**ASSESSMENT OF THE GENETIC DIVERSITY OF THE ACACIA TREE SPECIES IN KENYA USING MOLECULAR MARKERS FOR CONSERVATION GENOMICS.**

# **ABSTRACT**

Acacia trees are vital to Kenyan ecosystems, contributing to soil enrichment, biodiversity, and wildlife support. They belong to the Fabaceae family and include species like Acacia nilotica and Acacia xanthophloea, which are essential for agroecosystem restoration, land reclamation, and local livelihoods in arid areas. These trees offer resources such as fodder, medicinal products, timber, and honey, with some species also showing potential for new uses, like vegetable tannin from Acacia xanthophloea bark. Recent research using advanced DArTseq technology aims to explore the genetic diversity and population structure of Acacia trees in Kenya, providing crucial data for conservation and sustainable management.

Four populations containing seven samples of the ancient Acacia tree were used to investigate the genetic diversity through DArTSeq technology. The samples were collected from different locations and DNA extracted, libraries generated, and sequenced under the Illumina Hiseq 2500 system. The data was then filtered for SilicoDArT and SNP marker calling and generation.

The genetic diversity among Acacia samples was low, indicating minimal environmental and human impact on the species. Older tree samples from Kitui and Naivasha exhibited slight differences in unique alleles, contributing to variance within populations. The study revealed that while the DArT platform effectively genotyped indigenous Acacia species, the genetic diversity was low, suggesting potential vulnerability to environmental and genetic challenges. Despite this, high polymorphisms and moderate genetic differentiation indicate that Acacia species have not been significantly impacted by human activities, highlighting their potential for future research and conservation efforts.

*Keywords:* *Acacia trees, DArTseq, SNP markers, DNA extraction, Genetic diversity, Conservation, Population structure, Sequencing*

# **Abbreviations**

AMOVA - Analysis of Molecular Variance

ASAL - arid and semi-arid lands

DArT - Diversity Arrays Technology

DArTseq - Diversity Array Technology Sequence

DNA - Deoxyribonucleic acid

GBS - Genotyping by Synthesis

HWE - Hardy-Weinburg Equilibrium

MAF - Minor Allele Frequency

PCR - Polymerase chain reaction

PCA - Principal Component analysis

PIC - Polymorphism Information Content

SNP - Single Nucleotide Polymorphism

UPGMA - Unweighted Pair Group Method with Arithmetic Mean

# **INTRODUCTION**

Acacia trees are prominent components of ecosystems in Kenya, playing crucial roles in soil enrichment, biodiversity maintenance, and supporting numerous wildlife species. The acacia classification is of the kingdom: Plantae, order: Fabales, family: Fabaceae, genus: Vachellia, and species: V. *nilotica*. The Family Fabaceae or Leguminosae includes plants like Pea, bean or legume family, is the third largest Angiosperm (flowering plants) family with over 700 genera and about 20 000 species.

This tall tree reaches a height of up to 30 meters and is characterized by its smooth, yellow/green photosynthetic bark. The small bipinnate leaves feature paired straight stipules that are white and spinescent. The numerous bisexual flowers form round yellow spikes, each exhibiting regularity. The flowers contain exserted stamens and pistils with a superior ovary and extending style. The fruit is a non-sickle-shaped, flattish pod, tardily dehiscent, measuring up to 13cm in length. The tree has a dense spherical crown, with stems and branchlets often dark to black in color, fissured bark, and a greyish-pinkish slash that releases reddish low-quality gum. Young trees display thin, straight, light-gray spines in axillary pairs, typically ranging from 3 to 12 pairs long and 5 to 7.5 cm in length. Mature trees, on the other hand, usually lack thorns. The bipinnate leaves have 3-6 pairs of pinnulae and 10-30 pairs of leaflets, each leaflet measuring 4-5 mm long and exhibiting +/- tomentose characteristics. The rachis bears a gland at the bottom of the last pair of pinnulae. The flowers are arranged in globulous heads, 1.2-1.5 cm in diameter, of a bright golden-yellow color, either axillary or whorly on peduncles 2-3 cm long located at the end of the branches. The pods are grey, thick, softly tomentose, straight or slightly curved, measuring 5 to 15 cm long on a pedicel, and 0.5 to 1.2 cm wide (David Becking, 2023).

In Kenya, the most dominant species are the *Acacia Senegal, Acacia xanthophloea, Acacia nilotica,* and the *Acacia brevispica*. The arid and semi-arid land (ASALs) of Africa is mostly degraded due to human interference, and climate change. They barely receive adequate rainfall annually (less than 400 mm). Hence the Acacia tree species has been detrimental in ensuring both agroecosystems restoration, land reclamation through nitrogen fixation, and providing local communities with survival income (Omondi et al., 2010).

Acacia trees play a vital role as a valuable natural resource for rural communities inhabiting arid regions worldwide. These trees serve multiple purposes, including providing livestock fodder, medicinal resources, timber, poles, charcoal, and fuel wood. Acacia pollination is by insects, and they later develop fruits after 4 to 6 months. Additionally, Acacia plants contribute to sustaining various life forms while offering pollen and nectar for honey production. In the Arid and Semi-arid Lands of Kenya, specific Acacia species serve as crucial livelihood sources. In Kitui County, Kenya, efforts have been made to explore wild silk production, but the primary significance of Acacia woodlands lies in the generation of high-quality honey. The honey, renowned for its exceptional quality, experiences strong demand both locally and nationally, making honey production a significant source of livelihood for the communities in the area. (Warui et al., 2018). Acacia xanthophloea bark tannin could be a potential new source of vegetable tannin agent (Cheloti et al., 2023).

In India, there are more than 1500 medicinal plants and half of these are being effectively used in curing different diseases. And the leaves of the *Acacia nilotica* have been tested to have high levels of total phenolic content, higher antioxidant activity, and higher protein content, compared to the pods and bark. Hence the A. *nilotica* is being used in the control and cure of diabetis melitus as it contains anti-diabetic properties (Sadalage et al., 2023).

Understanding the genetic diversity and population structure of Acacia trees is essential for effective conservation and sustainable management. According to (Omondi et al., 2010), few studies have been done on the genetic diversity of the acacia trees of Kenya. One study of *A. senegal* using random amplified polymorphic DNA (RAPD) and inter-specific simple sequence repeat (ISSR), resulted in a moderate level of diversity (H = 0.283) of the tree species.

