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RESEARCH ARTICLE

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## ASSOCIATION OF KAPPA-CASEIN GENOTYPE AND THE LINEAR PARAMETER IN TWO INDIGENOUS BOS INDICUS AND BOS TAURUS CATTLE IN NIGERIA

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### ABSTRACT

Kappa-casein as a mammalian milk protein is involved in several important physiological processes and it's about 80% of the total protein in cow milk. This study aimed at genotyping bovine Kappa casein (*CSN3*) in two indigenous Nigerian cattle populations and to determine the frequency distribution of Kappa casein variants as detected across the animals examined and their association with the body measurement. DNA was extracted from 100 blood samples of 50 White Fulani and 50 N'dama cattle for identification and genotyping of kappa-casein gene by polymerase chain reaction restriction fragment length polymorphism (PCR-RFLP) test using *HindIII* restriction endonucleases. The PCR products of the specific primer K-F and K-R for the two cattle breeds give 530bp specific band. Digestion of 530bp amplified products of White Fulani and N'dama by restriction endonuclease *HindIII* generated three fragments of 530-, 370- and 160- bp each for the two breeds. Results of the cuts with this enzyme show the presence of genotypes AA, AB and BB in the samples. These findings suggest that BB genotype could be selected for increase body conformation and protein content of milk.

**Keywords:** Cattle, Genotyping, Kappa-Casein Gene, N'dama, (PCR-RFLP), White Fulani

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## INTRODUCTION

Casein is one of the members of milk proteins family that exists in different molecular forms and is the main protein present in the cow's milk (Alipanah *et al.*, 2005). It is also a member of phosphoproteins family ( $\alpha$ S1,  $\alpha$ S2,  $\beta$ ,  $\kappa$ ). Each of the first four caseins ( $\alpha$ s1,  $\alpha$ s2,  $\beta$  and  $\kappa$ ) manifests variability at the level of Phosphorylation and glycosylation. Phosphorylation is a key factor responsible for the stabilization of calcium phosphate nanoclusters in casein micelles (De Kruif and Holt, 2003; Huppertz, 2013). In the intestine, the protein ingested is divided into a non-dissolved peptide (Para kappa-casein) and a soluble hydrophilic glycopeptide (caseinomacropeptide) (Ageitos *et al.*, 2006). Caseinomacropeptide has been identified to be responsible for higher digestion efficiency, prevention of newborn hypersensitivity to ingested proteins and inhibition of gastric pathogens (Ageitos *et al.*, 2006). Kappa-casein is responsible for the formation, stabilization and aggregation of the casein colloidal aggregate thereby changing the manufacturing properties and digestibility of milk (Jann, 2004).

Kappa casein is different from other caseins in structure and other properties (Azevedo *et al.*, 2008). Two allelic variants, *A* and *B* is seen on exon IV of the bovine kappa casein gene on point mutation (Alipanah *et al.*, 2007). These variants can be differentiated by polymerase chain reaction and restriction fragment length polymorphism (PCR-RFLP) analysis (Rachagani and Gupta, 2008). Also, *CSN3* gene has been seen to be highly polymorphic in bovine and according to recent review of milk protein nomenclature (Caroli *et al.*, 2009). The allele *A* and *B* have different amino acid and the positions of these amino acids differs (Alexander *et al.*, 1988). The variation has been associated with processing properties like cheese production (Alipanah *et al.*, 2007) and physiological processes such as antibacterial and cytotoxic effects (Hamza *et al.*, 2010). PCR-RFLP is one of the most frequently used methods for genetic polymorphism studies because it's simple, (Yahyaoui, 2003) and it involves the amplification of a target DNA region including the polymorphic restriction enzyme sites by PCR afterward digesting the amplicon with the respective restriction enzymes. One of the downsides of PCR-RFLP when compared with RFLP analysis is that it's difficult in finding polymorphisms within limited size of the PCR amplified fragments (Agarwal *et al.*, 2008). Over the years, body measurements have been used to interpret growth and production factors, to describe size inheritance and types of breeds or strains, and to estimate weight in beef cattle (Lasisi *et al.*, 2002 and Ndumu *et al.*, 2008). Morphological descriptions have also been used to evaluate breeding goals, to assess type and function and to estimate the animals' value as potential breeding stock (Mwacharo *et al.*, 2006). Linear body measurements (LBM) can be used in assessing growth rate, feed utilization and carcass characteristics in farm animals (Adeyinka and Mohammed, 2006; Yunusa *et al.*, 2013). Linear body measurements are divided into skeletal and tissue measurements (Essien and Adesope, 2003 and Hamito, 2009).

