Agrosearch (2013) 13 No.1: 149 - 163 Http://dx.doi.org/10.4314/agrosh.v13i1.14

THE NUTRIGENETIC EFFECTS OF *Moringa oleifera* SEED MEAL ON THE BIOLOGICAL GROWTH PROGRAMME OF YOUNG BROILER CHICKENS

A. A. Toye[1], F.E. Sola-Ojo, O.M. Olaniyan and V. Ojo
Quantitative, Molecular and Functional Genetics Group, Department of Animal Production,
Faculty of Agriculture, University of Ilorin, Kwara State, Nigeria.
[1]Corresponding Author: ayo.toye@btinternet.com

ABSTRACT

A Nutrigenetic study of the effects of graded levels (0%, 5% and 10%) of undecorticated undefatted Moringa oleifera Seed Meal (UUMOSM) on the biological growth programme of 48 young broilers of two genotypes (Marshall and Arbor Acres) was conducted. Rates of change (%) of Body Weight (WTR), Length (BLR) and Girth (BGR), and Lengths of Shank (SLR), Thigh (TLR), Wing (WLR) and Keel (KLR) between 1 and 4 weeks age were measured. The effect of Genotype and Diet on growth rate was defined by fitting a univariate General Linear Model, while the strength of relationship between traits was examined by use of Pearson's bivariate correlation method. Only BLR was significantly (P<0.05) affected by genotype, while diet significantly (P<0.05) determined WTR, BGR, TLR, WLR, and KLR. Significant (P<0.05) effects of Genotype x Diet interaction on WTR, BLR, BGR, WLR and KLR were observed. The level of correlation between trait rates varied with increasing levels of UUMOSM in both genotypes; exhibiting a direct, inverse, parabola or inverted parabola shaped relationship curve. These results showed that subtle variations in dietary levels of UUMOSM significantly influence the biological growth programme of young broilers, with implications for size and interrelationship of body parts, including shape/conformation. They further showed that substructures within populations such as clusters with non-overlapping nutritional habits (voluntary or forced) influence overall population estimates of inter-trait relationships. The transcriptomic (gene expression) and metabonomic correlates of the phenomenon reported here will be examined in further studies and should yield evidence of underlying mechanisms.

Keywords: *Moringa oleifera* seed meal, Broiler, Growth rate, Correlationand Regression.

INTRODUCTION

Poultry farming remains a potential panacea to the chronic problem of animal protein insufficiency in Nigeria (Babatunde, 1980);, other Parts of Africa, and developing countries across the world. It constitutes a significant portion (104,247,960 birds) of Nigeria's livestock resource (RIMS, 1992). If poultry farming in Nigeria is to realize and maintain its high potentials, there is the continuing need for genetic improvement of the highly adapted Nigerian local chicken. Though this bird is characterised by poor production, they are highly adapted to stress, disease and the local specific flora and fauna that constitute a significant portion of its diet within the extensive management system in which it is typically reared. Equally, genetics can play a significant role in the improvement of imported highly productive exotic genotypes which are however poorly adapted to the Nigerian environment.

Methods of animal improvement which include cross breeding and/or selection as well as genome manipulation through molecular studies require sound judgment of the consequences of genome (genotype) manipulation in the context of standard and/or alternative diets. Equally, the vast improvement in animal productivity which has resulted from past and continuing improvements in animal nutrition is the product of empirical measurement of the effects of diet on health and productivity in specific genotypes of poultry.

A growing wealth of scientific evidence, in human and laboratory and farm animals, suggests that not all genotypes respond equally to the same drug and/or nutritional regime., This has primed the emerging view that within target groups, the utilization of resources are best effective across the board when an individualized approach to nutrition (nutrigenomics) and medicine (pharmacogenomics) applies.

In the context of poultry farming, it seems reasonable to posit that changes in diet as a result of substitution of feed constituents (including sources of macro and micro nutrients, minerals, vitamins and additives) can profoundly alter production and performance of animals, though not always equally in all genotypes, and there is therefore the need for increasing care in prescription, avoiding the one-size fits all approach, and adopting nuance in prescription (founded in empirical genotype comparisons and genotype specific tests) such that effects are maximized when deployed. The introduction of relatively inexpensive non-conventional feedstuffs into poultry diets, which is driven by a need to keep poultry production profitable and viable through competitive pricing of product in the face of demand driven upward pressure on the price of conventional feedstuffs which constitute over 65% of the cost of production, must increasingly harness improvements in technology to define the genotype-specific effects of diet manipulation so as to maximize profit even further.