In this project, however, we were inclined to utilizing the latest, highly reproducible, and powerful DArTseq sequencing technology to assess the genetic variation among 30 Acacia tree samples collected from diverse regions in Kenya. DArTseq uses the genotyping-by-sequencing (GBS) technology to sequence and generate data from novel non-referenced genomes. This then generates single-nucleotide polymorphisms (SNP) and DArTseq markers called silicoDArTs. This technology has proved over many studies to be robust, and of high quality in genomics studies across various species and applications (Cai et al., 2020).

Thus, the objective of this research is to; (1) assess the genetic diversity of Acacia trees in Kenya using DArTseq technology; (2) identify the population structure and relatedness of Acacia tree species across different regions in Kenya, and (3) provide valuable data for the formulation of effective conservation strategies and further research for Acacia trees in the region.

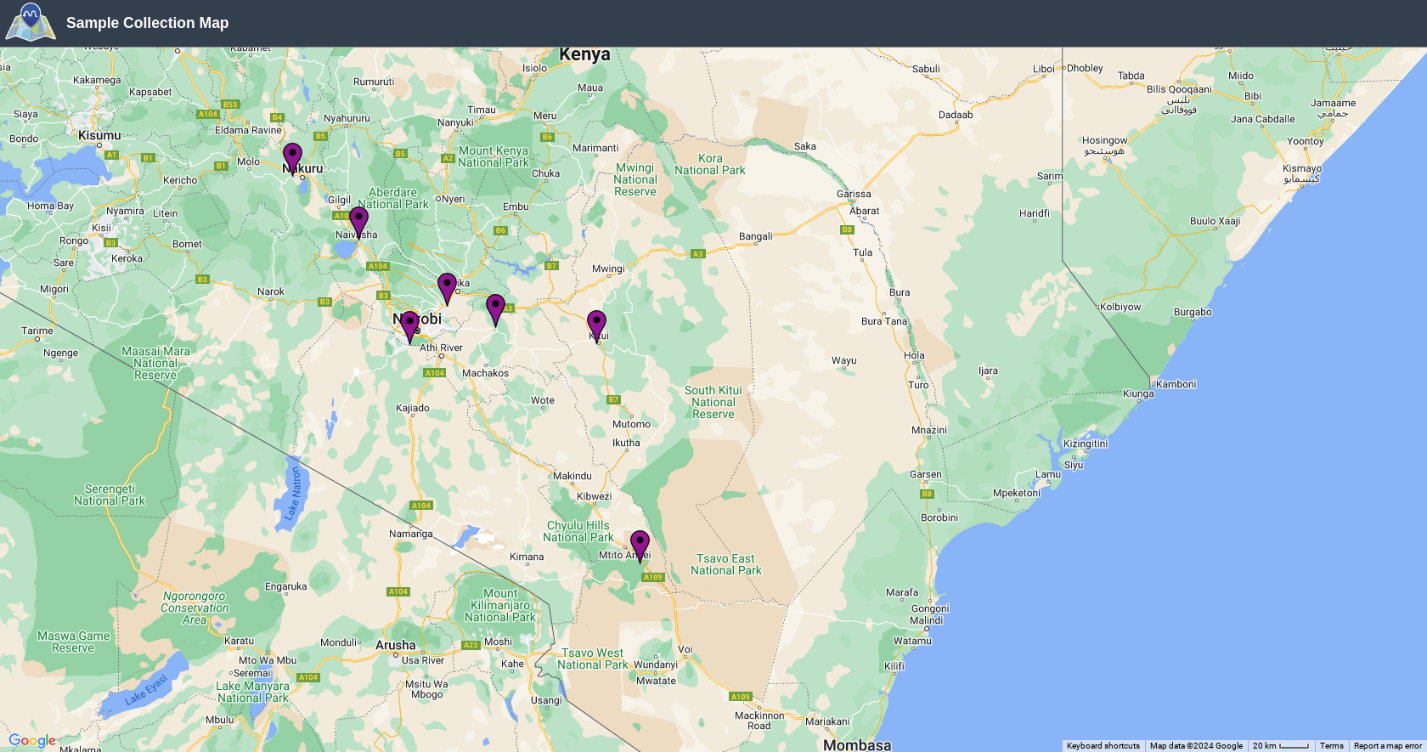
# **2. MATERIALS AND** **METHODS**

## **2.1 Plant Material:**

A total of 7 Acacia tree leaf samples were randomly collected from different ecological zones across Kenya, ensuring representation from distinct habitats. Their geographical position co-ordinates were recorded. The low number is due to the wild and unchartered nature of some of these tree locations including wildlife game reserves. To ensure collection of ancient samples, the trees had to have a DBH (diameter at breast height) greater than 90 cm.

**Table 1: Origin, collection sites and geographical coordinates of Acacia samples from Kenya used in this study**

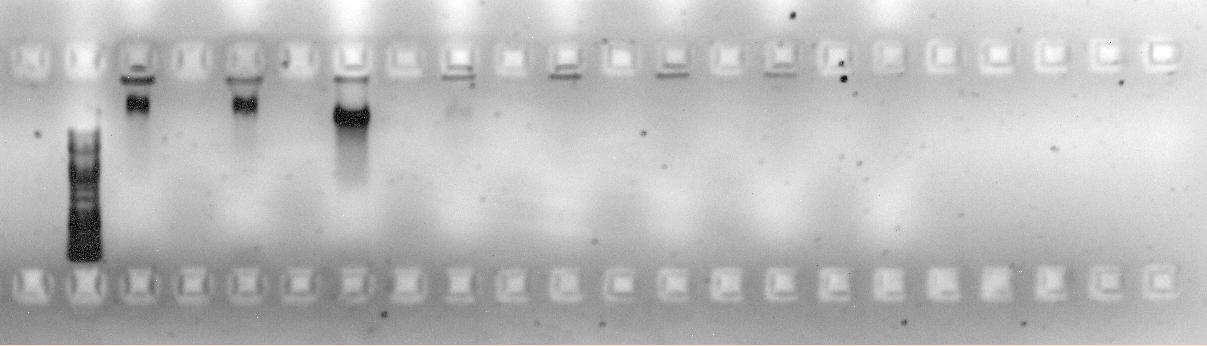
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Sample type | County | Area Name | Co-ordinates |
| SBK1 | Leaf | Kitui | Kitui | -1.379637, 37.987279 |
| SBK2 | Leaf | Taita taveta | Tsavo | -2.800206, 38.262899 |
| SBK3 | Leaf | Nakuru | Kaptembwa | -0.295316, 36.019097 |
| SAK1 | Leaf | Nakuru | Naivasha | -0.709782, 36.446686 |
| SAK2 | Bark | Machakos | Tala | -1.272193, 37.329637 |
| SAK3 | Bark | Kiambu | Juja | -1.135752, 37.020516 |
| SAK4 | Bark | Kajiado | Ongata Rongai | -1.384197, 36.775701 |



