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Differences in growth and fat deposition between White Plymouth Rock and Nagoya breeds as a tool for QTL analysis

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A B S T R A C T

Two breeds of chickens were used in this study *White Plymouth Rock* (WPR) and *Nagoya* (NAG) in addition to tracking of their crossbred (♀ WPR X ♂ NAG) of two generations (F1and F2) for evaluating the differences in growth characteristics and fat deposition. Body weights were measured weekly from the first day (hatch day) till 4 weeks of age and different weight gains were also calculated. In addition to feed intake (for the period of 3-4 weeks of age) and feed conversion ratio were estimated. At four weeks of age, birds were dissected and the major internal organs including liver and gizzard were weighed, moreover the parts of breast muscle were also recorded. The results showed that, WPR was significantly higher in body weights, body weight gains and feed intake than NAG chicken. Also, WPR showed significantly larger sizes for liver, gizzard, pectoral muscles, abdominal fat (AF), ventriculus fat (VF), subcutaneous fat (SF) and total fat weight than NAG chicken. The correlation analysis showed that body weight at one week of age and body weight gain of the first week of age were found to have positive correlation with liver triglycerides and serum triglycerides levels in WPR while it was associated with decreasing of level of total cholesterol in serum in NAG. These results served as evidence for elucidating the major differences observed between the two breeds concerning growth and fat deposition. In addition to the relationship between increasing body weight and fat deposition was established. Thus, future QTL analysis can be performed for identification of chromosomal regions controlling growth and fatness traits and subsequently candidate gene influencing these traits could be revealed in further investigations.

Keywords: Breeds, Fat, Growth, Nagoya, White Plymouth Rock.

1. Introduction

A significant progress has been continuously made in the broiler's selection programs which based on rapid weight gain as a tool for reducing market age. In 1953, broiler was required more than 70 days to attain an acceptable body weight for slaughter (1.5 kg). Recently, broilers took only 42 days as a fattening period to reach 2.5 kg body weight (Fouad and El-Senousey, 2014). However, this rapid gain in body weight associated with an excessive fat deposition. Excessive fatness negatively affects broiler industry through depressing feed efficiency, lowering chicken meat yield, difficult meat processing and subsequently cause economic loss. In addition, it has many health hazards causing serious diseases and therefore consumer rejection. Thus, fatness obviously undesirable both economically and socially (Tatsuda and Fujinaka 2001a,b; Jennen et al., 2004; Tůmová and Teimouri, 2010; Wang et al. 2012) . In chickens, over 85% of body fat is stored in the adipose tissue as abdominal, subcutaneous and intramuscular fat. Inside these tissues, fat used as a source of energy when needed, heat insulator and protective cushion (Jennen, 2004). Moreover, the heritability of fatness is high between 0.4 and 0.7 (Le Bihan-Duval et al., 2001; Zerehdaran et al., 2004), providing strong evidence for presence of genetic basis for fat deposition and related traits in broiler chickens. Inside chickens' cells fat is stored as triglycerides and liver is the main site for fat lipogenesis and triglycerides synthesis. Nonetheless, liver is responsible for synthesis of HDL which important for increase uptake of triglycerides and bring free cholesterol into the plasma. In addition, many studies referred to the role of lipogenesis in increasing fat deposition (Jennen, 2004). Nevertheless, fatness measurement is laborious and expensive due to cost of slaughtering and dissection so the use of molecular based technique will be of great value for analysis of fatness or even identification of possible candidate gene/s (Ikeobi et al., 2002; Lagarrigue et al., 2006). QTL analysis provides information about the position and effects of QTL and this knowledge would be of great value for marker assisted selection and understanding the genetic basis for studied phenotypes (Liu et al., 2007).

Nagoya is a popular native Japanese chicken reared in the *Aichi Prefecture*, and used as a dual-purpose breed with good quality meat and eggs. During the period between 1868 and 1912 the *Cochin* (Chinese breed) was crossed with some native Japanese breeds to produce *Nagoya Cochin* then in period around (1912 – 1926) the *Nagoya* breed was developed by removing leg feather from *Cochin* breed which now is extinct (Tsudzuki, 2003).

