Nigerian J. Anim. Sci. 2020, 22 (1): 91-100

Polymorphisms of growth hormones gene and their associations with growth traits of crossbred pigs in humid tropical environment

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Target Audience*; Pig Breeders, Researchers and Pig Farmers*

Abstract

This study was undertaken to identify and analyse the polymorphism of growth hormone genes in pigs and to determine the associations of these growth hormone genes with growth traits such as body weight and linear body measurement of crossbred pigs. Blood of sixty (60) randomly selected crossbred pigs from six different genotypes (Local pigs x Local pigs, Landrace x Landrace, Large white x Large white, Local pigs x Landrace, Local pigs x Large white and Large white x Landrace) was used for DNA extraction. Polymerase Chain Reaction (PCR) was performed. Sequences were aligned and Single Nucleotide Polymorphism (SNPs) detected using Mega 6.0. DNA polymorphism was determined by DNAsp version 5 and the association between growth traits and growth hormone genes was done using Genstat v12. The effects of G>A mutation and interaction of growth hormone genes (GH) on growth performance of crossbred pigs at birth, weaning (6 weeks) and 16 weeks were obtained, with no significant differences (P>0.05) between genotypes GG (normal) and GA (mutant) among the pigs in association with body weight (BW) and linear body measurements. Results revealed that GH gene genotype GA had higher growth trait values than genotype GG at birth, weaning and 16 weeks. Consequently, these SNPs may be useful indicators in selection of pigs for higher growth rate and meat production. GA genotypes had a stronger correlation to higher body weight than GG genotypes in pigs.

Key words: *GH gene, genetic polymorphism, body measurements, Crossbred pigs*

Description of Problem

Advances through genetic engineering in various areas of animal production (management, nutrition, environment, sanitary control and genetic breeding) have led to improvements in the pig production chain (1). Genetic breeding of herds is done by selecting animals with high production potential based on their phenotype. The alternative method for the choice of the best animals to be used as foundation stocks of the subsequent generation is to recognize genes or loci governing economically important characters and to integrate this material into traditional breeding techniques (2).

Growth hormone (*GH*) displays an essential part in regulating tissue growth and metabolism in animal. Although, most amino acids of the *GH* protein are preserved, many single nucleotide polymorphisms are also found in characters of growth, lean rate and milk production (3). The *GH* plays a significant part in the growth of livestock as well as other genetic procedures such as metabolism, lactation and reproduction (4), and the form of which, shows an essential part in postpartum longitudinal growth and development, tissue

growth, lactation, reproduction as well as protein, lipid, and carbohydrate metabolism (5).

The growth hormone has many physiological purposes, such as stimulating muscle growth (6), bone growth and enlargement (7), controlling fat content (8) and metabolism (9). Therefore, the GH gene is a promising candidate gene worth reviewing for its influences on growth associated traits (1). Growth hormone gene could be potential candidate marker for marker assisted selection programs. Thus few study has examined the association between SNPs and growth traits in pigs especially in Nigeria content. The objective of this study was to investigate the possible associations of growth hormone gene polymorphisms on pigs with reference to body weight to identify a potential marker for use as a complementary parameter in the selection of pigs

Materials and Methods

Experimental Site

The field work was carried out at the piggery unit of University of Port Harcourt, Rivers State, Nigeria. Rivers state is located at latitude 4.8943 N and longitude 6.9105 E. The altitude is 15m above sea level. Rivers state has a tropical wet climate with very short dry seasons with annual rainfall of 2708mm, average temperature is between 25 – 28^{o}C and relative humidity is above 85%. (Department of Geography, University of Port Harcourt) While, laboratory analysis were performed using facilities at the Department of Animal Science laboratory, University of Port Harcourt, Rivers State and International Institute of Tropical Agriculture (IITA), Ibadan, Oyo State, Nigeria respectively.

Experimental Animals

The experiment involved three breeds of pigs namely Local pigs, Landrace (Lr) and Large White (Lw). A total of thirty – six breeding pigs consisting six boars and thirty gilts were used to generate progenies for the experiment according to the mating scheme below:

Local pigs x Local pigs, Landrace x Landrace, Large white x Large white, Local pigs x Landrace, Local pigs x Large white and Large white x Landrace.

