

Molecular characterization using SSR markers points to population admixture of genetic variation among introduced Cashew (*Anacardium occidentale* L.) in Northern Cameroon

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Short Report

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Abstract

Understanding the genetic diversity of cashew (*Anacardium occidentale* L.) is crucial for effective conservation and breeding programs. This study aimed to assess the genetic variability of 74 cashew genotypes collected from five provenances across three regions of northern Cameroon using 13 SSR markers. All primers successfully amplified DNA, producing an average of 2.5 polymorphic bands. The SSR markers revealed a low level of polymorphism, with two to three alleles per locus, which is relatively noteworthy for an introduced species.

Discriminant Analysis of Principal Components (DAPC) showed that the first two components explained 43.9% of the total variability, allowing clear discrimination of genotypes and revealing structured genetic variation. The genotypes were partitioned into seven clusters. Cluster analysis based on Nei's genetic distance confirmed these results, highlighting genetic structuring among populations. Genotypes from Ngaoundéré (Ng) were largely assigned to specific clusters, while those from Garoua (Ga) and Yagoua (Ya) were distributed across several clusters, indicating genetic differentiation, structure, and admixture. Most genotypes displayed strong cluster membership ($\geq 90\%$), but a subset showed admixed ancestry, suggesting human-mediated propagation or multiple introduction events of cashew germplasm into northern Cameroon.

The observed genetic variation likely reflects the combined influence of environmental factors, local adaptation, and historical cultivation practices. This study provides the first insights into cashew genetic diversity in northern Cameroon, offering a valuable basis for future production, conservation, and breeding efforts.

Introduction

Cashew (*Anacardium occidentale* L.), commonly called cashew or caju, is a tropical fruit tree widely cultivated across warm regions of the world Johnson (1973); Mitchell and Mori (1987). It belongs to the Anacardiaceae family, which comprises about 75 genera and nearly 700 species Nakasone and Paull (1998); Asna and Menon (2024). The genus *Anacardium* itself contains eight species native to tropical America, of which *A. occidentale* is the most economically significant Azam-Ali and Judge (2001). This species, with a chromosome number of $2n = 42$, has become the leading tropical nut crop due to its broad social and economic importance. Today, cashew cultivation is established in more than 40 countries across Africa, Asia, Latin America, and the Caribbean UNCTAD (2021).

In Cameroon, cashew was first introduced in 1975 in the northern regions through an initiative of the National Office for Forest Development (ONADEF) as part of a reforestation and environmental protection program. For several years, its adoption remained limited. Renewed interest emerged in the early 2000s, driven by farmers and government policies that sought to diversify agricultural income sources and reduce dependence on cotton, the dominant cash crop in northern Cameroon. Farmers in the North and Far North regions began integrating cashew into their farming systems, often intercropping it with vegetables and food staples Noiha *et al.* (2017). To consolidate this momentum, the

Cameroonian government adopted a national strategy in 2018 to promote the cashew value chain, later revised in 2024 with the ambition of positioning the country among the world's leading producers by 2030 Adeniyi et al. (2019); Noiha *et al.* (2017). Ongoing projects in the Far North highlight cashew's potential as a source of revenue for rural households, particularly in regions where poverty rates remain among the highest in the country.

The cashew tree is highly versatile, with multiple uses across its organs: wood for furniture, bark and leaves for traditional medicine, and kernels as the principal commercial product Haiwa et al. (2024). Surveys in northern Cameroon indicate that commercial and food uses dominate, while medicinal and artisanal applications are less common (Nnanga et al. (2023). Despite its growing economic relevance, research on cashew production and processing in Cameroon remains limited. Interest is, however, expanding, especially among policymakers and researchers, who view cashew as both a livelihood and environmental asset. For example, the Cotton Development Company (SODECOTON) and the Institute of Agricultural Research for Development (IRAD) are working to integrate cashew into cotton production systems to strengthen rural economies while improving environmental sustainability Madou et al. (2020).

As with other perennial crops, evaluating genetic variability is a prerequisite for effective breeding programs. The success of selecting superior genotypes depends on the diversity of traits within the gene pool. In cashew, fruit set and yield can be influenced by genetics, pollination, agronomic practices, and environmental conditions Yaman and Uzun (2020). Constraints such as low productivity, use of heterogeneous planting materials, limited breeding efforts Moumouni *et al.* (2022), and the occurrence of pests and diseases Wonni et al. (2017) often aggravated by climate instability Ben Zaied and Ben Cheikh (2015) further underscore the need for improved varieties. Developing and disseminating high-yielding and resilient genotypes is therefore essential to meet increasing market demands Tarpaga et al. (2020); Moumouni *et al.* (2022).

Molecular tools offer a reliable means to characterize genetic diversity in tree crops. DNA based markers are particularly valuable because they are not affected by environmental conditions or plant developmental stages He et al. (2014). In cashew, several marker systems such as Random Amplified Polymorphic DNA (RAPD) Santhosh *et al.* (2009); Jena et al. (2016), Amplified fragment length polymorphism (AFLP) (Archak et al. (2003), microsatellites, single nucleotide polymorphisms (SNPs) Savadi *et al.* (2023); Mukhebi et al. (2025) and sequence-specific amplification polymorphism (SSAP) Syed et al. (2005) have been employed to assess genetic variability and construct linkage maps. Among these, microsatellite markers are especially useful due to their codominant inheritance, reproducibility, and high polymorphism, making them suitable for fingerprinting and diversity studies Sultana et al. (2022); Savadi et al. (2025).