White Plymouth Rock, western broiler chicken with significant body weight gain and higher fat deposition. It was commonly used as a parental breed for broilers with excellent body gain (Tatsuda and Fujinaka, 2001a). Few literatures are available on the differences between those breeds regarding to body weight and growth characteristics and implementation of this knowledge for QTL analysis and revealing chromosomal regions controlling these phenotypes.

The objective of the present study was to state the differences between *Nagoya* and *White Plymouth Rock* breeds in growth related traits and body fat deposition and the effect of these traits on various biochemical parameters. Additionally, F1 and F2 were developed from both breeds for tracking the inheritance of growth and fatness related traits under investigation. Therefore, the possibility of their usage as parental breeds for developing resource populations for QTL analysis and identification of genes which may control growth and fatness in chickens.

2. Material and methods

2.1. Animals

This experiment was started with incubating of 55 WPR, 55 NAG and 35 F1 fertile eggs; this incubation was allowing us to obtain about 29 WPR, 17 NAG, and 8 F1 chicks from different hatches, in addition to 239-day-old chicks for F2 generation (produced by crossing between *Nagoya* males and *White Plymouth Rock* females). The eggs were kept under the optimum incubation conditions for 18 days then transferred to the hatchery three days before hatching. On hatching day, chicks were identified by id number and their body weights were recorded as the initial body weight (BW0). The hatched chicks were kept in the brooder for three weeks and the body weights were measured weekly from hatch day till 4th week of age. The brooding temperature started at 33°C at hatching day, then lowered by 3°C weekly till reach around 21 °C at 4 weeks of age. The light was kept continuous throughout the first week then the lightening

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Table 1. Performance traits in WPR, NAG, and their cross breed for two generation

Parameter	Performance traits in gram ± SE			
	WPR	NAG	F1	F2
BW 0	46.82±0.61[a]	44.43±0.83[a]	*	41.81±0.21[b]
BW1	136.08±2.25[a]	89.9±3.03[d]	121.81±4.29[b]	104.49±0.79[c]
BW2	290.21±5.04[a]	187.96±6.79[d]	253.79±9.60[b]	228.13±1.76[c]
BW3	529.55±9.18[a]	320. 43±12.37[d]	438.05±17.49[b]	381.95±3.20[c]
BW4	746.65±16.61[a]	502.88±22.36[c]	641.50±31.63[b]	563.98±5.80[b]
WG1	89.06±2.19[a]	50.23±2.95[c]	*	62.83±0.77[b]
WG2	148.84±3.26[a]	99.66±4.40[c]	132.47±6.22[ab]	124.03±1.15[b]
WG3	245.67±6.06[a]	117.95±8.16[d]	198.59±11.54[b]	153.30±2.12[c]
WG4	236.87±9.55[a]	156.07±12.86[b]	240.81±18.19[a]	187.60±3.33[b]
WG total	624.15±18.67[a]	493.17±25.13[b]	*	524.19±6.51[b]
Feed intake (3-4 week)	604.23±18.45[a]	408.02±24.85[c]	607.57±37.57[ab]	511.29±7.28[b]
FCR (3-4 week)	3.19±0.16[a]	3.51±0.21[a]	3.22±0.30[ab]	2.73±0.06[b]

BW0= body weight at hatch. BW1= body weight at 1 week. BW2= body weight at 2 weeks. BW3= body weight at 3 weeks. BW4= body weight at 4 weeks. WG1= weight gain from day 0 to one week of age. WG2= weight gain from 1-2 weeks of age. WG3= weight gain from 2-3 week of age. WG4= weight gain from 3-4 week of age. WG total= weight gain from day 0 to 4weeks of age. FCR = feed conversion ratio for 3-4 weeks of age. *Missed data due to initial weight for F1 was lost. a-c means carrying different superscripts in the same raw were significantly different (P<0.05).

