

2 - 4 April 2025 | Manthabiseng Convention Centre Maseru, Kingdom of Lesotho

Genetic Diversity of Grain Sorghum Accessions in Lesotho Using Single Nucleotide Polymorphisms (SNP) Markers





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INTRODUCTION

- Sorghum production in Lesotho declined despite an increase in acreage (4013 tons in 2022, 6735 tons in 2021; 8466 ha in 2021 to 15 420 ha in 2022(FAOSTAT, 2022).
- Lesotho has a rich and diverse sorghum germplasm. This genetic diversity resource is untapped, under-utilized and has not been fully documented as a result, there is a need to assess the underlying genetic diversity and structure in the germplasm to develop ideal breeding strategies for sorghum quality improvement.

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- Therefore, the objectives of this study were to
 - (1) assess the extent and patterns of genetic diversity among sorghum accessions collected in Lesotho and
 - (2) determine the population structure of the thirty-two sorghum accessions.
- The information generated will be valuable for sorghum pre-breeding by identifying diverse parental germplasm for core breeding.

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MATERIALS AND METHODS

32 sorghum accessions collected across Lesotho DNA extracted using CTAB protocol

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Genotyped using SNP markers (DArTseq Technology) at SEQART AFRICA in Nairobi, Kenya.

SNP markers filtered for minor allele frequency (MAF > 0.05)

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DATA ANALYSIS

- Genetic diversity parameters estimated using KDCompute Population pluggin (Liu and Muse, 2005).
- Analysis of Molecular Varience (AMOVA) was done using the KDCompute pluggin.
- The principal coordinates analysis (PCoA) was done using Plugin in KDCompute from Sequart Africa (kdcp_standalone_ ClusteringDendrogram).
 - Clustering was done with hamming distance method and manhatton dissimilarity methods was constructed to identify the diversity within the population.

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RESULTS AND DISCUSSIONS

GENETI	GENETIC PARAMETERS				
STATISTICS	MEAN	LOWER	UPPER		
Polymorphic Information Content (PIC)	0.31	0.06	0.50		
Gene Diversity (GD)	0.34	0.04	0.53		
Expected Heterozygosity (H _e)	0.28	0.07	0.49		
Observed Heterozygosity (H _o)	0.24	0.04	0.48		
Minor Allele Frequency (MAF)	0.23	0.05	0.50		
Major Allele Frequency (MaF)	0.77	0.50	0.95		

GENETIC PARAMETERS AND MARKER CHARACTERISTICS

- 2113 SNP markers were selected and used to estimate the genetic diversity of the accessions.
 - PIC mean 0.31 with the range 0.06 to 0.50, these results show that the SNP markers were moderately informative and polymorphic (Botstein *et al.*, 1980).
 - These findings are comparable with values reported on sorghum in previous studies (Yahaya *et al.*,2023).
 - The GD of the SNP markers exhibited a range of 0.04 to 0.53, with an average of 0.34, indicated a high level of diversity.
 - These informative markers can be effectively used for genotyping populations in genetic diversity studies (Salem and Sallam, 2016).
 - The H_o value of 0.28 obtained in this shows a moderate genetic diversity. This is in line with the findings of Afolayan *et al.* 2019 and Yahaya *et al.* 2023 but higher than results from Enyew *et al.* 2022, who also used SNP markers for sorghum genetic diversity analysis.
- MAF ranged from 0.05 to 0.50, with mean of 0.23 which indicates that there is moderate diversity.

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POPULATION STRUCTURE

AMOVA Table				
	SSD	MSD	%SS	df
Accessions	1.36	0.12	63.8	11
Error	0.77	0.04	36.2	20
Total	2.12	0.07	100	31

ANALYSIS OF MOLECULAR VARIANCE (AMOVA)

- The result of the AMOVA demonstrated the genetic variation among populations.
- The AMOVA indicated that 63.8% of the variance was due to the differences amongst accessions.
- The present study revealed the presence of very high genetic differentiation among populations of sorghum ($F_{st} = 0.45$) Wright (1965).
- The collection was based on geographical and agronomic merits. This indicates that a considerably varying population was selected for the study.

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CLUSTER ANALYSES OF INDIVIDUAL ACCESSIONS



- PCA revealed 78% of variations explained by the first two axes. The first and second principal coordinate axes showed 61% and 17%, respectively.
- The total genetic variation of the first two PCA recorded in this study highlights the possibility of highly informative and selective SNP markers for genetic studies in sorghum, which may aid in conservation and future breeding efforts.









- Distinct clusters are formed.
- The genetic structure of sorghum populations in Lesotho has not been studied. The accessions might have evolved from ancestors from the East Africa and also from other parts of Africa.
- Sorghum use is similar across the country and is planted across similar micro-climates hence differentiation observed.
- The differentiation is rather based on combination of factors such as microclimate and taste preferences per location.



CONCLUSION

- There is a moderate variation observed among the sorghum accessions in Lesotho which could be the foundation for developing and generating desirable new sorghum varieties with superior wide adaptability.
- However, phenotypic evaluations should be conducted to establish underlying genetic basis of phenotypic variation.
- Accessions used in this study may be used to design and conduct gene discovery which may lead to the discovery of genes controlling sorghum quality traits and tolerance to biotic and abiotic stresses.



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THANK YOU



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