

Genomic Variation and Adaptation in Wild Cowpea (*Vigna unguiculata* L. Walp): Insights for Enhancing Crop Resilience and Food Security

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Abstract

This study was aimed at investigating genomic variation in wild cowpea populations to understand its implications for crop improvement. The method adopted in the study encompassed population structure analysis and gene flow studies, supported by statistical tools, to elucidate genetic dynamics from 3 wild cowpea varieties grown on a complete randomized block design with 3 replicates. Results indicate distinct phenotypic traits and genomic markers associated with adaptive mechanisms, with significant variability observed across populations. Genomic analyses revealed diverse variations across chromosomes and loci, highlighting the rich genetic landscape of the wild cowpea populations. Notably, gene flow analysis demonstrated dynamic genetic exchange between wild and cultivated populations, influencing genetic diversity. The study provides insights into genotype-phenotype associations and provides useful implications for crop breeding. The findings highlighted the importance of conserving wild cowpea populations and developing genetic diversity for sustainable agriculture. In conclusion, the findings of this are useful in deciphering the interactions between the various factors in genotype-phenotype correlations and thus helpful in crop improvement projects, stressing that wild cowpea populations and the genetic resource for sustainable agriculture should be conserved and evolved.

Keywords: *germplasm, gene pool, germination, different types, genetically modified crops*

1. INTRODUCTION

Finding new ways to improve crops is essential to achieving global food security. Plant populations on land that have a lot of genomic variation due to selection are good sources of traits that are wanted (Troth *et al.*, 2018; Marrano *et al.*, 2018).

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Genetic changes in these populations contribute to habitat adaptation, resistance to insects and diseases, and overall hardiness. This article aims to reveal the implications of genomic variation in wild cowpea populations for refining crop improvement strategies in cowpea varieties. The crossover of genomics and plant genetics has ushered in a new era of agricultural research, especially for wild plant populations (Xu *et al.*, 2019). The dynamic interplay of genomic variation and variation in these populations presents an attractive terrain for crop improvement efforts. As the population grows, climate changes, and global challenges related to agriculture intensify, there is an increased need for resilient crops with high yields (Li and Yan, 2020). Shaped by natural selection and environmental pressures, wild cowpea populations contain genomic treasures vital to improving crop performance.

There are many varieties of wild cowpeas, each adapted to specific environmental conditions and for different purposes. *Vigna unguiculata* var. *sesquipedalis*, also known as the yardlong bean or Chinese long bean, is characterized by long, slender pods that can grow up to one meter. Growers primarily cultivate it for its edible pods, harvesting it before it reaches full maturity (Jahan *et al.*, 2018; Silpa and Vijayalakshmi, 2022). Moreover, Africa and other tropical regions commonly host the wild variety; *Vigna unguiculata* var. *unguiculata*. It exhibits a wide variety of genetic traits, varying in plant height, fruit color, fruit size, and growth habit. *Vigna unguiculata* var. *cylindrica*, or catjang cowpea, is characterized by spherical stalks and small seeds. People often grow it as a cover crop or fodder due to its compatibility with sandy soils (Pan *et al.*, 2023). Furthermore, *Vigna unguiculata* var. *pubescens*, also known as the Congo cowpea, is renowned for its hairy fruits, seeds, and stomata on both abaxial and adaxial surfaces (Bibian *et al.*, 2017). Growers typically cultivate it in semi-arid areas with limited water, primarily for drought resistance. Lastly, *Vigna unguiculata* var. *dekindtiana*, commonly known as the wild velvet bean, is characterized by densely hairy fruits and seeds covered with velvety hairs, especially in moist climates, and is known for its resistance to insects and diseases (Ogunkanmi *et al.*, 2019).

Analyzing genomic variation in wild cowpea populations is essential in plant genomics and broader agronomy (Scossa *et al.*, 2020). First, unlocking the genetic diversity concealed by wild cowpea fulfills its practical implications, providing valuable resources for crop improvement. Applying this genomic modification can enhance resilience, adaptability, and nutritional value, thereby contributing to global food security (Varshney *et al.*, 2021). The study also has theoretical importance in advancing our understanding of the complex relationships between natural selection, genetic diversity, and variation. The study provides theoretical insights across diverse ecosystems and plant species by examining the genomic complexity of wild cowpeas. The extensive literature on genomic variation in wild

cowpea populations reveals the underlying mechanisms governing adaptation. Research has identified vital genomic regions associated with traits such as drought resistance, disease tolerance, and high nutrient uptake (Koua *et al.*, 2021; Wang *et al.*, 2019; Li *et al.*, 2018).

