

CLASSIFICATION OF DONKEY STRAINS IN NORTHWESTERN NIGERIA THROUGH EUCLIDEAN DISTANCE MEASUREMENTS

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ABSTRACT

Proper knowledge of variations and diversities between, among and within the populations of animals helps in classifying animals into their various genetic groups, which helps in identification and conservation of important alleles. A total of seven hundred (700) donkeys consisting of (280) adult, (210) young and (210) weaner donkeys were sampled from Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto and Zamfara States of Nigeria using a random sampling techniques. Biometric traits measured among sampled donkeys were body weight, head length, head width, ear length, neck length, neck circumference, shoulder width, height at withers, heart girth, body length and tail length. Data obtained were subjected to statistical analysis to determine the genetic distance estimate across the strains. The classification of Black (Duni), White (Fari), Brown (Idabari), Red (Auraki) and Brown-white (Idabari-fari) donkeys (by using Euclidean as the distance measurement, Single Linkage, Average Linkage, and Complete Linkage were applied, and the obtained results were compared. The simple discriminant analysis procedure was used to classify the strains using the R 2.13.0 (R Development Core Team) package. Homogeneous genetic distance was observed for head width (16, 16) and shoulder width (21, 21) in male red donkeys. Female donkeys showed similar and closed genetic distances for ear length in red (26, 21), black (21, 26) and brown (26, 21) and male Red (26,22), Black (22, 25), White (26, 22) and Brown (22, 25) across the strains. Heart girth, body length and height at wither showed high level of genetic variability among the strains. Heaviest body weight was recorded in male red (141.90kg) donkey strain with a distance of 6.75cm compared to other strains of donkeys. Further classification of donkeys into various genetic groups should employ heart girth, body length and height at wither.

Keywords: Donkey, genetic distance, classification, strain, Nigeria.

INTRODUCTION

Knowledge of morphometric characteristics marks the first step in classification of Farm animal genetic resources (FAnGR) (Delgado *et al.*, 2001). Genetic distance is a measure of the genetic divergence between species or between populations within a species, whether the distance measures time from common ancestor or degree of differentiation (Nei, 1987). Populations with many similar alleles have small genetic distances. This indicates that they are closely related and have a recent common ancestor. Genetic distance is useful for reconstructing the history of populations. For example, evidence from genetic distance suggests that Sub-Saharan Africa and Eurasian people diverged about 100,000 years ago (Nei, 1974). Genetic distance is also used for understanding the origin of biodiversity. For example, the genetic distances between different breeds of domesticated animals are often investigated in order to determine which breeds should be protected to maintain genetic diversity (Ruane, 1999). Since donkey population has suffered substantial decline in its size, it is expected that the levels of inbreeding and risk of extinction may be high which necessitates a genetic study to assess variability among donkey populations for their conservation along with their breed assignment, better utilization, production and management practices. This study aimed at determining the genetic clustering, extent of genetic diversity and classification of donkeys into various genetic groups using biometric traits.

MATERIALS AND METHODS

Seven hundred donkeys (700) donkeys comprising 280 adults, 210 young and 210 weaner donkeys were used. The study was carried out in the North West of Nigeria. The States where donkeys were sampled were Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto and Zamfara States of Nigeria using random sampling techniques. These States in North West Nigeria were selected for this study because of existence of high population of donkeys. The age of the donkeys was determine using teeth count in combination with the information provided by donkey owners. Biometric traits measured were

body weight, head length, head width, ear length, neck length, neck circumference, shoulder width, height at withers, heart girth, body length and tail length using a flexible tailor's tape. The classification of Black (Duni), White (Fari), Brown (Idabari), Red (Auraki) and Brown-White (Idabari-fari) donkeys (by using Euclidean as the distance measurement; Single Linkage, Average Linkage, and Complete Linkage were applied, and the obtained results were compared. The cluster analysis procedure was used to classify the strains using the R 2.13.0 (R Development Core Team, 2015) package. DISCRIM procedure was used to calculate the probabilities of including an animal in determining the strain, taking into account the error made in classification of the strain. Stepwise discriminant procedure (STEPDISC) was applied to determine, which performance traits were used in the final clustering analysis.

RESULTS AND DISCUSSION

The classification by the application of Euclidean to measure distance among biometric traits of male and female donkeys are shown in Table 1. In male black donkey, homogeneous genetic relationships were observed for head width (16, 16), between cluster 1 and 2, and shoulder width (21, 21) in male red donkey. Similar genetic relationships were observed between cluster 1 and 2 for ear length in male red (26, 22), Black (22, 25), White (26, 22), and Brown (22, 25). In female donkeys, the genetic distance between cluster 1 and 2 for ear length in Red (26, 21), Black (21, 26), Brown (26, 21) and Brown-white were similar for neck length (38, 36) and head length (38, 35). Closer and similar genetic distances were also observed for head width in female Black (11, 14) and White (11, 14). Heart girth, body length and height at wither showed high level of genetic variability across the strains. Similar report was observed in the findings of Nei, 1987 who reported genetic divergence among animal populations with many similar alleles having small genetic distances. This indicates that they are closely related and have a common ancestor.

The classification by the application of single, average and complete linkage are shown in Table 2. The heaviest body weight was recorded in male red (141.90kg) donkey strain with a distance of 6.75cm compared to other strains of donkeys. Male donkey with the smallest body weight was recorded in white (123.55kg) with a distance of 12.01cm.

