of the 32 accessions of *D.edulis* based on combination of ISSR and SCoT markers.



erally exhibited higher polymorphism information content (PIC) and gene diversity (GD) values, with mean PIC and GD of 0.75 and 0.77, respectively, as compared with 0.51 and 0.55 for SCoT. Primers such as UBC-840 and UBC-851 were particularly effective, revealing more variable loci and contributing substantially to overall diversity, while SCoT primers, though lower in average indices, have captured variation within gene-associated regions, enhancing functional resolution across the accessions.

The differences observed between the two marker systems likely reflect variation in primer binding efficiency and targeted genomic regions. The primers with PIC values above 0.5 indicated strong discriminatory ability in accordance with the classifications of Botstein & al. (1980) and Ganapathy & al. (2012). Comparable trends were reported by Abd El-Moneim & al. (2021), who found higher mean PIC values for ISSR (0.77) than for SCoT (0.62) in quinoa, confirming the greater capacity of ISSR markers to detect polymorphism. El-Moneim (2019) similarly reported higher informativeness for ISSR than SCoT in wheat. The present study follows the same pattern, with ISSR revealing broader genome-wide variability and SCoT contributing valuable gene-related information. Together, these results demonstrate the effectiveness of combining the two marker systems in capturing a comprehensive view of *D. edulis* genetic diversity.

Clustering analyses (Figs 3-5) have further illustrated population structuring corresponding to ecological gradients. Accessions from similar environments tended to group together, whereas those from contrasting habitats have formed distinct but related clusters. This suggests that gene flow occurs more readily among geographical-

ly proximate populations and declines gradually across the environmental gradients. Given that all accessions originated from South Nigeria, a continuous range rather than isolated regions, the observed differentiation likely reflects ecological heterogeneity and local adaptation rather than strict geographic isolation.

Environmental and historical factors appear to underlie those patterns. The humid, densely vegetated conditions of Cross River and Akwa Ibom contrast with the more seasonal and open habitats of Oyo and parts of Edo, representing clear microclimatic variation within the species' range. Such contrasts may impose selective pressures that influence allelic distribution, while pollen and seed dispersal maintain gene flow and prevent pronounced differentiation (Dick & al. 2008). Tchinda & al. (2016) similarly reported high within-population diversity and low population differentiation in *D. edulis*, attributing that pattern to extensive pollen movement and predominant cross-pollination. Similar trends were noted by Al-Yasi & al. (2024), who reported that geological and climatic variations significantly shaped the genetic structure of *Juniperus* accessions. Moreover, human-mediated dispersal through the frequent exchange of *D. edulis* fruits and seedlings among neighbouring communities likely reinforces this genetic connectivity, consistent with observations in the earlier studies (Waruhiu & al. 2004; Makueti & al. 2015).

Earlier molecular studies on *D. edulis* have primarily relied on SSR and ISSR markers, which provided limited resolution of population relationships. The present ISSR–SCoT approach, therefore, offers a broader genome-wide perspective and greater insight into the population-level diversity across South Nigeria. While this study provides some valuable baseline information, further efforts and expanded geographic sampling would bolster understanding of the gene flow and evolutionary dynamics across the species' full range.

Generally, the combined use of ISSR and SCoT markers has revealed a rich, interconnected genetic base in *D. edulis*, shaped by environmental variation, ongoing gene exchange, and human influence. These findings fulfil the study's objective of characterising the species' genetic structure and emphasise the importance of conserving its diverse germplasm across natural habitats to support future breeding and sustainable utilisation.

Conclusion

ISSR and SCoT markers jointly provide reliable insights into the genetic diversity of *Dacryodes edulis* from South Nigeria. ISSR markers have revealed broader genome-wide variability, while SCoT markers have captured variation within gene-associated regions. Their combined application highlights the genetic structuring shaped by ecological gradients and local adaptation across the species' continuous natural range. These findings reaffirm the usefulness of both marker systems for assessing population structure and supporting the conservation and improvement of *D. edulis* germplasm.