The present study considered the effects of introducing undefatted undecorticated *Moringa oleifera* seed meal (UUMOSM) into the diet of two genotypes of broiler chicken, specifically measuring the effect on growth rate as measured by Bodyweight rate, which is a trait on which systematic selection by geneticists acts to produce year-on-year improvement in the rate to market weight of broilers.

Because growth as measured by body weight rate arises as a result of changes in linear growth rate and mass of body components (parts) as well as body part proportions (Length and mass), overall body weight may vary depending on genotype and/or diet. Also, overall profit on each bird depends on the proportion contributed by various body parts to overall bodyweight (for example breast meat carries very high value in western economies while thigh and drumstick are highly valued in Nigeria). The knowledge of the effect of diet on the relationship between rates of growth of various body parts, and between body Weight rate and rates of growth of body parts is essential. This study therefore examined the effect of genotype, diet, andthe interaction of genotype levels of UUMOSM on growth rate of individual body parts of broiler chicken, and also assessed the relationship between rates of change of body weight and linear measures of body parts by use of a bivariate correlation method.

MATERIALS AND METHODS

All experiments were implemented in accordance with Institutional guidelines on the care and use of animals for scientific studies, and in compliance with generally accepted rules of best practice world wide.

Origin and management of experimental birds

Moringa Seed Meal: Moringa seeds were obtained from an open market in Kaduna, Kaduna State, crushed by pounding in a mortar by pestle, and air dried at room temperature ($23^{o}C$) for 12 days. This was reground to increase particle size homogeneityand then incorporated into a broiler starter diet that was formulated to NRC (1984) standards, at 0%, 5% and 10% of the overall feed weight.

Experimental Birds: Forty eight (48) day old Arbor Acres and Marshall Broiler chicks were obtained from Obasanjo and Toivic Farm Ibadan, Oyo State, Nigeria. They were randomly allocated to diet groups/cage compartments such that within each genotype, eight birds were assigned an experimental diet containing 0%, 5% or 10% UUMOSM which they were fed from day old to the end of their fourth week of age (day 28, at which the conventional broiler started phase ends). Feed and water were supplied ad libitum, and cage housing density, routine medication and vaccination regimes and management were as previously descibed (Atteh, 2004, MVM, 1996), from day old to four weeks.

Data Collection

Body weight (BW): Body weight in gram (g) was recorded to two decimal places, by use of a sensitive weighing scale (Scout II brand)

Body length (BL): Body length, was taken as the nostril to pygostyle distance measured in centimetre (cm) units when a tape measure is stretched from a bird's nasal opening, along its gently stretched neck, and along its back, to the tip of its pygostyle.

Body girth (BG): Body girth, was taken as the distance in centimetre (cm) units covered when a tape measure is looped round the region of the breast, taking care to run the tape under (rather than over) the Wing.

Shank length (SL): The shank length was taken as the distance in centimetres (cm) between the foot pad and the hock joint, measured by use of a set of Venire callipers.

Thigh length (TL): Thigh length was taken as distance between the tip of the tarsus and the ball joint, measured in centimetre (cm) units by use of a tape measure.

Keel length (KL): This was taken as the distance between the cranial and caudal termini of the Keel bone, measured in centimetre (cm) units by use of a tape measure.

Wing length (WL): Wing length was taken as the distance from the humerus-coracoid junction to the distal tip of the phalange digits, and was measured in centimetre (cm) units by the use of a tape measure.

Growth rate: For body weight (g), and each of the linear measures of body growth recorded (cm), growth rate/velocity/potential for a 3-successive-week period (Day 7 28) was determined by the use of an adapted version of the formula of Maciejowski and Ziêba (1982),

$I = [(T2\ \ T1) / (T2 + T1)/2] \times 100$ ………………………………………………………… (1)

Where:
I= Growth rate per unit period (%).
$T1$= Average initial reading for the stated period (g or cm).
$T2$= Average final reading for the stated period (g or cm).

Least squares means and standard error values of growth rate for each trait in each treatment group were determined by the use of Microsoft Excel 2007, and all data were further subjected to analysis by the use of the General linear model procedure of SPSS Version 17 (IBM SPSS, 2008). The Effects of genotype, diet, and their Interaction GxE_d were examined. The following model was specified:

$Y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + e_{ijk}$ ………………………………………………… (2)

Where Yijk = Rate of the dependent trait
μ= overall mean.
α_i = effect of the i^{th} genotype.
β_j = effect of j^{th} diet.
$\gamma_{ij}= \alpha\beta_{ij}$ =effect of the interaction between the i^{th} genotype and the j^{th} diet.
e_{ijk}= residual effect.

For each factor (Genotype and Diet) in which more than two levels existed (Diet in the current study), significantly different means ($p<0.05$) were separated by use of the Duncan's Multiple Range procedure option in SPSS 17 (SPSS IBM).