Table 2. Slaughter weight in WPR, NAG, and their cross breed for two generation

Item as an absolute weight (g)	Weights (g) ± SE			
	WPR	NAG	F1	F2
Liver	22.84±0.61[a]	15.35±0.80[c]	19.54±1.14[ab]	18.71±0.21[b]
Gizzard	15.05±0.45[a]	10.93±0.60[b]	13.18±0.85[ab]	14.76±0.15[a]
AF	5.19±0.26[a]	2.92±0.35[b]	5.08±0.50[a]	3.24±0.09[b]
VF	5.54±0.23[a]	2.87±0.32[b]	4.86±0.45[a]	3.35±0.08[b]
SF	5.91±0.25[a]	3.44±0.34[b]	5.70±0.48[a]	3.78±0.09[b]
Total fat weight	16.47±0.68[a]	8.07±0.92[b]	16.52±1.31[a]	10.33±0.24[b]
Total fat weight%	0.02±0.09[b]	0.01±0.12[b]	0.02±0.17[b]	1.80±0.03[a]
Average pectoralis minor	18.15±0.50[a]	10.91±0.67[b]	16.86±0.95[a]	11.84±0.17[b]
Average pectoralis major	63.57±1.61[a]	39.45±2.17[b]	56.97±3.07[a]	43.35±0.56[b]
Total breast muscles	83.53±2.07[a]	50.39±2.79[c]	69.04±3.95[b]	54.89±0.72[c]
Item as a percent from slaughter weight	**Weights (%) ± SE**			
Liver%	10.12±0.12[b]	10.09±0.16[ab]	10.04±0.23[ab]	10.50±0.04[a]
Gizzard%	8.21±0.16[b]	8.53±0.21[b]	8.39±0.30[b]	9.33±0.05[a]
AF%	4.64±0.13[a]	4.30±0.18[ab]	5.03±0.25[a]	4.27±0.04[b]
VF%	4.83±0.12[a]	4.23±0.17[b]	4.99±0.24[ab]	4.37±0.04[b]
SF%	5.0±0.12[a]	4.70±0.16[ab]	5.34±0.23[a]	4.65±0.04[b]
Total fat weight%	8.37±0.20[a]	7.13±0.27[b]	9.23±0.39[a]	7.70±0.07[b]
Average pectoralis minor%	8.96±0.09[a]	8.42±0.13[b]	9.25±0.18[a]	8.32±0.03[b]
Average pectoralis major%	16.94±0.16[a]	16.04±0.2٢[b]	17.62±0.31[a]	16.07±0.05[b]
Total breast muscles%	19.54±0.18[a]	18.21±0.25[b]	19.04±0.35[ab]	18.15±0.06[b]

AF = abdominal fat VF = ventriculous fat SF = subcutaneous fat
a-c means carrying different superscripts in the same raw were significantly different (P<0.05)

Table 3. Some biochemical measurements in WPR, NAG and their cross breed for two generation

Item	Means (mg/dl) ± SE			
	WPR	NAG	F1	F2
Liver TG	8.57±0.63[a]	4.48±0.90[b]	9.96±1.27[a]	5.89±0.22[b]
Liver TC	2.95±0.05[a]	2.97±0.07[a]	2.92±0.10[ab]	2.67±0.02[b]
Serum TG	39.41±1.94	38.24±2.62	34.65±3.96	37.25±0.68
Serum TC	136.50±3.51[b]	153.56±4.73[a]	140.48±7.16[a]	131.62±1.23[b]
Serum HDL	128.44±3.86[ab]	115.01±5.19[b]	128.65±7.86[ab]	133.62±1.35[a]
Serum glu	188.49±3.29[b]	187.45±4.43[b]	201.13±6.70[ab]	207.58±1.15[a]

a-c means carrying different superscripts in the same raw were significantly different (P<0.05)
TG= triglycerides TC= total cholesterol HDL= high density lipoproteins. glu= glucose

conditions adjusted to 14 hours light and 10 hours dark through the remaining period of rearing. All the chicks have free access to tap water and feed. One week before dissection, the chicks were transferred to separate cages and feed intake was recorded individually. The eggs and the chicks were kept at the chicken housing facility at Graduate School of Bio Agricultural Sciences, Nagoya University, Japan.

2.2. Growth performance and carcass traits measurements

Average body weight of chicks was determined at 0 day (initial weight) and then weekly until the end of the experiment. The gain in body weight was calculated weekly by finding the difference in weight between two successive weights. Feed intake was measured from 3rd week till 4th week of age and Feed conversion ratio was also calculated for the same period by dividing feed intake on the bird weight gain though this period (3-4 weeks). A total of 292 birds from all groups (29 WPR, 16 NAG, 8 F1 and 239 for F2 generation) were weighed and slaughtered at 4 weeks of age, after fastening for 2-3 hours before dissection then anesthetized by isoflurane and dissected. The absolute weights of abdominal fat inside the peritoneal cavity (AF), Ventriculus fat surrounding the gizzard (VF), subcutaneous fat surrounding neck (SF) and total fat were measured and were expressed as a percentage of body weight at slaughter. In addition, to the liver (the site of lipogenesis) and the gizzard weights were also recorded. Pectoralis minor and major from the left and the right sides of breast muscle and the total breast muscle weight were recorded and were expressed as a percentage from body weight.

