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# Factor analysis of biometric traits of Tonga cattle for body conformation characterization

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**ABSTRACT:** The Tonga is one of the recognized breeds of the Zambian cattle. This is a multi-purpose breed found in the southern part of the country. The present study was undertaken to study the different body measurements and relationships among different body measurements and to develop unobservable factors (latent) to define which of these measurements best represent body conformation in cows of this breed. The two extracted factors factors which accounted for 54.4% of total variance represented the body and the distal conformation of the cow. The communalities estimates indicated that cephalic conformation did not contribute effectively to explain body conformation, while the remaining traits contributed effectively, and these traits could be considered to explain the body conformation of the Tonga cow. The result suggests that the principal component analysis could be used in breeding programs with a drastic reduction in the number of biometric traits needed to explain the body conformation.

Keywords: biometry, correlation, indices, sanga, Zambia.

# INTRODUCTION

Biometric traits are used to characterize body conformation of different breeds of livestock, compare growth in different individuals and also describe an individual or population in a better way than the conventional methods of weighing and grading (Pundir, 2011). Body dimensions have been used to indicate breed, origin and relationship or shape and size of an individual (Pundir, 2011). EAAP and FAO have used height at withers as a prime indicator for their type. Recently, alternative body measurements and indices estimated from different combinations of different body traits produced a superior guide to weight and were also used as an indicator of type and function in domestic animals (Schwabe & Hall, 1989; Salako, 2006). Body shapes measured objectively could improve selection for growth by enabling the breeder to recognize early-maturing and late-maturing animals of different size (Brown, 1973; 1974). The exploitation of body dimensions could be achieved by grouping them more meaningfully. Significant differences in different body measurement/biometric traits due to age and sex were reported by many workers in different species and breeds: Gilbert, (1993), Shahin, (1995), Pundir, (2007a, b,c and 2008), Singh, (2008) and Yakubu, (2009) in cattle; Biedermann & Schmucker (1989), Jakubec, (1999) and Miserani, (2002) in horses; and Salako, (2006) in sheep.

Analysis of variance and correlations are used to obtain relationships among different body measurements, and the factor and principal component analysis (PCA) can explain relationships in a better way when the recorded traits are correlated This analysis transforms an original group of variables into another group, principal components, which are linear combination of original variables The purpose of factor analysis is to reduce a set of data that may describe and be used easily (Pundir, 2011). For genetic improvement, the principal components simultaneously consider a group of attributes which may be used for selection purpose. Fumio, (1982), Hammock, (1986), Karacaroen, (2008) and Yakubu, (2009) used factor analysis to study the different biometric traits in Japanese Black cattle, beef cattle, Swiss dairy cattle and White Flauni cattle, respectively. Salako (2006) and Sadek, (2006) used factor analysis to study the principal component factor analysis of the morpho-structural traits in Uda sheep, and factor analysis of body measurements in Arabian horses, respectively.

The Tonga is one of the recognized breeds of the Zambian cattle. This is a multi-purpose breed found in the southern part of the country. It provides a livelihood to many people as a source of meat, milk and draught power. Brownlee (1977) reported that the Tonga cattle were in Zambia before the Bantu migrations from Central Africa. It is a short-horned Sanga, largely found in the southern region of Zambia between the Kafue and Zambezi rivers. This breed has undergone a lot of uncontrolled crossbreeding because of the concentration of commercial ranches in this region. It was estimated to contribute about 52% of the indigenous cattle population in Zambia, but these numbers have greatly declined in the last three decades due to indiscriminate crossing with exotic breeds (Mwenya, 2001). The hump is on the neck and chest and is small in the male and may be absent in the female. The dewlap is moderately developed. The body is not deep and the legs are long. At Mochipapa Research Station, mature weights of 560 kg and 360 kg for Tonga breed bulls and cows at 4 years of age were recorded, respectively. Traditional herds, however, reach only 500 kg for bulls and 300 kg for cows at 4 years of age. The Tonga cattle is a adapted all-purpose breed for smallholders farmers, and because of its affirmed worthiness under low level management, there is an urgent need to implement measures to preserve it.

Presently, the size of the cow, represented by different body measurements, is one of the important criteria in selection of elite animals. There is an urgent need to describe the body conformation by recording a minimum number of body measurements/biometric traits which reduce the cost, labor and time of selection.