The levels of correlation between trait rates in the Arbor Acres and Marshall broilers irrespective of genotype and diet (ALL), in Arbor Acres irrespective of diet (Arbor Acres - All), and same for Marshall (Marshall All), and within diet level for each of the genotypes (Arbor Acres 0%, 5% and 10% UUMOSM, and Marshall 0%, 5% and 10% UUMOSM) were determined by the use of the Pearson's method (Falconer, 1989) implemented in SPSS 17 (IBM SPSS, 2008) :

$$rP = \frac{Cov(PxPy)}{VVxvVy} \quad \text{……………………………………………………………………(3)}$$

Where:

rP	= Phenotypic correlation.
Cov (PxPy)	= Phenotypic covariance of traits x and y.
Vx	= phenotypic variance of trait x.
Vy	= Phenotypic variance of trait y.

RESULTS

Of the seven growth rate parameters examined, only body length rate (BLR) was significantly ($P<0.05$) determined by Genotype (Arbor Acres>Marshall), Table 1. In contrast, diet significantly ($P<0.05$) determined rates of change of body weight (WTR), body girth (BGR), thigh length rate (TLR), Wing Length (WLR), and Keel Length rate (KLR) (Table 1). Genotype x Diet interaction (G x E_d) contributed to variation in rates of change of Bodyweight, Body Length, Body Girth, Wing Length and Keel Length (Table 1)

Within genotype, Levels of the inclusion of UUMOSM in the diet of young chicks at starter phase significantly determined performance as measured by rates of growth of Body Weight and Body parts (Table 2). In Marshall Broilers, BLR and BGR did not vary significantly with diet, whereas WTR, BGR, TLR and WLR varied in the order 10% UUMOSM > 5% and 0% UUMOSM. In contrast, no significant difference of Keel Length growth rate was observed between Marshall Chickens fed 0% or 10% UUMOSM diets, and both exhibited lower rates of Keel Length growth than the 5% UUMOSM group (Table 2). In Arbor Acres broilers, WTR, GLR, SLR and TLR did not differ significantly ($p<0.05$) between the 3 dietary groups (Table 2), whereas BLR and WLR differed in the order 0% UUMOSM >5% and 10% UUMOSM). The rate of growth of Keel Length (KLR) of Arbor Acres birds fed 5%UUMOSM was intermediate between, but did not differ from that observed for 0% UUMOSM which was higher in value, and 10% UUMOSM which was lower, while KLR was significantly higher for Arbor Acres fed 0% UUMOSM than the 10% UUMOSM group.

Correlation between rates of growth of Bodyweight and Lengths of Body Parts

0% UUMOSM: Significantly ($p<0.05$) high correlations (.810) existed between the rate of BGR and WTR in Marshall strains of chicken at 0% UUMOSM level, other relationships exhibited low to medium levels negative or positive correlation (-.325 to .660) which were not significant ($p>0.05$) in the Marshall broiler (Table 4). In the Arbor Acre strains there was no significant correlation between the rate of weight gain and those of other linear parts measured (Table 4).

5% UUMOSM: In the Marshall strain, a very high significant ($p<0.01$) and positive correlation (.918) was observed between BGR and WTR at 5% UUMOSM, and the relationship between WLR and TLR was also significant ($p<0.05$) and high (.801), while no significant correlation was observed between all the Body parts measured in Arbor Acre Strain.

10% UUMOSM: At 10 % UUMOSM inclusion level, there exists a significantly high correlation between weight traits rate and other Body parts measured (WTR vs. BLR, WTR vs. SLT, WTR vs. TLR, BLR vs. SLR, BLR vs. TLR, BLR vs. KLR, SLR vs. TLR and KLR, TLR vs. KLR exhibited correlation levels .716, .817, .802, .891, .753, .796, .899, .755, .826 respectively). In Arbor Acres strain, a significantly ($P<0.05$) high and negative correlation exists between BLR and SLR (-.752), Table 5.

Table 1: The Effects of genotype, diet,, and their interaction on growth rate as measured by Body Weight and Body part rates of growth from 1 - 4 weeks of age in Arbor Acres and Marshall broilers.

