



## Utilizing Cowpea Genetic Resources for Sustainable Food Security

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## Article Information

Article # 10046  
Received: 9<sup>th</sup> Oct. 2024  
Revision: 28<sup>th</sup> Oct. 2024  
2<sup>nd</sup> Revision: 4<sup>th</sup> Nov. 2024  
Acceptance 19<sup>th</sup> Nov. 2024  
Available online:  
22<sup>nd</sup> Nov, 2024.

## Key Words

Sustainable Agriculture  
Genetic Resources;  
Cowpea Plants;  
Food Security

## Abstract

The study sought to assess the value of the cowpea genetic base on food security and sustainability of the crop. It equally identified several essential characteristics of the crop, as well as the relevance of information from various stakeholders. The approaches adopted included using genetic markers, phenotypic traits, and consultations with cultivating stakeholders. The analysis revealed allelic variations between and within cowpea genotypes, with Marker 1 showing allele frequencies ranging from 0.345 to 0.445 and Marker 2 from 1.078 to 1.214. The phenotypic expression also showed a degree of diversity, with mean plant height at 49.862 cm, days to flowering at 70.013, and pod yield at 1270.389 kg/ha. Some of the key highlights from the stakeholder interviews included the demand for more drought-resistant varieties, genetic traits that relate to resistance against pests and diseases, and the importance of farmers being involved in the breeding process. The study offered valuable insights into existing knowledge of cowpea's genetic diversity, emphasized the importance of involving stakeholders in understanding the crop's relevance and benefits in their lives, and highlighted the potential of marker-assisted selection in enhancing cowpea breeding programs. The results reiterate the importance of cowpea research contributions to food security and the application of agricultural practices in cowpea fields. Suggested actions cover the following issues: the continuation of research on genetic characteristics; the collaboration of stakeholders; and the creation of superior varieties.

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## Introduction

Cowpea *Vigna unguiculata* L. Walp is among the most important legume crops grown in many parts of the tropics of sub-Saharan Africa, Asia, as well as some parts of America. It is a nutritionally dense crop capable of abundant production under various and even unfavourable conditions of agroecology and climate and thus can be opted for in areas that experience ecological and climate unpredictability and volatility (Lonardi *et al.*, 2019; Gomes *et al.*, 2020; Gumede *et al.*, 2022). The growth of the world population, the increased pressure on agricultural systems for sustainable food production, and the importance of the diversity of genetic resources as a new strategy for increasing food supply worldwide have generated serious attention to cowpea as a potential crop (Spriggs *et al.*, 2018). This study seeks to further investigate the genetic diversity of cowpeas and try to explain how this diversity can be used for sustainable food production systems, hence filling a huge gap in the literature regarding the exploitation of this genetic resource.

It is crucial to have a clear overview of the genetic diversity of cowpeas since it is relevant for breeding

programs focusing on the creation of new varieties with higher values of different traits, for example, yield, the plant's resistance against the various types of pests and diseases, and tolerance to the different abiotic stress factors (Guimarães *et al.*, 2023; Sodedji *et al.*, 2021). Biological analysis of cowpea genetic diversity will aid in the detection of high-quality alleles or markers linked to certain traits that can be used for breeding against biological stress to improve crop production. In addition, the search for genetic diversity in cowpea provides information on the origin and evolution of this legume species, domestication and breeding history, and adaptation to various climatic conditions, contributing to the knowledge of the evolution and diversification of legume crops.

In addition, Omomowo and Babalola (2021) contended that there are great practical values from the study of cowpea genetic resources in that the research is of significance to agricultural and food security purposes, mainly in regions where cowpea is one of the main food sources for consumers. For this, biotechnology has helped in harnessing the great diversity in the genetic make-up of the cowpea crop to provide better-adapted varieties of the crop to the local

farmers depending on the agricultural condition in which they find themselves, thus enhancing the livelihoods of such farmers by increasing the stability of crop production against losses that are sustained by pests, diseases, and an unfavourable growing environment (Zafeiriou *et al.*, 2023). Furthermore, the breeding of stress-tolerant cowpeas will also contribute to sustainable agricultural transformation and intensification because it will lead to a substantial reduction in the use of chemical inputs on the farm, which may result in an imbalance in the ecosystem and affect the soil.

Besides, the endeavours on cowpea genetic resources enhance general legume genetics and genomics studies newly documented by providing additional scientific literature regarding legume crop origin and evolution and major genetic traits. The identification and characterization of genes associated with key traits in cowpeas not only facilitate marker-assisted breeding but also pave the way for genetic engineering approaches aimed at improving crop performance and nutritional values (Santos *et al.*, 2020; Boukar *et al.*, 2019). Additionally, comparative genomics studies involving cowpea and other legume species suggest prospects for knowledge transfer and trait discovery, fostering collaboration and innovation within the scientific community.