The present study was undertaken to study the different body measurements and relationships among different body measurements and to develop unobservable factors (latent) to define which of these measurements best represented body conformation in Tonga cattle

## MATERIALS AND METHODS

#### Data

Data consisted of 21 different body measurements on 31 adult Tonga adult cows from their native zone of the Gwembe Valley in Southern Zambia. All the cows recorded were from 12 different herds in Lusitu district. All measurements were taken by different recorders, but since the measurements are defined anatomically, authors do not believe that this fact could effect any systematic differences. The circumference and horn length measurements were taken by a tape while the other measurements were taken by a mapping stick. The recorded body measurements were body length (BL), cannon perimeter (CP), cranial length (CrL), cranial width (CrW), distance between horn tips (HoD), dorsosternal distance (DE), ear length (EL), facial width (FcW), head width (HdW), head length (HdL), heigth at rump (RH), heigth at fetlock (FH), heigth at hip (HiH), height at tail base (BT), height at withers (HW), hip length (HiL), hip width (HiW), horn perimeter (HoP), horn length (HoL), shoulder distance (SD), and thoracic girth (TG). Ethical approval was considered not necessary as animals were measured without any invasive or painful procedure after informed consent of the voluntarily participating owner. Data are available at the following address: peremiquelp@prodan.udl.cat.

#### Statistical analysis

Factor analysis is a general expression for a group of statistical techniques dealing with the reduction of a set of observable variables in terms of a small number of latent factors. It includes both factor and principal component analyses. They are functionally the same and used for the same purpose. However, they are quite different in terms of underlying assumptions. Factor analysis assumes that a variable's variance can be decomposed into two parts (Johnson & Wichern, 1982). The first part is called common variance (Communality Factor) that is shared by other variables included in the model. The estimate of communality for each variable measures the proportion of variance of that variable explained by all the other factors jointly. The second part is called specific variance (Unique Factor) as it is specific to a particular variable and includes the error variance. Factor analysis deals only with the common variance of the observed variables. However, principal component analysis considers both the total variance and unique variance and does not make any differentiation between these two. The objective of factor analysis is the reduction of the original variables into a limited number of unobservable latent factors (variables) that are extracted to account for inter-correlation among the observed variables and to explain why these variables are correlated with each other. It assumes that the unique variance represents a significant portion of the total variance. On the other hand, the objective of principal component analysis is to account for the maximum portion of the variance represents a small portion of the total variance. Multivariate statistical analyses were performed with the PAST software (Hammer, 2001).

## **Rotation of factors**

Rotation of principal factors was through the transformation of the factors to approximate a simple structure. Two factor analysis using promin rotation was used. Variables with coefficient of correlation < [0.4] were excluded from this analysis. Kaiser's measure of sampling adequacy (KMO) was used to determine whether the common factor model was appropriate (Johnson & Wichern, 1982). A loading below 0.3 was not accepted. All the analysis were carried out using the Factor v. 7.00 software package (Lorenzo-Seva & Ferrando, 2006) statistical package.

## **RESULTS AND DISCUSSION**

#### **Biometric traits**

The descriptive statistics for all the biometric traits are presented in Table 1. The coefficient of variation for different biometric traits ranged from 4.8 (height at tail base) to 29.9 (distance between horn tips). As expected, it was observed that horn traits, that is horn length, horn diameter and distance between tips, and ear length, had more variability which may be due to the fact that selection was not applied for these traits (horn traits) or that these parts respond more to the environment than others (ear length). Head traits had middle variability.

Table 1. Means (cm) with standard deviation (SD) and coefficient of variation (CV) of different traits (measurements in cm). Abreviations in

	the text	
Traits	X±SD	CV (%)
TG	138.8±13	9.4
CP	12.5±1.7	13.6
EL	13.9±2.3	16.8
HiW	34.7±3.1	9.1
HiL	37.7±2.6	6.9
HW	$105.9 \pm 5.8$	5.4
RH	$110.7 \pm 5.4$	4.9
HiH	111.7±6.2	5.5
BT	$107.0\pm5.1$	4.8
FH	42.6±2.5	5.8
BL	117.2±7.7	6.6
DE	52.3±3.3	6.4
SD	22.7±3.0	13.3
CrW	$15.4 \pm 1.2$	7.7
HdW	18.0±1.3	7.1
FcW	$12.8 \pm 1.4$	11.0
HdL	43.5±2.6	5.9
CrL	12.7±1.6	12.8
HoP	15.8±2.4	14.9
HoL	25.8±6.9	26.7
HoD	49.4±13.6	27.5

#### Phenotypic correlations

The correlation coefficients between studied biometric traits are given in Table 2. A total of 210 correlations (in all combinations) were estimated. The correlation coefficients ranged from 0.002 (EL-DE) and -0.003 (HdL-HoD) to >0.7 (DE-HiL, HW-RH, HiH-BT and RH-HiH), showing a straight back line. Among these, only height were significant ( $r_s$ <0.6), of which none were negative correlations. Heights had the highest phenotypic correlations for cows. The positive and significant (p<0.05/0.01) correlations among different biometric traits suggest high predictability among the different traits. The variables TG, FH, SD, CrW, HoL and HoD presented no  $r_s$ >0.4.

