Journal of Agriculture, Food, Environment and Animal Sciences
Tarım, Gıda, Çevre ve Hayvancılık Bilimleri Dergisi
http://www.jafeas.com, ISSN: 2757-5659

J. Agric. Food,
Environ. Anim.
Sci.5(2): 330-343, 2024

Udder Diversity: A Genetic Exploitation across Cattle Breeds under Extensive Management System in Nigeria

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Research Article

Article History:
Received:23 June 2024
Accepted:09 December 2024

Keywords:
Breeds
Cattle
Diversity
Genetic
Udder

ABSTRACT

This study evaluates the genetic diversity of udder traits in three Nigerian cattle breeds: Red Bororo, White Fulani, and Sokoto Gudali, raised under extensive management systems. A total of 270 cows, 90 from each breed, were assessed for udder length, width, depth, and teat length. Mahalanobis squared distances (D^2) quantified genetic divergence between breeds. Canonical discriminant analysis validated the data, with Wilks Lambda (0.349, 0.910) and Bartlett's chi-square test results significant at $p<0.001$ for function 1 and $p<0.05$ for function 2. Function 1 explained 94.2% of the variance, with a canonical correlation of 0.785, outperforming function 2's 69.16% variance and 0.300 correlation.Five discriminating traits were; udder depth, udder width, hind teat length, front teat length, and udder length—were identified as discriminating variables among the breeds. Hind teat length (0.966) was the most significant contributor to function 1, followed by udder length (0.549). In function 2, udder length (0.883) and front teat length (1.321) were most influential. Genetic distances revealed significant divergence between Sokoto Gudali and Red Bororo (34.713), and Sokoto Gudali and White Fulani (45.428), while the distance between Red Bororo and White Fulani (1.995) was non-significant. Classification accuracy was highest for Sokoto Gudali (88.9%), followed by White Fulani (73.3%), and Red Bororo (42.9%). These findings suggest potential for exploiting udder diversity in breeding programs to enhance milk production in these cattle breeds.

To Cite: Dauda A, Okon B., 2024. Udder Diversity: A Genetic Exploitation across Cattle Breeds under Extensive Management System in Nigeria. Agriculture, Food, Environment and Animal Sciences, 5(2): 330-343.

INTRODUCTION

Udder morphology is a critical trait in dairy cattle, influencing both milk production and ease of milking. Understanding the genetic diversity of udder characteristics across different cattle breeds can provide valuable insights for improving dairy production through selective breeding. In Nigeria, a country with diverse cattle breeds adapted to various ecological zones, this aspect of genetic research is particularly pertinent (Dauda, 2021).

Mostly located in the semi-arid areas of northern Nigeria, Sokoto Gudali cattle are renowned for their resilience and flexibility. They may produce both milk and meat because of their moderately sized udders and evenly spread teats. Research has indicated that their genetic composition enables them to function effectively in vast systems with modest inputs, underscoring their potential for dairy improvement (Bello et al., 2021).

Rahaji, or red Bororo cattle, are renowned for their ability to withstand dry conditions. Compared to other breeds, they have larger udders, moderate teats and Nigerian pastoralists frequently milk the animals of their milk ability. According to research by (Abubakar and Akinyele, 2022), the breed's udder characteristics are associated with higher milk yield, which makes them a useful genetic resource for dairy production in large-scale systems.

One of the most popular and commercially important breed of cattle in Nigeria is the White Fulani, which thrives on the savannah. Their udder characteristics show a great deal of genetic variability, which affects their capacity to produce milk. White Fulani cattle exhibit significant variation in udder size and shape, suggesting potential for selective breeding to improve dairy production in conditions of extensive grazing, according to a study (Yusuf et al., 2020).

Several studies have emphasized the importance of characterizing and utilizing the genetic diversity within indigenous cattle breeds to enhance productivity and sustainability in the livestock sector (Rege, 1999; Yakubu et al., 2010). This research aims to explore the genetic diversity of udder traits among various cattle breeds in Nigeria using discriminant analysis. By leveraging this analytical approach, the study seeks to uncover significant morphological variations and their genetic bases, providing a framework for targeted genetic improvement and conservation of indigenous cattle breeds.