**Figure 1: The geographical map of Acacia sample collection locations in Kenya used in this study**

## **2.2 DNA Extraction:**

High-quality genomic DNA were extracted from the leaves of each collected sample using using the NucleoMag 96 Plant genomic DNA extraction kit (Macherey–Nagel, Du¨ren, Germany), following the manufacturer’s instructions. The quantification of the extracted DNA was then checked manually using 0.7% agarose



**Figure 2: DNA Quality Check showing bands on 0.7% Agarose Gel for the 7 Acacia samples**

**Table 2: DNA quality and purity was measurements recorded using a DeNovix spectrophotometer.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Sample type | Concentration (ng/ul) | 260/280 | 260/230 |
| SBK1 | Leaf | 9.760 | 1.79 | 1.08 |
| SBK2 | Leaf | 202.150 | 1.58 | 0.56 |
| SBK3 | Leaf | 42.529 | 1.17 | 0.87 |
| SAK1 | Leaf | 31.660 | 1.59 | 0.50 |
| SAK2 | Bark | 28.149 | 1.114 | 0.24 |
| SAK3 | Bark | 3.894 | 1.37 | 0.42 |
| SAK4 | Bark | 7.532 | 1.38 | 0.36 |

## **2.3 Library Preparation and Sequencing:**

The genomic DNA samples underwent DArTseq library preparation, which is a genome representation method that targets specific genomic regions, mostly exons due to methylation sensitivity. This technology allows for the simultaneous screening of thousands of loci, providing extensive coverage of the genome. 2ul of DNA, in full replication was digested using a combination of the rare cutting endonuclease enzyme PstI (5`-CTGCA|G-3`) in combination with the frequently cutting restriction enzyme MseI (5`-T|TAA-3`). The resulting digested DNA fragments were ligated to other pieces of fragments like the barcoded adaptors (4-9 bp) and sequencing adapter overhangs. The new fragments were then amplified in a Polymerase Chain Reaction (PCR) machine using optimized settings for 35 cycles. The PCR products were then checked for quality and correct fragment size by running them in a 1.2% agarose gel.



**Figure 3: Acacia library quality control check in agarose showing failed sample SAK3**

Sample SAK3, failed quality check, due to poor DNA concentration and purity as shown in the quality scores highlighted above.

The samples that passed the quality check were then pooled together, purified and loaded on to the cBot (Illumina, Inc., San Diego, CA, USA) for cluster generation via bridge amplification on a single read flowcell. The sequencing was then carried out on an Illumina HiSeq2500. Allele calling was done using the proprietary analytical pipeline called DArTsoft14, developed by DArT Pty Ltd, Canberra, Australia. SNP and DArT markers are then generated where DArTseq markers scored a ‘0’, ‘1’, ‘and ‘- ‘, representing presence, absence, and no-zero count. The SNP markers were scored as ‘1’ for the SNP allele homozygote, ‘0’ for reference allele homozygote, and ‘2’ for heterozygotes presence.

## **2.4 Genetic Diversity and Population**

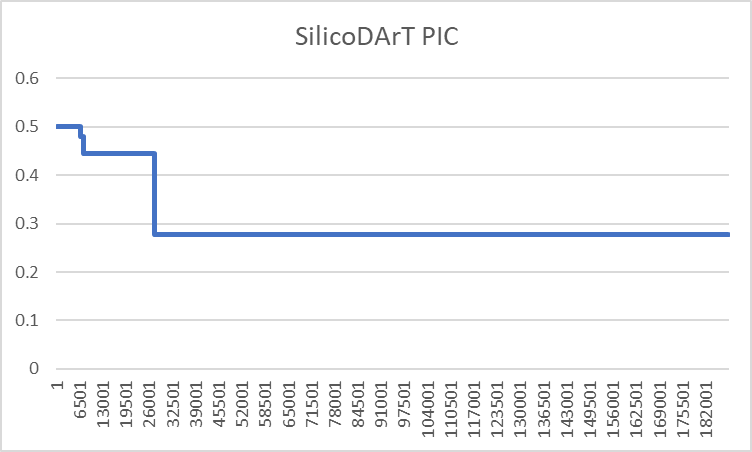
Genetic diversity and population structure was calculated from the 6 samples using both DArTseq and SNP data. Using the new version of dartR for genetic data analysis and visualization, diversity indices such as inbreeding coefficient, total gene diversity, and heterozygosity was determined. Using the SNP and DArTSeq, a neighbor-joining tree was built. The hierarchical structure analysis was supported by the use of hierarchical analysis of molecular variance (AMOVA), principal components analysis (PCA), and a pairwise genetic distance matrix of the accessions. Estimating the pairwise fixation index (Fst) allowed for the analysis of genetic divergence between the Acacia populations.