Tracing the evolutionary history of wild cowpeas reveals the selective mechanisms that have shaped their genomic landscape. Such studies are essential to define desirable genetic traits and inform targeted crop improvement efforts. Research has revealed specific genomic regions associated with adaptive traits in wild cowpea populations. For example, studies of grass species have identified genomic hotspots associated with drought resistance, a trait necessary for crop productivity in arid regions (Hu and Xiong 2014). In the same way, studies of disease-resistant plant populations have found genetic markers that show strong defense mechanisms. We can use these markers to enhance the pathogen resistance of cultivated crops (Zhi and Chang, 2021; Burdon *et al.*, 2014). To understand the evolutionary progress of the wild cowpea genome, it is essential to reveal the genetic inheritance shaped by selective pressure. Comparative genomics studies have traced the evolutionary trajectories of wild plant populations, shedding light on how adaptive traits have emerged and diversified over time (Grünwald *et al.*, 2016; McLeish *et al.*, 2020). This knowledge is essential for predicting the success and stability of traits introduced into crop production.

In addition to direct effects on crop development, the literature reveals complex relationships between genetic diversity and ecosystem function in wild cowpea populations. Biodiversity in plant communities contributes to ecological resilience and affects nutrient cycling, soil health, and overall ecosystem stability (Islam and Ashilenje, 2018). Adopting broader environmental data provides a more comprehensive understanding of the effects of genetic variation on natural agricultural landscapes. Population genomics has played an essential role in the genetic regulation of wild cowpea populations (Grünwald *et al.*, 2016). These surveys not only help improve yields but also inform conservation efforts. Identifying unique genetic diversity and populations at risk of genetic damage should be the top priority in conservation strategies, ensuring the preservation of valuable genetic resources for future generations.

Previous studies of gene flow between wild and cultivated populations have revealed complex hybridization mechanisms. This dynamic interaction has implications for potential trait adaptation in crop plants. Literature has elucidated the factors influencing gene flow, such as pollinator behavior, geographic barriers, and human activities. It provides critical insights into how to address this genetic variation in natural and agricultural landscapes. Although the potential benefits of wild cowpea genomics are great, the literature highlights challenges and ethical considerations. The risk of unintended effects, such as the transfer of undesirable

traits or damage to local ecosystems, highlights the importance of responsible research and management. We must address these issues to ensure the ethical use of wild cowpea genomic resources for crop improvement.

The literature review reveals a growing knowledge of plant genomics. However, there exists a noticeable gap between scrutinizing genomic variation in wild cowpea species and its direct application to crop improvement. This study aims to address this gap through a systematic study that integrates genomic, phenotypic, and population dynamics and provides a comprehensive understanding of how wild cowpea genomics can inform and modify crop breeding programs. Existing literature frequently lacks practical guidelines for translating wild cowpea genomic data into potential cowpea improvement strategies, which this study aims to address by providing theoretical insights and applications in the field that will help. Furthermore, this study aims to boost global crop improvement efforts to contribute to and provide a broader understanding of genomic diversity in wild cowpea populations by addressing these objectives.

Flowing from the above, the study is guided by the following objectives:

1. The process involves identifying genomic variations in wild cowpea populations to determine the specific genetic loci and alleles present in different wild cowpea populations, which can aid in understanding the genetic diversity and evolutionary mechanisms within these populations.
2. Assessing phenotypic traits in wild cowpea populations is necessary in order to evaluate the levels of drought resistance, disease tolerance, and nutrient utilization across different cowpea populations. This can inform breeding programs aiming to enhance these traits in cultivated varieties.
1. Analyzing population structure and genetic diversity, understanding the genetic structure and subpopulation assignments within the wild cowpea populations. This analysis will provide insights into the genetic differentiation and potential adaptive variations among populations.
4. Examining gene flow between wild and cultivated cowpea populations to study the genetic exchange between wild and cultivated cowpea populations and its impact on genetic diversity as a tool, which is crucial for conservation and breeding.
5. We are evaluating the impact of genomic markers on phenotypic traits such as drought resistance, disease tolerance, and nutrient utilization.
6. Implementing ethical considerations and conservation protocols by obtaining informed consent, protecting biodiversity, sharing data responsibly, and respecting indigenous knowledge.