The present study aims to investigate the genetic diversity and relationships among 74 cashew genotypes collected from Adamawa, North, and Far North regions of Cameroon using SSR markers. This

work provides baseline knowledge that could support breeding, conservation, and sustainable development of cashew in the country.

Materials and Methods

Plant material

A total of seventy-four (74) cashew (*Anacardium occidentale* L.) genotypes were collected from three experimental orchards located in the northern regions of Cameroon (Adamawa, North, and Far North). Nut samples were obtained from farmers' plantations during February 2019 Madou *et al.* (2020). The collection comprised 16 genotypes from Yagoua (Ya), 15 from Garoua (Ga), 15 from Touboro (Tb), 14 from Ngaoundéré (Ng), and 15 of undetermined provenance (Tv) (Figure 1). The cashew germplasm cultivated in these regions was originally introduced in 1975 as part of a reforestation and agricultural diversification program Patrice *et al.* (2020); Dooh *et al.* (2021).

DNA extraction

Young, healthy leaves were collected from single trees representing each cashew morphotype. Genomic DNA was isolated from 100 mg of fresh leaf tissue using the cetyltrimethylammonium bromide (CTAB) protocol Doyle and Doyle (1990). The quality and integrity of the extracted DNA were assessed by electrophoresis on a 2% (w/v) agarose gel.

SSR amplification

Thirteen microsatellite markers previously developed by Croxford *et al.* (2006) and Jaime *et al.* (2007) were used to evaluate genetic diversity (Table 1). These markers were chosen because of their high polymorphic information content reported in earlier cashew diversity studies Cavalcanti and Wilkinson (2007a); Aliyu (2012); Kouakou *et al.* (2020).

Polymerase chain reaction (PCR) amplification was performed using the AccuPower® PCR Premix kit (Bioneer, Korea) in a 20 µL reaction mixture containing 3 µL of template DNA, 1 µL of each primer (forward and reverse), and nuclease-free water. Reactions were carried out in an Applied Biosystems 2720, using a reaction AccuPRC volume of 25 µL containing 5 µL of 5X Promega buffer, 0.5 µL of each primer, 0.5 µL of dNTPs, 0.05 µL of Taq polymerase and 2 ng of DNA. The thermal cycling profile consisted of an initial denaturation step at 94 °C for 5 min, followed by 35 cycles of denaturation at 94 °C for 1 min, annealing at primer-specific temperatures for 1 min, and extension at 72 °C for 1 min, with a final extension at 72 °C for 7 min. PCR products were separated on 2% agarose gels alongside a 100 bp DNA ladder to verify amplification and product size.

Table 1. Details of the 13 microsatellite (SSR) loci used for *Anacardium occidentale* genotyping, including primer sequences and optimal annealing temperatures (Ta) as reported by Croxford *et al.* (2006) and Jaime *et al.* (2007).

Data analyses

DNA profiles were scored visually from the gel images. The fragments generated by SSR amplification were treated as molecular markers, and each individual was genotyped by direct inspection of the bands. Polymorphic fragments were coded in a binary format, and the resulting dataset was compiled in a Microsoft Excel spreadsheet to generate the analysis matrix.

Genetic diversity parameters, including the number of alleles and polymorphism information content (PIC), were calculated to evaluate genetic variation among cashew genotypes. Discriminant analysis of principal components (DAPC) and cluster analysis were performed to explore population structure.

Nei's genetic distance was computed to quantify genetic divergence between pairs of individuals based on allele frequencies. The resulting genetic distance matrix was used to construct a Neighbor-Joining (NJ) tree, which provided insights into clustering patterns among cashew accessions. The observed clusters were subsequently compared with the known geographical origins of the accessions in order to assess the influence of provenance on genetic structure.

RESULTS

SSR Polymorphism

All 13 SSRs successfully generated at least one allele in the region of the expected size for cashew genotypes. Size of markers ranging from 100 and 250 bp.

The number of amplified bands per marker for all genotypes ranged from 33 to 52. The lowest number of bands was observed in mAoR7 (33 bands) and one band per genotype was found. The marker mAoR17 produced a total of 52 bands, with 2 bands per genotype in such cases. All the markers proved to be polymorphic. No marker produced monomorphic bands in all 74 introduced genotypes.

The markers mAoR6 and mAoR11 were detected in nearly 75% of the cultivars, whereas mAoR41 was absent in about 60% of all cultivars analyzed. In the accessions from Ngaoundere, the Aocc14 marker was present in only one individual, while mAoR41, mAoR47, and mAoR29 were absent in 86% of the genotypes.

Polymorphism was high enough to enable discrimination of all thirteen markers, showing that the 13 markers used were polymorphic. Significant allelic variations were also observed, 6 SSR markers presented 2 alleles and 7 markers presented 3 alleles. All the varieties could be discriminated by SSR profiles.

Polymorphism Information Content (PIC) value represents the relative informativeness of each marker. In the present study, the average of PIC value was found to be 0.46. The highest genetic diversity is explained by the genotypes included in this study with the mean PIC value ranged between 0.38 for marker mAoR6 to 0.50 for markers mAoR48 and mAoR44.

Table 2. Number of alleles, amplified bands, and Polymorphism Information Content (PIC) values for 13 SSR loci in 74 cashew (*Anacardium occidentale* L.) genotypes.