# **3. RESULTS**:

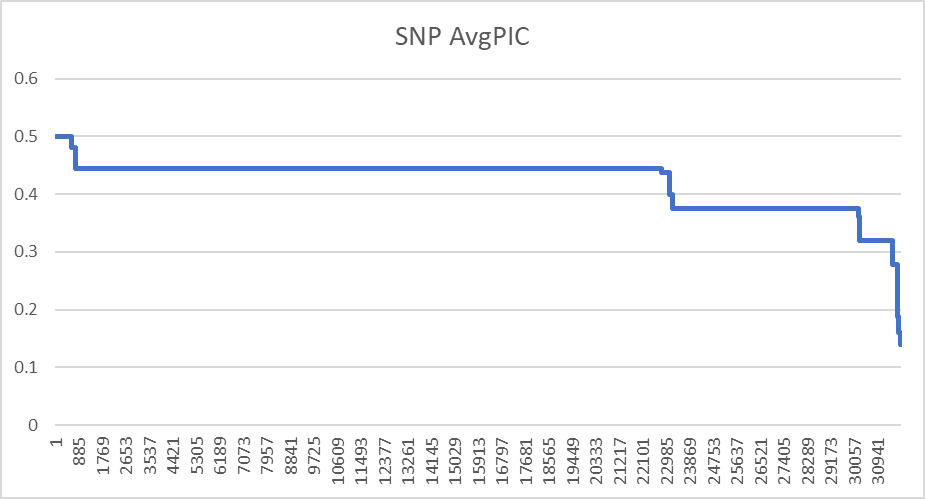
## **4.1 DArTseq and SNP Detection**

After sequencing was done in the HiSeq2500, a total of 49,678 SNP markers were generated. A final selection of 31,823 markers were selected with over 90% reproducibility, and above 90% call rate. DArTseq markers were reduced to 188,499 from a total of more than 500,000 markers. The file was too large to work with due to many low call rate markers below 70%. The average call rate was observed at 99% while reproducibility for the markers was observed at 95%. This was all done automatically from the proprietary DArTSoft14 algorithm program after sequencing is complete.

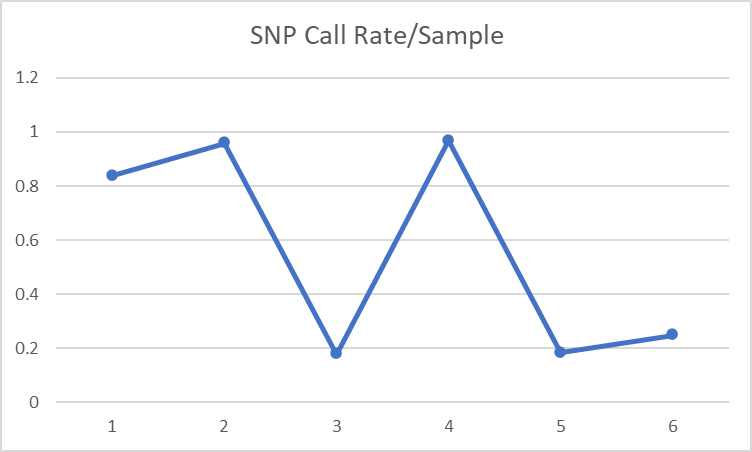
The summary of polymorphism information content (PIC) for SNP markers was between 0.5 and 0.14 with an average of 0.42. For the DArTseq markers, the PIC ranged from 0.5 to 0.27, with an average PIC of 0.30.



**Figure 4. Observed PIC of silicoDArT data**



**Figure 5. Observed PIC of SNP data**



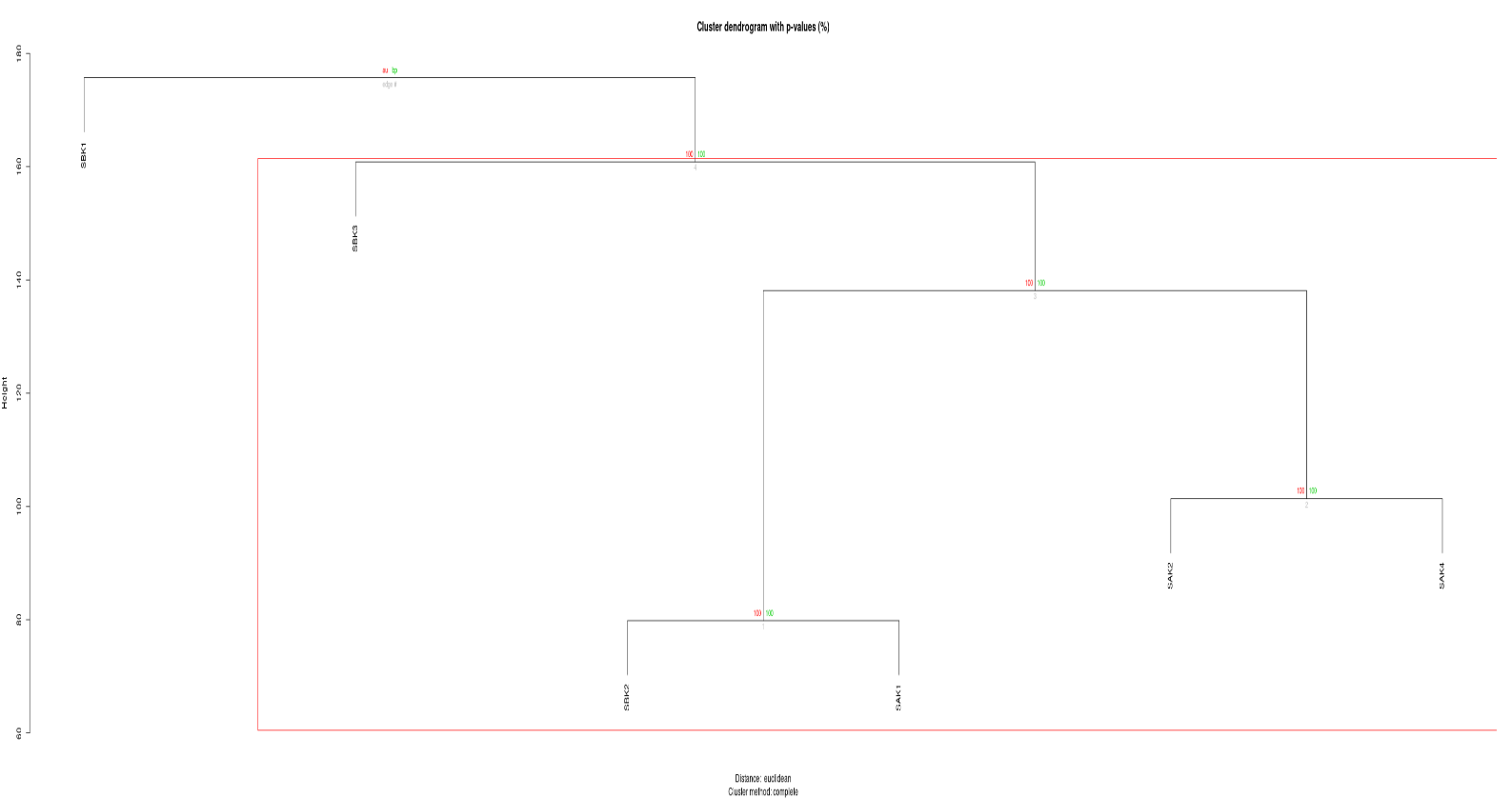
**Figure 6. Observed SNP call rate per sample**