MATERIAL and METHOD

Study Area

The study was conducted in Maiduguri and its environs, located in the northeastern region of Nigeria. The experiment was carried out between the months of October and

April (from the early dry season when there is abundance of dry grasses and farm residue to the peak of the dry season when feed is limited). The state is located between the Sudan Savanna and Sahel Savanna vegetation zones at latitudes 11°32′ North and 11°40′ North and latitudes 13°20′ East and 13°25′ East. This area is characterized by a semi-arid climate, with distinct wet and dry seasons (BMLS, 2016).

Study Population

A total of 270 cows were included in the study, comprising 90 cows from each of the three breeds: Red Bororo, White Fulani, and SokotoGudali. These breeds were chosen for their economic and cultural importance in the region. The animals were grouped based on their parity. All measures were take one technician for consistency and to avoid errors from human judgements.

Sampling Method

Cows were randomly selected from various herds within Maiduguri and its surrounding areas. The selection was done to ensure a representative sample of each breed, accounting for variations in age and lactation status.

Data Collection

Data on udder traits were collected through physical examination and measurements. The following traits were recorded:

- ✓ Udder length: measured from the rear attachment of the udder, near the escutcheon, to the front of the udder where it blends smoothly with the body.
- ✓ Udder width: measured as a distance between two lateral lines of attachment of the udder to abdominal wall, beneath the flank. The measuring tape was kept in position on one side of the cow, under flank, near the stifle joint and it was passed over in between fore and rear teats to the other side.
- ✓ Udder depth: measured by subtracting distance from the barn floor to the udder floor from distance from the barn floor to the base of the udder.
- ✓ Teat length: measured from the upper part of the teat, where it hangs perpendicularly from the quarter to the tip.
- ✓ Front teat length: Measured using a measuring tape from the base of the front teat to the tip.
- ✓ Hind teat length: Measured using a measuring tape from the base of the hind teat to the tip.
- ✓ Distance between front and hind teat: Measured using a measuring tape between the bases of the front and hind teats.
- ✓ Distance within front teats**:** Measured using a measuring tape between the bases of the front teats.
- ✓ Distance within hind teats: Measured using a measuring tape between the bases of the hind teats. Measurements were taken using a flexible measuring

tape to ensure accuracy and consistency. Measurements were taken for six (6) months, between the months of October to April. All measurements were taken by one technician for consistency and to avoid errors from human judgements.

Measurements were taken using a flexible tape measure, ensuring precision and consistency. Each cow was measured in the same manner to reduce measurement bias.

Statistical Analysis

Discriminant Analysis (Mahalanobis Genetic Distance)

The Estimation of Mahalanobis squared distances (D2) between different breeds in same location were obtained using Candisc procedure of SAS (2000). Squared distance (D2) between the different breeds in same location was estimated by the following relationship D2 (i/j) = (xi – xj) cov-1 (xi - xj). Where D2 = genetic distance between populations in an m- dimensional space. I/j = the element of the i^{th} row and the j^{th} column of the inverse matrix. xi–xj= mean sets of original variables, Cov = covariance of the original data set.