Genetic variation analysis

Polymorphisms among the 74 cashew cultivars was detected by 13 SSR markers. Discriminant analysis of principal components (DAPC) sorted the genotypes into different groups according to the polymorphic banding pattern (Fig. 2)

The association of the 74 genotypes was examined using genetic distance matrix data of 13 SSR markers. The Discriminant Analysis of Principal Components was employed to gain insight into the germplasm and genetic relationship of the population. The first two principal Components contributed to explain the variation (Fig. 3 and Fig. 4).

The results show there is a diversity between and within the regions of collected samples.

A second component with eigenvalue separated the germplasm into 7 clusters which identified the population structure. Cluster 1 consisted of highest 17 genotypes from 4 different origins. Cluster 3 retained 8 genotypes from 4 different origins.

With the max membership probability, MCLUST, implemented in a R package analysis based on the SSR marker genotypes revealed its potential in producing distinct membership probability to unequivocally assign individuals of an admixed population to subgroups.

This approach allowed us to estimate the membership probabilities of each genotype in distinct genetic clusters. The analysis was carried out under an admixture model with correlated allele frequencies, where multiple independent runs were conducted for each assumed number of clusters.

Our results indicated that most genotypes displayed high membership probabilities (greater than 90%) for a single cluster, suggesting well-defined and distinct genetic groups. However, a subset of genotypes exhibited admixed ancestry, with membership probabilities distributed across two or more clusters. This finding that is consistent with the clustering observed in the Neighbor-Joining tree constructed using Nei's genetic distance.

Cluster and origin analysis

The genetic relationship between the 74 genotypes was assessed using a clustering analysis based on the genetic dissimilarity matrix obtained from SSR markers. Discriminant analysis of principal components (DAPC) divided these genotypes into seven clusters (Figure 3). Cluster 1 contained the largest proportion of individuals, comprising 50% of accessions from Ngaoundéré, 28.57% from Touboro, 14.28% from Yagoua, and 7.14% from Garoua. Cluster 2 contained 12 genotypes, 44.44% of which were from Garoua. Cluster 3 included 42.86% of genotypes originating from Touboro. Cluster 4 contained 25% of accessions from Yagoua and 25% from Garoua. Cluster 5 was composed of 38% genotypes from

Yagoua. Cluster 6 had a high proportion of accessions of undetermined origin (83.33%). Finally, cluster 7 contained 38% accessions from Touboro and 38% from Garoua. Overall, genotypes from Garoua and Yagoua are distributed across six of the seven identified clusters, while those from Ngaoundéré are concentrated in three clusters, with 86% in clusters 1 and 2. Hence, closed genetic relation was seen between the accessions of Touboro and Garoua grouped in Cluster 1,2,3,4 and 7 due to genetic resemblance.

Diversity and structuring of cashew tree through probabilistic membership analysis

Analysis of cluster membership (Figure 4) reveals marked contrasts between provenances. The accessions from Yagoua and Garoua are distributed across several genetic groups, indicating high diversity and admixture. Those from Touboro show intermediate diversity, while the accessions from Ngaoundéré exhibit pronounced genetic homogeneity. Accessions of undetermined origin are scattered across all clusters. The membership probability of assigning genotypes estimates the likelihood that a genotype belongs to a given cluster. In this study, the results reveal that some accessions are distributed across several clusters, while others show a high probability (up to 80%) of belonging to a single cluster. Accessions such as Ya11, Ga7, Ga10, Ga14, Tv5, Ng2, and Tv10 show membership probabilities distributed across three clusters, while Tv8 spans four clusters. This pattern suggests potential crossing or genetic exchange between provenances

Phylogenetic analysis of cashew genotypes based on Nei's genetic distance

The phylogenetic tree constructed using the Neighbor-Joining based on Nei's genetic distance (Fig. 5). It graphically represents the genetic proximity or divergence among different accessions. Individuals or populations sharing a low Nei's distance cluster together in neighboring branches. This tree reveals a distinct grouping of cashew tree accessions into several branches, reflecting the genetic diversity highlighted by SSR markers. Genotypes from Garoua and Yagoua are distributed across several branches, suggesting high intra-provenance heterogeneity and possible gene flow between populations. In contrast, some accessions from Ngaoundéré appear grouped in tighter branches, reflecting greater genetic homogeneity. Accessions of undetermined origin (Tv) are scattered across different clades.

Discussion

Genotypic variability of cashew accession from the three northern regions of Cameroon

The present study represents the first attempt to characterize the genetic diversity of cashew populations in northern Cameroon, a region where little information is available compared to other production zones. The study focused on 74 accessions genotyped with 13 SSR markers to investigate the extent of genetic variability and population structure.

The results of this study highlight a high degree of genetic structuring among the 74 cashew accessions analyzed, collected from different provenances (Ga, Tb, Ng, Ya, and Tv). The absence of monomorphic markers and the relatively high number of alleles (2 to 3 per locus) indicate a high degree of polymorphism, confirming the relevance of the SSRs chosen for characterizing genetic diversity. This diversity is particularly notable for an introduced species, undoubtedly reflecting the multiplicity of sources of introduction and/or exchanges of plant material between farmers Meyer et al. (2021).

The discriminant analysis of principal components (DAPC) provided further insight into the genetic relationships, with the first two axes explaining 43.9% of the total variance (35.2% and 8.7%, respectively). The DAPC partitioned the accessions into seven clusters comprising genotypes of different provenances, thereby highlighting the existence of distinct genetic groups. Importantly, most individuals displayed strong membership probabilities (> 90%) to a single cluster, supporting the presence of clearly differentiated genetic groups. Nonetheless, a subset of accessions showed admixed ancestry, with membership probabilities distributed across multiple clusters. Such admixture patterns, as similarly observed in alpaca populations managed under community-based systems Peralta et al. (2025), suggest historical gene flow and the exchange of planting material between different cashew-growing regions. This is particularly plausible in northern Cameroon, where farmers frequently exchange seeds and grafting material, favoring the introduction of alleles from diverse origins.

