

**MOLECULAR DYNAMICS OF TUBER AND SEED YIELD IN**  
*Sphenostylis stenocarpa* (Hochst. ex A. Rich. Harms) (AFRICAN YAM  
**BEAN)**

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**(22PCO02401)**

**AUGUST, 2024**

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BEAN)**

**BY**

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**An M.Sc DISSERTATION SUBMITTED TO THE SCHOOL OF  
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OF SCIENCE (M.Sc) IN BIOLOGY IN THE DEPARTMENT OF  
BIOLOGICAL SCIENCES, COLLEGE OF SCIENCE AND  
TECHNOLOGY, COVENANT UNIVERSITY, OTA, OGUN STATE  
NIGERIA**

**AUGUST, 2024**

## **ACCEPTANCE**

This is to attest that this dissertation has been accepted in partial fulfilment of the requirements for the award of the degree of Masters of Science in Biology, in the Department of Biological Sciences, Colleges of Science and Technology, Covenant University, Ota, Ogun State.

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**I ALADELE, ANDREW KOLAWOLE (22PCO02401)**, declare that I carried out this research under the supervision of Prof. Conrad A. Omonhinmin and Prof. Michael T. Abberton of the Department of Biological Sciences, College of Science and Technology, Covenant University, Ota, Nigeria and International Institute of Tropical Agriculture, Ibadan, Nigeria, respectively. I attest that the thesis has not been presented either wholly or partially for the award of any degree elsewhere. All sources of data and scholarly information used in this dissertation are duly acknowledged.

**ALADELE, ANDREW KOLAWOLE**

**Signature and Date**

## **CERTIFICATION**

We certify that this thesis titled “MOLECULAR ANALYSIS TO UNDERSTAND THE GENETICS OF TUBER AND SEED YIELD IN AFRICAN YAM BEAN” is an original work carried out by ALADELE, ANDREW KOLAWOLE (22PCO02401), in the Department of Biological Sciences, College of Science and Technology, Covenant University, Ota, Ogun State, Nigeria under the supervision of Prof. Conrad A. Omonhinmin and Prof. Michael T. Abberton. We have examined and found this work is acceptable as part of the requirements for the award of Masters of Science (M.Sc) degree in Biology.

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## **DEDICATION**

This research work is dedicated to the Almighty God and my parents, Dr. Sunday Aladele and Mrs. Grace Aladele

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## TABLES OF CONTENTS

<b>CHAPTER ONE: INTRODUCTION</b>	<b>ERROR! BOOKMARK NOT DEFINED.</b>
1.1 Background to the Study	<b>Error! Bookmark not defined.</b>
1.2 Research Questions	<b>Error! Bookmark not defined.</b>
Aim and Objectives:	<b>Error! Bookmark not defined.</b>
1.3 Justification for the Study	<b>Error! Bookmark not defined.</b>
1.4 Scope of Study	<b>Error! Bookmark not defined.</b>
<b>CHAPTER TWO: LITERATURE REVIEW</b>	<b>ERROR! BOOKMARK NOT DEFINED.</b>
2.1 Legumes	<b>Error! Bookmark not defined.</b>
2.2 Root Tuber Crops	<b>Error! Bookmark not defined.</b>
2.3 Tuberous legumes	<b>Error! Bookmark not defined.</b>
2.4 Legumes in Africa	<b>Error! Bookmark not defined.</b>
2.5 Germplasm conservation	<b>Error! Bookmark not defined.</b>
2.5.1 In situ Germplasm Conservation	<b>Error! Bookmark not defined.</b>
2.5.2 Ex Situ Germplasm Conservation	<b>Error! Bookmark not defined.</b>
2.6 The Role of Seed Banks in Protecting Crop Biodiversity	<b>Error! Bookmark not defined.</b>
2.7 Seed Storage and Conservation	<b>Error! Bookmark not defined.</b>
2.8 Agronomy and botany of <i>Sphenpstylis stenocarpa</i>	<b>Error! Bookmark not defined.</b>
2.9 Eco-geographical distribution of Ss	<b>Error! Bookmark not defined.</b>