Female donkey with the heaviest body weight was recorded in brown donkey strains (123.07kg) with a distance of 16.78cm while the female donkey with the smallest body weight was recorded in brown-white (52.25kg). The high level of genetic variability observed among strains of donkeys signifies that the higher the genetic distance estimates among the strains, the further the genetic distances and the more or better the chances for selection in the population. The result of this study is similar with the findings of John *et al.* (2017) who reported similar and closed genetic distance estimates in the qualitative traits of donkeys.

Table 1: Classification by the application of euclidean to measure distance among biometric traits of male and female donkeys

Red cluster				Black cluster				White cluster				Brown cluster				Brown-white cluster			
Sex	Traits	1	2	Sex	Traits	1	2	Sex	Traits	1	2	Sex	Traits	1	2	Sex	Traits	1	2
Female	HG(cm)	118	92	Male	HW(cm)	110	105	Male	HG(cm)	111	82	Female	HG(cm)	114	73	Female	HW(cm)	89	84
Male	HG(cm)	114	104	Male	BL(cm)	109	100	Male	BL(cm)	109	87	Female	BL(cm)	106	70	Female	HG(cm)	88	79
Male	BL(cm)	109	99	Male	HG(cm)	108	101	Male	HW(cm)	105	80	Female	HW(cm)	104	79	Female	BL(cm)	84	76
Female	BL(cm)	109	89	Female	BL(cm)	87	107	Female	HW(cm)	86	105	Male	HW(cm)	77	99	Female	NC(cm)	49	42
Female	HW(cm)	108	85	Female	HG(cm)	82	115	Female	HG(cm)	84	112	Male	BL(cm)	73	101	Female	TL(cm)	49	42
Male	HW(cm)	107	97	Female	HW(cm)	80	106	Female	BL(cm)	84	112	Male	HG(cm)	69	108	Female	NL(cm)	38	36
Female	NC(cm)	71	35	Male	NC(cm)	62	50	Male	TL(cm)	64	35	Female	TL(cm)	65	39	Female	HL(cm)	38	35
Male	NC(cm)	65	51	Male	HL(cm)	48	46	Male	NC(cm)	60	50	Female	NC(cm)	60	38	Female	EL(cm)	24	22
Female	TL(cm)	63	22	Male	NL(cm)	47	43	Female	NC(cm)	47	61	Female	HL(cm)	49	34	Female	SW(cm)	14	16
Male	TL(cm)	60	49	Male	TL(cm)	46	68	Male	HL(cm)	47	36	Female	NL(cm)	47	33	Female	HW(D)(cm)	11	10
Male	NL(cm)	49	35	Female	TL(cm)	45	61	Male	NL(cm)	45	35	Male	NC(cm)	39	47				
Female	HL(cm)	49	28	Female	NC(cm)	40	65	Female	TL(cm)	38	68	Male	TL(cm)	33	53				
Male	HL(cm)	48	39	Female	NL(cm)	33	46	Female	NL(cm)	38	46	Male	NL(cm)	32	47				
Female	NL(cm)	47	27	Female	HL(cm)	32	48	Female	HL(cm)	36	48	Male	HL(cm)	28	48				
Male	EL(cm)	26	22	Male	SW(cm)	24	22	Male	EL(cm)	26	22	Female	EL(cm)	26	21				
Female	EL(cm)	26	21	Male	EL(cm)	22	25	Female	EL(cm)	23	26	Male	EL(cm)	22	25				
Female	SW(cm)	24	14	Female	EL(cm)	21	26	Male	SW(cm)	20	17	Female	SW(cm)	20	12				
Male	SW(cm)	21	21	Male	HW(D)(cm)	16	16	Female	SW(cm)	15	25	Female	HW(D)(cm)	17	11				
Male	HW(D)(cm)	16	12	Female	SW(cm)	15	19	Male	HW(D)(cm)	13	11	Male	SW(cm)	13	23				
Female	HW(D)(cm)	15	11	Female	HW(D)(cm)	11	14	Female	HW(D)(cm)	11	14	Male	HW(D)(cm)	11	15				
HL: Head length; HWD: Head width; EL: Ear length; NL: Neck length; NC: Neck circumference; SW: Shoulder width; HW: Height at withers; HG: Heart girth; BL: Body length; TL: Tail length. The values for each of the five groups were ranked; the first level of ranking was cluster 1 while the second level was cluster 2.																			

HL: Head length; HW(D): Head width; EL: Ear length; NL: Neck length; NC: Neck circumference; SW: Shoulder width; HW: Height at withers; HG: Heart girth; BL: Body length; TL: Tail length. The values for each of the five groups were ranked; the first level of ranking was cluster 1 while the second level was cluster 2.

Table 2. Classification by the application of single, average and complete linkage

Sex	Strain	Body weight (kg)	Distance
Male	Brown	130.29	16.64
	Red	141.90	6.75
	Black	137.87	9.32
	White	123.55	12.01
Female	Brown	123.07	16.78
	Red	115.90	10.91
	Black	109.60	11.40
	White	113.45	12.09
	Brown-white	52.25	0.00

CONCLUSION AND RECOMMENDATION

High level of genetic distance estimates were recorded for heart girth, body length and height at wither among donkey strains in the studied populations. Further classification of donkeys into various genetic groups should employ heart girth, body length and height at wither.

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