Our results suggest a high level of genetic variability within the cashew germplasm of northern Cameroon, making it a valuable resource for the creation of improved hybrids. The analysis of membership probabilities and genetic distances provides valuable insights into the genetic diversity of the germplasm, which is essential for developing targeted breeding strategies. The higher variability among these cashew genotypes is particularly noteworthy, as it may provide a valuable resource for breeding programs aimed at enhancing resilience to climate change and disease. The ability of SSR markers to reliably differentiate genotypes confirms their relevance for genetic characterization and marker-assisted selection, and paves the way for the rapid identification of divergent parental lines. This approach would allow hybrid vigor to be exploited and a large genetic pool to be maintained, as has been observed in other perennial species Gelaye and Luo (2024); Zhou et al. (2024).

However, the high diversity obtained should be interpreted with caution, as they may be influenced by sample size, the number and type of loci studied, and the allelic richness of the markers used Moumouni *et al.*, (2022); Das et al., (2025). Although the SSRs used proved to be sufficiently polymorphic to describe genetic diversity, the future integration of high-density markers, such as SNPs, would allow for a better understanding of genomic variability and refine our understanding of population structure.

Origin of cashew genotypes

The genetic structure of the 74 cashew genotypes indicates significant differentiation among provenances,, confirming the hypothesis that environmental pressures and evolutionary history influence genetic diversity Manel et al. (2003); Muller et al. (2006); Miller et al. (2012). The DAPC analysis highlights contrasts between provenances. Some show pronounced genetic homogeneity, while others

display a more diverse structure, reflecting distinct dispersal dynamics Bohonak (1999); Mushtaq et al. (2022). The Ng and Tb provenances, in particular, reveal high genetic homogeneity. This result could reflect uniformity linked to systematic factors such as collection methods or environmental conditions (Salgotra and Chauhan (2023); Velasco et al. (2025)). The very low diversity observed in the genetic material of cashew trees from the Ng provenance could also be explained by self-pollination (Samal et al. (2003); Bhadra et al. (2019)).

Conversely, the Ya and Ga provenances show higher genetic variability, probably linked to regional differences or variations in classification criteria (Asna and Menon (2024); Lahai et al. (2025)). In this results accessions: Ya11, Ga7, Ga10, Ga14, Tv5, Ng2, Tv10 and Tv8 show membership probabilities distributed across three and four clusters. This pattern suggests potential crossing or genetic exchange between provenances reflecting genetic admixture Kong et al. (2024); Guo *et al.* (2024); Żukowska and Lewandowski (2025). In practice, when a provenance shows high genetic diversity, it is recommended to first confirm the selection on a large natural population rich in diversity, then identify the best-performing individuals Fu (2015); Bhandari et al. (2017). In this study, cultivars from Ng were grouped into a separate cluster. This specificity could be explained by the reproductive mode of the cashew tree, whose flowers are adapted to cross-pollination but can, in the absence of pollen donors, resort to insect-facilitated self-pollination, thus promoting genetic recombination Cavalcanti and Wilkinson (2007b); Lahai et al. (2025). Furthermore, the absence of strict geographical isolation could contribute to the homogenization of genes between provenances Chen et al. (2023).

The phylogenetic tree constructed using the Neighbor-Joining method based on Nei's genetic distance provides important insights into the genetic structure of cashew accessions. The clear separation of accessions into distinct branches reflects the genetic diversity revealed by SSR markers, confirming their effectiveness in assessing population differentiation Kouakou et al. (2020); Savadi *et al.* (2021). The distribution of genotypes from Garoua and Yagoua across multiple branches indicates a high level of intra-provenance heterogeneity. This pattern may be explained by extensive gene flow among populations, possibly mediated through natural pollination or seed exchange by farmers. In contrast, the clustering of certain accessions from Ngaoundéré into more compact branches suggests higher genetic homogeneity within this provenance, which could be the result of a narrower genetic base or more intensive selection practices. Interestingly, the accessions of undetermined origin (Tv) are dispersed across different clades, highlighting their admixed ancestry and potential role as genetic bridges between populations. Overall, these findings provide evidence of both genetic differentiation and connectivity among cashew provenances, which are key elements for guiding breeding programs and conservation strategies.

However, these interpretations remain hypothetical and require further genetic and ecological investigations to confirm these mechanisms and clarify their determinants.

Local adaptation and historical influences of accessions in production areas

The variability observed in the cashew genetic material collection could result from the genetic history of the populations, their geographical origin, and the selection of traits sought by farmers Mohana et al. (2023); Asna and Menon (2024). The genotypes from Garoua and Yagoua are distributed across six of the seven identified groups, while those from Ngaoundéré are concentrated in three groups, with 86% in groups 1 and 2. This structure likely reflects local adaptation phenomena or the influence of historical events on the genetic diversity of these populations.

A close genetic relationship has been observed between the Touboro and Garoua accessions, grouped in groups 1, 2, 3, 4, and 7. This genetic proximity could result from historical gene flow or shared agricultural practices in these regions, promoting greater genetic homogeneity within their populations Bøhn et al. (2016); Mukhebi et al. (2025). Such structuring could also reflect local adaptation or historical processes influencing the genetic diversity of these populations Mopper and Strauss (2013). This pattern is consistent with results obtained for other crops, where geographical proximity and common farming practices facilitate gene exchange (Smolders (2006); Mukhebi et al. (2025).