RESULTS and DISCUSSION

Summary of Canonical Discriminant Function of Cows on Breed Effect

Table 1 shows two discriminant functions: Eigen values, variance proportion, canonical correlation, and the standardized discriminant coefficient of the most discriminating variables. The significance of the discriminant function extracted was tested with Wilks Lambda (0.349, 0.910) and Bartlett's test chi-square 84.823 at level of significance ($P<0.001$) for function 1 and 7.597 at level of significant ($P<0.05$) for function 2, which provides validity for the canonical discriminant analysis. The percentage of share variance of 94.20 in function 1 is higher than 69.16 in function 2. The canonical correlation of function 1 is also higher (0.785) than 0.300 in function 2. The high percentage of the shared variance (eigen value) and the total variation in the grouping of discriminant function 1 in this study could be attributed to the differences among the three cow populations in their udder and teat traits and evidence of high genetic variability among them. This also implies that discriminant function 1 indicated that the model in function I was more efficient in explaining the variation existing in the grouping variable than the models of function 2. The efficiency of the higher canonical correlation, which measures the strength of the model to explain the variation existing in the grouping variables, was also indicated. The two canonical functions (linear combinations of the continuous variables that summarize variation between the three cattle breeds) obtained could be used as criteria for establishing udder and teat traits standards for Nigerian cows. Hair (1998) also reported that canonical correlation measures the strength explaining the variation in the grouping variables, which implied that the higher the value of the canonical correlation, the higher the variation between the breeds in their udder and teat traits. Thus, the higher the value of the canonical correlation, the higher the strength (Ebegbulum et al., 2018).

Table 1. Summary of canonical discriminant function of cows on breed effect

Function	Eigen value	Variance proportion	Canonical correlation	Λ	X^2	Sig
1	1.610	94.20	0.785	0.349	84.823	0.00
2	0.099	69.16	0.300	0.910	7.597	0.05

X^2 =Bartlett's test chi-square, Λ= wilk’s lambda

Morphological Variables Selected by Stepwise Discriminant Analysis to Separate The Cows Into Genetic Groups

Table 2 presents the results of the stepwise discriminant analysis, showing Wilk’s lambda, F-values, probability, and tolerance statistics. The discriminant analysis based on significant F-values indicated that five steps were involved in the selection of the five most discriminating variables (Udder depth, Udder width, HTL, FTL, and Udder length) that discriminate the Sokoto Gudali, Red Bororo, and White Fulani cows into their genetic groups. Thus, when the five most important morphometric variables for separating the three genotypes were selected, Wilk’s Lambda dropped from 0.581 to 0.329 with a significant difference between the three breeds with a significant ($P < 0.001$) F-value (from 29.610 to 4.353). The high standard deviation for some of the independent variables suggested that they were good discriminators as the separation was large (Gwazaet al., 2013).The significant ($p < 0.05$) differences between means of udder depth, udder width, hind teat length, front teat length, and udder length producing high F values in descending order indicate that these variants have high discriminating power and better ability to differentiate the groups. This udder and teat diversity pattern could be a result of the inherent genetic potential of each breed (Gizawet al., 2007; Sun et al., 2004; Barrett et al., 1989). These variables can be used to characterize and differentiate between the three breeds of cattle. Morphological variables are easy to monitor and may facilitate the use of ethnological characterization and, at the same time, institute reliable racial discrimination (Frankhamet al., 2002).

Table 2. Morphological variables selected by stepwise discriminant analysis to separate the cows into genetic groups

Step	Traits selected	Wilk Lambda	F to remove	Tolerance	P-value
1	Udder depth	0.581	29.610	1.000	0.000
2	Udder width	0.464	10.210	0.949	0.000
3	HTL	0.417	4.437	0.930	0.000
4	FTL	0.365	5.634	0.217	0.000
5	Udder length	0.329	4.353	0.536	0.000

FLT=Front teat length, HLT=Hind teat length,

Total Standardized Canonical Coefficient and Total Variance Explained by Each Canonical Variable