2.3. Biochemical Assays

At 4 weeks of age and just before dissection, fresh blood samples from wing vein (without anticoagulant) were kept for serum separation and analysis of triglycerides (TG), total cholesterol (TC), high density lipoprotein (HDL) and glucose in serum. Serum TG and TC measured using triglyceride E-test Wako and cholesterol E-test Wako, respectively. Serum HDL measured by HDL cholesterol E-test wako and serum glucose measured by Auto kit glucose (Wako Pure Chemical Industries Ltd., Osaka, Japan). In addition, liver samples were kept for analysis of TG and TC in liver using Folch's method, (Folch et al., 1957) by triglyceride E-test Wako and cholesterol E-test Wako (Wako Pure Chemical Industries Ltd., Osaka, Japan), respectively.

2.4. Statistical analysis

Raw data was analyzed by using the JMP Pro software version 13.2.0 *(SAS Institute Japan Ltd., Tokyo, Japan*). The effects of two environmental factors including sex and hatching date on the different phenotypes were tested using a linear model of the JMP software. The hatching date treated as random effect while the sex treated as fixed one. Then data were fitted into final mixed model containing hatching date as random effect and sex as a fixed effect for explanation the effect of those variables on the dependent variables and correction of the effects showing significance at 5% level. The fitted data were finally analyzed by one-way analysis of variance (ANOVA) test using JMP software to study the effect of the 4 groups on the traits under investigation followed by Tukey's honestly significant difference (HSD) post hoc test to compare means among groups. Pearson's correlation analysis carried out to examine the relationship between the growth and carcass traits and biochemical levels detected among the two parental strains, their F1 and F2.

3. Results

3. 1. Growth traits

The ANOVA results for body weight analysis represented in table (1). There was no significant difference was observed between WPR and NAG breed, but both breeds had significantly higher hatch weight compared to F2 generation. Successive body weights (BW1, BW2 and BW3) were significantly differed among all groups; WPR showed the highest body weight means on the other hand, NAG breed revealed the lowest means in body weights. In general, the phenotype (high body weights in WPR) was deteriorated after crossing from generation to another toward the light body weight of NAG chicken. Regarding to body weight gain 0-1 (WG1), WPR significantly differed from F2 generation which showed significant difference compared to NAG. Body weight gain within 1-2 weeks (WG2) and feed intake, had no significant differences between WPR and F1 OR F1 and F2 generation while all of them showed significant differences compared to NAG breed. In addition, WPR was found to be significantly different from F2 generation. While, body weight gain at 2-3 (WG3), had no obvious differences between F1 and F2 generations while, both of them were significantly different from NAG chicken. Nevertheless, WPR had the highest significant weight gain at this period (2-3 week). For body weight gain at WG4 (3-4 week), there were no statistical differences were observed between WPR and F1 generation or between F2 generation and NAG birds. Moreover, WPR and F1 were significantly different from both F2 and NAG. The analysis of body weight gain for 0-4 period showed that, there was no statistical difference between F2 generation and NAG breed in contrast; there was significant difference between WPR and both groups. Lastly for FCR, the results revealed that, no significant difference could be observed between any pairs of groups except between NAG breed and F2 generation of crossing.