Dependent Variable	Source	Mean Square	Sig.	Partial Eta Squared	Observed Power[b]
Bodyweight rate (WTR)	Corrected Model	479.833	.003	.343	.943
	Mean	558952.631	.000	.992	1.000
	Genotype (G)	814.626	.009	.150	.759
	Diet (E_d)	431.693	.027	.158	.677
	G x E_d	360.577	.047	.135	.593
Body Lengh Rate (BLR)	Corrected Model	227.728	.000	.399	.983
	Mean	35622.507	.000	.954	1.000
	Genotype (G)	580.542	.000	.253	.958
	Diet (E_d)	94.156	.112	.099	.443
	G x E_d	184.892	.016	.178	.742
Body Girth Rate (BGR)	Corrected Model	418.775	.000	.447	.995
	Mean	10842.938	.000	.807	1.000
	Genotype (G)	12.999	.649	.005	.073
	Diet (E_d)	600.261	.000	.316	.975
	G x E_d	440.177	.002	.253	.914
Shank Length Rate (SLR)	Corrected Model	172.102	.095	.194	.617
	Mean	179497.005	.000	.980	1.000
	Genotype (G)	427.270	.030	.107	.591
	Diet (E_d)	157.873	.169	.081	.365
	G x E_d	58.747	.507	.032	.159
Thigh Length rate (TLR)	Corrected Model	497.986	.000	.455	.996
	Mean	135809.766	.000	.978	1.000
	Genotype (G)	238.730	.074	.074	.433
	Diet (E_d)	728.049	.000	.328	.981
	G x E_d	397.551	.007	.210	.831
Wing Length Rate (WLR)	Corrected Model	430.288	.000	.524	1.000
	Mean	117595.783	.000	.984	1.000
	Genotype (G)	1.854	.843	.001	.054
	Diet (E_d)	503.180	.000	.340	.986
	G x E_d	571.614	.000	.369	.993
Keel Length Rate (KLR)	Corrected Model	995.834	.000	.437	.994
	Mean	127826.087	.000	.952	1.000
	Genotype (G)	109.935	.401	.017	.132
	Diet (E_d)	1228.648	.001	.277	.943
	G x E_d	1205.970	.001	.273	.939

b. Computed using alpha = .05

Table 2: Least Squares Means[*] of Growth Traits Velocity from 1 - 4 weeks age in Marshall and Arbor Acres Broilers.

		Marshall			Arbor Acres		
Sn.	Trait	0% UUMOSM	5% UUMOSM	10% UUMOSM	0% UUMOSM	5% UUMOSM	10% UUMOSM
1	Bodyweight Rate WTR (%)	109.46 ± 3.61(8)^{a}	105.58 ± 2.55(8)^{a}	121.05 ± 4.3(8)^{b}	97.16 ± 4.58(8)	108.19 ± 3.34(8)	106.03 ± 3.45(8)
2	Body Length rate, BLR (%)	22.53 ± 2.3(8)	24.25 ± 1.43(8)	24.52 ± 2.58(8)	37.09 ± 1.02(8)^{b}	25.73 ± 2.98(8)^{a}	29.34 ± 2.58(8)^{a}
3	Body Girth Rate, BGR (%)	6.3 ± 3.02(8)^{a}	12.12 ± 3.31(8)^{a}	28.23 ± 1.96(8)^{b}	14.14 ± 1.5(8)	13.77 ± 3.24(8)	15.62 ± 3.1(8)
4	Shank Length Rate, SLR (%)	65.28 ± 2.97(8)	60.87 ± 2.14(8)	66.27 ± 0.26(8)	54.94 ± 5.16(8)	56.46 ± 2.15(8)	63.1 ± 4.37(8)
5	Thigh Length Rate, TLR (%)	47.85 ± 1.13(8)^{a}	41.1 ± 2.46(8)^{a}	63.93 ± 3.4(8)^{b}	55.25 ± 3.96(8)	53.74 ± 3.83(8)	57.28 ± 2.04(8)
6	Wing Length Rate, WLR (%)	46.37 ± 2.37(8)^{a}	44.14 ± 2.27(8)^{a}	57.38 ± 2.06(8)^{b}	59.81 ± 1.84(8)^{b}	41.92 ± 2.86(8)^{a}	47.34 ± 2.87(8)^{a}
7	Keel Length Rate, KLR (%)	58.65 ± 3.69(8)^{b}	33.3 ± 4.92(8)^{a}	58.32 ± 4.59(8)^{b}	62.75 ± 2.31(8)^{b}	53.13 ± 6(8)$_{a,b}$	43.47 ± 3.81(8)^{a}

* Group mean, standard error and count are presented as; Means ± s.e.m (n).

A,b, Means with different superscripts within genotype within row are significantly

Arbor Acre and Marshall broilers irrespective of diet: Table 6 shows the correlations between measures of trait velocity in Arbor Acres and Marshall broilers irrespective of diet. in this examination format, Marshall strains showed some significantly moderate and high correlation, specifically, between WTR and BLR, BGR, TLR, WLR and KLR (.428, .745, .690, .480, .589 respectively), while other Body parts such as the TLR and BGR, WLR vs. BGR and TLR, KLR vs. SLR, TLR, and WLR) also showed positive moderate and high correlations (.631, .448, .742, .572, .599, and .530). In the Arbor Acre strain, significant (p<0.05) and positive moderate correlation existed between WTR and TLR (.473) and SLR vs. TLR, while significant (p<0.01) high and positive correlation existed between BLR and WLR (0.617).