Blood Collection and DNA Isolation

Two (2) ml of blood sample was collected from the ear vein of ten (10) randomly selected progenies from the six different genotypes used for investigation into EDTA tube and stored in a freezer at 20^{o}C until the DNA is extracted. DNA was extracted from the whole blood collected using Zymo Bead TM Genetic DNA kit (Irvine, C A, USA) following the procedure of the manufacturer. DNA was quantified using spectrophotometric and concentration was adjusted to 50ng µl. The quality of DNA was checked on 1.0% agarose gels and tainted with ethidium bromide (10).

DNA Extraction/Isolation and Purification

Total DNA was isolated from whole blood samples using a Zymo Bead ™ Genomic DNA Kit following the protocol as recommended by the manufacturer (ZYMO RESEARCHCORPORATIONemail:info@zymoresearch.com,websitewww.zymoresearch.com). The following procedures were taken for the purification of DNA from 50 µl whole blood:

1. The ZymoBead™ slurry was fully re-suspended using the vortexing machine. In a 1.5 ml tube, 200 µl of Genomic Lysis Buffer was added to 50 µl of blood, then 10 µl Zymo Beads™ was added. Mixed by inversion, and then incubated at room temperature for 5 minutes. Centrifuged the tube at 1,500 x g for 1 minute. The supernatant was cautiously removed without disturbing the bead pellet. (The Genomic lysis

buffer was used for breaking the cell open, usually known as cell lysis, to uncover the DNA within. Chemical method was applied to achieve this as both physical and chemical techniques may possibly be used for cell disruption. This was done with detergent known as Sodium dodecyl sulphate (SDS), which helped in removal of cell membrane lipids).

2. 200 µl of Genomic Lysis Buffer was added to the ZymoBeads™. Pellet was resuspended by pipetting up and down. Then centrifuged at 1,500 x g for 1 minute. The supernatant discarded.
3. 200 µl of DNA Pre-Wash Buffer was added to the ZymoBeads™. The pellet resuspended, moved to a new tube, and then centrifuge at 1,500 x g for 1 minute. The supernatant was discarded.
4. 500 µl of g-DNA Wash Buffer was added to the ZymoBeads™. The pellet resuspended and then centrifuged at 1,500 x g for 1 minute. The supernatant discarded. Recentrifuged briefly and residual wash buffer was removed.
5. 35 µl of Elution Buffer was added; pellet was resuspended through pipetting up and down, and then centrifuged at 10,000 x g for 1 minute.
6. At this point, the supernatant was collected. The supernatant contains purified DNA which was stored (at -20ºC) for PCR (Polymerase Chain Reaction). DNA quality and quantity were controlled using analysis on agarose gels.

DNA Concentration and Quantification

Deoxyribonucleic acid (DNA) quantification is generally done to decide the normal concentrations of DNA present in a mixture as well as their purity. In DNA evaluation, DNA is needed in specific quantities and concentrates for optimal performance. Spectrophotometric quantification method was used to establish the concentration of DNA solution for this study (10).

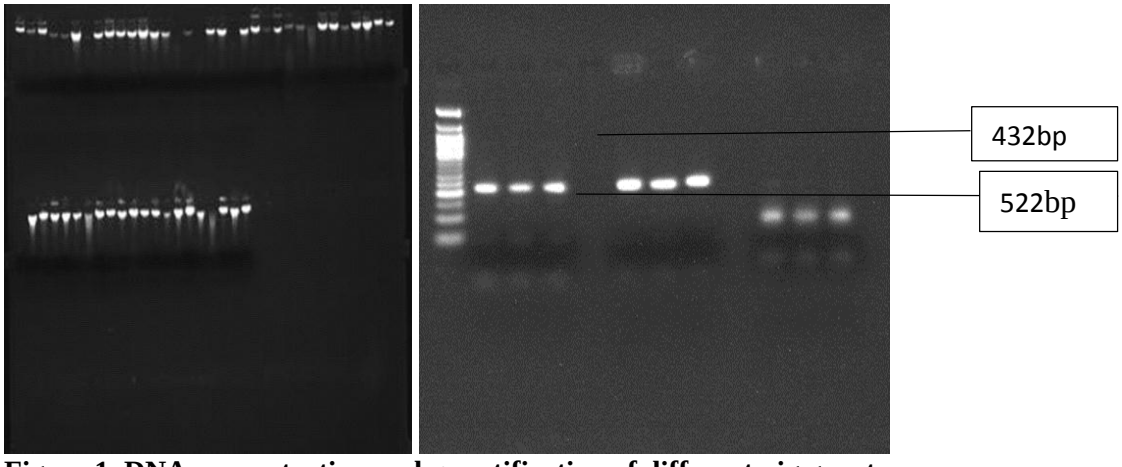

Figure 1. DNA concentration and quantification of different pig genotypes
Amplification of GH Gene by PCR.