## **4.2 Genetic Diversity**

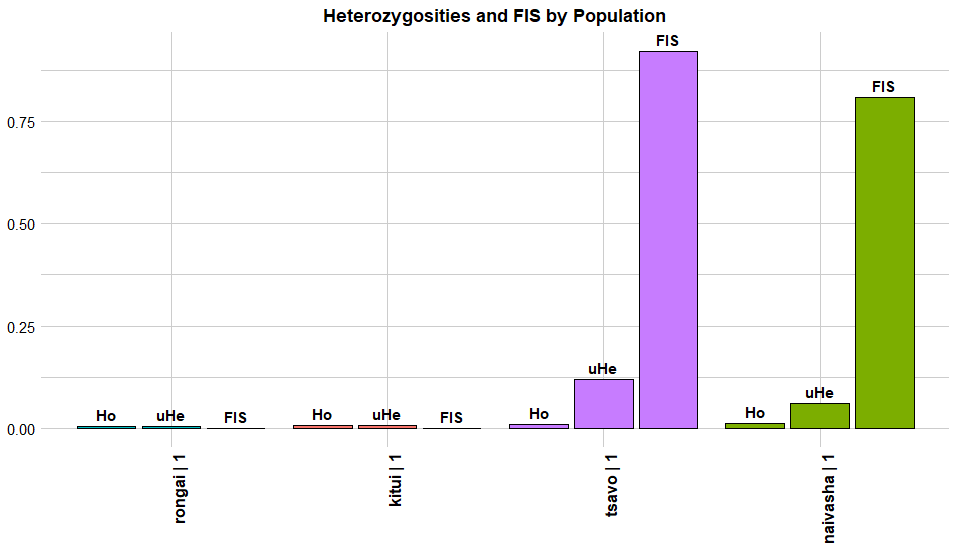
The expected heterozygosity (He) for SNP markers in the population ranged from 0.0029 to 0.068. The mean observed heterozygosity (Ho) and the He, were in synchronization with the high PIC values described above.

**Table 3. SNP observed and expected heterozygosity based on population**

|  |  |  |  |
| --- | --- | --- | --- |
| pop | Ho | He | Fis |
| kitui | 0.005848 | 0.002924 | 0 |
| naivasha | 0.011558 | 0.034802 | 0.809228 |
| rongai | 0.00443 | 0.002215 | 0 |
| tsavo | 0.009414 | 0.068719 | 0.921739 |



**Figure 7. Hierarchical clustering dendrogram with bootstrap P-values Acacia SNP data**



**Figure 8. SNP observed heterozygosity per population**

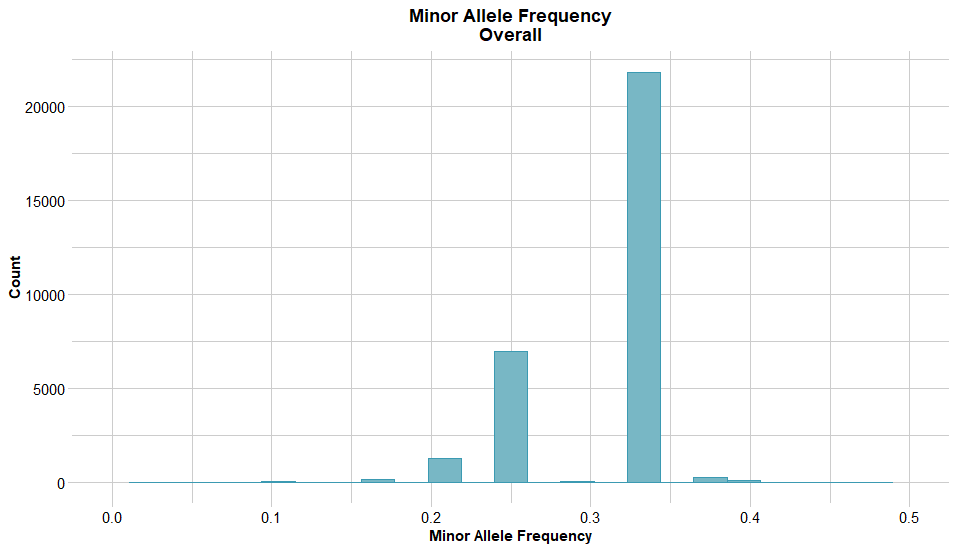
## **4.3 Population Structure Analysis**

Similarities in the genetic makeup among the Acacia samples were assessed using the SNP markers exposing 5 clusters. This is being strictly supported by the delta-k plot. A neighbor joining tree was developed showing similar clustering between the SNP and SilicoDArT data. The phylogenetic tree grouped the populations into three groups, with two internal nodes (Figure 12). The locus minor allele frequency (MAF) for the SNP data set scores between 0.08 and 0.5, with a mean of 0.3. Allelic richness (q =0) of the acacia samples was calculated, including Shannon information (q = 1), and heterozygosity (q = 2). Population Structure analysis using the STRUCTURE software, revealed 3 variated group structures within SNP marker data as shown below.

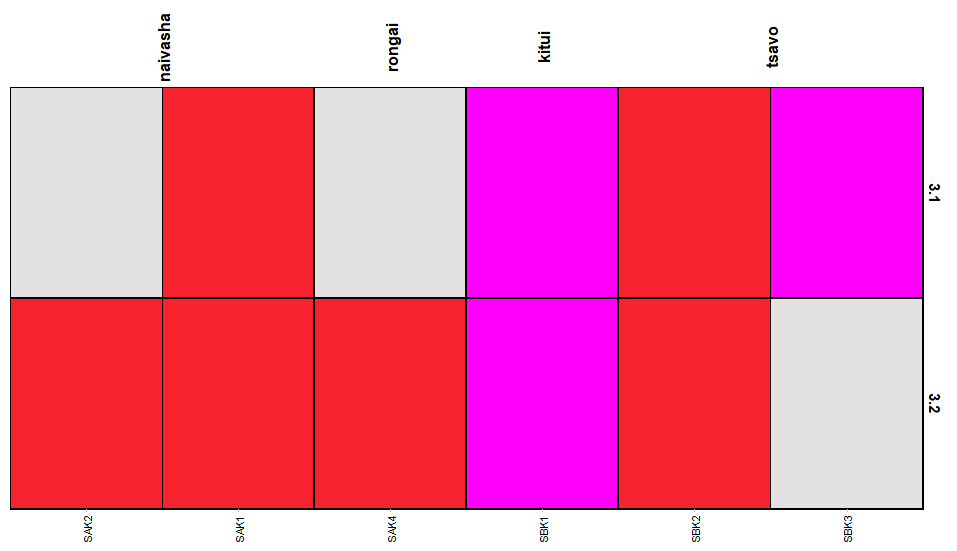
Genetic diversity of individual samples was backed up by principal coordinate analysis (PCA) despite individuals per population being too little, with the minimum required being ten individuals per population. These showed a substantial variance in diversity gap between the various populations based on combined SNP and SilicoDArT data.