Table 3 presents the total sample standardized canonical coefficient and the total variance explained by each canonical variable. The first canonical function (Can1.), or fisher linear discriminant function, explained 94.20% of the total variation, while canonical function 2 (Can2) explained 100.00% of the total variation. The canonical discriminant analysis performed in this study will help in weighing each original trait's contribution to each of the two canonical variables. The first canonical variable (Can 1) loaded highly for hind teat length, udder length, and udder depth in the inverse, while Can 2 loaded highest for front teat length, followed by hind teat length and udder width. These traits that are high in Can1 and Can2 demonstrate their relevance in discriminating between the genotypes. Variables with a loading power of 0.30 (or higher) are considered to contribute significantly as discriminating variables. The standardized canonical discriminant coefficient provides information on the importance and strength of each predictor for the discriminant function (Meritexellet al., 2003).The aforementioned traits are adequate to be used in discriminating and identifying udder variation between the populations of three breeds of cattle (Red Bororo, White Fulani, and Sokoto Gudali). In particular, the multiple correspondence analyses showed that the variation was accounted for by CAN1 and CAN2. Thus, the canonical discriminant analysis was successful in identifying variations in udder and teat traits among breeds. Those udder and teat traits were the traits that separated and differentiated the breeds in particular, the front teat length and the hind teat length. In addition, the differentiation of the three breeds due to udder and teat traits is strongly due to genetic or breed differences.

Table 3. Total standardized canonical coefficient and total variance explained by each canonical variable

Traits	Function	
	Can. 1	Can. 2
FTL	-0.809	0 .958
HTL	0.819	-1.337
DSBFT and HT	0.280	0.411
DSWTFT	-0.122	0.115
DSWTHT	0.016	-0.443
Udder Width	0.040	0.641
Udder Length	0.504	0.071
Udder Depth	0.370	-0.169
Total variance	94.20	100.00

FTL=front teat length, HTL=hind teat length, DSBFT and HT=distance between front teat and hind teat, DSWTFT=distance within front teat, DSWTHT=distance within hind teat.

Standardized Canonical Discriminant Function Coefficients

Table 4 presents the standardized Canonical Discriminant Function Coefficients. The results showed that hind teat length (0.966) was the highest, followed by udder length (0.549) and udder depth (0.348) in their standardized canonical discriminant coefficients in function 1, whereas udder length had the highest (0.883), followed by front teat length (1.321) in function 2. The standardized canonical discriminant coefficient provides an index of the importance of each predictor and the direction of the relationship (Dauda et al., 2018a). Hind teat lengths were the strongest predictors, while udder, udder length, udder depth, and front teat length were next in importance as predictors. Thus, the first function will contribute significantly to the discriminant process. The second function does not contribute much significantly to the discrimination process as compared to that of the first function. In other words, this factor does not help much in discriminating between the groups. This result agreed with Boaheng and Sam (2016) who opined that the derived discriminant functions provided maximum (canonical linear discriminant function) separation among breeds. Canonical discriminant analysis allowed an understanding of udder and teat traits, taking into account the total (co)variation between traits jointly, which is biological and physiologically accepted because performance traits are naturally correlated (Rosario et al., 2008). Although the practical interpretation of the canonical variables is difficult at first, their process of extraction is based on the distinguished weighing of original traits, which normally have biological and economic importance. This fact was extremely important to elucidate the practical interpretation of these variables and make the evaluation of treatments easier (Rosario et al., 2008).

Table 4. Standardized Canonical Discriminant Function Coefficients

Traits	Function	
	1	2
FTL	-0.792	1.321
HTL	0.966	-1.574
Udder Length	0.549	0.883
Udder Depth	0.348	-0.285

FTL=front teat length, HTL=hind teat length,

Derived Linear Discriminant Models for The Sokotogudali, Red Bororo and The White Fulani Cows

Table 5 presents the linear discriminant equations of the three breeds investigated. Each equation comprises constant and derived partial regression coefficients that explain the contribution of a variable in predicting group membership. A higher partial regression coefficient indicates a higher contribution of the associated variable to the prediction of group membership. From Table 3, D1 = -164.22 + 6.95FTL -8.70HTL