The PCR cocktail mix consist of 2.5ul of 10x PCR buffer,1ul of 25mM MgCl2, 1ul each of forward primer and reverse primer, 1ul of DMSO, 2ul of 2.5mMDNTPs, 0.1ul of 5u/ul Taq DNA polymerase, and 3ul of 10ng/ul DNA. The total reaction volume was made up to 25ul using 13.4ul Nuclease free water. Initial denaturation at 94˚C for 5mins, followed by 36

cycles of denaturation at 94˚C for 30sec, annealing at 56˚C for 30secs and elongation at 72˚C for 45sec. Followed by a final elongation step at 72˚C for 7 minutes and hold temperature at 10 ˚C forever. Amplified fragments were visualized on Safe view-stained 1.5% agarose electrophoresis gels (11). The magnitude of the amplicon is about 1500bp and the DNA ladder used is 50bp from NEB. The polymorphism was performed by Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) as proposed (12). The sequences of the forward and reverse primers for the amplification of the GH gene were:

Forward: 5'-TCA GCA GAG TCT TCA CCA AC-3'.

Reverse: 5'-CAA CAA CGC CAT CCT CAC-3'.

GAAATTTTTTGGGGGGTTCGCTGTTTTA
ATTCTTTTGTGTACGGGCTGGGTTTAGC
ACGCAGGGTCTAGGGTGATTAATAAGC
GCAGATCAGGGGCCGTTCCAGAATCCC
TGGACCCAGCTCCGCAGACCACTCAGG
GACCTGTGGACAGCTCACCGGCTGTGA
TGACTGCAAGGAAGTGCCCTAAAATCC
CAGTGGGCTTGGTGTGTTCTGAAGGGT
GACGTGGGGGCCATGCAGACGGAGGG
GCACCAACCTTGGCTTGGGGGTTCCGA
ATGTGAGCATGATATCTACCCTTAATAT
GCGGCAAGTTTAATGTCCTGGGAAGGA
AGAGAGGAAAGGTTGTGGACCAAGCCT
CTTGTCTCTGGTCCTCTCTCAGGCCTCC
GGTCTCTAGCATGGACTCGGCTCCTGGT
TTGCCCGGTCGCTGCCTGATAGGGGGG
AGCTGTCCAGCTTCCTTGCCACTTTTGC
ATGCGGGCCGGCCGACTGACATGGGCC
GACAAAATGTTGAGCCAGAA

Figure 2: Fasta format of *Sus scrofa* growth hormone gene that was sequenced

Experimental Design and Statistical/Data Analysis Procedure

Genotypes were calculated in all the progenies of the crossbred pigs used for the study. The data obtained were employed to relate the influence of polymorphism of *GH* gene on body weight and some linear body measurements of pigs at birth, weaning (6 weeks) and 16 weeks, these were verified with the use of a model with the consequence of each genotype at *GH* locus assessed in different crossbred pigs.

To investigate the association of the studied *GH* gene polymorphism with linear body measurements traits, the relationship between BW and some body measurements with known genotypes in pigs at birth, weaning and 16 weeks were analysed using Genstat v12. The effect of mutation on growth data was analysed by SAS (2001) using significant differences separated. DNA sequences were aligned using Mega 6.0. DNA polymorphism was determined by DNAsp version 5.