## MATERIALS AND METHODS

### BLOOD AND MORPHOMETRIC DATA COLLECTION

Blood samples were collected from a total of 100 healthy animals belonging to two indigenous *Bos indicus* and *Bos taurus* cattle. White Fulani (n=50) and N'dama (n=50). Blood was drawn from the ventral region of the tail from each animal into a 10ml EDTA bottle containing (Ethylene Di amine Tetra acetic Acid) as an anticoagulant and kept on ice until transferred to -40C freezers. Also, data on seven metric traits (Body length, chest girth, withers height, ear length,

tail length, leg length and head circumference) were taken in centimeter (cm) on individual cattle with the aid of a tape rule. The Animals were restrained by running them into the crunch and their sexes were also taken into consideration. Measurements was taken early in the morning prior to grazing.

### GENOMIC DNA EXTRACTION AND PCR-RFLP ASSAY FOR KAPPA-CASEIN GENOTYPES

The Genomic DNA was extracted from whole blood using the DNA Genomic kit (Bioline) following the manufactural's protocol. DNA fragment was amplified by PCR, using Kappa casein forward primer as K-F:5'-ATAGCCAAATATATCCCAATTCAGT-3' and reverse primer as K-R:5'TTTATTAATAAGTCCATGAATCTTG-3'.

The PCR reaction volume of 50µl contains 3µl of genomic DNA, 1µl of each primer, 10µl of NFW and 10µl of Master Mix to a final volume of 50µl. the amplification conditions include: pre –denaturation at 94°C for 4 minutes, annealing temperature at 54.74°C for 30s, extension of DNA at 72°C for 30s, final extension at 72°C for 4minutes, ending at 4minutes to keep it cool and the cycle repeated for 35 times. For genotyping, PCR products were digested with *HindIII* restriction enzyme which was used for the determination of kappa-casein *A* and *B* alleles.

### STATISTICAL ANALYSIS

Data analysis was performed to examine the effects of breed, sex and genotype on body weight and linear measurements of the experimental animals with Analysis of Variance (ANOVA) using the General Linear Model (GLM) from the Statistical Analysis Software (SAS vs 9.2).

The statistical model used was:

$$Y_{ijkl} = \mu + B_i + S_j + G_k + BS_{ij} + BG_{ik} + SG_{jk} + BSG_{ijk} + e_{ijkl}$$

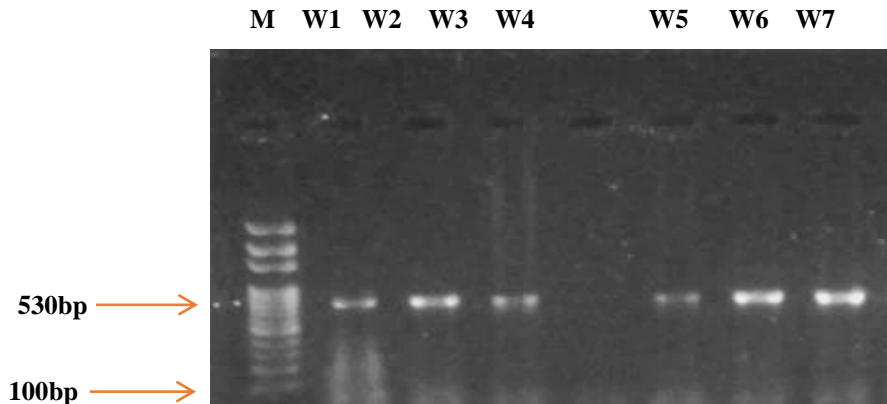
Where  $Y_{ijkl}$ , is the individual observation,  $\mu$ - general mean,  $B_i$  – breed effect,  $S_j$ - sex effect,  $G_k$ - genotypic effect,  $BS_{ij}$  – effect of breed and sex interaction,  $BG_{ik}$ - effect of breed and genotype interaction,  $SG_{jk}$  – effect of sex and genotype interaction,  $BSG_{ijk}$ - effect of breed, sex and genotype interaction and  $e_{ijkl}$ , is the experimental error.