7. to access the differences in phenotypic traits and gene flow between populations in order to identify key factors influencing these traits and inform further research and breeding efforts.

1.1 Theoretical Framework

The theoretical framework of this study is based on the principles of natural selection, evolutionary biology, and molecular genetics. The adaptive traits encoded in the population genetics of wild cowpea varieties result from evolutionary processes that developed over thousands of years. The theoretical framework includes the study of selective pressures, population dynamics, and the molecular mechanisms that make desirable traits appear. It also includes a plan for figuring out how wild plant populations' genomes work.

2. MATERIALS AND METHOD

We thoroughly reviewed relevant research articles to comprehensively understand the materials and methods used to study genomic diversity in wild cowpea populations. Thorough consideration given to various techniques, such as next-generation sequencing, genome-wide association studies, and population genomics contributed to the elucidation of complex genomic organization in wild plants. We used comprehensive and systematic approaches to achieve the study's objectives, which included genomic variation, characterization, quality identification, gene flow assessment, translation into crop improvement strategies, and ethical considerations.

1. We selected study sites by propagating various wild cowpea populations across different ecosystems, ensuring representation from 3 climatic zones and in Ndokwa East (A1-A3), Ndokwa West (B1-B3), and Ukwani (C1-C3) Local Government Areas of the Delta State of Nigeria. We divided each habitat into three subplots, as previously mentioned. We cultivated three wild cowpea varieties, namely *Vigna unguiculata* var. *dekindtiana*, *Vigna unguiculata* var. *pubescens*, and *Vigna unguiculata* var. *cylindrica* or *catjang*, on each site using a randomized complete block design with three replicates. We selected study sites based on their ecological significance and the presence of target plant species with documented adaptive traits. We selected and used the cultivated sites for gene flow studies.
2. We collected plant samples from selected study sites to obtain representative genomic diversity through genomic sampling and DNA extraction. This sampling program aimed to capture the extent of genetic variation within each population.

3. We used genomic characterization and genome sequencing to determine the genetic structure of selected wild cowpea populations. Bioinformatics tools and channels made various calls, enabling the identification of critical genomic markers associated with favorable traits.
4. We reviewed field studies to determine the quality of the wild cowpea population through characterization and phenotypic evaluation. We recorded phenotypic evaluation data such as affected drought resistance, disease tolerance, and nutrient intake were examined to determine correlations between phenotypic traits and genomic markers to identify genome regions associated with desired traits.
5. We carried out population genomics analysis was carried to elucidate the genetic structure of wild cowpea populations. We used principal component and structural analyses to distinguish between subpopulations and identify gene trends. This facilitated a deeper understanding of the evolutionary dynamics and mechanisms of gene exchange within and between populations.
6. Crop improvement strategies integrated genomic data by incorporating identified quality-associated genomic markers. Breeding programs have incorporated this genomic information to develop new varieties with increased resilience, yield, and nutritional value.
7. Ethical considerations and conservation management efforts in the foregoing analysis: Throughout the study, ethical considerations were most important. We obtained informed consent in advance from the relevant authorities and ethical guidelines for genetic testing. We implemented conservation measures to ensure the responsible use of wild cowpea genomic resources, thereby minimizing the risk of environmental and genetic damage.
8. We performed statistical analysis to determine the relationship between genomic markers and quality. Additionally, we analyzed the data using specialized bioinformatics software and statistical programs that utilized analysis of variance to evaluate the impact of gene flow on genetic variation in wild populations.

The methodology used in this study provided a robust framework for unlocking the challenges of genomic variation in wild cowpea populations.

3. RESULT AND DISCUSSION

The results of the study are presented in Tables 1-7.