The genetic effects of *GH* gene polymorphism of body weight and some linear body measurements were analysed with the following model:

$Y_{ij} = \mu + Gi + e_{ij}$

Y_{ij} = growth parameters

μ = the overall mean,

Gi= the fixed effect of the ith genotype for *GH* gene, e_{ij} = the random residual error

Results and Discussion

Table 1; Effect of G>A Mutation in growth hormone gene on Growth Traits of Crossbred Pigs at Birth

MUTATION	Body Weight(kg)	Body Length(Cm)	Height at wither(Cm)	Heart Girth (Cm)	Rear Girth (Cm)
GG (Normal)	1.25±0.02	30.78±0.57	22.23±0.13	22.56±0.16	22.61±0.23
GA(Mutant)	1.31±0.02	32.49±0.65	23.34±0.15	23.17±0.18	23.31±0.56

The effects of G>A mutation in growth hormone gene (*GH*) on growth traits of crossbred pigs at birth is as shown in Table 1. The results indicated no significant differences (P>0.05) between genotypes GG (normal) and GA (mutant) among the pigs in association with body weight (BW), body length (BL), height at wither (HTW), rear girth (RG) and heart girth (HG) while numerically, the crossbred pigs with genotype GA (mutant) had higher values for all the growth traits compared to genotype GG (normal). Therefore, genotype GA might be the most beneficial for growth traits in crossbred pigs used for this study and this implies no significant association of genotype GG (normal) and GA with the growth traits at birth. However, since no information about the G>A mutant growth hormone genes is available in the literature. The current result of non-significant effect of genotypes observed on body weight of crossbred pigs at birth was in agreement with the findings of (13) who reported that pigs with homozygote AA genotype had more birth weight (1.23±0.25 kg) than genotype AB (1.20±0.21 kg) and BB (1.18±0.27 kg) in Nanchang White. While, Large Yorkshire had the same body weight at birth for genotype AA and AB (1.47±0.24 kg) at birth than pigs with BB genotypes. Meanwhile, this present non significant effect of GH gene polymorphism on growth traits of pigs was contradicted to the findings of (14) who reported (14) significant differences in growth traits of the two genotypes (GG and GA) in their discoveries that polymorphism in 5´ flanking region had a significant influence on growth characters such as linear body measurements and body live weight. Pigs with GA genotypes had superior growth characteristics numerically. This significant influence of the various genotypes on BW, HTW, BL, HG and RG in this study concurs to the declaration that insulin- like growth factor-1(IGF-1) is an essential controller of cell proliferation, differentiation and apoptosis, it also has severe insulin-like metabolic impacts and is imperative for growth and development all over the body.

Table 2; Effect of G>A Mutation in growth hormone gene on Growth Traits of Crossbred Pigs at Weaning

Mutation	Body Weight(kg)	Body Length(Cm)	Height at wither(Cm)	Heart Girth(Cm)	Rear Girth(Cm)
GG (Normal)	5.79±0.17	51.27±1.01	29.54±0.53	34.28±1.19	34.60±1.24
GA(Mutant)	5.92±0.19	52.47±1.14	30.19±0.60	36.88±1.34	37.27±1.40

Table 2 showed the effect of G>A mutation on growth traits of crossbred pigs at weaning. The result obtained follows the same trend with the result obtained at birth. However, no significant (P>0.05) differences were observed among the growth hormone (GH) gene genotype GG and GA for BW, BL, HTW, HG and RG at weaning (6 weeks). While, the GA genotype was higher numerically in BW, HTW, BL, HG, and RG. This observation of non- significant effect of *GH* gene polymorphism on growth traits was in line with the study of (15) who reported that heterozygote genotypes (GA) for two GH polymorphism seemed beneficial for traits of muscularity and adiposity in the breeding program. Association of GH gene polymorphism in genotype GG and GA with BW and other linear body measurements showed no significant difference. The result also implied that mutant GA genotype is responsible and more associated for growth rate among the breeds of pigs used for the experiment than GG.