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		~											~~	~	Hd			~ -		Но	Ho
	TG	СР	EL	H1W	HıL	HW	RH	H1H	BT	FH	BL	DE	SD	CrW	W	FcW	HdL	CrL	HoP	L	D
TO		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.57
TG	0	./68	.354	.967	.118	.722	.6/3	.684	.857	.420	.409	.150	.692	.918	.040	./55	.481	./01	.596	.439	0
CD	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CP	.055	0	.018	.167	.529	.461	.225	.192	.927	.901	./41	./12	.1/8	.621	.334	.375	.847	.288	.000	.598	.257
EI	-0	0		0	514	0	0	0	0	0	0	0	0	0	570	0	0	190	0	0	504
EL	.172	.423	0	./19	.514	.260	.073	.418	.291	.989	.099	.992	.255	.423	.579	./4/	.815	.489	.071	.197	.504
HI W	-0	-0	067		002	0	108	007	072	720	105	0	400	404	017	001	005	665	028	110	0
	.008	.234	.007	0	.005	.008	.198	.007	.072	.720	.195	.014	.409	.404	.017	.001	.005	.005	.058	.110	.920
т	287	-0	-0	510		005	054	005	010	0 912	002	000	626	411	014	000	025	716	547	572	606
ь ц	.207	.110	.122	.510	0	.005	0.054	.005	.019	.012	0.002	.000	.020	.411	.014	.009	.035	./10	.547	0	.090
W	067	138	209	332	189		000	000	000	906	013	021	187	698	086	035	030	104	805	076	530
**	.007	-0	0	0	0	0	.000	0	0.000	0	0	0	0	0	0.000	0.055	0.050	0	0	0	0
RH	079	224	327	237	349	719		000	000	625	159	025	406	180	072	174	075	208	835	654	817
Hi	-0	-0	0	0	0	0	0	.000	0	0	0	0	0	0	0	0	0	0	0	0	0
н	076	241	151	473	493	697	723		000	468	072	024	778	170	173	053	002	207	702	829	947
	0	-0	0	0	0	0	0	0	.000	0	0	0	0	0	0	0	0	0	0	0	0
вт	.034	.017	.196	.328	.418	.609	.591	.703		.229	.131	.013	.188	.952	.091	.003	.030	.063	.874	.982	.693
	-0	-0	-0	0	0	0	0	0	0	,	0	0	0	0	0	0	0	0	0	0	0
FH	.150	.023	.003	.067	.044	.022	.091	.135	.222		.386	.258	.921	.284	.421	.333	.671	.573	.970	.824	.111
	0	-0	-0	0	0	0	0	0	0	-0		0	0	0	0	0	0	0	0	0	0
BL	.154	.062	.302	.239	.537	.442	.259	.327	.277	.161		.008	.265	.532	.068	.070	.014	.270	.546	.956	.350
	0	-0	0	0	0	0	0	0	0	-0	0		0	0	0	0	0	0	0	0	0
DE	.265	.069	.002	.437	.752	.414	.401	.406	.441	.210	.468		.752	.313	.014	.017	.026	.765	.416	.609	.110
	0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0		0	0	0	0	0	0	0	0
SD	.074	.248	.211	.154	.091	.244	.155	.053	.243	.019	.207	.059		.639	.337	.106	.667	.490	.858	.343	.630
Cr	0	-0	-0	0	0	-0	-0	-0	-0	-0	0	0	0	0	0	0	0	0	0	0	0
W	.019	.093	.149	.155	.153	.073	.247	.253	.011	.199	.117	.187	.088	.000	.093	.176	.492	.301	.895	.037	.960
Hd	0	-0	0	0	0	0	0	0	0	-0	0	0	-0	0		0	0	0	0	0	0
W	.371	.179	.104	.424	.438	.314	.327	.251	.309	.150	.332	.437	.179	.307		.000	.028	.084	.633	.746	.191
Fc	-0	-0	0	0	0	0	0	0	0	0	0	0	-0	0	0		0	0	0	0	0
W	.058	.165	.060	.546	.461	.379	.251	.350	.523	.180	.330	.424	.296	.249	.615		.000	.009	.432	.782	.274
Hd	-0	0	0	0	0	0	0	0	0	-0	0	0	-0	0	0	0		0	0	0	0
L	.131	.036	.044	.487	.380	.390	.324	.527	.389	.079	.435	.399	.080	.128	.395	.617		.054	.850	.571	.986
Cr	0	-0	-0	0	0	0	0	0	0	-0	0	0	-0	0	0	0	0		0	0	0
L	.072	.197	.129	.081	.068	.298	.232	.233	.338	.105	.204	.056	.129	.192	.315	.462	.350		.199	.955	.968
Ho	0	0	0	-0	0	0	-0	-0	0	0	0	0	-0	-0	-0	-0	-0	-0		0	0
P	.099	.596	.328	.374	.112	.046	.039	.072	.030	.007	.113	.151	.033	.025	.089	.147	.035	.237	0	.496	.043
Ho	0	-0	0	0	0	0	0	0	0	-0	-0	0	-0	0	0	0	-0	-0	0		0
	.144	.099	.238	.293	.105	.524	.084	.041	.004	.042	.010	.096	.1/6	.3/6	.061	.052	.106	.011	.12/	0	.088
Ho	0	0	0	-0	0	0	0	0	-0	-0	0	0	-0	0	-0	-0	-0	-0	0	0	
D	.106	.210	.125	.01/	.073	.11/	.043	.013	.074	.292	.1/4	.293	.090	.009	.241	.203	.003	.008	.365	.311	