### RESULTS

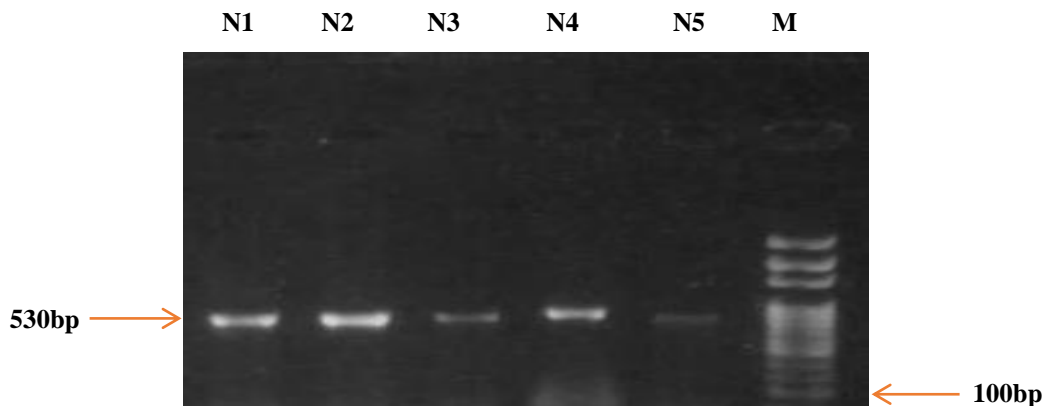
The genomic DNA extraction protocol used in this study gave a reasonable quality and quantity of DNA. Upon gel electrophoresis on 1.5% agarose gel, sharp high molecular weight bands suitable for PCR-RFLP analysis were observed. Also, PCR amplification using Kappa casein Forward and Reverse primers yielded a high molecular weight band of 530 bp DNA fragment of *CSN3* gene from all tested animals. The amplified products from the two indigenous *Bos indicus* and *Bos taurus* cattle, after the digestion with *HindIII* endonuclease generated three different DNA fragments of 530bp, 370bp and 160bp. The restriction digest of *CSN3* with *HindIII* endonuclease reveal three distinct genotypes. Genotype *AA* with a single undigested fragment of 530-bp, genotype *AB* has two digested fragments of 370- and 160-bp and genotype *BB* with three fragments of 530-, 370- and 160- bp. Hence, two kappa casein variants *A* and *B* were identified in this study (Fig. 1-4).

The *CSN3* variants detected in this study and their frequencies are presented in Table 1. The genotypic frequencies and gene frequencies of the *CSN3* variants varied across the two breeds examined. Genotypes *AA* and *AB*

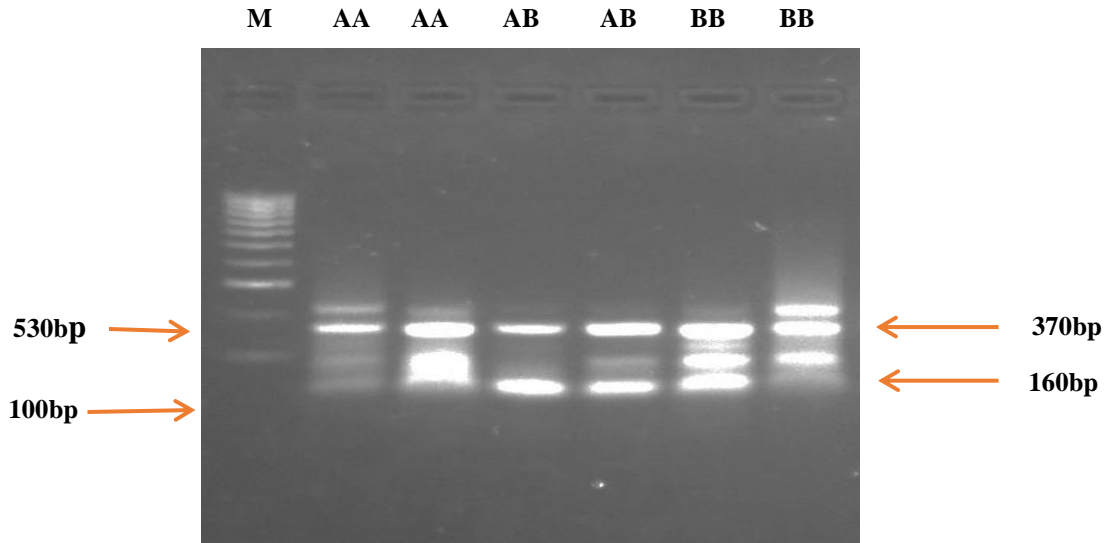
were more predominant compared to genotype *BB* in the two breeds examined in this study. In all, genotypic variant *BB* was less frequent in the two breeds but appears more frequent in the N'dama breed (0.20) than in the white Fulani breed (0.18) (Table 1). In White Fulani breed, the genotypic frequency of the *BB* and *AB* variants were found to be identical (0.18) and (0.64) for *AA* variant. While for N'dama cattle has *AA* (0.52), *BB* (0.22) and *AB* (0.26). Also, allele frequencies *A* and *B* were found on both breeds. Allele *A* was predominant than allele *B* in the two-breed population in this study. The allele frequencies for the White Fulani are *A* (0.73) and *B* (0.27) and that of N'dama, *A* (0.66) and *B* (0.34). The highest frequency of *B* allele (0.34) was found in the N'dama breed.