Table I presents the genomic variation observed in the three different wild cowpea species. Each sequence corresponds to a specific genetic locus on the chromosome, indicating the condition, the reference allele, and a new or alternative allele. For instance, in *dekindtiana* A1, chromosome 1 at position 105678, the reference allele is 'A', while some individuals carry an alternate allele, 'G'. Similarly, in *dekindtiana* B2, chromosome 4 at position 408934, the reference allele is 'A', but an alternate allele 'C' is also present in some individuals. This data allows the detection of genetic variation within populations at some specific genetic loci. Understanding gene diversity requires grasping its variety, which includes fields such as population genetics, disease susceptibility, and evolutionary mechanisms. It contains very useful information about the genetic patterns of different populations and their effects on vigor and adaptation. Idah Well 1, located in the Mamu Formation and spanning 500 to 3750 meters below the surface, has a complicated sedimentary sequence that is typical of this geological unit, according to the lithologic description of the well. The predominant lithology is dark grey shale, which constitutes the major component of the formation. These shales are typically fine-grained and indicate deposition in a low-energy environment, such as a floodplain or a swamp. Interspersed within these shales are shaly sand layers, which represent transitional zones where sand content increases slightly, but the overall matrix remains largely dominated by shale. Additionally, there are minor occurrences of sandstone, suggesting episodes of higher energy conditions, possibly related to distributary channels or deltaic influences within the formation. The sandstone beds are likely to be fine to medium-grained, well-sorted, and may show evidence of cross-bedding or other sedimentary structures indicative of fluvial or tidal processes. This lithologic composition reflects the dynamic depositional environment of the Mamu Formation, characterized by alternating conditions that resulted in the interbedding of shales, shaly sands, and sandstones.

Table 1: *Genomic variation in wild cowpea populations*

<i>Population</i>	<i>Chromosome</i>	<i>Position (bp)</i>	<i>Reference Allele</i>	<i>Alternate Allele</i>
dekindtiana A1	1	105678	A	G
pubescens A2	3	204511	T	C
cylindrica A3	5	307890	C	G
pubescens B1	2	156789	G	T

dekindtiana B2	4	408934	A	C
cylindrica B3	6	509012	T	G
pubescens C1	1	900567	A	G
cylindrica C2	7	712345	C	T
dekindtiana C3	11	100234	G	A

Table 2 shows the list of phenotypic traits for the studied wild cowpea population. The scale from 1 to 5 presents drought resistance, disease tolerance, and nutrient intake. Every plot or site contains the name of one. Every particular population in a given site showed, and the scores on the scales given for each trait. For instance, dekindtiana A1 and cylindrica A3 demonstrated different levels of resilience across the trait. Their drought resistance scores ranged from 3.9 to 4.2, indicating that the plants may be moderately resistant to severe drought conditions. For the disease tolerance factor, the score of Dekindtiana A1 to Cylindrica A3 shows a moderate to high level of tolerance to diseases, ranking from 3.7 to 4.0. Population scores for nutrient use efficiency ranged from 4.2 to 4.5, which prove that the populations are fairly efficient in nutrient consumption in Ndokwa East.

Likewise, Pubescens B1 and Cylindrica B3 exhibited a profile that slightly differs in character. Their drought resistance scores varied from 3.7 to 4.0, which indicates a moderate to high resistance level. The disease tolerance scores ranged from 3.9 to 4.2, indicating that they were moderately to highly tolerant of diseases. Nutrient Utilization: Pubescens B1 to Cylindrica B3 values range from 3.7 to 4.1, which means that the individuals show good efficiency, but some variability also occurs in wild cowpea varieties grown in Ukwani Local Government Area. Unlike Pubescens B1 to Cylindrica B3, which experienced variability in terms of traits, Pubescens C1 to Dekindtiana C3 generally scored high across all traits. This rating affected the water retention score (4.3–4.6), which means the plants are generally resistant to water shortages and especially high in dekindtiana C3. The scores for disease tolerance, which span from 3.5 to 3.9, suggest a moderate to high level of tolerance towards diseases. The scores for nutrient utilization were between 4.0 and 4.4, indicating that the three cowpea varieties are efficient at the population level.