Table 2. Coefficients of Spearman's correlation. Abreviations in the text

### Factor analysis

The measure of sampling adequacy, Kaiser-Meyer-Olkin (KMO), was 0.648 (mediocre) when variables TG, FH, SD, CrW, HoL and HoD were excluded. Yakuba, (2009) reported estimates of sampling adequacy as 0.90 and 0.92 in age groups of 1.5 to 2.4 years and 2.5 to 3.6 years, respectively, in White Fulani cattle. The estimate of sampling adequacy KMO revealed the proposition of the use in different biometric traits caused by the underlying factors. The overall significance of the correlations tested with Bertlett's test of Sphericity for the biometric traits (chi-square = 250.8; df = 105; P = 0.000010) was significant and provided enough support for the validity of the factor analysis of data. The determinant of the matrix was 0.000031066736478.

The estimated factors loading extracted by factor analysis are presented in Table 3. The two factors accounted for 54.4% of total variance. Yakuba, (2009) extracted two factors in the age group of 1.5 to 2.4 years which accounted for 85.37% of total variation, and four factors in the age group of 2.5 to 3.6 years explained 86.47% of the total variation by studying the 14 morphostructural traits of White Flauni cattle. Salako (2006) extracted two factors from 10 different biometric traits in Uda sheep which accounted for 75% of total variation. Sadek, (2006) extracted three factors for Arabian mares and stallions separately by studying 14 different traits and these explained 66% and 67% of total variation. In the present study, the first factor accounted only for 39.9% of the variation out of 15 accepted measurements. The second factor accounted for 14.4% of total variability. The first factor gave different weights and positive sign to all the traits except cannon perimeter. This factor represents the general shape and size of the cow. The second factor assigned positive weights to cannon perimeter, ear length, height at withers and horn perimeter and seemed to be representing the distal conformation of the cow. Yakuba, (2009) reported that the second factor explained 6.38% and 7.68% of total variation, while Salako (2006) reported that the second factor explained 11.03% of total variations, and 17% of total variation in Arabian mares and stallions, and stallions, and set all conformation in Category and set all conformation of the second factor explained 11.03% of total variation. respectively. The communality ranged from 0.166 (Cranial Length), 0.268 (Ear Length) and 0.284 (Head Width) to 0.825 (Horn Length) (Table 4). Higher estimates of communality (ranged from 0.79 to 0.93) were observed by Yakuba, (2009) and approximate high estimates of communality (0.42 to 0.87 and 0.32 to 0.83) were reported by Sadek, (2006).

Variable		F1		F2	
СР		-0.520		0.676	
EL				0.529	
HiW		0.719			
HiL		0.683			
HW		0.467		0.467	
RH		0.609			
HiH		0.722			
BT		0.616			
BL		0.609			
DE		0.627			
HdW		0.503			
FcW		0.603			
HdL		0.704			
CrL		0.413			
HoP				0.929	
			Sample		Total
Axis	Eigenvalue		variance		sample
					variance
1	5.994		39.9		39.9
2	2.168		14.4		54.4

Table 3. Rotated loading matrix (loadings lower than absolute 0.300 omitted). Abreviations in the text

Table 4. Communalities
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Variable	Communality
CP	0.577
EL	0.268
HiW	0.541
HiL	0.618
HW	0.530
RH	0.454
HiH	0.578
BT	0.529
BL	0.434
DE	0.473
HdW	0.284
FcW	0.436
HdL	0.547
CrL	0.166
HoP	0.825

## CONCULSION

The two extracted factors determine the source of shared variability to explain body conformation in Tonga cows. These factors represent the body and the distal conformation of the cow. The communalities estimates indicated that cephalic conformation did not contribute effectively to explain body conformation, while the remaining traits contributed effectively and these traits could be considered to explain the body conformation of the Tonga cow. The result suggests that the principal component analysis (PCA) could be used in breeding programs with a drastic reduction in the number of biometric traits needed to explain the body conformation.

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#### Conflict of interest statement

None of the authors of this paper has a financial or personal relationship with other people or organisations that could inappropriately influence or bias the content of the paper.

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