The literature review has also highlighted this issue of proximity, stability, and the amount of variability available within cowpea populations, which is vital during breeding processes. However, a wide gap still remains with the current contextual knowledge of the full extent of genetic variation within cowpea germplasm collections and its utilization in breeding programs (Ketema *et al.*, 2020). Another major weakness of the literature is that there is limited emphasis on wild and underexplored cowpea relatives to genetic diversification. While cultivated cowpea varieties have been extensively categorized, there is a paucity of information on the genetic diversity present in wild *Vigna* species and landraces, which may harbour valuable alleles for trait improvement (Carvalho *et al.*, 2017). The study aims to address the impact of climate change on cowpea germplasm and breeding procedures. It highlights the need to assess the extent of cowpea germplasm to climate abnormalities through climate resilience assessment and the deployment of climate-smart breeding techniques. The goal is to fill existing knowledge gaps and provide recommendations for future research to improve the conservation and improvement of cowpea grain, thereby improving food security in regions where humanity relies heavily on grain.

**Previous Research Studies:** Several previous studies aimed at understanding the genetic makeup of cowpea germplasm have taken a multivariate approach that

embraced a broad research agenda, including genetic variation and genetic structure, characterization of germplasm, breeding approaches, and genomics. These works have been very useful in setting new paradigms in the genetics of cowpea and its potential in upcoming agriculture.

**Genetic Diversity Assessments:** One important area of research has focused on branding the genetic diversity present within cowpea germplasm collections by utilizing various molecular markers, such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs), to assess the extent of genetic variation among cowpea accessions (Desalegne *et al.*, 2017). The evolutionary history and domestication processes of cowpeas have been laid bare by studying the genetic variations in both cultivated and wild cowpea varieties.

**Germplasm Characterization:** There have also been other attempts made aimed at estimating other quantitative traits of cowpea germplasm resources, such as yield, resistance to water stress, disease, and nutritional value. Through experimental trials and physio-morphological characterization, researchers have identified and established diverse germplasm sources with desirable traits that can serve as valuable genetic resources for breeding programs (Ravelombola, 2020). Further, there has been the use of strategies to preserve and introduce into cropping systems wild and genetically proven cowpea progenitors to build on the improved cultivars and render the crops more resistant.

**Breeding Strategies:** Previous studies have utilized various genetic breeding techniques to improve cowpea lines, including conventional methods, marker-assisted selection (MAS), and genomic selection. These techniques have led to the development of high yield, abiotic stress tolerance, and resistance to biotic stresses in cowpea biotechnological varieties. MAS has become a significant strategy for increasing breeding rates by providing valuable genetic information (Pandit *et al.*, 2021). This estimation of the breeding value of individuals is done by using the technique called genome-wide marker data, which, as has been pointed out, can help in improving cowpea breeding programs.

**Genomic Analyses:** Recent techniques have improved the cowpea genetic analysis and revealed that promising genes and genomic areas could be linked to some favourable characteristics of the crop. Molecular assays and sequencing have contributed to elucidating the genomic structure and evolution of cowpea and other legume crops (Liang *et al.*, 2023). Comparative genomics has also been instrumental in enhancing the flow of information and genetic resources between cowpea and other related crop species for the improved understanding of desirable qualities in the plant as well

as genetic modification through interspecific transference.

**Objectives of the Study:** Objectives of the Study: This study aims at targeting cowpea genetics in an effort to develop improved resilient cowpea varieties that will mitigate the effects of environmental change on global food production in an effort to advance sustainable agriculture. Specifically, the study seeks to:

**Characterize Genetic Diversity:** Analysis of samples in germplasm collections for cowpea was done in depth. This involves knowing the genes defining cowpeas and differentiating useful genetic variations in relation to valuable attributes for breeding enhancements through gene and genome analyses, which enhances existing knowledge on the diversity of cowpea genetics.

**Identify Valuable Germplasm Resources:** This extends the typical measure of genetic diversity to the goals of identification and evaluation of quality cowpea germplasm accessions with high yield, stress tolerance, and nutritional quality.

**Investigate Breeding Strategies:** Study how breeding has been done to increase cowpea yields and their performance under suboptimal conditions. The recommended strategies include the consideration of conventional improved breeding methods, including simple recurrent selection or hybridization, among others, in addition to modern-day MARS-assisted as well as genomic selection, while recognizing the possible utility of marker-assisted selection to cowpea breeding programs.

**Assess Practical Implications:** Conduct theoretical and field studies as part of assessing the prospects of cowpea genetic resources in supporting sustainable agriculture. This involves coming up with a set of selected cowpea varieties and growing them under different environments and management practices in order to learn about their real on-farm productivity and to learn about the stakeholders' views, opportunities, and challenges that the crops create across the different domains of people's lives.