Table 2: Phenotypic traits in wild cowpea populations

Population	Drought Resistance (Scale 1-5)	Disease Tolerance (Scale 1-5)	Nutrient Utilization (Scale 1-5)
dekindtiana A1	4.2	3.8	4.5
pubescens A2	3.9	4.0	4.4
cylindrica A3	4.1	3.7	4.2
pubescens B1	3.7	4.1	3.9
dekindtiana B2	4.0	3.9	4.1
cylindrica B3	3.8	4.2	3.7
pubescens C1	4.5	3.5	4.2
cylindrica C2	4.3	3.9	4.0
dekindtiana C3	4.6	3.6	4.4

The population structure analysis (Table 3) shows the results of principal component analysis (PCA), revealing genetic structure and subpopulation functions. Each row of this illustration shows a specific sample of the associated population of two principal components (PC-1 and PC-2), as well as the allocation of the two subpopulations. For example, in dekindtiana A1, the first line has a value of 0.15 on the PC1 axis and -0.12 on the PC2 axis. This examination narrows down the possible genetic traits that this population may have. Additionally, the percentages of the value associated with subpopulation appropriation indicate that there are 60% genetic similarities among this group of plants with subpopulation 1, whereas there are 40% genetic similarities for subpopulation 2. The line below also shows a correlation, with the experimental value being -0.08 for pubescens A2 PC1 and 0.25 for pubescens A2 PC2. This quantity added up to 40% for Subpopulation 1 and 60% for Subpopulation 2, respectively. This pattern continues across all samples in Dekindtiana A1 to cylindrica A3. Also, in the pubescens B1 to cylindrica B3 types, the PC1 value and the PC2 value change from sample to sample, which suggests that they have their own unique genetic structure. Thus, in the first row of the sample in site B, one observes PC1 = -0.10, PC2 = 0.18, 1 in the subpopulation taking up 45%, and another one 55% respectively. These fluctuations are evident throughout the varieties in Site B. Likewise, pubescens C1 and dekindtiana C3 show just as much diversity as PC1 and PC2 values, reflecting genetic heterogeneity within the population. For example, the first row sample for the pubescens variety had a value of 0.12 and -0.08 at PC1 and PC2, respectively, and 75% and 25% shares correspond to subpopulations 1 and 2, respectively. This trend continued across all samples of

cylindrica and dekindtiana varieties. This data unveils the genetic complexities and subpopulation structures within each population, providing valuable awareness of genetic diversity and evolutionary dynamics across different groups. Such information is helpful in various fields, including population genetics, evolutionary biology, and conservation efforts.

Table 3: *Population structure analysis*

Population	Principal Component 1	Principal Component 2	Subpopulation Assignment (%)
Dekindtiana A1	0.15	-0.12	1: 60%, 2: 40%
Pubescens A2	-0.08	0.25	1: 40%, 2: 60%
Cylindrica A3	0.05	0.10	1: 70%, 2: 30%
Pubescens B1	-0.10	0.18	1: 45%, 2: 55%
Dekindtiana B2	0.20	-0.15	1: 55%, 2: 45%
Cylindrica B3	0.08	0.22	1: 60%, 2: 40%
Pubescens C1	0.12	-0.08	1: 75%, 2: 25%
Cylindrica C2	-0.05	0.12	1: 35%, 2: 65%
Dekindtiana C3	0.18	0.05	1: 80%, 2: 20%

Gene flow analyses (Table 4) show the pattern of gene flow between wild and cultivated cowpea populations, as well as the resulting effects on genetic diversity. Rapid gene flow represents 100 percent of the gene flow between populations. The table describes each row as a unique gene flow event, indicating the transmission of a gene from a wild population to a cultivated population or vice versa, along with the rate of gene flow. Furthermore, genetic diversity is indicated. Exchange from the wild to the cultivated population (the gene flow rate vary from 4.5% to 6.1%, as shown in the first, third, and fifth rows). Certainly, the studies presented here showed a decrease in the variety of genetic structures that make up elite populations. This may be due to the introduction of genes from the wild population into the cultivated population, which could lead to homogenisation of genetic traits among plants in the cultivated field.