Table 3; Effect of G>A Mutation in growth hormone gene on Growth Traits of Crossbred Pigs at Week 16

Mutation	Body Weight (kg)	Body Length (Cm)	Height at wither (Cm)	Heart Girth (Cm)	Rear Girth (Cm)
GG (Normal)	13.29±0.41	72.44±0.57	39.48±0.63	49.71±1.03	49.66±1.00
GA(Mutant)	13.05±0.46	73.43±0.64	38.43±0.71	51.55±1.17	52.05±1.13

The Table 3 showed effect of G>A mutation on growth traits of crossbred pigs at 16 weeks. The result indicated no significant (P>0.05) differences among the GH gene genotype GG and GA for BW, BL, HTW, HG and RG at week 16. The non significant result observed agreed with the findings of (16). The authors claimed that growth hormone genotype was not associated with growth traits after investigating the progenies of purebred and crossbred sires of pigs. However, the homozygotes GG (normal) genotype values were superior in BW (13.29±0.41 kg) and HTW (39.48±0.63 cm) to BW (13.05±0.46 kg) and HTW (38.43±0.71 cm) observed in genotype GA. While, BL, HG, and RG were superior in GA than in GG genotype. This obtained results was in line with the observation of (15) who reported that heterozygote genotypes for two *GH* polymorphism is more valued for characters of sturdiness and adiposity in the breeding plan. Association of *GH* gene polymorphism in genotype GG and GA with BW and other linear body measurements exhibited no significant difference. (17) reported that growth performance traits in Duroc, Landrace and Tao-Yun pig breeds were highly associated with their growth hormone genotypes. The finding implied that the candidate gene tactic is one of the various approaches appropriate for investigating the association between growth hormone genes, which is one of the favorable scheme for the genetic improvement of economically important quantitative traits.

Table 4; Interaction Effect of Crossbred Pigs and Mutation (SNP (G>A) on Growth

Progeny Genotypes	GenotypesSnp (G>A)	Body Weight(kg)	Body Length(cm)	Height At Wither(cm)	Heart Girth(cm)	Rear Girth(cm)
Large white x Large white	NORMAL(GG)	1.34±0.15	29.29±4.29	23.02±0.12	22.76±0.34	23.15±0.15
	MUTANT(G>A)	1.39±0.05	34.31±0.42	22.56±0.62	23.12±0.71	23.36±0.58
Landrace x Landrace	NORMAL(GG)	1.26±0.00	34.57±0.00	24.14±0.00	22.00±0.00	22.14±0.00
	MUTANT(G>A)	1.41±0.05	34.47±0.04	23.34±0.17	23.04±0.71	23.00±0.00
Local pigs x Local pigs	NORMAL(GG)	0.89±0.03	27.25±0.25	17.13±0.13	20.75±0.25	20.75+0.25
	MUTANT(G>A)	-	-	-	-	-
Large white x Landrace	NORMAL(GG)	1.47±0.04	33.73±0.10	23.67±0.23	24.29±0.16	23.40±0.47
	MUTANT(G>A)	-	-	-	-	-
Local pigs x Landrace	NORMAL(GG)	1.10±0.00	27.90±0.00	23.00±0.00	22.88±0.00	22.70±0.00
	MUTANT(G>A)	1.145±0.02	28.90±1.00	22.86±0.25	23.28±0.40	22.71±0.24
Local pigs x Large white	NORMAL(GG)	1.24±0.01	31.92±0.32	22.43±0.14	22.67±0.40	23.52+0.41
	MUTANT(G>A)	1.28±0.00	32.27±0.00	24.63±0.00	23.17±0.00	24.17±0.00

Performance of At Birth

SNP = Single Nucleotide Polymorphism G>A mutant

Table 4 showed the interaction effect of crossbred pigs and mutation (G>A) on growth performance at birth. Crossbred (Large white x Landrace) with GG genotypes were higher in BW (1.47±0.04 kg) and HG (24.29±0.16 cm) than those in GA genotype. Purebred (Local pigs x Local pigs) with GG genotype had the least BW (0.89±0.03 kg) and HG (20.75±0.25 cm) respectively. The result indicated that no mutant GA was observed in Large white x Landrace crossbred and Local pigs x Local pigs purebred in BW and other LBMs. The result also revealed that *GH* gene genotype GA had higher growth trait values than genotype GG at birth. It was also observed that genotype GG from Landrace x Landrace recorded the longest BL (34.57±0.00 cm) and HTW (24.14±0.00 cm). However, normal GG genotype from Local pigs x Local pigs had the least BL (27.25±0.25 cm) and HTW (17.13±0.13 cm). Also, the mutant (GA) genotype from Local pigs x Large white crossbred had the highest value for RG of (24.17±0.00 cm). While, normal GG genotype from Local pigs x Local pigs recorded the least RG (20.75±0.28 cm). Genotype GA produced higher values for BW among the breeds of pigs studied. Also, GA genotype had higher values for BL, HG and RG among Large white x Large white, Local pigs x Landrace and Local pigs x Large white. Whereas, normal (GG) recorded higher values for HTW among the breeds of pigs. The findings reported by (13) agreed with the result obtained in this study where no significant effect of genotypes was recorded on the White Nanchang and Large Yorkshire at birth in body weight. These authors also found that pigs possess AA genotype had higher birth weight (1.23±0.25 kg) than genotype AB (1.20±0.21 kg) and BB (1.18±0.27 kg) in Nanchang White while, Large Yorkshire had the same body weight at birth for genotype AA and AB (1.47±0.24 kg). (16) claimed that growth hormone genotype was not associated with growth traits. However, the outcomes of findings of (17) disclosed that growth performance traits in Landrace and Duroc and Tao-Yun pig breeds were highly associated with their growth hormone genotypes.