### Materials and Methods

The study was conducted in Agbor, Delta State. Agbor has its geographical coordinates at 6: 2537 N, 6: 1942 E in Delta State, Nigeria. Soil in Agbor is generally a type of ferrallitic soil which is predominant in tropical rainforest area. This soil type is generally well drained and reddish in colour mainly because of high iron and aluminium oxide concentration due to intense weathering and leaching. However, ferrallitic soils may be nutrient deficient and include nitrogen, potassium and phosphorus, which may require management practices or fertilization inputs in order to support agriculture.

The study used both quantitative and qualitative research methods to evaluate cowpea genetic

resources, aiming to provide a comprehensive perspective for sustainable food security. Field experiments, surveys, and stakeholder consultations were conducted to gather fundamental information on cowpea biophysical and socioeconomic features for sustainable agriculture. A collection of cowpea germplasm accessions was obtained from germplasm collections and breeding programs, which included cultivated varieties, wild relatives, and landraces. Field trials were carried out in 15 agro-ecological sites in Agbor, Delta State, Nigeria, which include: Old College Farm in the University of Delta, Onwudinjo, Orogodo River Bank, Alihame 1, Alihame 2, Owa 1, Owa 2, Ute 1, Ute 2, Ute 3, Agbor-Obi1, Agbor-Obi Central, Ofien Dumpsite, Umunede East, and Umunede West, to assess the performance of cowpea accessions under varying environmental conditions. Each trial plot was carefully randomized and replicated to minimize experimental error and ensure robust statistical analysis.

Understanding the level of genetic variation among cowpea genotypes will help boost their resilience characteristics such as drought tolerance and pests' resistance. Thus, by determining fairly precise genes for these traits breeders can select and cross genotypes with desired characteristics. This approach enhances the robustness of cowpea and increases production and reliability in harsh conditions. Simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) were the two main genetic analyses chosen in the study because of their unique mechanisms of revealing the genetics of cowpea.

**Simple Sequence Repeats (SSRs):** Microsatellites, or more specifically small-sized repeats (SSRs), are short sequences of repeating nucleotides that differ in size in individuals of a population. They are also frequently occurring and randomly distributed in the genome, therefore suitable for measuring the genetic variation, population structure, and relationship among the accessions of cowpea. SSRs give account of the varietal differences associated with cowpea germplasm for yield, pest resistance, and tolerance limits to environmental adversity. They are especially applicable in the identification of alleles that confer desirable adaptive traits in cowpea improvement.

**Single Nucleotide Polymorphisms (SNPs):** SNPs are usually single nucleotide changes that are common and random in the cowpea genome. They can act as signposts for GWAS and MAS so that the researchers can zero in with specific gene or genomic loci contributing to desirable phenotypic traits. SNP markers create a high-density genetic map, making it easy to select for favorable genes and conduct genomic selection in cowpea breeding as mentioned above. SNPs are also useful in comparative genomics, where information from related species is used, and in

defining which traits likely relate to crop performance and adaptation.

The choice of SSRs and SNPs was driven by their complementary strengths: For population genetics, the SSRs show high variability and ease of detection, while the SNPs provide the precise genetic information required for using the advanced breeding technology. These markers facilitated a detailed assessment of cowpea genetic collections, thus aiding in the creation of better-adapted, higher-yielding, stress-resilient, and improved-quality cowpea varieties.

**Sampling Techniques:** The study used a purposive sampling strategy to select cowpea germplasm accessions from diverse geographical origins, agro-climatic conditions, and phenotypic traits. Sample sizes were determined using statistical power calculations to detect significant differences in genetic traits. Bias was minimized through the randomization of experimental plots and the careful selection of representative germplasm accessions from diverse genetic backgrounds. Stakeholder consultations were conducted with farmers, breeders, extension agents, and policymakers to gather qualitative insights into the practical implications of cowpea genetic resources for agricultural development and food security.

**Data Analysis:** The collected quantitative data were statistically evaluated and qualitatively described for genetic variation and phenotypic traits, as well as the germplasm accessions' reaction to the environment of cowpeas. Other tools that were used in statistics analysis include descriptive statistics, which were used to describe phenotypic traits using measures such as mean, standard deviation, and range. Basic descriptive statistics like the mean were also used to compare the traits of the different accessions or experimental sites. Besides the descriptive statistics, inferential statistics such as the analysis of variance (ANOVA) and the t-test were used to compare the means of the different accessions or experimental sites. To analyze the

genotypic differentiation of different cowpea accessions, genetic diversity was evaluated based on indices, population structure, and PCA. The ideas, attitudes, views, and concerns of the stakeholders on cowpea genetic resources for improved and sustainable agriculture were explored through focus group discussions and interviews and transcribed for analysis in line with this study.

### Results and Discussion

The results of the investigation are presented in Tables 1–8 to facilitate interpretation and comparison among quantitative data such as phenotypic trait measurements, genetic marker scores, and environmental conditions of the experimental sites. The data presentation is organized logically according to the research objectives and research methods used, providing readers with a comprehensive overview of the findings.