In contrast, genotypes from other regions showed greater genetic variability, potentially reflecting differences in adaptation or exposure to distinct environmental pressures. The marked genetic differentiation between genotypes from different provenances supports the idea that geographical barriers or environmental factors influence genetic variation in cashew trees Sexton et al. (2015).

The genetic proximity between these genotypes highlights the potential for utilizing these populations in breeding programs targeting specific traits shared between these provenances. Conversely, genotypes from more distant origins showed greater genetic variability, suggesting that they may exhibit adaptive traits linked to unique environmental conditions or historical factors that have shaped their genetic makeup Xiang et al. (2020); Putnins and Androulakis, (2021).

Conclusion

This preliminary study revealed significant genetic diversity among 74 cashew genotypes from northern Cameroon using 13 SSR markers. The analyses revealed high polymorphism, marked genetic structuring, and regional groupings reflecting the influence of geographical origin, local adaptation, and evolutionary history. These results highlight the value of SSR markers for characterizing and conserving genetic diversity, guiding variety improvement programs, and enhancing the sustainability of cashew cultivation in Cameroon.

Declarations

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Author contributions

All the authors contributed to the study conception and design. Material preparation, data collection and data analysis. The first draft of the manuscript was written by ZAIYA ZAZOU Arlette and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Conflict of interest

The authors declare no conflicts of interest of relevance to this topic.

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Tables

Table 1. Details of the 13 microsatellite (SSR) loci used for *Anacardium occidentale* genotyping, including primer sequences and optimal annealing temperatures (Ta) as reported by Croxford et al. (2006) and Jaime et al. (2007).

Locus	Primer Sequence (5'-3')	Repeat Motif	Annealing Temp (°C)
mAoR6	F: CAAAACTAGCCGGAATCTAGC R: CCCCATCAAACCCTTATGAC	(AT) ₅ (GT) ₁₂	58.2
mAoR7	F: AACCTTCACTCCTCTGAAGC R: GTGAATCCAAAGCGTGTG	(AT) ₂ (GT) ₅ AT(GT) ₄	58.2
mAoR11	F: ATCCAACAGCCACAATCCTC R: CTTACAGCCCCAAACTCTCG	(AT) ₃ (AC) ₁₆	60.3
mAoR17	F: GCAATGTGCAGACATGGTTC R: GGTTTCGCATGGAAGAAGAG	(GA) ₂₂	56.1
mAoR29	F: GGAGAAGAAAAGTTAGGTTTGAC R: CGTCTTCTTCCACATGCTTC	(TG) ₁₀	61.0
mAoR41	F: GCTTAGCCGGCACGATATTA R: AGCTCACCTCGTTTCGTTTC	(GGT) ₈	58.2
mAoR42	F: ACTGTCACGTCAATGGCATC R: GCGAAGGTCAAAGAGCAGTC	(CAT) ₉ TAT(CTT) ₇	60.3
mAoR44	F: CACGTTCGCATCATCCAA R: CGTCAGAGATTACGGCATTG	GTG(GT) ₃ GCT(GGT) ₄	58.2
mAoR46	F: CGGCGTCGTAAAGCAGT R: TCCTCCTCCGTCTCACTTTC	(ACC) ₇ (AC) ₃	61.0
mAoR47	F: AAGAGCTGCGACCAATGTTT R: CTTGAACTTGACACTTCATCCA	(TAAA) ₂ (TA) ₇ (AAT) ₅	58.2
mAoR48	F: CAGCGAGTGGCTTACGAAAT R: GACCATGGGCTTGATACGTC	(GAA) ₆ (GA) ₃	58.2
mAoR55	F: TGACTTTCAAATGCCACAAC R: CTCAAGCTTTCATGGGGATT	(AC) ₂ CC(AC) ₅ (TTAT) ₆	58.2
Aocc14	F: AATTGAAGAGTGATTTGGTTG R: AATAACATGCTTACTTACTCAAAT	(AT) ₂ (GT) ₅ TA(TG) ₉	56.0

Table 2. Number of alleles, amplified bands, and Polymorphism Information Content (PIC) values for 13 SSR loci in 74 cashew (*Anacardium occidentale* L.) genotypes.

Locus	Number of Alleles	Number of Amplified Bands	PIC Value
mAoR6	3	56	0.38
mAoR7	3	33	0.49
mAoR11	2	55	0.39
mAoR17	3	52	0.43
mAoR29	2	46	0.47
mAoR41	2	28	0.47
mAoR42	3	48	0.46
mAoR44	3	38	0.50
mAoR46	2	50	0.44
mAoR47	2	43	0.49
mAoR48	3	37	0.50
mAoR55	2	45	0.48
Aocc14	3	47	0.47