Table 5: Interaction Effect of Crossbred Pigs and Mutation SNP (G>A) on Growth Traits at Weaning (6weeks)

Progeny genotypes	Snp (G>A)	Body Weight(kg)	Body Length(cm)	Height At Wither(cm)	Heart Girth(cm)	Rear Girth(cm)
Large white xLargewhite	NORMAL(GG)	5.75±0.95	53.94±6.06	29.82±1.68	36.38±3.63	36.67±3.17
	MUTANT(G>A)	5.86±0.02	57.88±0.02	32.20±3.09	41.06±4.01	41.31±4.02
Landrace x Landrace	NORMAL(GG)	4.72±0.00	52.00±0.00	28.54±0.00	33.71±3.00	34.43±0.00
	MUTANT(G>A)	4.82±0.26	49.02±0.31	28.40±0.39	36.70±3.13	36.52±2.81
Local pigs x Local pigs	NORMAL(GG)	3.45±0.23	42.75±0.75	25.44±0.06	27.04±0.40	29.54±2.46
	MUTANT(G>A)	-	-	-	-	-
Large white x Landrace	NORMAL(GG)	8.98±0.16	60.48±1.35	32.59±0.36	38.92±2.10	38.48±2.22
	MUTANT(G>A)	-	-	-	-	-
Local pigs x Landrace	NORMAL(GG)	5.87±0.00	53.48±0.00	33.63±0.00	35.10±0.00	34.25±0.00
	MUTANT(G>A)	6.78±0.60	56.48±1.21	32.44±1.84	37.50±1.50	37.84±1.91
Local pigs x Large white	NORMAL(GG)	5.99±0.14	44.99±1.34	27.22±0.05	34.53±0.57	34.23±0.49
	MUTANT(G>A)	6.24±0.15	46.52±0.25	27.60±1.35	32.25±1.70	33.43±0.95

SNP = Single Nucleotide Polymorphism G>A mutant

Table 5 showed the interaction effect of crossbred pigs and SNP (G>A) on growth traits at weaning (6 weeks). The result revealed that GH gene GG genotype from Large white x Landrace crossbred had highest BW (8.98±0.16 kg) and BL (60.481.37 cm), while, Local pigs x Local pigs purebred had the least BW (3.45±0.23 kg) and BL (42.75±0.75 cm) respectively. The result also indicated that heterozygote G>A genotypes had higher growth traits in progenies from Large white x Large white, Landrace x Landrace, Local pigs x Landrace this showed that growth hormone genes containing the GA genotype grew more rapidly related to GH genes which comprise the GG genotypes. Based on this results, it is concluded that the GG genotype of growth hormone genes represents the selection genotype for smaller size. No significant difference (P>0.05) was observed among the progenies of crossbred pigs in association with the growth traits through the BW and other linear body measurements. The result also showed that Local pigs x Local purebred pigs and Large white x Landrace crossbred do not have mutant genotype GA in BW and other linear body measurements, this revealed that GG genotype is highly conserved the progenies of Large white x Landrace and Local pigs x Local pigs, it could also be as a result of lengthy natural selection and improvement. Mutant (GA) genotype is superior in BW, HTW, HG and RG for Large white x Large white. Mutant (GA) genotype also had higher values in HG and RG for Landrace x Landrace and Local pigs x Local pigs. Likewise, GA genotype recorded higher values for BW and BL in Local pigs x Large white than GG genotype. The result also showed that there were association between growth hormone *GH* gene and the growth traits among the various progenies of crossbred pigs. This result is in accordance with the observations of (17) who indicated that growth traits in Landrace, Tao-Yun pig and Duroc genotypes were extremely linked with their growth hormone genes.