References

Abd El-Moneim, D., ELsarag, E.I.S., Aloufi, S.; El-Azraq, A.M., ALshamrani, S.M., Safhi, F.A.A., Ibrahim, A.A. 2021. Quinoa (*Chenopodium quinoa* Willd.): Genetic Diversity According to ISSR and SCoT Markers, Relative Gene Expression, and Morpho-Physiological Variation under Salinity Stress. – Plants, **10**, 2802.

Ajibesin, K.K. 2011. *Dacryodes edulis* (G. Don) H. J. Lam: A review on its medicinal phytochemical and economical properties. – Res. J. Med. Pl., **5**(1): 32-41.

Climate-Data.org. 2018. Climate data for Abia, Akwa Ibom, Cross River, Edo, Enugu and Oyo States, Nigeria. Retrieved from https://en.climate-data.org/

Dick, C.W., Hardy, O.J., Jones, F.A., Petit, R.J. 2008. Spatial scales of seed and pollen-mediated gene flow in tropical rain forest trees. – *Tropical Plant Biology*, **1**: 20-33.

El-Moneim, D.A. 2019. Characterization of ISSR and SCoT markers and TaWRKY gene expression in some Egyptian wheat genotypes under drought stress. – J. Pl. Prod. Sci., **8**(1): 31-46.

Etminan, A., Pour-Aboughadareh, A., Mohammadi, R., Ahmadi-Rad, A., Noori, A., Mahdavian, Z., Moradi, Z. 2016. Applicability of start codon targeted (SCoT) and inter-simple sequence repeat (ISSR) markers for genetic diversity analysis in durum wheat genotypes. – Biotechnol. Biotechnol. Equip., **30**: 1075–1081.

Ganapathy KN, Gomashe SS, Rakshit S, Prabhakar B, Ambekar SS, Ghorade RB, Patil JV (2012). Genetic diversity revealed utility of SSR markers in classifying parental lines and elite genotypes of sorghum (*Sorghum bicolor* L. Moench). – Austr. J. Crop Sc., **6**(11): 1486-1495.

Hassan, F.A.S., Ismail, I.A., Mazrou, R., Hassan, M. 2020. Applicability of inter-simple sequence repeat (ISSR), start codon targeted (SCoT) markers and ITS2 gene sequencing for genetic diversity assessment in *Moringa oleifera* Lam. – J. Appl. Res. Med. Aromat. Pl., **18**:100256.

Jaccard, P. 1908. Nouvelles recherches sur la distribution florale. – Bull. Soc. Vaud. Sci. Nat., **44**: 223-270.

Luz, G.C.; Strioto, D.K.; Mangolin, C.A.; Machado, M.D.F.P. 2020. ISSR markers to assess genetic diversity of cultivated populations from artificial selection of *Stevia rebaudiana* (Bert.) – Bertoni. Breed. Sci., **70**: 508–514.

Makouate, H. F., & Lekagne, J. B. D. 2022. African Pear (*Dacryodes edulis* (G. Don) HJ Lam). Physical characteristics, nutritional properties and postharvest management: – Rev. Agric. Conspect. Sci., **87**(1): 1-10.

Makueti, J. T., Otieno, G., Tchoundjeu, Z., Muchugi, A., Tsobeng, A., Asaah, E., & Kariba, R. 2015. Genetic diversity of *Dacryodes edulis* provenances used in controlled breeding trials. – J. Pl. Breed. Crop Sci., **7**(12): 327-339.

Kadji, B. R. L., Kone, F. M. T., Sika, A. E., and Dabonne, S. 2016. Physico-chemical properties of Safou (*Dacryodes edulis*) fruits grown in Côte d'Ivoire. – J. Appl. Biosci. **105**: 10103-10110.

Odesola, K.A., Olawuyi O.J., Paliwal R., Oyatomi, O.A & Abberton, M.T. 2023. Genome Wide association analysis of phenotypic traits in Bambara groundnut under drought-stressed and non-stressed conditions based on DArTseq SNP. – Front. Plant Sci., **14**: 1104417.