All birds irrespective of genotype and diet: The correlations between measures of trait velocity when all birds were considered irrespective of genotype and diet showed that WTR was significant (p<0.01) and moderately correlated with BGR, SLR and TLR, (.559, .405, .474 respectively) and positive but low correlation was observed between WTR and KLR (.313) . BLR had a low but positive correlation with WLR (.341) while the association between BLR and SLR was low and negative (-.345) but significant (p<0.05). BGR had a moderate and low but significant (p<0.01) correlations with TLR and WLR respectively (.507 and .289 respectively), while TLR had a significant (p<0.05)) but low correlation with SLR, WLR and KLR (.299, .338, and .336 respectively), and WLR was significantly (p<0.01) and moderately correlated with KLR (.457).

Effect of diet on the strength of correlation between traits in Arbor Acres broilers: The effect of diet on the strength of relationship between traits is illustrated in Figure 1. The strength of relationship between WTR and BGR increased with the increasing levels of UUMOSM (a direct relationship) in the diet of Arbor Acre birds (Figure 1A). Conversely, increasing levels of UUMOSM in the diet reduces the level of WTR vs. TLR, BLR vs. BGR, BGR vs. WLR, SLR vs. TLR, and SLR vs. WLR correlation (Figure 1 B). A parabolic trend was observed between increasing levels of dietary UUMOSM and the pairwise relationships between WTR and

Table 3:Correlation between measures of traits velocity in Arbor Acres and Marshall Broilers Fed 0% UUMOSM (Arbor Acres strain Lower diagonal, Marshall Strain Upper diagonal).

Traits	WTR	BL	BGR	SLR	TLR	WLR	KLR
WTR	1	.345	.810*	.210	-.196	.204	.660
BLR	-.552	1	.274	-.137	-.295	-.164	-.325
BGR	.157	.601	1	.140	.102	-.140	.500
SLR	.405	-.185	.014	1	-.359	.258	.449
TLR	.658	-.626	-.253	.661	1	.064	-.303
WLR	.337	.272	.444	.580	.239	1	.348
KLR	.696	-.253	.433	.266	.399	.248	1

*= p<0.05, **=p<0.01.

Table 4: Correlation between measures of trait velocity in Arbor Acres and Marshall broilers fed 5% UUMOSM (Arbor Acres Lower diagonal, Marshall Upper diagonal).

	WTR	BLR	BGR	SLR	TLR	WLR	KLR
WTR	1	.107	.918**	.235	.276	.150	.312
BLR	.661	1	.409	-.197	-.133	-.163	-.545
BGR	.466	.355	1	.150	.211	.155	.135
SLR	.219	.042	.629	1	.275	.440	.693
TLR	.455	.097	.654	.496	1	.801*	.267
WLR	-.004	.206	.149	.032	-.407	1	.447
KLR	.188	.525	-.451	-.703	-.320	.089	1

*= $p<0.05$, **=$p<0.01$.

Table 5: Correlation between measures of trait velocity in Arbor Acres and Marshall Broilers fed 10 % UUMOSM (Arbor Acres lower Diagonal, Marshall Upper diagonal).

	WTR	BLR	BGR	SLR	TLR	WLR	KLR
WTR	1			.817*	.802*	.078	.646
BLR	.193	1		.891**	.753*	-.064	.796*
BGR	.695	-.080	1	.456	.453	-.564	.205
SLR	.347	-.752*	.461	1	.899**	.103	.755*
TLR	.453	.090	.360	.399	1	.357	.826*
WLR	.418	.467	.141	-.110	-.129	1	.533
KLR	.604	-.381	.301	.628	.135	.409	1

*= $p<0.05$, **=$p<0.01$.

Table 6: Correlation between measures of trait velocity in Arbor Acres and Marshall Broilers irrespective of the diet. (Arbor Acres strain Lower diagonal, Marshall Strain Upper diagonal).

Traits	WTR	BLR	BGR	SLR	TLR	WLR	KLR
WTR	1	.428	.745**	.327	.690**	.480*	.589**
BLR	-.104	1	.324	-.075	.230	-.036	.025
BGR	.333	.151	`	.210	.631**	.448**	.252
SLR	.364	-.311	.334	1	.299	.389	.572**
TLR	.473*	-.009	.331	.517**	1	.742**	.599**
WLR	-.170	.617**	.120	-.002	-.063	1	.530**
KLR	.103	.338	-.133	-.099	-.101	.402	1

*= $p<0.05$, **=$p<0.01$.