Figures

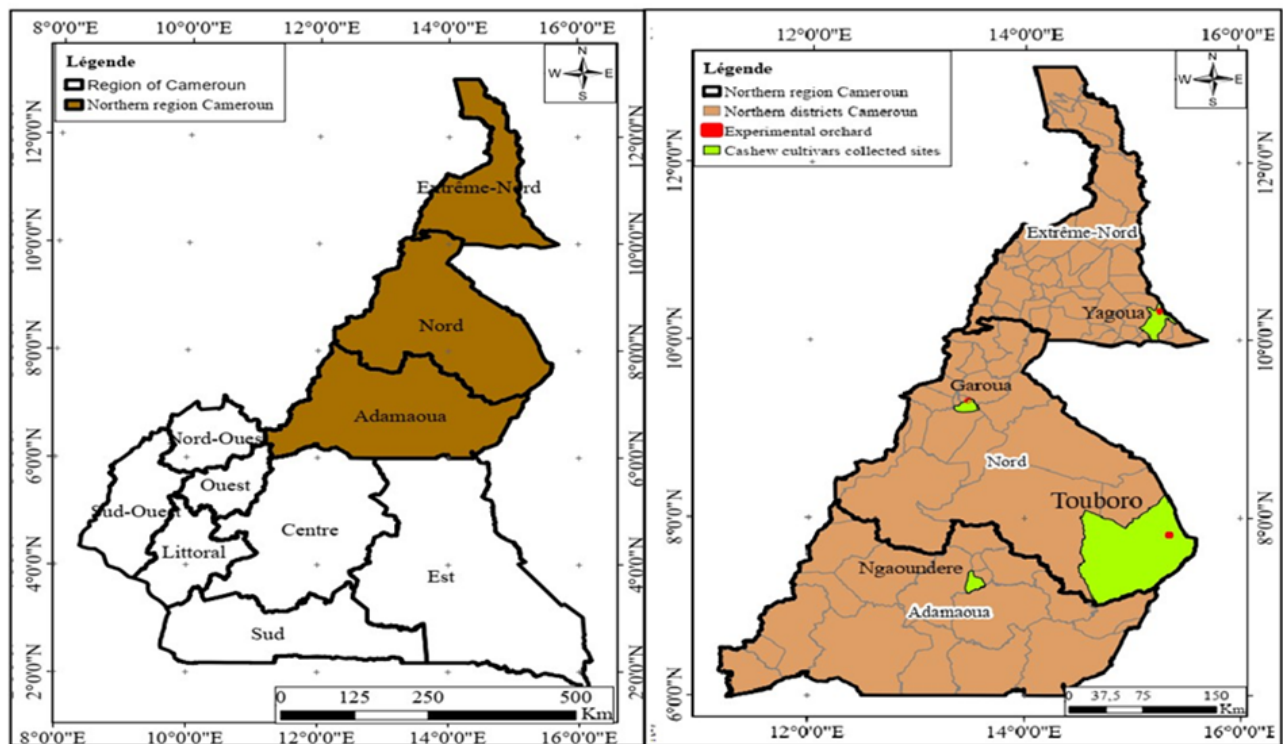


Figure 1

Geographical location where cashew accessions were collected.