3.2. Carcass traits and fat deposition

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The results of carcass traits were summarized (Table 2). The results showed that regarding to the absolute liver weight the WPR was non-statistically different with the F2 generation, but it was the highest significantly than NAG and F2 generation (22.84±0.61, 15.35±0.35 and 18.71±0.21 respectively), while by comparing liver weight percentage the difference was significant only between WPR and F2 generation in liver weight percentage (10.12% VS 10.50%). the F2 generation was differed significantly in gizzard weight percentage (9.33%) compared to the other groups (WPR, NAG and F1 generation). By comparing of absolute fat weights (g) the result showed that WPR breed and its F1 crossbred had the highest fat weight in all different parts of carcass (AF 5.19 and 5.08, VF5.54 and 4.86, SF 5.91and 5.70 and total fat 16.47and 16.52g for WPR and F1 crossbred, respectively) and then this effect is disappeared in the F2 generation (F2 generation and NAG breed were being non-significant). AF %, VF %, SF % and total fat weight percent between the four groups, were in general following the same trend of absolute fat weights especially in VF% and total fat % (VF 4.83% and 4.99% total fat percentage 8.37% and 9.23% for WPR and F1 generation, respectively).

The results of ANOVA test for breast muscles weights and percentages were represented in tables (2). For average weight of pectoralis minor and major muscles, there was no significant difference between F2 and NAG. Although there was no difference observed between WPR and F1 generation, both of them were significantly differed from the other two groups. The analysis total breast muscles weight showed no difference between F2 and NAG while WPR showed significant differences when compared to all groups. For average pectoralis minor % and average pectoralis major%, both F1 and WPR different significantly from NAG and F2 with no difference could be observed between F1 and WPR or between NAG and F2. Moreover, WPR found to be significantly different from NAG and F2 when comparing the percentage of total breast muscles. Generally, the breast muscles and its parts follow the same trend of the fat deposition between all groups either in its absolute weigh or its percentage to the slaughter weight measurements.

3. 3. Biochemical analyses

The results of ANOVA test for different biochemical parameters in serum and liver were summarized in table (3). For liver TG, both WPR and F1 were significantly different from NAG and F2 with no difference observed between both or between NAG and F2. The results of liver TC analysis indicated differences between both WPR and NAG comparing to F2 with no further significances could be reported between the groups. The analysis of serum TG showed no differences between any of the groups under investigation with F ratio equal 0.56. For serum TC, only NAG showed significant difference when compared to WPR and F2. Concerning serum HDL, only F2 was significantly different from NAG with no differences observed between any of the remaining groups. For serum GLU, no differences reported between WPR, NAG and F1 or between F1 and F2. Only F2 were found to be significantly different from NAG and WPR.

3. 4. Relationships between growth parameters, body fatness and different biochemical assays

According to Pearson's correlation coefficient computed between different pairs of traits in all groups (WPR, Nag and their F1and F2 generations) some traits affects the biochemical parameters detected in liver and serum positively while the other had negative effects. The results of Pearson's correlation analysis in WPR were represented in table (4) which showed only WG4 correlated negatively with levels of glucose in serum. According to the results of correlation analysis carried out for NAG which summarized in table (5), BW1, BW2, WG1, total fat, VF% and total fat% responsible for increased liver TG. However, BW4, WG1, WG4, AF and VF cause reduction of liver TC. Similarly, WG4 cause reduction of serum TC. On the other hand, BW3 and BW4 were found to be correlated positively with serum HDL.

The results of F1 correlation analysis were summarized in table (6) which showed that, the level of liver TG correlated negatively with different fat content, total fat content, AF% and SF%. Serum HDL was found to have negative correlation with BW3, WG2 and WG3 while BW1 reduced serum glucose levels. F2 results presented in table (7), liver TG only affected with hatching weight while there were positive correlations between liver TC and BW1, BW2, WG2 and AF. Moreover, AF and AF% were found to be negatively correlated with serum TG. Serum TC only had negative correlation with WG4.

4. Discussion

Concerning the growth traits, *White Plymouth Rock* breed showed an increased in most growth parameters that were represented by its higher body weight and body weight gain at all ages and periods of ages,

Table 4. Pearson's correlation analysis between different biochemical parameters and body weight and fatness traits in *White Plymouth Rock* breed