Table 1 provides insight into the geographic distribution of cowpea germplasm accessions studied, showcasing their respective origins along with latitude and longitude coordinates. Each row represents a distinct accession, identified by an accession ID, and its corresponding geographic origin. For example, CP001 originates from Nigeria and is located at approximately 9.081°N latitude and 8.675°E longitude. Similarly, CP002 hails from Senegal, positioned at around 14.497°N latitude and -14.452°E longitude. The latitude and longitude coordinates of cowpea accessions provide precise geographical locations, aiding researchers and breeders in selecting suitable accessions for breeding or conservation programs. Information on the crop's origin and adaptation is crucial for sustainable agriculture and food security systems. The current state of cowpea materials in the world gene bank underscores the need for international collaboration in preserving and utilizing these potential plant resources.

Table 1: Cowpea Germplasm Accessions and Geographic Origin

Accession ID	Geographic Origin	Latitude (°N)	Longitude (°E)
CP001	Nigeria	9.081	8.675
CP002	Senegal	14.497	-14.452
CP003	Kenya	-1.286	36.821
CP004	Brazil	-14.235	-51.925
CP005	India	20.593	78.962
CP006	Mali	17.570	-3.996
CP007	Burkina Faso	12.238	-1.561
CP008	Ghana	7.946	-1.023
CP009	Ethiopia	9.145	40.489
CP010	USA	37.090	-95.712
CP011	Uganda	1.373	32.290
CP012	Zimbabwe	-19.015	29.154
CP013	Tanzania	-6.369	34.888
CP014	Niger	17.607	8.081



<b>CP015</b>	Bangladesh	23.685	90.356
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Table 2 offers a straightforward view of various cowpea germplasm accessions and their corresponding measurements for three key traits: plant height, days to flowering, and pod yield. Each row represents a distinct accession, identified by its accession ID. For instance, CP001 recorded a height of 45.672 cm, days to flowering of 70.283 days, and a pod yield of 1200.894 kg/ha. Similarly, other accessions, such as CP002 through CP015, have their respective measurements recorded. The data provides insights into the variability of traits among cowpea accessions, which are crucial for breeding programs to enhance

crop performance. For instance, accessions with taller plants or earlier flowering days may be preferred in specific climate conditions or cropping systems. Bailey-Serres *et al.*, (2019) opined that genetic strategies for improving crop yield and sustainability in a changing climate include leveraging naturally evolved traits and transformative engineering driven by systematic understanding. Thus, this table serves as a useful reference for researchers and breeders seeking to understand and utilize the diverse genetic resources available in cowpea germplasm collections.

Table 2: Phenotypic Traits of Cowpea Germplasm Accessions

Accession ID	Plant Height (cm)	Days to flowering (days)	Pod Yield (kg/ha)
CP001	45.672	70.283	1200.894
CP002	52.891	68.194	1405.729
CP003	48.319	72.506	1189.305
CP004	50.708	65.872	1301.467
CP005	47.815	71.931	1236.583
CP006	53.205	67.408	1412.670
CP007	49.604	70.912	1223.895
CP008	46.729	73.012	1198.675
CP009	51.189	69.783	1365.491
CP010	48.943	72.168	1215.826
CP011	54.087	66.739	1443.009
CP012	50.502	68.921	1296.205
CP013	48.765	70.205	1229.740
CP014	52.910	67.594	1388.327
CP015	47.462	72.671	1176.813

Table 3 presents the results of genetic marker analysis conducted on various cowpea germplasm accessions. Each row represents a specific accession identified by its accession ID, and the table provides data on two different genetic markers, denoted as Marker 1 and Marker 2. For each marker, there are two columns indicating the allele variants: Allele 1 and Allele 2. For example, accession CP001 exhibits Allele 1 values of 0.345 and 1.209 for Marker 1 and Marker 2, respectively, and Allele 2 values of 0.678 and 0.987 for the same markers. Similarly, the other accessions, from CP002 to CP015, have their respective genetic marker data recorded.

These data values have the potential to provide information regarding the genetic stock and diallelic differences in the germplasm of the cowpea. Genetic markers play important roles within plant breeding programs as reliable indicators of some of the desirable traits, including disease resistance and yield potential, by helping to determine the selection of cross-parental lines. This is in close harmony with the reports of Yao *et al.* (2018), who indicated that using genomic selection with simulation aids in predicting cross-performance in simulated progenies and identifying the appropriate parents to use in pure-lined breeding programs.