Okafor I. Variety delimitation in *Dacryodes edulis*. 2003. – Internl. Tree Crops J., **20** (2):255-265.

Oluwaniyi, O.O., Nwosu, F.O. & Okoye, C.M. 2017. Comparative study of the constituents of the fruits pulps and seeds of *Canarium ovatum, Persea americana* and *Dacryodes edulis*. – Jordan J. Chem., **12**(2): 113-125.

Olawuyi, O.J. & Azeez, A.A. 2019. Molecular evaluation of Garcinia kola Heckel accessions using RAPD markers. – Am. J. Mol. Biol., **9**(2): 41-51.

Olufemi, S., Odesola, K.A. & Olawuyi, O.J. 2024. Genetic diversity among selected Kersting's groundnut accessions based on SSRr, SCoT And RAPD Markers. – Ife J. Agric., **36**: (1).

Osman S.A. & Ali., H.B. 2020. Genetic diversity of five Lathyrus species using RAPD, ISSR and SCoT Markers. – Asian J Pl. Sci.**19**:152–65.

Rimlinger, A., Marie, L., Avana, M.L., Bouka, G. U. D., Zekraoui, L., Mariac, C., Carrière S. M. & Duminil, J. 2020. New microsatellite markers for *Dacryodes edulis* (Burseraceae), an indigenous fruit tree species from Central Africa. – Mol. Biol. Rep., **47**: 2391-2396.

Rohlf, F.J.j 2000. NTSYS-pc: numerical taxonomy and multivariate analysis system, version 2.1. Exeter Software, Setauket, New York

Saghai-Maroof, M. S., Soliman, K. M., Jorgensen, R. A., & Allard, R. W. 1984. Ribo-somal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chro-mosomal location, and population dynamics. – Proc. Nat. Acad. Sci 81: 8014-8018

Sika E.A., Kadji, R.L., Ouattara, L., Dabonné, S. & Koffi-Nevry, R. 2021. Antioxidant and Antimicrobial Activities of Various Extracts from Safou (*Dacryodes edulis*) Cultivated in Côte d'Ivoire. – Microbiol. Res. J. Int., **31**(8): 1-8.

Silou, T., Rocquelin, G., Mouaragadja, I. & Gallon, G. 2002. Chemical composition and nutritional characteristics of safou (*Dacryodes edulis*) of Cameroon and the Congo-Brazzaville, the Congo-Kinshasa and Gabon. – Riv. Ital. Sost. Grasse., **79**: 177-182.

Singh, R.B. Mahenderakar, M.D., Jugran, A.K., Singh, R.K. & Srivastava, R.K. 2020. Assessing genetic diversity and population structure of sugarcane cultivars, progenitor species and genera using microsatellite (SSR) markers. – Gene., **753**: 144800.

Soliman, E.R.S., El-Shazly H.H., Börner, A. & Badr, A. 2021. Genetic diversity of a global collection of maize genetic resources in relation to their subspecies assignments, geographic origin, and drought tolerance. – Breed Sci. **71**(3): 313–25.

Sowunmi, F.A., & Akintola, J.O. 2010. Effect of Climatic Variability on Maize Production in Nigeria. Res. J. Environ. Earth Sci., **2**(1): 19-30.

Tchinda, N.D., Wanjala, B. W., Muchugi, A., Fotso., Nzweundji, G., Ndoumou, D.O. & Skilton, R. 2016. Genetic diversity and gene flow revealed by microsatellite DNA markers in some accessions of African Plum (*Dacryodes edulis*) in Cameroon. – Afr. J. Biotechnol., **15**(13): 511-517

Waruhi, A.N., Kengue, J., Atangana, A. R., Tchoundjeu, Z. & Leakey, R.R.B. 2004. Domestication of *Dacryodes edulis*: 2. Phenotypic variation of fruit traits in 200 trees from four populations in the humid lowlands of Cameroon. – J. Food Agric. Env,, **2**(1): 340-346.