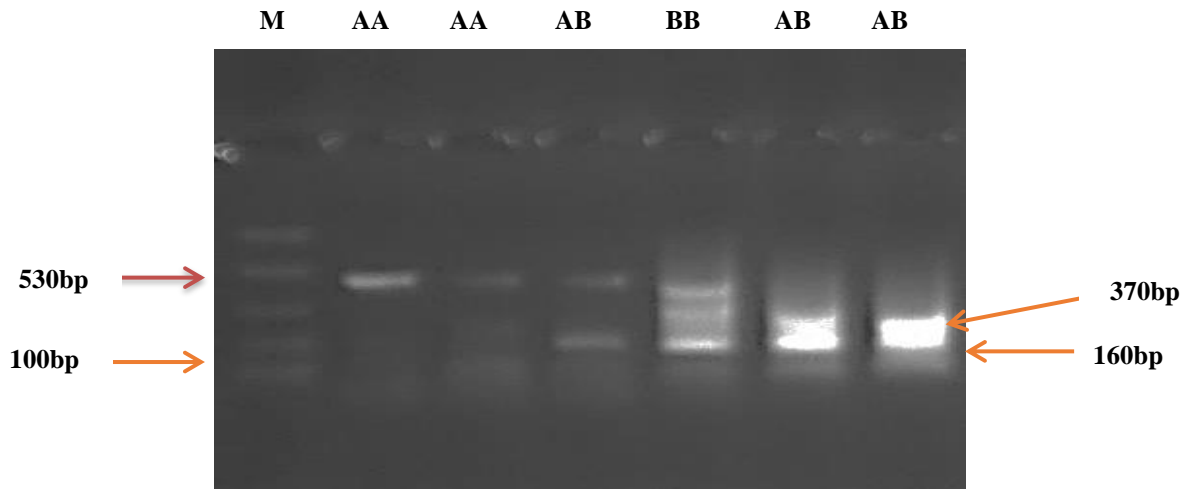
**Figure 1:** Gel electrophoresis showing 530 bp *CSN3* fragments generated by PCR amplification of genomic DNA using *CSN3* specific primers. Lane M is a 100 bp DNA marker. Lanes from W1-W7 are those taken from White Fulani breeds. 2µl of the amplicons were loaded on each lane.



**Figure 2:** Gel electrophoresis showing 530bp *CSN3* fragments generated by PCR amplification of genomic DNA using *CSN3* specific primers. Lane M is a 100 bp DNA marker. Lanes from N1-N5 are those taken from N'dama breeds. 2µl of the amplicons were loaded on each lane.



**Figure 3:** Restriction fragment patterns of kappa casein gene with the White Fulani cattle after digesting with endonuclease *HindIII* and running on 2.5g agarose gel. The corresponding genotypes are shown at the top of each lane and the lane M is a 100 bp DNA ladder.



**Figure 4:** Restriction fragment patterns of kappa casein gene with the N'dama breed after digesting with endonuclease *HindIII* and running on 2.5g agarose gel. The corresponding genotypes are shown at the top of each lane. Lane M is a 100 bp DNA ladder.