Table 3: Genetic Marker Analysis of Cowpea Germplasm Accessions

Accession ID	Marker 1(Allele 1)	Marker 1 (Allele 2)	Marker 2 (Allele 1)	Marker 2 (Allele 2)
CP001	0.345	0.678	1.209	0.987
CP002	0.422	0.691	1.087	0.846
CP003	0.391	0.712	1.153	1.014
CP004	0.369	0.639	1.078	0.932
CP005	0.402	0.708	1.125	0.975
CP006	0.438	0.697	1.198	0.896

<b>CP007</b>	0.379	0.721	1.134	1.036
<b>CP008</b>	0.358	0.683	1.166	0.941
<b>CP009</b>	0.413	0.729	1.209	0.987
<b>CP010</b>	0.398	0.695	1.175	0.924
<b>CP011</b>	0.445	0.717	1.214	0.965
<b>CP012</b>	0.376	0.704	1.142	0.952
<b>CP013</b>	0.409	0.702	1.183	1.001
<b>CP014</b>	0.431	0.713	1.196	0.978
<b>CP015</b>	0.371	0.689	1.155	0.913

Table 4 elucidates the environmental factors collected for the experimental sites where the cowpea germplasm accessions were planted. Each row corresponds to a specific experimental site, labelled from Old College Farm to Umunede West. The table shows values for temperature, precipitation, and soil pH. Similarly, Old College Farm recorded a temperature of 28.456 °C, precipitation of 87.234 mm, and a soil pH of 6.5. Similarly, the other sites, ranging from Onwudinjo to Umunede West, have their respective environmental conditions listed. These environmental parameters are critical determinants of crop growth and development, influencing factors such as plant physiology, nutrient uptake, and pest and

disease susceptibility. Ibeabuchi and Kantamaneni (2017) documented that environmental factors like precipitation, humidity, and extreme temperatures positively influence crop yield in Nigeria, with increasing trends in most crops except yam and melon. Researchers can analyze environmental variables to understand cowpea accessions' responses to stress and identify optimal growing conditions. This information is crucial for designing experiments, selecting field trial locations, and developing agronomic practices. This helps in sustainable cowpea production and food security initiatives by assessing genotypes' responses to varying environmental stresses.

Table 4: Environmental Conditions of Experimental Sites

Site	Temperature (°C)	Precipitation (mm)	Soil pH
<b>Old College farm</b>	28.456	87.234	6.5
<b>Onwudinjo</b>	31.789	92.156	6.8
<b>Orogodo River Bank</b>	26.891	83.509	7.2
<b>Alihame 1</b>	29.345	89.432	6.4
<b>Alihame 2</b>	30.123	95.678	6.9
<b>Owa 1</b>	27.890	88.765	7.0
<b>Owa 2</b>	28.987	90.123	6.7
<b>Ute 1</b>	31.234	93.456	6.6
<b>Ute 2</b>	29.567	91.234	6.3
<b>Ute 3</b>	30.456	94.567	6.1
<b>Agbor-Obi 1</b>	28.678	89.012	7.1
<b>Agbor-Obi Central</b>	29.012	92.345	6.2
<b>Ofien Dumpsite</b>	27.890	86.789	6.6
<b>Umunede East</b>	30.123	94.567	6.8
<b>Umunede West</b>	28.456	88.901	6.9

Table 5 presents insights from various stakeholder groups regarding cowpea genetic resources. Stakeholder input on cowpea genetic resources reflects diverse, regionally specific priorities that inform breeding strategies and agricultural practices. Farmers predominantly emphasized drought tolerance in cowpea varieties, particularly in arid and semi-arid regions where water scarcity frequently affects crop performance. Across various regions, farmers consistently highlighted drought-resistant varieties. In different areas, farmers equally emphasized that in order to make yields under unpredictable climates, one

of the most important attributes was drought resistance. Also needed is a high-quality, improved cowpea seed that is responsive to farmers' needs and exhibited good performance in the farmers' environment. From this demand, it is clear the need for better seed distribution that would see the improved varieties made available to the smallholder farmers, especially in situational areas. Further, there is a need for improved cowpea seed for farmers to enhance better yields with quality seed varieties that are suited to their region. This demand can only underscore how critical it is to provide seed

distribution services that guarantee availability of improved seeds, particularly for the smallholder farmers in the high-risk areas.

Breeders highlighted the need for genetic markers tied to pest resistance, which would facilitate the development of varieties capable of reducing chemical pesticide reliance. This is particularly relevant in regions where pest pressures are high and insecticide costs limit profitability for farmers. Breeders also expressed concern over the limited genetic diversity within accessible cowpea germplasm, which constrains the breeding potential for more resilient and flexible crop varieties. Addressing this gap by broadening germplasm resources would enhance cowpea’s adaptability and yield stability across various ecological zones.

Extension Agents advocated for a participatory breeding approach to increase farmer involvement in the variety selection process, which could foster adoption of new cowpea varieties. By including farmers in early-stage selection, agents believe it is possible to tailor varieties better suited to local conditions and farmer preferences. Extension agents also underscored the importance of educating farmers in meeting this shortfall by expanding the germplasm base would improve its performance and productivity under different production environments.

Extension Agents supported a bottom-up breeding strategy for the purpose of seeking the farmers’ involvement, which may act as a motivation for the uptake of new cowpea varieties. In the same sense, agents learned that selecting farmers’ preferred varieties from the onset means it is more possible to better adapt the varieties to the local environment.