Table 6: Interaction Effect of Crossbred Pigs and Mutation SNP (G>A) on Growth Traits at 16 Weeks

Progeny genotypes	SNP (G>A)	Body Weight(kg)	Body Length(cm)	Height At Wither(cm)	Heart Girth(cm)	Rear Girth(cm)
Largewhite xLargewhite	NORMAL(GG)	14.05±1.51	75.39±2.79	39.79±1.42	53.82±2.34	53.75±2.75
	MUTANT(G>A)	12.32±1.79	73.48±1.70	38.84±1.42	53.47±1.98	53.67±0.67
Landrace x Landrace	NORMAL(GG)	13.13±0.00	75.86+0.00	41.43±2.01	51.86±0.00	51.29±0.00
	MUTANT(G>A)	13.31±0.21	75.72±0.29	38.67±1.42	54.50±2.67	54.31±5.00
Local pigs x Local pigs	NORMAL(GG)	8.35±0.35	57.50±0.50	35.13±1.42	39.54±0.13	39.54±0.04
	MUTANT(G>A)	-	-	-	-	-
Largewhite x Landrace	NORMAL(GG)	18.30±0.62	80.02±0.91	44.06±0.90	54.21±0.34	54.63±1.37
	MUTANT(G>A)	-	-	-	-	-
Local pigs x Landrace	NORMAL(GG)	13.64±0.00	74.67±0.00	40.06±2.01	52.80±0.00	53.33±0.00
	MUTANT(G>A)	13.81±0.17	73.65±0.55	40.57±1.42	52.00±0.97	53.13±0.80
Local pigs x Largewhite	NORMAL(GG)	12.26±0.09	71.20±0.15	36.16±1.16	46.04±1.34	45.38±1.52
	MUTANT(G>A)	12.75±0.85	70.87±0.37	35.65±1.42	46.24±0.30	47.11±1.28

SNP = Single Nucleotide Polymorphism G>A mutant

Table 6 revealed the interaction effect of crossbred pigs and mutation SNP (G>A) GH gene on growth performance at week 16. The results showed that progenies with GA had higher BW and other linear body measurements compared to genotype GG among the crossbred pigs. Normal GG from Large white x Landrace had the highest values for BW, BL, HTW, HG and RG while, Local pigs x Local pigs had the least values for BW, BL, HTW, HG and RG. The result indicated that all growth traits were influenced by the growth hormone genes as these traits are positively correlated. The result also showed that there was association between the growth hormone gene and growth traits among the pigs studied and genotypes GA seems to be beneficial genotype for body weight and other growth traits in crossbred pigs. The result suggested that *GH* could be used as a genetic marker for marker assisted selection (MAS) for outstanding growth traits during animal breeding procedure. The *GH* genes can also be used as a candidate gene for reviewing pigs polymorphism and their association in relation to growth. The result obtained also correspond to the discoveries of (18) where the results of the association with growth characters showed that *IGF-1* mutation affected the BW, BL and HG of pigs at 16 weeks. The authors found that homozygote TT genotype grew more rapidly compared to *IGF-1* genes containing the heterozygote TC genotype. This notion supports the previous findings in other species of animals that *GH* gene can be promoted as candidate gene to improve animal performance such as body weight

Conclusion and Application

1. The results obtained showed that there were associations between growth hormone *GH* gene and the growth traits among the various progenies of crossbred pigs.
2. The progenies with GA had higher BW and other linear body measurements compared to genotype GG among the crossbred pigs.
3. The results also suggested that *GH* genes could be used as a genetic marker for marker assisted selection (MAS) for outstanding growth traits during animal breeding procedure. *GH* genes can as well be used as a candidate gene for reviewing pigs polymorphism and their association in relation to growth.
4. The finding of this study implied that the candidate gene tactic is one of the various approaches appropriate for investigating the association between growth hormone genes, which is one of the favorable scheme for the genetic improvement of economically important quantitative traits.

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