**Table 1: Genotypic and allele frequencies of CSN3 genetic variants**

Breeds	Genotypic frequency		Allele frequency		
	<i>AA</i>	<i>BB</i>	<i>AB</i>	<i>A</i>	<i>B</i>
White Fulani	0.64	0.18	0.18	0.73	0.27
N'dama	0.52	0.22	0.26	0.66	0.34

**Table 2: Effects of breeds, genotype and sex on linear measurements (cm)**

Breeds	Ear length	Body length	Chest girth	Height at withers	Leg length	Tail length	Head circumference
White Fulani	21.88 ± 0.47 <sup>a</sup>	152.56 ± 5.03 <sup>a</sup>	150.92 ± 4.84 <sup>a</sup>	67.75 ± 2.04 <sup>a</sup>	80.84 ± 1.41 <sup>a</sup>	96.06 ± 2.53 <sup>a</sup>	96.43 ± 2.50 <sup>a</sup>
N'dama	19.95 ± 0.41 <sup>a</sup>	128.50 ± 4.41 <sup>b</sup>	121.11 ± 4.21 <sup>b</sup>	58.87 ± 1.78 <sup>a</sup>	66.70 ± 1.23 <sup>b</sup>	78.25 ± 2.22 <sup>b</sup>	78.22 ± 2.19 <sup>b</sup>
Genotype							
<i>AA</i>	21.09 ± 0.36 <sup>a</sup>	137.70 ± 3.83 <sup>b</sup>	135.86 ± 3.68 <sup>b</sup>	65.02 ± 1.55 <sup>a</sup>	74.61 ± 1.07 <sup>a</sup>	88.36 ± 1.92 <sup>a</sup>	89.66 ± 1.90 <sup>a</sup>
<i>BB</i>	20.35 ± 0.63 <sup>a</sup>	137.32 ± 6.72 <sup>b</sup>	139.21 ± 6.46 <sup>a</sup>	63.12 ± 2.72 <sup>a</sup>	74.36 ± 1.88 <sup>a</sup>	84.25 ± 3.38 <sup>a</sup>	84.84 ± 3.33 <sup>a</sup>
<i>AB</i>	21.31 ± 0.60 <sup>a</sup>	146.58 ± 6.40 <sup>a</sup>	132.97 ± 6.15 <sup>b</sup>	61.79 ± 2.59 <sup>a</sup>	72.35 ± 1.79 <sup>a</sup>	88.85 ± 3.22 <sup>a</sup>	87.46 ± 2.17 <sup>a</sup>
Sex							
Male	21.01 ± 0.47 <sup>a</sup>	140.89 ± 5.03 <sup>a</sup>	133.13 ± 4.83 <sup>b</sup>	61.03 ± 2.04 <sup>a</sup>	72.84 ± 1.41 <sup>a</sup>	86.32 ± 2.53 <sup>a</sup>	86.76 ± 2.49 <sup>a</sup>
Female	20.82 ± 0.41 <sup>a</sup>	140.18 ± 4.42 <sup>a</sup>	138.89 ± 4.24 <sup>a</sup>	65.58 ± 1.79 <sup>a</sup>	74.71 ± 1.24 <sup>a</sup>	87.99 ± 2.22 <sup>a</sup>	87.88 ± 2.19 <sup>a</sup>

<sup>a</sup>Means with same superscripts on the same column are not significantly different ( $p \geq 0.05$ ) from each other. Means with different superscripts on the same column are significantly different ( $p \leq 0.05$ ) to each other.

The association of the various genotypes and the body parameters are presented in Table 2. The result shows the effects of the breeds, sex and genotypes on their linear body measurement. This result indicated that the breeds effects on the linear measurements of the animals had no significant ( $P \geq 0.05$ ) effect on the ear length and height at wither of both the white Fulani and the N'dama breed but it had significant ( $P \leq 0.05$ ) effect on the body length, chest girth, leg length, tail length and head circumference with the white Fulani breed having the highest values. For body length, White Fulani has 152.56cm and N'dama 128.50cm for, chest girth 150.92cm and 121.11cm, leg length 80.84cm and 66.70cm, tail length 96.06cm and 78.25cm and head circumference 96.93cm and 78.22cm. Furthermore, this result shows that the genotypes Kappa casein had no significant ( $P \geq 0.05$ ) effect on the ear length, height at wither, leg length, tail length and head circumference but there was significant ( $P \leq 0.05$ ) effect on the body length and chest girth with genotype *AB* recorded the highest value in the body length as 146.58cm while no significant ( $P \geq 0.05$ ) effect exist between genotype *AA* and *BB*. For the chest girth, the highest value was seen on the genotype *BB* as 139.21cm with genotype *AA* and *BB* having no significant difference as well. The sex effect on the linear measurement, there was no significant ( $P \geq 0.05$ ) effects on the linear measurements except for the chest girth with the female having the highest value recorded as 138.89cm over the male 133.13cm.