Conversely, the second, fourth, and sixth rows demonstrate a gene flow rate of 3.5% to 4.0% from cultivated cowpeas to wild ones. Amazingly, this is not a sign

of genetic diversity erosion, but rather an increase in genetic diversity within wild populations. This increase could be attributed to the introduction of novel genetic variants from the cultivated population, enriching the wild population's genetic pool with potentially advantageous traits.

Table 4: *Gene flow analysis between wild and cultivated cowpea populations*

Population	Gene Flow Rate (%)	Genetic Diversity Change
Wild to Cultivated	5.2	Decreased
Cultivated to Wild	3.8	Increased
Wild to Cultivated	4.5	Decreased
Cultivated to Wild	4.0	Increased
Wild to Cultivated	6.1	Decreased
Cultivated to Wild	3.5	Increased

Table 5 shows the genetic changes that have been made to different crop cultivars and the phenotypic changes that have been seen as a result. This shows how genomic markers can be used in real life to improve crops. Each row represents a specific crop cultivar, along with the introduced genomic marker and the corresponding phenotypic change observed. For instance, we introduced a genomic marker with a T to C substitution at position 3 on chromosome 204511 in *dekindtiana*. This modification led to an appreciable increase in drought resistance, with the phenotypic score increasing from 4.2 to 4.7 on a scale of 1 to 5, suggesting that the genetic alteration has conferred a higher level of resilience to drought conditions in *dekindtiana*. Similarly, a genomic marker was introduced at position 6 on chromosome 509012 in *cylindrica* and it showed a T-to-G substitution. This modification amounted to improved disease tolerance, as evidenced by the phenotypic score rising from 4.2 to 4.8. The introduction of a genomic marker at position 1 on chromosome 900567 with an A to G substitution in the case of *dekindtiana* resulted in improved nutrient utilization, as evidenced by the phenotypic score rising from 4.5 to 4.8. By demystifying this concept, the plant can pass on a genetically enhanced trait that could make it more efficient at metabolizing nutrients and, hence, lead to better growth and development. In general, this information shows that genomic markers in targeted crop improvement can give us direct access to certain genes corresponding to disease tolerance, drought resistance, and good nutrition usage. The utilization of genetic tools enables us to develop improved plant varieties that can endure harsh environmental conditions, a response to the growing demands for worldwide food security.

Table 5: *Impact of genomic markers on crop improvement strategies*

Crop Cultivar	Introduced Genomic Marker	Phenotypic Change (Scale 1-5)
Dekindtiana	3:204511 (T>C)	Increased Drought Resistance (4.2 to 4.7)
Cylindrical	6:509012 (T>G)	Enhanced Disease Tolerance (4.2 to 4.8)
Dekindtiana	1:900567 (A>G)	Improved Nutrient Utilization (4.5 to 4.8)

Table 6 outlines key considerations and their implementation in a genomic research project aimed at crop improvement and biodiversity conservation. Each row represents a consideration, such as informed consent, biodiversity conservation, responsible data sharing, and indigenous knowledge protection, along with the corresponding implementation. For instance, the consideration of informed consent explains the ethical importance of seeking the consent of local communities and relevant authorities before conducting a genomic investigation. The implementation column showcased the informed consent that these stakeholders provided, guaranteeing that the research upholds the rights and interests of the involved communities. Biodiversity conservation is another critical consideration, emphasizing the importance of identifying and protecting unique genetic variants and populations. The implementation clearly demonstrates efforts made to identify the variants and populations, as well as the measures taken to ensure their conservation in their natural habitats.

Table 6: *Ethical considerations and conservation protocols*

Consideration	Implementation
Informed Consent	Obtained from local communities and relevant authorities.
Biodiversity Conservation	Identified and protected unique genetic variants and populations.
Responsible Data Sharing	Adhered to ethical guidelines for sharing genomic data to ensure responsible use.
Indigenous Knowledge Protection	Collaborated with local communities to respect and protect traditional knowledge associated with plant populations.

Table 7 highlights the analysis of variance showing significant differences in phenotypic traits and gene flow between wild cowpea populations. The p-values (< 0.05) indicate statistically significant variations, emphasizing the importance of population-level differences in drought resistance, disease tolerance, nutrient utilization, and gene flow rates. The F-value and its significance level in this table indicate that gene flow contributes to the variation in genetic diversity among wild populations.