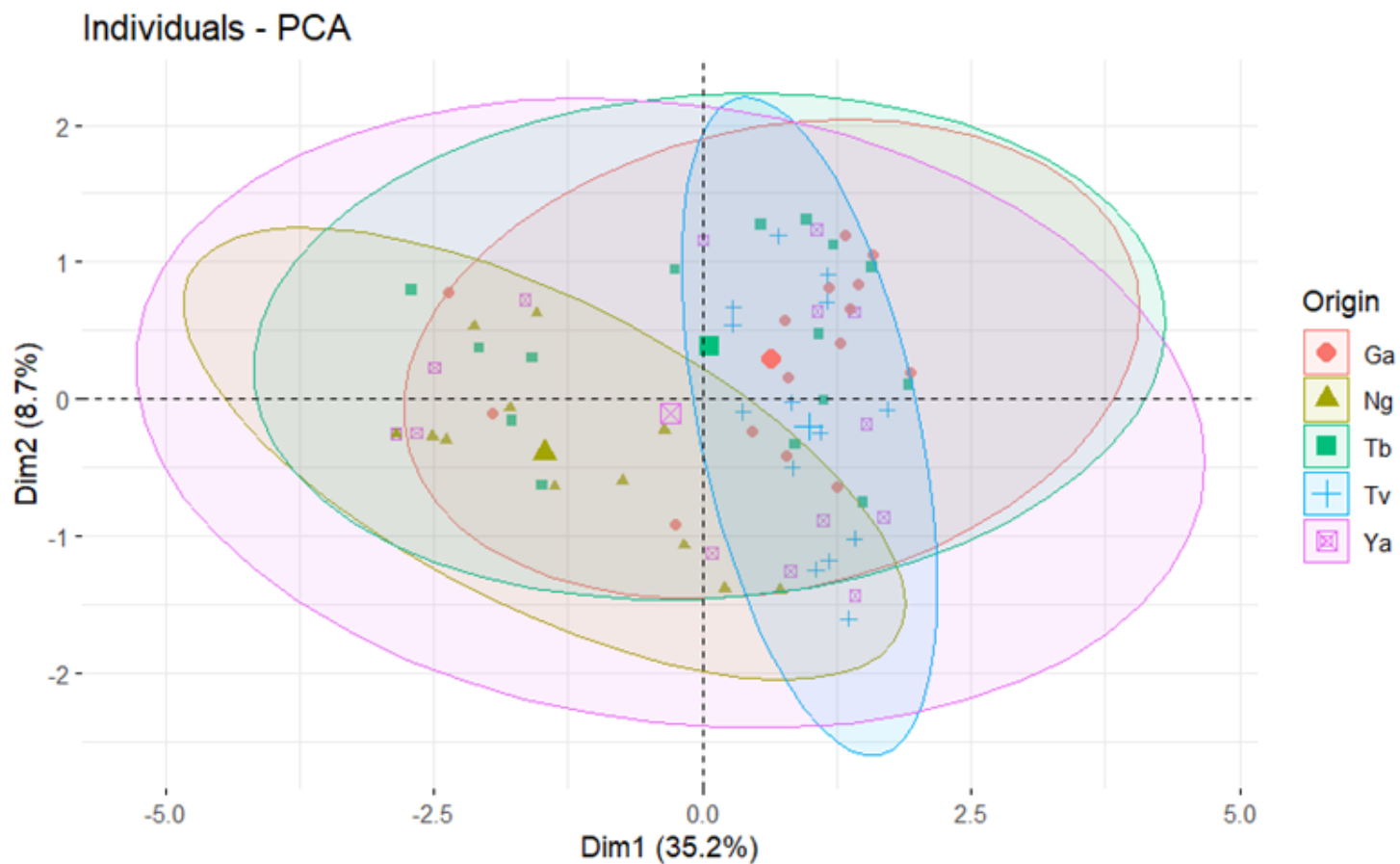


Figure 2

Discriminant analysis of principal components (DAPC) for 74 Cashew genotypes of the germplasm collection of collected from cashew-growing regions of Cameroon. Each colour represents the different provenances identified each dot represents an individual. Ga: Garoua Origin; Ya: Yagoua origin; Tb: Touboro origin; Ng: Ngaoudéré origin and Tv: Indeterminate origin.