+ 4.81DSBFF -1.56DSWFT + 2.77DSWTHT + 0.46UW + 1.60UL + 4.88UD, D2 = -133.57 + 7.95FTL -9.52HTL + 4.06DSBFF -1.46DSWFT + 2.94DSWTHT + 0.33UW + 1.17UL + 4.63UD, and D3 = -129.59 + 9.21FTL -11.21HTL + 4.28DSBFF -1.37DSWFT + 2.65DSWTHT + 0.49UW + 1.10UL + 4.49UD were the equations for predicting group membership of SokotoGudali, Red Bororo, and White Fulani cows, respectively. The higher values of front teat length and distance between front and hind teat were morphological modifications created by genetic differences that might have occurred through random sampling, genetic drift, and selection. Due to genetic variations between the three breeds' populations, the superior cow in front teat length can be selected to improve milk yield since teat length and width are factors that determine milk yield from a cow (Anon, 2019).Since the relationships between udder characteristics and milk yield can be useful tools in selecting animals for dairy production systems (Mingoas et al., 2017), A positive correlation existed between the average daily milk yield and the various teat measurements, such as teat length, teat diameter, and the distance between the front and hind teats (Prasad et al., 2010).

Table 5. Derived linear discriminant models for SokotoGudali, Red Bororo and White Fulani cows

Traits	D 1	D2	D3
Constants	-164.22	-133.57	-129.59
FTL	6.95	7.95	9.21
HTL	-8.70	-9.52	9.21
DSBFT and HT	4.81	4.06	4.28
DSWTFT	-1.56	-1.46	-1.37
DSWTHT	2.77	2.94	2.65
Udder Width	0.46	0.33	0.49
Udder Length	1.60	1.17	1.10
Udder Depth	4.88	4.63	4.49

FTL=front teat length, HTL=hind teat length, DSBFT and HT=distance between front teat and hind teat, DSWTFT=distance within front teat, DSWTHT=distance within hind teat

Pairwise Mahalanobis genetic distance between the SokotoGudali, Red Bororo and the White Fulani cows

Table 6 presents the Mahalanobis genetic distance between the SokotoGudali, Red Bororo, and White Fulani cows. Genetic distance, which is the degree of genetic difference (genomic difference) between breeds, species, or populations, is measured by some numerical method (Dauda et al., 2018b). The pairwise genetic distance between SokotoGudali and Red Bororo was 34.713 at the 0.001 significance level, SokotoGudali and White Fulani were 45.428 at the 0.001 significance level, and 1.995 was the genetic distance between Red Bororo and White Fulani at the 0.143 significance level. The highest genetic distance is between SokotoGudali and White Fulani (45.428), and the least is between Red Bororo and White Fulani (1.995). The longer distance between SokotoGudali and White Fulani revealed that udder and teat differences are maintained in part by the reduction of gene flow among populations separated by large distances as well as physical-ecological barriers. The high genetic distance observed between SokotoGudali and White Fulani could be due to natural selection, artificial selection, and adaptation to environmental conditions.Thus, crossbreeding between SokotoGudali and White Fulani may produce positive heterosis, whereas the lower genetic distance between Red Bororo and White Fulani could be due to genetic exchange that has taken place over time and has reduced the genetic distance that would have theoretically described their differences. This could have been facilitated by geographical proximity, whereby there was unrestricted and indiscriminate crossbreeding among local populations (Yakubu and Ibrahim, 2011). The low genetic distance between White Fulani and Red Bororo could also be due to ethnic farming communities arising from selection induced by differing ethnic cultural practices. The closeness between Red Bororo and White Fulani compared to SokotoGudali might also be a result of near biometric convergence, which may function as a guide to genetic and evolutionary relationships between the two breeds. Thus, crossbreeding between Red Bororo and White Fulani might not produce desirable heterosis with regard to udder traits. Genetic distance is important to determine the hybrid vigor (heterosis) expected during crossbreeding (Yunusa et al., 2013).This agreed with the report of Traore et al., (2008). who opined that crossbreeding between animals with a high value of genetic distance will yield positive heterosis, while those with a small value of genetic distance will yield poor heterosis. In a related study, Tewe (1998) reported low genetic distance between the Sudan (Djallonke) and Sudan-Sahel (Mossi) sheep using Mahalanobis distance and attributed this to sustained introgression. Genetic diversity of livestock species allows animal production to be practiced in a range of environments and with a range of different objectives, which provides the raw material for survival and adaptability of a species (Dauda et al., 2018a).