The breeds and genotypes interaction effect on the linear measurement as seen in Table 3 below, shows that for the White Fulani cattle breed there was no significant ( $P \geq 0.05$ ) difference between genotypes on the ear length and head circumference but there was significant ( $P \leq 0.05$ ) effect among the genotypes under the body length, chest girth, height at wither leg length and tail length. For the body length, genotype *AB* has the highest recorded value as

162.56cm followed by genotype *BB* 151.10cm and then genotype *AA* 144.04cm for the chest girth, genotype *BB* had the highest value as 162.43cm followed by genotype *AA* 148.27cm and then the genotype *AB* 142.06cm. For height at wither, the genotype *AA* and *BB* has the highest value recorded as (69.84cm and 69.85cm respectively) and genotype *AB* has the lowest value 63.56cm. For leg length, genotype *BB* and *AA* also has the highest value recorded as (83.76cm and 80.29cm respectively) and the genotype *AB* 78.48cm has the lowest value. While the genotype *AB* has the highest value recorded as 103.48cm for tail length followed by the genotype *AA* 92.77cm and *BB* 91.93cm with no significant effect. In the N'dama breed, there was no significant ( $P \geq 0.05$ ) differences between genotypes on ear length, height at wither and leg length but significant ( $P \leq 0.05$ ) differences was on the body length, head circumference, chest girth and tail length. The body length and head circumference has the highest significant effect on genotype *AA* and *AB* with the body length having the highest recorded value on genotype *AA* and *AB* as (131.37cm and 130.60cm respectively) and *BB* as 123.53cm while for head circumference the genotype *AA* recorded the highest value as 81.88cm, while there was no significant ( $P \geq 0.05$ ) effect between genotype *AB* and *BB* 77.85cm and 74.73cm. And for the chest girth genotype *AB* and *AA* has the highest value (123.87cm and 123.45cm respectively) and genotype *BB* has the lowest recorded value as 116.00cm. The tail length has the highest value on genotype *AA* as 83.95cm and the genotype *BB* and *AB* has the lowest recorded value as (76.58cm and 74.23cm respectively).

**Table.3.** Effect of the interaction of breed and genotypes on linear measurement(cm)

Breeds	Genotypes	Ear length	Body length	Chest girth	Height at withers	Leg length	Tail length	Head circumference
White fulani	AA	21.89 ±0.47 <sup>a</sup>	144.04 ±5.07 <sup>c</sup>	148.27±4.87 <sup>b</sup>	69.84±2.05 <sup>a</sup>	80.29±1.42 <sup>a</sup>	92.77 ±2.55 <sup>b</sup>	97.45 ± 2.51 <sup>a</sup>
	BB	21.10 ±0.94 <sup>a</sup>	151.10±10.06 <sup>b</sup>	162.43±9.67 <sup>a</sup>	69.85±4.07 <sup>a</sup>	83.76±2.82 <sup>a</sup>	91.93 ±5.07 <sup>b</sup>	94.76 ± 4.99 <sup>a</sup>
	AB	22.65±0.94 <sup>a</sup>	162.56±10.06 <sup>a</sup>	142.06±9.67 <sup>c</sup>	63.56±4.07 <sup>b</sup>	78.48±2.82 <sup>b</sup>	103.48±5.07 <sup>a</sup>	97.06 ± 4.99 <sup>a</sup>
N' dama	AA	20.28 ±0.54 <sup>a</sup>	131.37±5.73 <sup>a</sup>	123.45±5.51 <sup>a</sup>	60.20±2.32 <sup>a</sup>	68.93±1.61 <sup>a</sup>	83.95 ±2.89 <sup>a</sup>	81.88 ± 2.84 <sup>a</sup>
	BB	19.60 ±0.84 <sup>a</sup>	123.53±8.92 <sup>b</sup>	116.00±8.57 <sup>b</sup>	56.39±3.61 <sup>a</sup>	64.96±2.50 <sup>a</sup>	76.58 ±4.49 <sup>b</sup>	74.93 ± 4.42 <sup>b</sup>
	AB	19.97 ±0.74 <sup>a</sup>	130.60±7.92 <sup>a</sup>	123.87±7.61 <sup>a</sup>	60.01±3.20 <sup>a</sup>	66.21±2.22 <sup>a</sup>	74.23 ±3.98 <sup>b</sup>	77.85 ± 3.93 <sup>a</sup>

<sup>a,b</sup> Means with same superscripts on the same column are not significantly different ( $p \geq 0.05$ ) from each other

Means with different superscripts are significantly different ( $p \leq 0.05$ ) to each other.