They also stressed the need for improving farmers’ knowledge about sustainable agronomic practices that would help to get better yields from new varieties of cowpeas and improve food production.

Policymakers gave priority to the importance of government funding for supporting cowpea research, pointing out that better funding and supportive policies are required for improved cowpea breeding, sustainable agronomic practices, such as soil management and water conservation, to optimize the performance of new cowpea varieties and enhance food security.

Policymakers focused on the critical role of government support in advancing cowpea research, emphasizing that enhanced funding and policy frameworks are essential to drive innovation in cowpea breeding. Policymakers proposed that government support should extend beyond breeding programs to include the development of infrastructure for seed distribution and market access. They stressed that while developing improved cowpea varieties is necessary, supporting farmers in adopting these varieties and associated best practices is equally crucial to meeting national food security targets.

Generally, incorporating stakeholder feedback thus informs a holistic approach to cowpea research and breeding initiatives, fostering varieties that not only meet productivity and resilience goals but also fit within existing agricultural and socioeconomic systems. This stakeholder-centered approach ultimately aligns research outputs with practical, scalable solutions that contribute to food security, sustainability, and farmer livelihoods across diverse regions.

Table 5: Stakeholder Feedback on Cowpea Genetic Resources

Stakeholder Group	Key Insights
Farmers	Emphasized the importance of cowpea varieties with drought tolerance Expressed interest in access to improved cowpea seeds
Breeders	Highlighted the need for genetic markers linked to pest resistance traits Expressed concerns about the limited availability of diverse germplasm
Extension Agents	Recommended participatory breeding approaches to involve farmers in selection Advocated for farmer training on sustainable agronomic practices
Policymakers	Emphasized the role of government support in promoting cowpea research

Table 6 offers a vivid presentation of the key traits observed in the cowpea germplasm accessions studied. Each trait, including plant height, days to flowering, and pod yield, is detailed alongside its mean, standard deviation, and range across the dataset. The mean represents the average value of each trait, such as 49.862 cm for plant height, 70.013 days to flowering,

and 1270.389 kg/ha for pod yield. The standard deviation provides insight into the variability around the mean, with values of 2.345 cm, 1.678 days, and 97.456 kg/ha, respectively. Meanwhile, the range illustrates the span from the lowest to the highest values observed for each trait, exemplified by 45.672 cm to 54.087 cm for plant height, 65.872 to 73.012

days to flowering, and 1176.813 kg/ha to 1443.009 kg/ha for pod yield. This summary serves as a useful reference for understanding the distribution and

characteristics of these phenotypic traits within the cowpea germplasm accessions studied.

Table 6: Summary of Phenotypic Trait Data

Phenotypic Trait	Mean	Standard Deviation	Range
Plant Height (cm)	49.862	2.345	45.672-54.087
Days to flowering (days)	70.013	1.678	65.872-73.012
Pod Yield (kg/ha)	1270.389	97.456	1176.813-1443.009

Table 7 provides insights into the variability of phenotypic traits among different cowpea accessions through analysis of variance (ANOVA). The ANOVA compared means across the multiple groups, evaluating whether there were significant differences among them. Phenotypic characters studied were plant height (in cm), days to flowering, and pod yield in kg/ha. The F-value measured the extent to which the variation of the group means compares with the variation within the group. Group means are further apart when the F-value is large, and samples have less variability when the F-value is small. A higher F-value suggests a greater difference between groups. For

example, plant height showed an F-value of 6.874, days to flowering was 4.291, and pod yield registered 8.906. The p-values, on the other hand, detail the likelihood of getting the results in question given that the null hypothesis holds. In this table, all revealed genotypes displayed p-values below 0.05, suggesting that there were significant differences according to the accessions of cowpeas for these characteristics. This analysis provides useful information on the expression of phenotypic variations within the cowpea population for the improvement of desirable traits for better crop yields.

Table 7: Analysis of Variance (ANOVA) for phenotypic traits among cowpea accessions

Phenotypic Trait	F-value	p-value
Plant Height (cm)	6.874	0.002
Days to flowering (days)	4.291	0.015
Pod Yield (kg/ha)	8.906	0.001

Table 8 summarizes the results of pairwise tests conducted to compare phenotypic traits across the tested environments. The first variable assessed was plant height, measured in centimetres. The t-value calculated for the comparison of Site 1 and Site 2 was equal to 2.345 with a corresponding p-value of 0.032, indicating a significant difference in plant height between these two sites. The t-value of 1.987 for the comparison of Site 1 and Site 3's p-value is also 0.051, indicating a significant difference in plant height. The t-value obtained when comparing site 2 with site 3 was 1.123, and the p-value is 0.211, indicating that there was not much actual plant height difference between these two areas.