Table 7:Correlation between measures of trait velocity of broilers irrespective of genotype and diet.

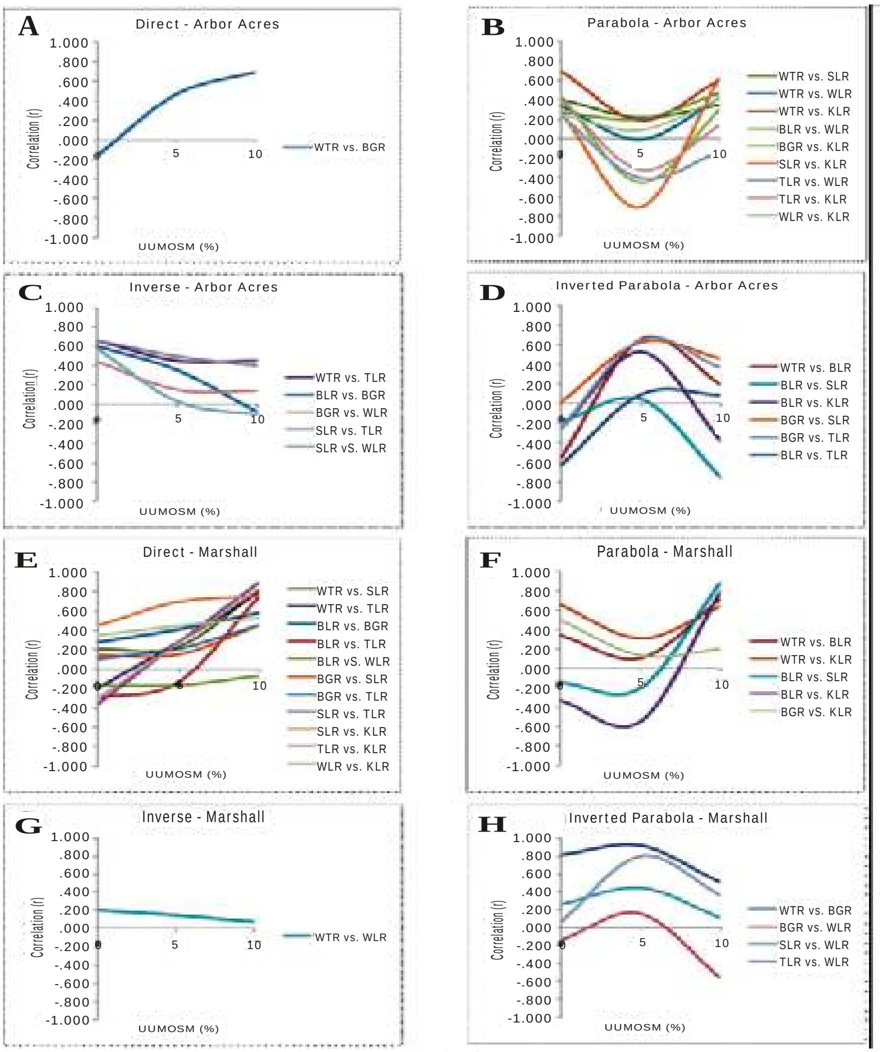
Trait	WTR	BLR	BGR	SLR	TLR	WLR	KLR
WTR	1						
BLR	-.050	1					
BGR	.550**	.179	1				
SLR	.405**	-.345*	.242	1			
TLR	.474**	.184	.507**	.299**	1		
WLR	.111	.341	.289*	.102	.338*		
KLR	.313*	.209	.115	.113	.336*	.457**	1

*= $p<0.05$, **=$p<0.01$.

SLR, WLR, KLR, and between BLR and WLR. The same parabolic trend was observed when BGR vs. KLR, SLR vs. KLR, TLR vs. WLR, TLR vs. KLR and WLR vs. KLR correlation levels were examined in Arbor Acres broilers (Figure 1B). An inverse parabolic trend was observed for the relationship between increasing levels of dietary UUMOSM and the correlation between WTR and BLR, BLR and SLR, BLR and KLR, BGR and SLR, BGR and TLR, and BLR and TLR in the same breed.