**Table 4. Basic SNP statistics for Acacia samples based on SNP data**

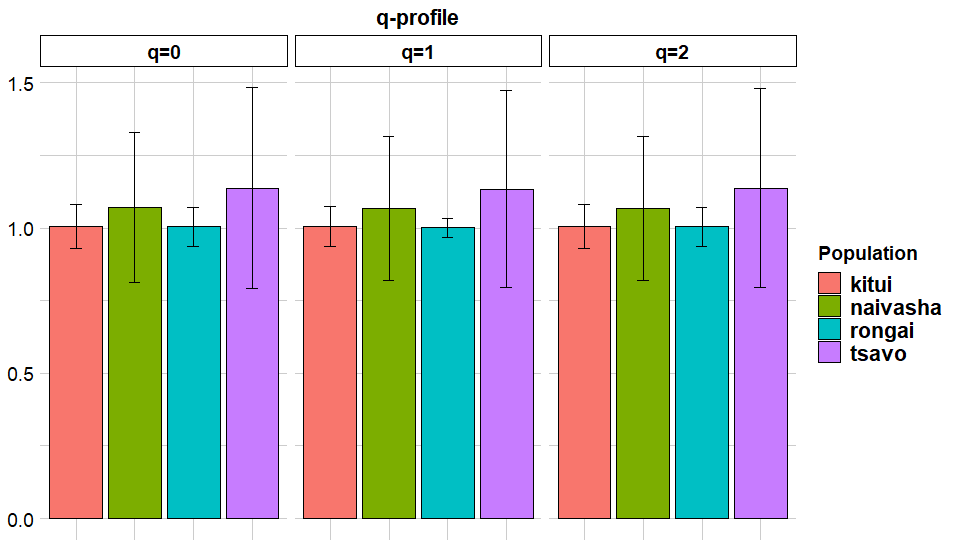
|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Ho** | **Hs** | **Fis** | **Ht** | **Dst** | **Fst** |
| 0.008 | 0.5631 | 0.9858 | 0.5459 | -0.0173 | -0.0316 |



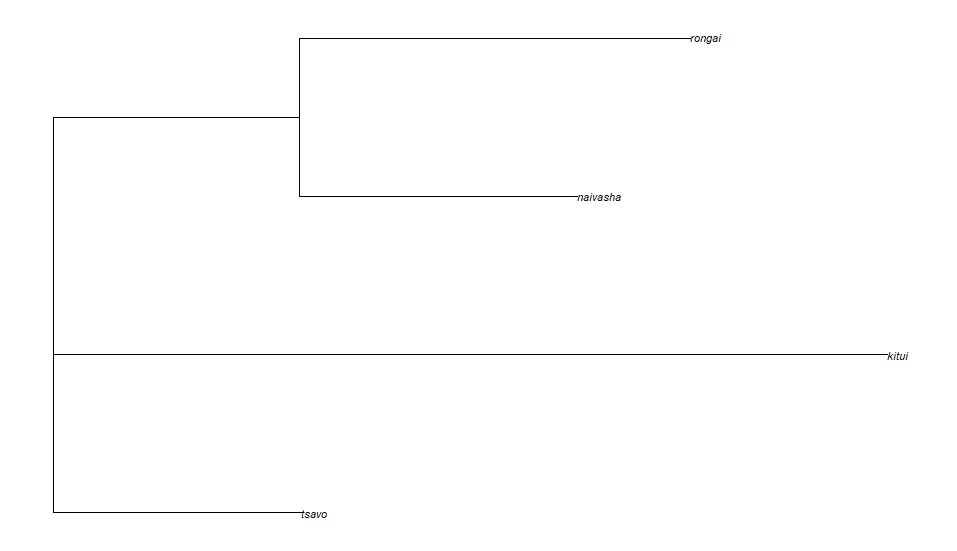
**Figure 9. The mean minor allele frequency (MAF) for all SNP loci**



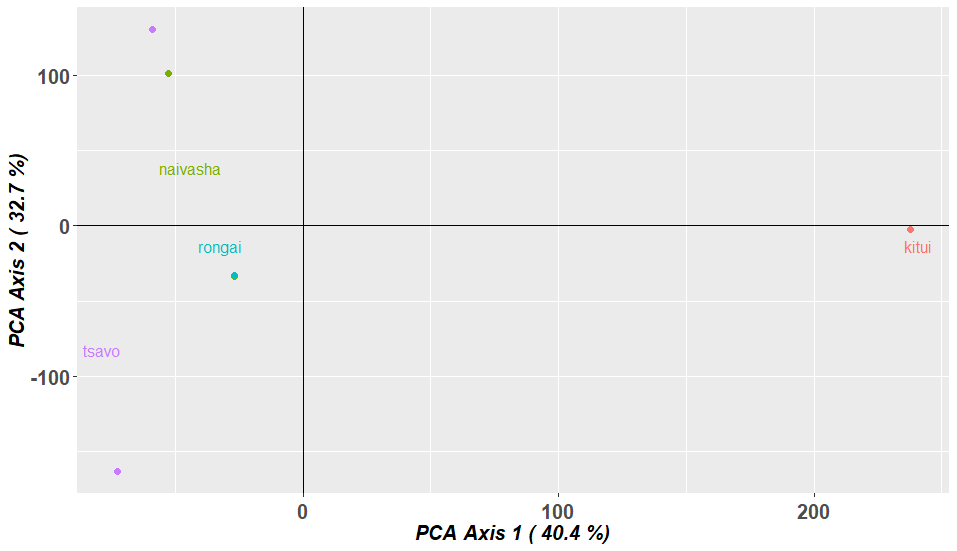
**Figure 10. SNP population structure heat map**