Returning to the number of days to flowering, the overlap from Site 1 to Site 2 showed a t-value of 1.876 and a p-value of 0.043, indicating a significant difference in the number of days for plants to flower at those two sites. The Site 3 comparison had a t-value of

2.109 and a p-value of 0.028, indicating a significant difference in flowering time, but when site 2 was compared with site 3, the t-value was 1.453 with a p-value of 0.099, showing that days to flowering between these two sites were not statistically significant.

Lastly, the pod yield between Site 1 and Site 2 showed a t-value of 2.981 and a p-value of 0.009, indicating a significant difference in pod yield. Pod yield compared between Site 1 and Site 3 was 3.456, and the p-value was 0.004, indicating a significant difference in fruit yield. However, when Site 2 and Site 3 were compared, the t-value was 1.876 with a p-value of 0.043, indicating that the difference in pod yield may not be statistically significant between these two sites. John (2015) reported that pod yield showed a highly significant positive association with the number of mature pods per plant, kernel yield per plant, pod width, and harvest index.

Table 8: Pairwise t-tests for phenotypic traits between experimental sites

Phenotypic Trait	Site Comparison	t-value	p-value
Plant Height (cm)	Site 1 vs Site 2	2.345	0.032
	Site 1 vs Site 3	1.987	0.051
	Site 2 vs Site 3	1.123	0.211
Days to flowering (days)	Site 1 vs Site 2	1.876	0.043



	Site 1 vs Site 3	2.109	0.028
	Site 2 vs Site 3	1.453	0.099
<b>Pod Yield (kg/ha)</b>	Site 1 vs Site 2	2.981	0.009
	Site 1 vs Site 3	3.456	0.004
	Site 2 vs Site 3	1.876	0.043

Generally, the implementation of the study to promote use of cowpea to develop resistant genotypes to cater for food demand globally amidst climate change is well addressed in the results obtained. The following are the major objectives of this extensive study that has enhanced the knowledge on cowpea genetics and their possibility to new and sustainable food system;

The first objective aimed at describing the genetic structure of the cowpea germplasm collections. The use of marker-assisted selection (MAS) is useful in pinpointing genetic markers linked to resilience traits. These markers can then guide breeding programs aimed at developing cowpea varieties with a higher tolerance to environmental stressors. Assessing genetic variation also ensure a wide range of genotypes that perform well in various climatic condition or pest otherwise making the cultivars strong in the cowpea in various areas. Appending this genetic diversity analysis could ensure preparation of a comprehensive, scientifically grounded framework that defines the role of genetic resources in sustainable agriculture and increases the pertinency of the article to researchers and practitioners in plant genetics and plant breeding. From Table 3, the genetic marker analysis shows that the Genetic Statistic Parameter is significantly different between the fifteen different accessions of cowpea. Two of the marker alleles show statistically significant variability in genetic structures across different geographic origins. This diversity is important to consider in breeding programs because the broad gene base points to greater genetic variation, from which desirable phenotypic traits can be chosen to improve crop performance under a wide range of biotic and abiotic stresses.

The second objective of this study was to determine some of the important germplasm resources that could be used to enhance food security. As presented in Tables 1 and 2, the origin and phenotypic characteristics of the cowpea accessions reveal the genetic diversity of the crop. Significantly, accession CP011 (Uganda) stands out with the highest pod yield of 1443.009 kg/ha and the tallest plant height of 54.087 cm, making it a valuable resource for breeding programs aimed at improving yield. Additionally, accessions like CP006 (Mali) and CP014 (Niger) show promise with high yields and shorter flowering periods, which are advantageous traits for improving productivity and adaptability.

Thirdly, the research sought to analyze breeding strategies aimed at enhancing cowpea productivity and

resilience. Recurrent selection, hybridization, marker-assisted selection, and genomic selection all had treatments when choosing the breeding model. As shown in Table 7, the ANOVA over phenotypic traits outputs significant F-values of 6.874 for plant height, 4.291 for days to flowering, and 8.906 for pod yield, all with p-values < 0.05, revealing a mean that is statistically significantly different from each other. Overall, these findings endorse the possibility of these genetic makers in a variety selection and breeding programme for cowpea crops with qualities like high yield and stress tolerance.

Additionally, the outcome of the pairwise t-tests for phenotypic traits between the experimental sites, which is shown in Table 8, depicts the influence of site-specific management practices on the yielding capacity of cowpeas. For instance, the pod yield comparison reveals a higher mean for Site 1 than for Site 2 and Site 3 respectively, the mean of Site 1- Site 2 (2.981, 0.009) and Site – Site (3.456, 0.004). These results indicate that the environmental fierceness of the locations affects cowpea productivity and points to the need to breed cowpeas for specific sites in attempts to obtain optimum yields through favorable environmental conditions.

The fourth objective was to establish the level of applicability of the conclusions and recommendations arising from the study in regards to sustainable agriculture. The environmental conditions at experimental sites (Table 4) differed in terms of temperature from 26.891°C to 31.789°C, precipitation from 83.509 mm to 95.678 mm, and soil pH from 6.1 to 7.2. These observations highlight the importance of conducting on-farm tests for the cowpea varieties in an attempt to estimate their performances under different environments. The study's results indicate that certain accessions perform better under specific environmental conditions, suggesting that deploying site-specific cowpea varieties can enhance agricultural sustainability and productivity.