**Table.4.** Effect of the interaction of sex and genotype on linear measurement

Sex	Genotype	Ear length	Body length	Chest girth	Height at withers	Leg length	Tail length	Head circumference
M	AA	21.21±0.55 <sup>a</sup>	136.45±5.89 <sup>b</sup>	133.13±5.66 <sup>b</sup>	65.71±2.38 <sup>a</sup>	74.59±1.65 <sup>a</sup>	86.28±2.96 <sup>a</sup>	91.55 ± 2.92 <sup>a</sup>
	BB	20.73±0.92 <sup>a</sup>	137.94±9.82 <sup>b</sup>	138.32±9.44 <sup>a</sup>	56.97±3.97 <sup>c</sup>	72.21±2.75 <sup>a</sup>	85.37±4.94 <sup>a</sup>	81.04 ± 4.87 <sup>c</sup>
	AB	21.10±0.92 <sup>a</sup>	148.26±9.82 <sup>a</sup>	127.95±9.44 <sup>c</sup>	60.43±3.97 <sup>b</sup>	71.71±2.75 <sup>a</sup>	87.31±4.94 <sup>a</sup>	87.69 ± 4.87 <sup>b</sup>
F	AA	20.96±0.46 <sup>a</sup>	138.95±4.89 <sup>b</sup>	138.59±4.70 <sup>a</sup>	64.33±1.98 <sup>a</sup>	74.62±1.37 <sup>a</sup>	90.44±2.46 <sup>a</sup>	87.78 ± 2.42 <sup>a</sup>
	BB	19.96±0.86 <sup>a</sup>	136.69±9.19 <sup>b</sup>	140.10±8.83 <sup>a</sup>	69.27±3.72 <sup>a</sup>	76.52±2.57 <sup>a</sup>	83.13±4.62 <sup>b</sup>	88.65 ± 4.56 <sup>a</sup>
	AB	21.52±0.77 <sup>a</sup>	144.90±8.21 <sup>a</sup>	137.98±7.89 <sup>a</sup>	63.15±3.32 <sup>a</sup>	72.98±2.30 <sup>a</sup>	90.40±4.14 <sup>a</sup>	87.22 ± 4.08 <sup>a</sup>

Means with same superscripts on the same column are not significantly different ( $p < 0.05$ ) from each other

Table 4 below, shows the interaction of sex and genotypes effect on linear measurement where for the male there was no significant ( $P \geq 0.05$ ) difference on the ear length, leg length and tail length but there was significant ( $P \leq 0.05$ ) effect on the body length with the highest value recorded on genotype *AB* as 148.26cm and no significant ( $P \geq 0.05$ ) difference existed between genotype *AA* and *BB* (136.45cm and 137.94cm).for chest girth the genotype *BB* has the highest value as 138.32cm followed by genotype *AA* 133.13cm and genotype *BB* has the lowest 127.95cm while for height at wither and head circumference, the genotype *AA* has the highest value as (65.71cm and 91.55cm) follow by genotype *AB* (60.43cm and 87.69cm) and genotype *BB* with the lowest value on both height at wither and head circumference as (56.97cm and 81.04cm respectively) while for the female it was observed that there was no significant ( $P \geq 0.05$ ) effect on the ear length, chest girth, height at wither, leg length and head circumference but the genotype had significant ( $P \leq 0.05$ ) effect on the body length. However, genotype *AB* recorded the highest value as 144.90cm while there is no significant ( $P \geq 0.05$ ) effect between genotype *AA* and *BB* which recorded (138.95cm and 136.69cm respectively). The genotype also had significant effect on the tail length with genotype *AA* and *BB* having the highest value as (90.44cm and 90.40cm respectively) while *AB* genotype recorded the lowest value 83.13cm for tail length.