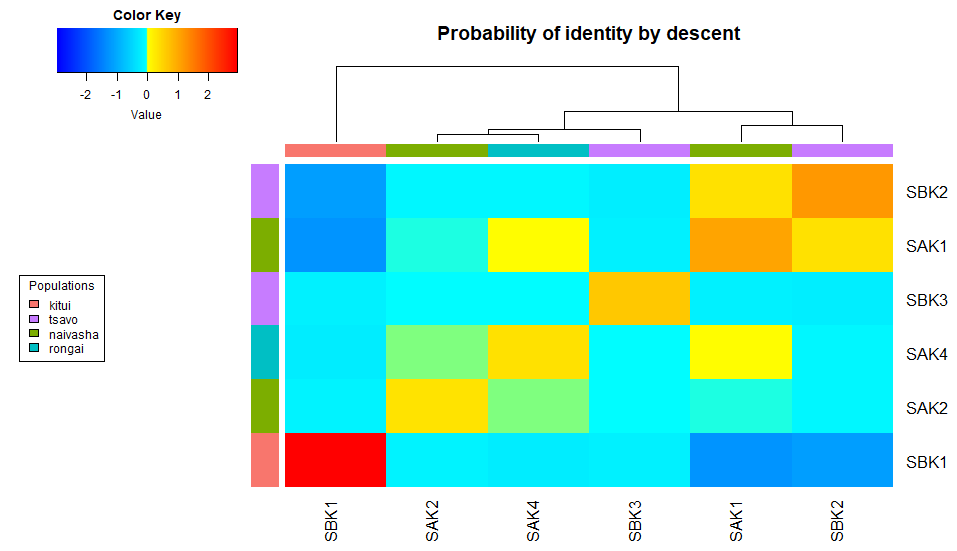
**Figure 11. SNP population diversity summary.**



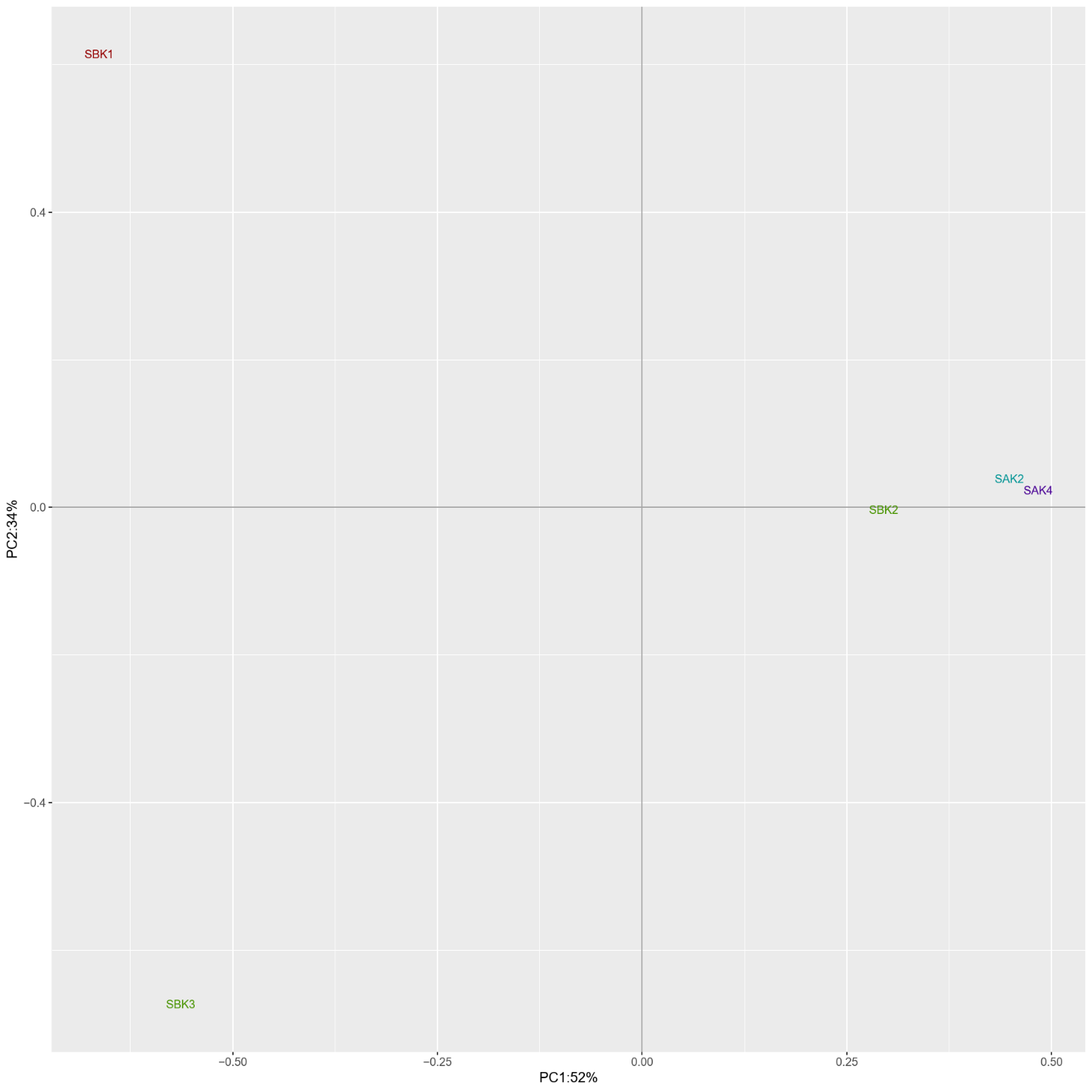
**Figure 12. A SNP neighbour joining tree of the Acacia population**