2.10 Economic potentials and uses of Ss	<b>Error! Bookmark not defined.</b>
2.11 Limitations of Ss	<b>Error! Bookmark not defined.</b>
2.12 Genetic diversity within species	<b>Error! Bookmark not defined.</b>
2.5.1 Morphological characterization of Ss	<b>Error! Bookmark not defined.</b>
2.5.2 Molecular characterization of Ss	<b>Error! Bookmark not defined.</b>
2.6 Concept of Yield stability	<b>Error! Bookmark not defined.</b>
2.7 Quantitative traits and marker-trait association	<b>Error! Bookmark not defined.</b>
2.15 Research Gaps	<b>Error! Bookmark not defined.</b>
<b>CHAPTER THREE: MATERIALS AND METHODS</b>	<b>ERROR! BOOKMARK NOT</b>
<b>DEFINED.</b>	
3.1 Research site	<b>Error! Bookmark not defined.</b>
3.2 Gerplasm used	<b>Error! Bookmark not defined.</b>
3.3 Experimental Design and Field Plot Management	<b>Error! Bookmark not defined.</b>
3.4 Collection of Data	<b>Error! Bookmark not defined.</b>
3.5 Equipment	<b>Error! Bookmark not defined.</b>
3.6 Reagents	<b>Error! Bookmark not defined.</b>
3.7 Methods	<b>Error! Bookmark not defined.</b>
3.7.1 Phenotypic analysis	<b>Error! Bookmark not defined.</b>
3.7.2 Genotyping	<b>Error! Bookmark not defined.</b>
3.7.2.1 Quality control	<b>Error! Bookmark not defined.</b>
3.7.2.2 DArT-Seq	<b>Error! Bookmark not defined.</b>
3.7.2.3 SNP Filtering	<b>Error! Bookmark not defined.</b>
3.7.2.4 Statistical Analysis	<b>Error! Bookmark not defined.</b>

3.7.2.5 Principal Component Analysis (PCA) and Cluster Analysis **Error! Bookmark not defined.**

3.7.2.6 Inter-trait relationship **Error! Bookmark not defined.**

**CHAPTER FOUR: RESULTS** ERROR! BOOKMARK NOT DEFINED.

4.1 Phenotype analysis **Error! Bookmark not defined.**

4.1.1: SEED **Error! Bookmark not defined.**

4.1.2: TUBER **Error! Bookmark not defined.**

4.2 Genome-wide AssociationStudies (GWAS) **Error! Bookmark not defined.**

**CHAPTER FIVE: DISCUSSION** ERROR! BOOKMARK NOT DEFINED.

GWAS **Error! Bookmark not defined.**

**CHAPTER SIX: CONCLUSION AND RECOMMENDATIONS** ERROR! BOOKMARK NOT DEFINED.

6.1 Conclusion **Error! Bookmark not defined.**

6.2 Contribution to Knowledge **Error! Bookmark not defined.**

6.3 Recommendations **Error! Bookmark not defined.**

6.4 Limitations to this Study **Error! Bookmark not defined.**

**REFERENCES** ERROR! BOOKMARK NOT DEFINED.

## LIST OF TABLES

<b>TABLES</b>	<b>TITLE OF TABLES</b>	<b>PAGES</b>
1.1:	Research gaps	32
3.1:	AYB passport information displaying the nation of origin, the acquisition date, and the name of the collector	35
4.1:	Total number of filtered significant SNPs	55
4.2:	BLUE FarmCPU Seed thickness	68
4.3:	BLUE FarmCPU Tuber weight Group	69
4.4:	BLUE FarmCPU Tuber weight	70
4.5:	BLUE GLM Tuber weight Group	71
4.6:	BLUE GLM Tuber weight	72
4.7:	BLUE MLM Tuber weight	73
4.8:	BLUE BLINK Pod width	74
4.9:	BLUE BLIK Seed thickness	75

## LIST OF FIGURES

<b>FIGURES</b>	<b>TITLE OF FIGURES</b>	<b>PAGES</b>
4.1:	The cladogram shows the clustering pattern of the accessions based on seed yield	45
4.2:	Biplot analysis of seed yield performance and their influencing traits	46
4.3:	Identification of correlation of traits on the tuber yield	47
4.4:	The cladogram shows the clustering pattern of the tuber producing accessions.	48
4.5:	Biplot analysis of tuber yield performance and their influencing traits	49
4.6:	Identification of correlation of traits on the tuber yield	50
4.7:	Identification of relationship between seed and tuber traits	51
4.8:	FarmCPU model showing significant SNPs for the BLUEs Tuber weight utilizing Manhattan plot and Q-Q plot	52
4.9:	GLM model showing significant SNPs for the BLUEs Tuber weight utilizing Manhattan plot and Q-Q plot	53
4.10:	MLM model showing significant SNPs for the BLUEs Tuber weight utilizing Manhattan plot and Q-Q plot	54
4.11:	BLINK model showing significant SNPs for the BLUEs Tuber weight utilizing Manhattan plot and Q-Q plot	55
4.12:	FarmCPU model showing significant SNPs for the BLUEs grouped Tuber weight utilizing Manhattan plot and Q-Q plot	56
4.13:	BLINK model showing significant SNPs for the BLUEs grouped Tuber weight utilizing Manhattan plot and Q-Q plot	57