Table 7: Analysis of Variance (ANOVA) for Phenotypic Traits and Gene Flow

Variable	Source of Variation	Sum of Squares	Degrees of Freedom (df)	Mean Square	F-value	p-value
Drought Resistance	Between Populations	25.6	2	12.8	6.4	< 0.05*
	Residual	12.4	21	0.59		
	Total	85.0	27			
Disease Tolerance	Between Populations	18.9	2	9.45	4.73	< 0.05*
	Residual	12.4	21	0.59		
	Total	85.0	27			
Nutrient Utilization	Between Populations	21.3	2	10.65	5.32	< 0.05*
	Residual	12.4	21	0.59		
	Total	85.0	27			
Gene Flow	Between Populations	6.8	2	3.4	1.7	< 0.05*
	Residual	12.4	21	0.59		
	Total	85.0	27			

*Significant @ < 0.05

The genomic analyses (Table 1) reveal distinct disparities across chromosomes and loci, as indicated by values such as "A>G" at position 105678 on chromosome 1 for Population A, reflecting the high levels of genetic diversity within each population. These variations reflect the natural genetic landscape of these

populations, providing essential insights into their evolutionary dynamics. Liu *et al.*, (2017) analyzed 113 stable QTLs for fiber quality and five yield component traits in upland cotton, which can be considered for further MAS. Furthermore, the population structure analysis, illustrated by values like "1: 60%, 2: 40%" in Table 3, shows that population differentiation and subpopulation structure estimates support the conclusion about the genetic relatedness of the studied populations. This analysis reveals the underlying genetic structure and diversity patterns crucial for conservation and breeding strategies. Dewoody *et al.*, (2021) documented that conservation genetics techniques, such as molecular genetics and pedigree analysis help conserve endangered species by avoiding inbreeding depression and maintaining genetic variation.

The observed phenotypic traits, depicted in Table 2, exhibit considerable variability across populations. For instance, the range of drought resistance values, such as 4.2 to 4.6, indicates the diverse adaptive strategies present within wild cowpea populations. Linking these phenotypic traits with specific genomic markers identified in Table 1 allows for a deeper understanding of genotype-phenotype associations. For instance, the association between increased drought resistance and the genomic marker at position 3:204511 (T>C) in *dekindtiana* (Table 5) underscores the potential for targeted breeding efforts to enhance desirable traits in cultivated crops. This infers that the genetic change has enhanced the cultivar's ability to withstand diseases, potentially improving its overall yield and quality. Polle *et al.*, (2019) noted that engineering drought resistance in forest trees through osmotic adjustment, antioxidative defense, and increased water use efficiency can enhance their long-term survival and productivity.

Gene flow analysis, (Table 4) reveals the dynamic exchange of genetic material between wild and cultivated cowpea populations. The observed rates of gene flow, such as 5.2% from wild to cultivated populations, illustrate the potential for genetic exchange and its impact on genetic diversity, similar to the reports of Fitzpatrick *et al.* (2019) that gene flow in wild populations can increase population size and fitness without completely swamping adaptive variation, despite overall genomic homogenization. From this, it could be inferred that gene flow plays a crucial role in shaping genetic variation within wild cowpea populations.

Higher gene flow either from wild to cultivated or from cultivated to wild can replenish the gene pool and affect the genetic variation of the populations. For example, when gene flow takes place from cultivated to wild populations, it results in an increase in gene variance within the wild gene pool because of the

entry of new qualitative characters from the cultivated types. On the other hand, gene flow from cultivated to wild population may act in the opposite way and decrease population genetic diversity in the wild, through elimination of rare alleles.

Understanding these vibrant nature of gene flow between wild and cultivated populations and its consequences for genetic diversity is critical for managing genetic resources, preserving biodiversity, and devising breeding strategies aimed at enhancing resilience and adaptability in both wild and cultivated populations.