Table 6. Pairwise Mahalanobis genetic distance of SokotoGudali, Red Bororo and White Fulani cows

Breeds	SokotoGudali	Red Bororo	White Fulani
SokotoGudali	0.00	34.713	45.428
Red Bororo	34.713	0.00	1.995
White Fulani	45.428	1.995	0.00

Summary of Classification Result After Cross-Validation

Table 7 shows the summary of the classification results for the three breed groups. 88.9% of the SokotoGudali cows were correctly classified. 42.9% of the Red Bororo cows were correctly classified, while 73.3% of the White Fulani cows were classified correctly into the genotype group. The low classification achievement rate of Red

Bororo in this study could be attributed to the absence of selection within the breeds. In addition, unhindered gene flow between the Red Bororo occurs through inter-regional trade and human movement, which promotes indiscriminant mating and the exchange of genetic materials among the breeds. The proportion of individuals correctly assigned to their respective populations is considered a measure of the morphological distinctness of the population (Pundir et al., 2015). The use of udder and teat measurements may greatly increase the reliability of the classification of different dairy cow breeds. Yakubu et al., (2010) were able to correctly allocate 85.48% of Bunaji cattle and 96.55% of SokotoGudali into their groups population using the nearest neighbor discriminant analysis.

Aziz and Al-Haur (2013), used discriminant analysis to correctly classify 100% of Ardi animals into their genetic group, and the percentages of animals assigned in Line 1 and Line 2 were 86.10 and 42.55, respectively. The present classification function is the first tool available to differentiate between SokotoGudali, White Fulani, and Red Bororo cows using udder and teat measurement under field conditions, which could aid their effective management and conservation. This is important because the potential capacity of populations to adapt and evolve as independent biological entities in different environmental conditions is restricted by the exchange of individuals between populations (Yakubu et al., 2010). The function provides important and informative variables (racial markers) that could be used to assign the three dairy cow breeds into distinct populations, thereby reducing the errors of selection in future breeding programs (Yakubu et al., 2010). The increasing activities of Fulani pastoralists lead to indiscriminate flock movement, traditional livestock exchange, and the transportation of livestock by traders from one part of the country to another, which could lead to genetic erosion. A proper classification of breeds will reduce variation. It did indicate that morphological measurements can be used to increase the consistency of individuals in a population and the separation of individuals between populations (Gwaza et al., 2013).The larger the variation of udder and teat traits between the cattle populations, coupled with the high correct assignment to their populations, is an indication that they belong to different populations. The use of multivariate discriminant analyses could therefore be successfully used in group membership classification. The genetic distinctiveness of an animal forms the basis for distinguishing it among different animal genetic resources and for assessing the available diversity (FAO, 1984). The present, future improvement, and sustainability are dependent upon the existing genetic variation (Benitez, 2002).

Table 7. Summary of classification result after cross-validation

Counts	Breed	SokotoGudali	Red Bororo	White Fulani	Total
Original count	SokotoGudali	24	2	1	27
	Red Bororo	6	12	10	28
	White Fulani	0	8	22	30
Percent count	SokotoGudali	88.9	7.4	3.7	100
	Red Bororo	21.4	42.9	35.7	100
	White Fulani	0	26.7	73.3	100

CONCLUSION

The study found a variation in udder characteristics (udder diversity) among cattle breeds raised in extensive management systems in Nigeria. The variation that existed could be due to genetic differences between the breeds. Sokoto Gudali and White Fulani had a wide Mahalanobis genetic distance, which implies that mating between the two breeds could result in high and positive heteroses, while White Fulani and Red Bororo had a close Mahalanobis genetic distance, which could be an exchange of genetic materials in the past and may not result in positive heteroses. The study has explored the possibility of exploiting this udder diversity for breeding purposes or to improve milk production in these systems.

Conflict of Interest

The authors have declared that there are no competing interests.

Authors Contribution

The authors contributed equally to the article.

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