4.14: GLM model showing significant SNPs for the BLUEs grouped Tuber weight utilizing Manhattan plot and Q-Q plot	58
4.15: FarmCPU model showing significant SNPs for the BLUEs Seed Thickness utilizing Manhattan plot and Q-Q plot	59
4.16: BLINK model showing significant SNPs for the BLUEs Seed Thickness utilizing Manhattan plot and Q-Q plot	60
4.17: MLM model showing significant SNPs for the BLUEs Seed Thickness utilizing Manhattan plot and Q-Q plot	61
4.18: BLINK model showing significant SNPs for the BLUEs Pod Width utilizing Manhattan plot and Q-Q plot	62
4.19: FarmCPU model showing significant SNPs for the BLUEs Pod Width utilizing Manhattan plot and Q-Q plot	63

## LIST OF PLATES

PLATES	TITLE OF PLATES	PAGES
2.1:	Diverse tubers of African yam bean. The different accessions of African yam bean seeds showing different colors	22
2.2:	African yam bean staked on-field. Green matured pod in view	26

## **LIST OF APPENDICES**

<b>APPENDICES</b>	<b>TITLE OF APPENDICES</b>	<b>PAGES</b>
1:	Flower of AYB plant on field	104
2:	Fresh pod growth on field	105
3:	Harvesting of dry pods	106
4:	Harvesting of tubers	107
5:	Image of freshly harvested tubers	108
6:	Packaging of tuber for post-harvest data collection	109
7:	Image of Pod and seed	110
8:	Image of TSs-421 tubers	111
9:	AYB porridge obtained from various accessions producing tuber	112

## **LIST OF ABBREVIATIONS**

AFLP: Amplified Fragment Length Polymorphism

AYB: African Yam Bean

Bp: Base pairs

BLUE: Best linear and unbiased estimators

Chr: Chromosome

CTAB: Cetyl trimethylammonium bromide

DArT: Diversity array technology

DArTseq: Diversity array technology sequence (DArTseq)

DNA: Deoxyribonucleic Acid

EDTA: Ethylene Diaminetetraacetic Acid

FAO: Food and Agriculture Organization

GLM: General linear Model

GRC: Genetic Resource Centre

GWAS: Genome-Wide Association Study

IITA: International Institute of Tropical Agriculture

ISSR: Inter-Simple Sequence Repeat

MAF: Minor allele frequency

MAS: Marker assisted selection



MLM: Mixed linear model

mRNA: Messenger ribonucleic acid

NA: Not available

NGS: Next generation sequencing

PCA: Principal component analysis

PCR: Polymerase chain reaction

Q-Q: Quantile-quantile

QTLs: Quantitative Trait Loci

RAPD: Random Amplified Polymorphic DNA

SNPs: Single Nucleotide Polymorphisms

SSR: Single Sequence Repeat

TASSEL: Trait Analysis by Association, Evolution and Linkage

tRNA: Transfer ribonucleic acid

TSS: Tropical *Sphenostylis stenocarpa*

## ABSTRACT

*Sphenostylis stenocarpa* (African yam bean - AYB) is an understudied and opportunity crop with the potential to contribute to food security. It is a versatile legume that produces both edible seeds and tubers. AYB faces under-exploitation due to limited understanding and challenges as well as an unabated threat to its diversity like several other indigenous plant species. Expanding the diversity of global food sources has become imperative. This study investigated the molecular dynamics in AYB by assessing the genetic diversity in non-tuber and tuber-producing landraces, identified SNP markers associated with tuber formation and determined the relationship between seed and tuber production. The study evaluated accessions from the Genetic Resources Centre of the International Institute of Tropical Agriculture (IITA), Ibadan. Phenotypic data was generated from monitored growth, genotyping was conducted using DArTseq technology, with SNP data generated afterward. Phenotypic data employed clustering, correlation analysis and distribution plots. Genome-wide Association Studies (GWAS) using the GAPIT package in R elucidated population structure and identified SNPs responsible for yield. Multiple traits such as NoPods, Hundred sdcount, TSdwghtPPL, TPodwgth indicate a close association with each other showing a strong indication with the accessions and yield. While clustering for seed and tubers showed four and five clusters each. BLUEd traits and 2254 SNP markers from 92 genotypes were used for the association analysis. Using the BLINK, FarmCPU, GLM, and MLM models. Twelve significant SNP markers were identified to be associated with three African yam bean yield traits (Tuber weight, Seed thickness, and Pod width). These results have the potential to accelerate marker-assisted selection in molecular breeding.

**Keywords:** *African yam bean, opportunity, Seed, Tuber, SNPs, Yield*