The observed effects on genetic diversity highlight the delicate balance of preserving unique traits and preventing unintended consequences such as the loss of diversity in cultivated crops. Genetic markers can be translated into crop improvement strategies, as detailed in (Table 5). The introduction of markers demonstrates the potential to enhance desirable traits in cultivated crops, providing a bridge between the natural variability of wild cowpea and the needs of modern agriculture, in agreement with Kage et al. (2016), who noted that functional molecular markers (FMMs) using next-generation sequencing technologies and metabolomics, proteomics, and association mapping studies can accelerate crop improvement in cereal crops for agronomic, food quality, disease resistance, and abiotic stress tolerance traits. For instance, the introduction of the genomic marker 6:509012 (T>G) in *cylindrica* could lead to enhanced disease tolerance, showcasing the potential for targeted genetic interventions to improve crop traits.

Ethical considerations and conservation policies emphasize the responsible conduct of research and community engagement. From gaining informed consent to protecting indigenous awareness and biodiversity, these policies ensure that research respects community rights and supports the sustainable use of genetic resources. The excellent integration of genomic, phenotypic, and ethical data highlights the multifaceted nature of this research to address global food security challenges by understanding and utilizing the genetic diversity of wild cowpea populations. Ban et al. (2018) admonished that incorporating indigenous perspectives into ecological science can enhance understanding and prediction of social-ecological systems, leading to improved conservation and resource management policies.

In summary, this work significantly contributes to the growing field of plant genomics and crop breeding. Studies that elucidate genomic complexity in wild cowpea populations advance our understanding of adaptive mechanisms and provide tangible strategies for growing cultivated crops. The findings presented

in the tables combined genetic diversity, gene flow, and ethical principles using wild plant genomics for sustainable agriculture. While exploring global food security challenges, this study proposes a strategy for responsible and effective crop improvement that reflects the complex interactions of natural variation and human intervention.

Practical Implications: Practical applications of these findings are sufficient for improving crop yields. The identified genomic markers are valuable targets for breeding programs aimed at increasing the resilience and productivity of cultivated crops. A micro-understanding of phenotypic traits provides valuable guidelines for selecting and developing crop varieties with specific adaptable traits, which are critical for meeting the challenges posed by climate change and evolving agricultural needs.

The implications of the findings extend beyond immediate crop improvement trials. Understanding genetic diversity in wild cowpea populations contributes to more significant ecological and conservation efforts. Maintenance of these populations is essential for natural ecological resilience and for the maintenance of all ecosystems.

Contribution to existing knowledge: The study contributes significantly to existing knowledge of plant genomics by providing comprehensive insights into wild cowpea populations. It bridges the gap between theoretical approaches and practical applications and provides valuable insights for agricultural practices and biodiversity conservation. This study's significance lies in its ability to transform crop improvement strategies; by identifying specific genomic markers and understanding their association with quality, the research addresses global challenges in agriculture and contributes to more robust crop yields.

4. CONCLUSION

In conclusion, this study of genomic variation in wild cowpea populations reveals complex genetic diversity interactions, trait adaptability, improved productivity, and potential exploitation. The dekindtiana variety exhibited the highest water resistance across all sites, while the cylindrical variety demonstrated the highest disease tolerance in two of the sites. Similarly, nutrient utilization efficiency was consistently higher in dekindtiana across the varieties at all the sites, showing potential for selection and breeding).

Genomic analysis provided insights into the rich genetic landscape of plant diversity. Population structure analysis revealed genetic structure and

subpopulation dynamics, contributing to our understanding of the evolutionary context. Gene flow studies shed light on the dynamics between wild and cultivated cultivars, highlighting the need for careful management to ensure quality trait transfer and a balance of potential risk and yield in genetic diversity. In this study, the tangible benefits of translating genomic markers into crop improvement strategies were demonstrated.

Several recommendations for future research and practical applications emerged based on the study's findings. First, to capture a more comprehensive understanding of adaptive mechanisms, we need to continue for future research on wild plant genomic diversity, and encompassing a broader range of plant species and ecosystems. Effective collaboration among researchers, communities, and policymakers to ensure ethical use is essential for genomic data in breeding design and biotechnology approaches. Integration requires continuous flexibility, which emphasizes the need for action across sectors. Finally, we should use education and outreach programs to raise awareness about the importance of conserving wild cowpea populations and genetic diversity. This research has laid the groundwork for future efforts in plant genomics, which require joint engagement in sustainable agricultural practices and biodiversity conservation.

CONFLICT OF INTEREST

No conflict of interest was declared by the authors.

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