## DISCUSSION

Many candidate genes have been identified and selected for analysis based on a known relationship with productivity traits. In this study, genetic polymorphisms of the bovine Kappa casein gene were analyzed in two indigenous breed of cattle and their genotypes determination was performed using PCR-RFLP technique in association with their linear parameters. The PCR-RFLP technique has been used to study the frequency of the *CSN3* genotypes (alleles) in both meat and dairy cattle (Alipanah *et al.*, 2005; Azevedo *et al.*, 2008). The identification of the variant genotypes of the *CSN3* gene in this study was performed through the PCR-RFLP method. Earlier studies have shown some restriction sites for endonucleases *HindIII* and other restriction enzyme on kappa-casein *AA*, *BB* and *AB* variants and the use of PCR-RFLP techniques for detecting polymorphism in kappa-casein gene (Mitra *et al.*, 1998; Otaviano *et al.*, 2005; Ahani *et al.*, 2006). The three genotypes *AA*, *AB*, and *BB* identified in this study were in accordance to other previous studies reporting the two variant A and B alleles of the *CSN3* gene as the two common alleles in *Bos taurus* dairy breeds (Beata *et al.*, 2008). From this study, genotypic frequencies of Kappa casein genotypes were: 32 cattle with the Kappa casein *AA* genotype, 9 with genotype *AB* and 9 with genotype *BB* for white Fulani while for N'dama, 26 cattle were detected with *AA* genotype, 14 with *AB* genotype and 10 with *BB* genotype. White Fulani and N'dama breeds showed a high degree of genetic variability for the kappa casein locus. In the two breeds examined, allele frequency of A was higher than that of B for White Fulani which had (0.73 vs. 0.27) and (0.66 vs. 0.34) for N'dama. The predominance of allele A over B has also been reported in numerous studies; Argentine and Patagonian Creole cattle breeds (Liron *et al.*, 2002), Holstein Friesian dairy cattle (Anggraeni *et al.*, 2010) and Russian Black and Red Pied cattle breed (Alipanah *et al.*, 2005). Significances of body weight, milk yield and body measurements in dairy cattle breeds have been studied by a number of researchers. Most of the investigators reported that larger and longer cows produced higher amount of milk (Yanar *et al.*, 2000). This corresponds to what is observed in this study that the cows with genotype *AB* and *BB* (allele B) have longer body length and larger chest girth and as such will produce higher



amount of milk which will contain higher milk protein and fat because of the *CSN3 B* allele that is positively correlated with milk protein and fat. Statistically significant differences were observed in kappa casein genotypes *AA*, *AB* and *BB*. The genotype *AA* appeared more in the cattle population than *AB* and *BB*. Next to genotype *AA* is the genotype *AB* and then the Genotype *BB* which has the least appearance but is the most closely associated with higher milk protein because of the homozygosity of the allele *B*. this correspond to Denisenko, 2004, work that say the *B* allele is correlated with higher protein milk content than allele *A*. Mean values of body measurement studied exhibited sexual dimorphism in favour of Female N'dama cattle, this may be due to physiological condition of the animals as it was not taken into consideration during the conduct of this research work, Females were significantly ( $P \leq 0.05$ ) superior to males in most of the body measurement taken, this observation is in line with submission of various workers ((Adeyinka and Mohammed, 2006; Yunusa *et al.*, 2013). Essien and Adesope (2003) and Seifemichael *et al.* (2014) submitted that the influence of sex on the body weight and some morphometric traits indicate the usual difference between sexes due to hormonal actions leading to different in growth rates. Whereas for the white Fulani cattle studied, the males were significantly ( $p \leq 0.05$ ) superior to females in most of the vital body measurement taken and this observation was contrary to the work submitted by Ndumu *et al.* (2008) and Seifemichael *et al.* (2014) and this condition may also be due to the physiological condition of the male animals which are known to be more muscular.

## CONCLUSION

The PCR-RFLP technique used was informative in distinguishing between the most widely reported *CSN3* variants, sequencing of the PCR fragments can also be done to reveal additional *CSN3* variants which were not previously identified through restriction digest analysis. The genotype frequency of *AA* was higher than that of *AB* and *BB* in the White Fulani and N'dama cattle population studied and the allele frequency of *A* was also higher than that of allele *B*. However, allele *B* is positively correlated with milk proteins and as such, the *AB* and *BB* genotype identified in *CSN3* gene is associated with higher milk protein and cows with *AB* and *BB* genotype were seen to have longer and larger and as such will produce higher amount of milk. Therefore, incorporation of these genotypes for *CSN3* may help to improve the milk yield and body conformation in the two indigenous *Bos indicus* and *Bos taurus* cattle population. Linear body measurements are important in predicting the contribution of cattle performance in improvement programs and for commercial production purpose. Linear body measurement traits in this study showed that sex is a main source of variation in the two cattle breeds.

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