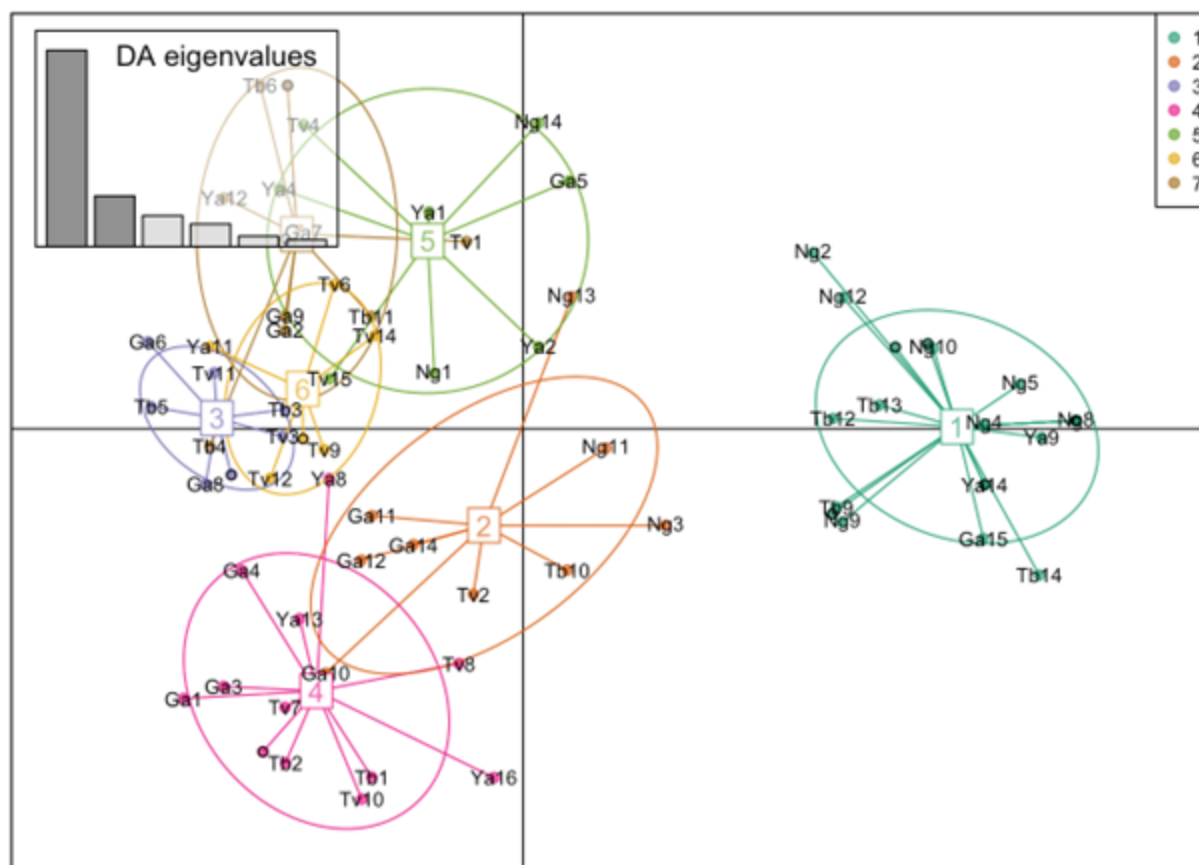
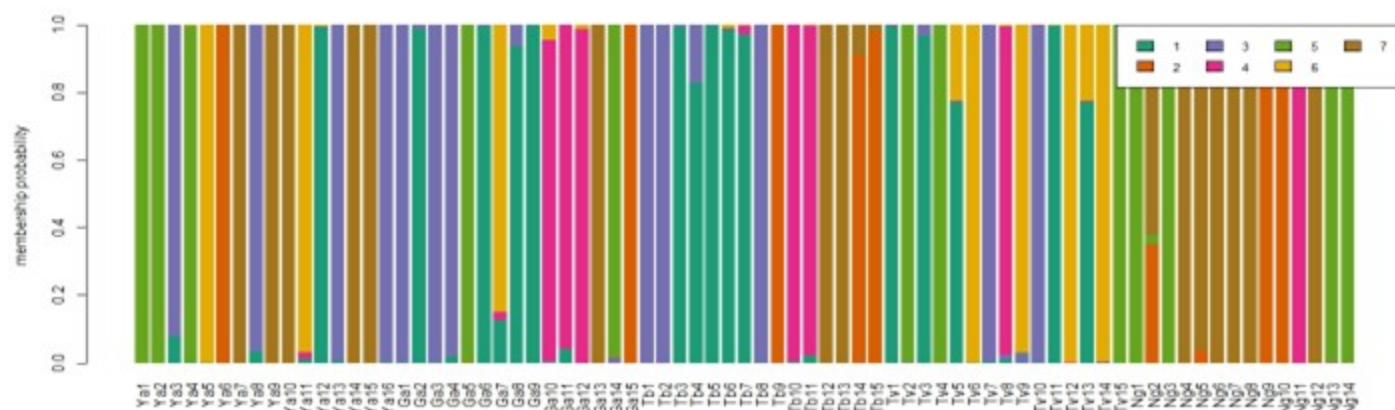
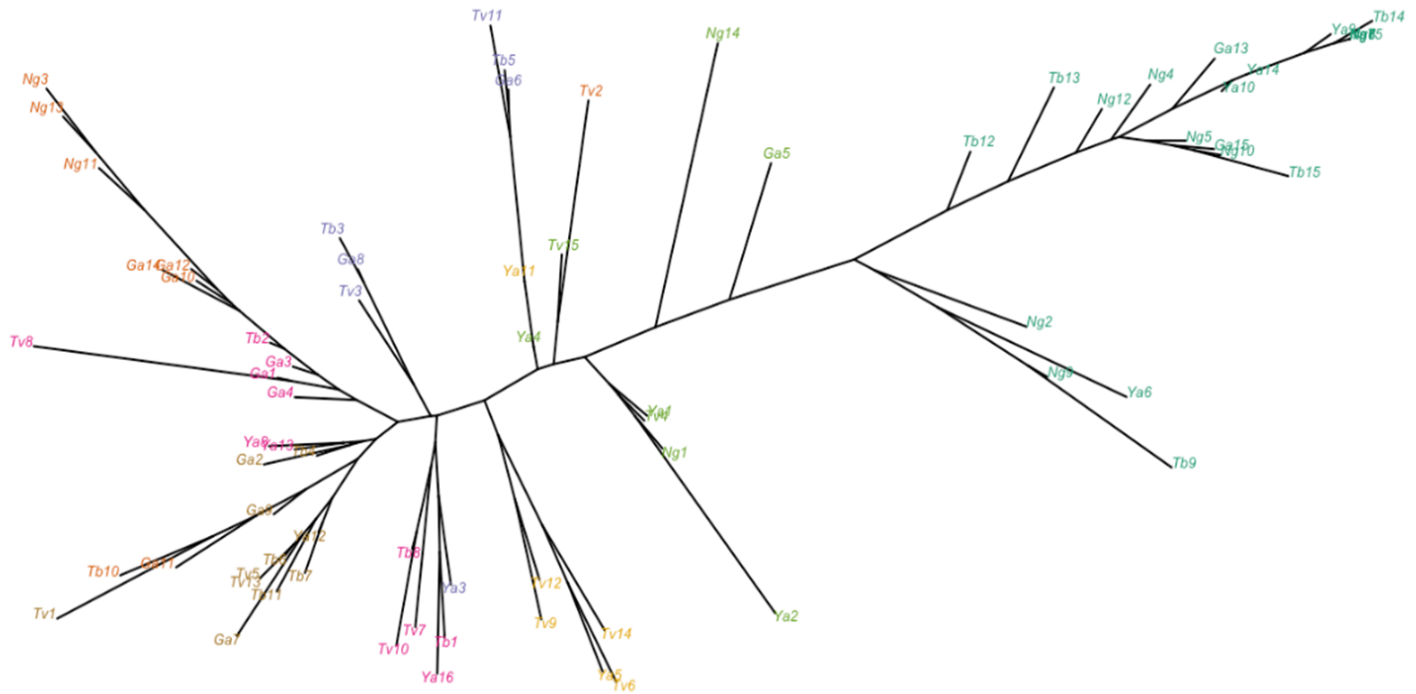


Figure 3

Grouping of genotypes based on Discriminant Analysis of Principal Components (DAPC), a multivariate method designed to identify and describe clusters of genetically related individuals. Results of the genetic structure analysis of 74 cashew nut genotypes based on their area of origin using the three-dimensional factorial correspondence analysis method according to the main plan. Each circle represents a cluster and each dot represents an individual. Each population is represented by its center of gravity. Ga: Garoua Origin; Ya: Yagoua origin; Tb: Touboro origin; Ng: Ngaoudéré origin and Tv: Indeterminate origin.



Membership probability of assigning genotypes Pattern of variation of 74 accessions based on 13 SSR markers. Bar lengths represent the membership probability of accessions belonging to different subgroups. Each colour represents a cluster. Ga: Garoua Origin; Ya: Yagoua origin; Tb: Touboro origin; Ng: Ngaoudéré origin and Tv: Indeterminate origin.



The neighbor-joining tree constructed from Nei's genetic distance revealed distinct clustering among the cashew. Use the Neighbor-Joining algorithm to construct a phylogenetic tree from the distance matrix. Ga: Garoua Origin; Ya: Yagoua origin; Tb: Touboro origin; Ng: Ngaoudéré origin and Tv: Undeterminate origin.