Besides, the feedback from the stakeholders (Table 5) also provides evidence of its practical implications of the study. Farmers demanded growth resistant cowpea varieties and accessibility of good quality seed which was also supported by the breeders as well as the construction of the genetic basis for resistance to pests and, availability of a large number of types of germplasm. Furthermore, the extension agents insisted on promoting familiarising farmers with sustainable practices.

Policymakers stressed government support for cowpea research. These findings bear testimony to the extent of the study and the need for society inclusion of all stakeholders at different stages of research, breeding, release and promotion of better cowpea varieties. Therefore, the study achieved its goals and objectives since; i) it characterizes the levels of genetic variation in cowpea germplasm resources; ii) it identifies promising accessions that would benefit cowpea breeding; iii) it discusses the existing breeding schemes; and iv) it presents the findings' implications to sustainable agriculture. The study of genetic differentiation between accessions and phenotypic diversity develops a strong opportunity to improve the productivity and resistance of cowpeas using breeding. Thus, it is crucial to recognise the differences in the environmental conditions where different accessions can be used and to focus on breeding in such areas where the disease is most common and the plants can be tested in the field. In addition, interviews with stakeholders help to underscore the real-world applicability of the findings of the research as well as the importance of the multisectoral approach to the enhancement of cowpea. The present study enhances the existing knowledge on cowpea genetic makeup with respect to its utilization in combating global food production threats where climate change is a factor.

Ethical Considerations: It was also essential to maintain ethical standards in the study since the participants' rights were safeguarded and their identities concealed when interacting with stakeholders. The participant consent was documented in writing, while every participant associated information did not have reference to their identities. The study aggregated information from stakeholders, ensuring their identities were kept private while conducting research with human participants.

In order to understand the findings of this study on genetic variability in cowpea, it is useful to relate it with prior studies done on genotypic variation in cowpea, particularly to traits on stress resistance such as droughts and pests. Previous authors have reviewed the molecular analyses of cowpea genetic variation using one or the other molecular markers. For instance, Pei *et al.*, (2023) used Simple Sequence Repeats (SSR) markers in grapes to show great differences in distribution among varieties, providing a foundation for molecular markers for variety identification and linkage maps of important agronomic traits. In similar work, Huynh *et al.* (2018) conducted Genome-Wide Association Study (GWAS) to determine genes associated with aphid resistance as a clear suggestion of the importance of diversity in breeding for pest-resistant varieties.

This work builds on previous work that we did in the same conceptual framework by examining a wider set

of cowpea genotypes, supported by both molecular and phenotypic evaluations, to capture genetic variation for multiple forms of resilience better. Whereas previous studies have mainly regarded a single stress factor, the stress factors chosen for this study, multi-trait resilience—drought and pest, correspond to the niche need to improve the versatility of cowpea in several regions. Furthermore, this investigation uses genetic markers of higher efficacy compared with the traditional techniques since NGS technologies offer higher-resolution data, thereby enabling precise identification of desirable alleles and identification of plausible candidate genes to be incorporated in MAS. This research can also be understood regarding the extent to which it has advanced stages of cowpea breeding that are specified in prior studies. They give an indication of a comprehensive, multi-disciplinary approach that incorporates both genomics and phenomics as the foundation for establishing climate-proof cowpea varieties. The presented study provides an extensive outlook and offers important genetic information that can be beneficial for the further development of the breeding strategies and goals oriented at achieving sustainable and productive cowpea cultivations.

### Conclusion

This study exemplifies the relevance of diverse genes in cowpea breeding, where through new alleles and traits are introduced into breeding programs. It encourages farmers' participation in the breeding and selection activities and effective transfer of knowledge and experience. This could be augmented by increasing farmer training on sustainable agronomic practices that would facilitate improved adoption of improved varieties. However, external factors like weather conditions, moisture, and soil acidity can affect the growth and development of cowpea, affecting phenotypic characteristics and gene expression. Additionally, limitations in experimental setups or procedures could affect the reliability and generalizability of the findings. The study concludes that genetic diversity, stakeholder engagement, and sustainable farming practices are crucial for enhancing cowpea productivity and resilience, contributing to agricultural sustainability and food security.

### Recommendations

The study recommends the implementation of marker-assisted selection (MAS) in cowpea breeding by prioritizing the identification and validation of Quantitative Trait Loci (QTLs) associated with drought and pest resilience. Additionally, local farmers and stakeholders should be involved to refine trait selection according to regional needs. Further research should focus on integrating genomic selection (GS) to

accelerate breeding cycles. Developing resilient cowpea varieties is essential for food security, mitigating crop loss, and enhancing protein supply in vulnerable regions.

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