The effects of diet on the strength of correlation between traits in Marshall Broilers: The effects of diet on the strength of relationship between traits are illustrated in Figure 1. Nine pairwise relationships (correlation) between traits (WTR vs. SLR, WTR vs. TLR, SLR vs. BGR, BLR vs. TLR, BLR vs. WLR, BGR vs. SLR, BGR vs. TLR, SLR vs. TLR, SLR vs. KLR, TLR vs. KLR and WLR vs. KLR) increased with increasing levels of UUMOSM (a direct relationship) in the diet of Marshall (Figure 1E). Conversely, increasing levels of UUMOSM in the diet reduce the level of WTR vs. WLR correlation (inverse relationship) (Figure 1 G). A parabolic trend was observed between increasing levels of dietary UUMOSM and the pairwise relationships between WTR and BLR, WRTR and KLR, BLR and SLR, BLR and KLR, and BGR vs KLR (Figure 1 F). Conversely, an inverse parabolic trend was observed for the relationship between increasing levels of dietary UUMOSM and the correlation between WTR and BGR, BGR and WLR, SLR and WLR, and TLR and WLR in the same strain Figure 1H).

Figure 1: The Effects of Graded levels of dietary Undefatted Undecorticated Moringa oleifera Seed Meal (UUMOSM) on inter trait-rate Correlation in Arbor Acres (A - D) and Marshall (E-H) Broilers.



DISCUSSION

The need to identify non-conventional feedstuffs to service increasing demand in animal agriculture for inexpensive feedstuffs, and to offset the increasing competition between animals and humans for established, safe and effective food/feed ingredients drives an increasing trend towards introduction of new products into the agricultural animal feed ingredient repertoire (The poultry site, 2008). One such alternative feedstuff worth investigating is Undecorticated Undefatted Moringa oleifera Seed Meal (UUMOSM) which was examined here. The present study examined the consequences of varying UUMOSM on growth metrics, specifically growth velocity as measured by rates of change of whole Bodyweight and Length of individual Body parts, and their interrelationship. Significant effects of genotype, dietary level of UUMOSM and their interaction observed here showed that subtle variations in dietary levels of UUMOSM significantly influence the biological growth programme of young broilers, with implications for overall size (mass) and size of individual Body parts, all contingent on genotype. Talha and Mohammed, 2012 had also reported a significant effect of Moringa oleifera Undecorticated seed powder on the performance of broiler chicks. A simplistic assumption that a one-size fits all approach for testing nonconventional feedstuffs may therefore not be appropriate for optimizing production (and in consequence, profit) across all possible permutations of commercial breeds of broiler and/or diet.

High correlations obtained between BGR and WTR for Marshall strain at zero and 5% inclusion levels of UUMOSM in this study corroborate the work of Ibe (1985) where actual Body Weight was reported to be highly correlated with breast width; and indicates the concordance of relative growth rate studies (as in the present study) and actual Body Weight and dimensions at market size as examined by Adeniji and Ayorinde, (1990). It was also evident from this study that some growth parameters such as BGR, BLR, SLR, TLR, WLR, KLR were significantly correlated with Body Weight rate in both strains, and this is in accordance with the study of Ibe (1985) in which 78% of the variation in Body Weight was accounted for by three variables, namely Keel Length, Thigh circumference and Shank Length.

The observation that that level of correlation between trait rates varied with the increasing levels of UUMOSM in both genotypes (exhibiting relationship curves that ranged from “direct” to “inverse”, to “parabola”, and “inverted parabola”) implies effects on relative size of Body parts, and overall Body shape/conformation, and specifies that the value of individual linear measurements as yardsticks (Markers) of overall performance in chickens is subject to dietary variation3. Inherently changes in the relative proportions of parts contributing to overall Body size may influence overall desirability, salability and profitability of whole bird or specialized “cuts” such as breast, thigh or drumstick positively or negatively and should therefore be considered in weighing up the adoption of new feedstuffs.

CONCLUSION

Collectively, these data highlighted the need for caution in adopting new feedstuffs for specific genotypes, emphasized the benefits of accounting for animal genotype and levels of inclusion in the considerations for adoption of new non-conventional feedstuffs into the standard repertoire of poultry feedstuffs by showing the marked consequences of each (genotype and diet) in a simple paradigm involving two genotypes of broiler chicken fed three levels of a novel feedstuff UUMOSM.

Inasmuch as birds fed UUMOSM (5% and 10% dietary inclusion) grew at least as rapidly, as those on a standard diet in both genotypes examined, it can be used to supplement broiler starter diets up to 10% inclusion level. The farmer is however urged to consider genotype-specific responses of individual Body parts and their overall relationship where specific proportions contributed by individual Body parts are important determinants of profitability, particularly in the Western world.