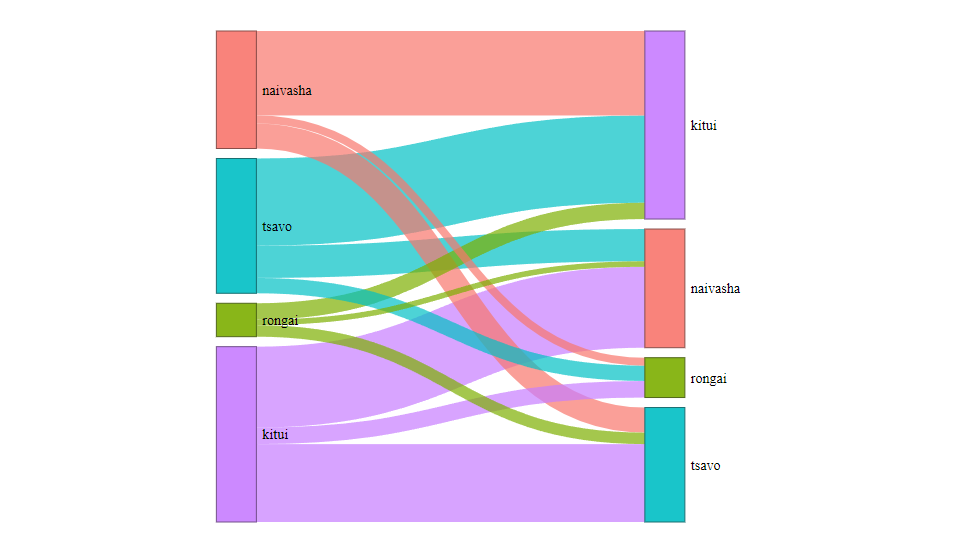
**Figure 13. PCA plot to infer group structure of Acacia based on SNP marker data.**



**Figure 14. Acacia SNP sample identity by descent matrix**



**Figure 15. PCA analysis based on samples.**



**Figure 16. SNP mean absolute allele frequency differences (AFD) between pairs of populations.**

## **4.4 Sequence Similarity**

The 31,823 SNP markers generated were exposed to a nucleotide blast search. The results were further filtered based on E-value (equal to 999), and Chromosome Position (equal to 0). This left a total of 1,896 SNP marker. All blast hits had an E-value greater than 1.24E-26. The SNP markers matched to various species such as *Acacia mellifera, Acacia mangium, Dichrostachys cinerea, Lupinus angustifolius, Lophophytum mirabile, Bretschneidera sinensis, Parapiptadenia rigida, Arachis duranensis,* *Acacia koa, and Anadenanthera colubrina.*

After E-value marker filtration, 3320 SilicoDArTs were selected for nucleotide blast, the markers were matching with *Acacia harpophylla, Acacia argyrophylla, Acacia mangium, Arachis duranensis, Dichrostachys cinerea,* *Millettia pinnata,* *Parkia javanica,* *Piptadenia communis, Pararchidendron pruinosum, Bupleurum falcatum,* and *Lophophytum mirabile.*

The blast results from the SNP and SilicoDArT markers showed similar species similarities which mostly consist of shrubs, trees, and herb species.

# **4. DISCUSSION**

Indigenous tree species like the Acacia, have been in existence for thousands of years and it is important to understand their genetic structure and genetic components for conservational purposes. Their potential for pharmaceutical use needs to be understood even from a genetic perspective. Affordable sequencing the Acacia tree samples using DArTSeq technology provided major insights on the genetic diversity of the tree species across the country of Kenya. Both silicoDArT and SNP markers showed high reproducibility (above 95%) on technical replicates, and high call rate for marker scoring therefore indicating their efficiency and reliability.

Genetic diversity measured using the proportion if polymorphism in the sequence data shows low genetic variance between the different Acacia samples. This also indicated low effects on the tree species from environmental and human factors. The observed (Ho) versus the expected heterozygosity (He) also showed little difference that was almost negligible (0.001). The SNP data averaged a PIC of 0.42, while silicoDArT was 0.30. This is high PIC translating to high genetic diversity within the populations due to high heterozygosity.

Older tree samples like the SBK1 from Kitui county and the SAK1 from Naivasha showed a little amount of significant difference in unique alleles as shown in PCA on Figure 15. Both populations have the highest amount of unique SNP markers hence contributing to their variance. This is also supported by the mean allele frequency of 0.31 as seen in Figure 9.

The observed genetic diversity (Hs) and the observed inbreeding coefficient (Fis), in Table 4, were calculated from the SNP markers. The average Fis being 0.98 meaning individuals in the populations are more alike to 98% similarity. The observed genetic diversity was also high at 0.561, showing less impact of human and ecological factors on the gene pool dilution of the species.

From the population structure analysis with the STRUCTURE software, we saw the populations being divided into three groups at K set to 5. This was supported by the population PCA analysis (Figure 13), and the neighbor joining tree (Figure 12). The MAF was calculated as 0.33 for the SNP data, indicating significantly high heterozygosity due to limited proliferation of seeds of Acacia tree species, as seed dispersal is via animals, especially migrating livestock, and wild animals. The seed is also very hard coated so dormancy is hard to break. Especially for the wild tree spepecies according to (Oginosako et al., 2005).

Genetic diversity (Dst) and genetic differentiation (Fst) was extremely low from the SNP data. AMOVA analysis also showed 1.4% significance for both silicoDArTs and SNP markers. The consistency of results generated by this analysis for both marker types was calculated using the Mantel test in dartR, which gave a significance score of 0.68. hence 68% significance showed good consistency between the two data types.

The blast search showed both data sets had close matches with similar tree species of Acacia, especially *Acacia mangium*, and *Acacia koa.* This shows potential of mapping this new data to some native Kenyan species and develop a Kenyan genetic map. This also shows significant pharmaceutical prospecting opportunities based on known traditional methods and new genetic gains.

# **5. CONCLUSION**

Understanding the genetic diversity of indigenous Acacia species is crucial for revealing their relationships with other plants and their genetic and phytochemical potentials. The DArT platform has proven effective in genotyping Acacia species affordably, using silicoDArTs and SNP markers which demonstrated high call rates and reproducibility. Results indicated low genetic diversity in Acacia, potentially affecting its ability to recover from environmental and genetic challenges.

Genetic diversity was assessed through polymorphic loci and heterozygosity measures, with PIC values ranging from 0.39 to 0.45, indicating high polymorphisms. The analysis showed that Acacia has not been significantly impacted by human activities, and the findings suggest that the species has moderate genetic differentiation and high diversity, with potential implications for future research and conservation.

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