Overall, growth rate is a major criterion used in the selection programme by breeders because of its ease of measurements (Ibe, 1985). However, the selection of individuals based on a composite phenotypic value incorporating the various growth criteria, Body Weight, Keel Length, and breast development is more valuable. The current study highlighted particular need for maintaining strict control over diet composition in breeding programmed because of the likely consequence on selection metrics. Equally, breeding programs can harness and highlight the beneficial effects of specific feedstuffs in recommendations for optimal productivity of their genetic stocks (individualized nutrition).

These data further showed that substructures within populations such as clusters with non-overlapping nutritional habits (voluntary or forced) influence overall population estimates of inter-trait relationships. The transcriptomic (gene expression) and metabonomic correlates of the phenomenon reported here will be examined in further studies and should yield evidence of underlying mechanisms.

REFERENCES

Adeniji, F.O and Ayorinde, K.L. (1990).Prediction of Body Weight of broilers at different ages from some linear Body measurements.Nig. *Journal of Animal Production*, 17: 42- 47.

Ajayi,F.O. (2010): Nigerian Indigenous Chicken: A Valuable Genetic Resource for Meat and Egg Production*. Asian Journal of Poultry Sci.*, 4:164-172.

Atteh, J.O. (2004). Principles and practices of Feed Manufacturing: *Publishers: Adlek printers*, Ilorin Kwara State: 30- 36.

Babatunde, G.M. (1980). Tottering Nigerian Livestock sector: Its problem and possibilities.*Inaugural Lecture University of Ibadan*: 9.

Boa-Amponsem, K., Sullivan, N.P.O., Gross, W.B. Dunnington, E.A., and Siegel, P.B. (1991). Genotype, Feeding Regimen and Diet Interactions in Meat Chickens.3.General Fitness.*Poult. Sci. Journal* 70:696-701.

Falconer, D.S. (1989).Introduction to Quantitative Genetics, 3rd *edition Longman Scientific and Technical, London.*

Ibe, S.N. (1985). Multivariate techniques for analyzing intercorrelated multiple traits in broiler data in Revitalizing Animal Production in Nigeria. *Proceeding of the 10th Annual conference of Nig.Society for Animal Production*: 1-8.

Maciejowski, J. and Zieba, J. (1982a). Genetics and Animal Breeding, Part A. Biological and Genetic Foundations of Animal Breeding.*Elsevier Scientific publishing co*. Amsterdam- Oxford- NewYork.PWN-Polish Scientific.

Meluzzi, A., Sirri, F., Castellini, C., Roncarati, A. Melotti, P. and Franchini, A. (2009).Influence of Genotype and Feeding on Chemical Composition of Organic Chicken Meat.*Ital. J. Anim.Sci*. Vol.8 (suppl.2), 766-768.

MVM. 1986.Handbook of Diagnostic Therapy and Disease Prevention and Control for the Veterinarian. *Merck Veterinary Manual*, 6th ed. Merial Services, Duluth, GA.

Pym, R.A.E.(1997). Effect of Genotype on Nutrient Utilization in Broilers. http//www.livestocklibray.com.au/bit stream/handle/1234/19828/97_toc.pdf. *Retrieved online* on 07/09/12.

RIMS, (1992).Nigerian Livestock Resource Vol. II National synthesis Annex.*Resource Inventory and Management Limited Executive Summary.*

SPSS 17.0 (2008): SPSS 17.0 Command Syntax Reference 2008, SPSS Inc., Chicago Ill.*http//http://www-01.ibm.com/software/analytics/spss/?prod_id=SPSS.*

Sterling, K.G., Pesti, G.M., and Bakalli, R.I. (2006).Performance of Different Broiler Genotypes Fed Diets with Varying Levels of Dietary Crude Protein and Lysine.*Poult. Sci. J.* 85: 1045-1054.

Swartland, H.J. (1984). Structure and development of meat animals.*Publ. Prentice, Hall. Inc*. Englewood Cliffs, New Jersey: 312-335.

Talha, E.A. and Mohammed, E.A. (2012). Use of Moringa oleifera seeds in Broilers Diets and its Effects on the Performance and Carcass Characteristics. *Int. J. App Poult. Res*, 1 (1): 1-4.

Tekeli, A., Celik, L., Kutlu, H.R., Gorgulu, M. (2002). Effect of Dietary Supplemental Plant Extracts on Performance, Carcass Characteristics, Digestive System Development, Intestinal Microflora and Some Blood Parameters of Broiler Chicks. *http//www.cabi.org/animalscience/uploads/file/Animalscience/additionalfiles/WPSAV erona/10283.pdf.retrieved online* on 08/09/12.

The Poultry Site (2008). Alternative Feed Ingredients: An Option to Combat High Feed Prices? *Http//www.thepoultrysite.com/articles/1185/alternative-feed-ingredients-an-option-to-combat-high-feed-prices. Retrieved* 08/09/12.