Parameter	Liver TG	Liver TC	Serum TG	Serum TC	Serum HDL	Serum GLU
BW 0	-0.05	-0.04	0.11	0.01	0.11	-0.15
BW 7d	0.12	0.05	0.32	-0.17	0.05	0.21
BW 14d	-0.04	0.22	0.01	-0.12	-0.07	0.04
BW 21d	-0.01	-0.15	0.29	-0.32	0.09	-0.04
BW 28d	0.06	-0.23	0.21	-0.15	0.34	-0.34
WG1	0.17	0.15	0.29	-0.27	-0.02	0.17
WG2	-0.08	0.22	-0.21	0.14	-0.07	-0.10
WG3	0.01	-0.30	0.26	-0.20	0.10	-0.09
WG4	0.03	-0.19	0.03	-0.25	0.20	-0.39*
WG total	0.09	0.10	0.16	0.17	-0.02	-0.11
Feed Intake 3-4 week	0.16	0.02	0.36	-0.09	0.27	0.01
FCR 3-4 w	0.02	0.26	0.17	-0.14	-0.10	0.24
Liver	0.17	-0.30	0.17	0.03	0.43	-0.09
Gizzard	-0.20	-0.04	-0.33	0.09	0.12	-0.31
AF	0.00	-0.06	-0.09	-0.12	0.40*	-0.16
VF	0.08	0.06	-0.03	-0.04	0.35	0.09
SF	-0.04	-0.03	-0.08	-0.14	0.30	-0.07
Total fat	-0.14	0.05	-0.11	-0.12	0.30	-0.04
Total PM minor	0.09	-0.24	0.04	-0.21	0.45	-0.41
Total PM major	0.14	-0.17	0.12	-0.20	0.39	-0.23
Total breast muscles	0.07	-0.19	0.04	-0.19	0.36	-0.32
Liver TG	1.00	-0.31	0.34	0.00	0.30	0.03
Liver TC	-0.31	1.00	-0.27	-0.08	-0.43	0.15
Serum TG	0.34	-0.27	1.00	-0.39	0.07	0.36
Serum TC	0.00	-0.08	-0.39	1.00	0.30	0.13
Serum HDL	0.30	-0.43	0.07	0.30	1.00	-0.06
Serum GLU	0.03	0.15	0.36	0.13	-0.06	1.00

* P<0.05

Table 5. Pearson's correlation analysis between different biochemical parameters and body weight and fatness traits in *Nagoya* breed

Parameter	Liver TG	Liver TC	Serum TG	Serum TC	Serum HDL	Serum GLU
BW 0	0.33	-0.22	-0.24	0.11	0.26	-0.22
BW 7d	0.77**	-0.48	-0.08	-0.48	0.14	0.04
BW 14d	0.60*	-0.42	-0.18	-0.42	0.34	0.04
BW 21d	0.23	-0.33	-0.23	-0.37	0.53*	-0.14
BW 28d	0.33	-0.59*	-0.06	-0.41	0.51*	-0.02
WG1	0.54*	-0.72**	-0.01	-0.39	0.45	0.23
WG2	0.38	-0.33	-0.26	-0.31	0.46	0.05
WG3	0.48	-0.21	0.02	-0.47	0.20	0.02
WG4	0.40	-0.63**	0.10	-0.51*	0.33	0.13
WG total	-0.43	0.20	-0.05	0.27	0.13	-0.09
Feed Intake 3-4 week	0.08	-0.32	-0.19	-0.26	0.19	-0.15
FCR 3-4 w	0.01	-0.07	-0.29	0.10	-0.10	-0.24
Liver	0.46	-0.55	0.08	-0.41	0.43	0.06
Gizzard	0.34	-0.34	0.17	-0.43	0.47	0.12
AF	0.40	-0.57*	-0.11	-0.25	0.16	-0.10
VF	0.53	-0.50*	-0.09	-0.48	0.25	-0.17
SF	0.47	-0.43	-0.13	-0.17	0.20	-0.27
Total fat	0.54*	-0.42	0.07	-0.46	0.37	0.21
Total PM minor	0.42	-0.56	-0.26	-0.35	0.42	-0.07
Total PM major	0.48	-0.43	-0.19	-0.51	0.27	-0.06
Total breast muscles	0.50	-0.43	-0.19	-0.51	0.27	-0.06
Liver TG	1.00	-0.32	0.08	-0.38	-0.04	-0.13
Liver TC	-0.32	1.00	0.26	0.18	-0.13	-0.05
Serum TG	0.08	0.26	1.00	-0.15	-0.04	0.53
Serum TC	-0.38	0.18	-0.15	1.00	0.07	-0.03
Serum HDL	-0.04	-0.13	-0.04	0.07	1.00	0.16
Serum GLU	-0.13	-0.05	0.53	-0.03	0.16	1.00

** P< 0.01 * P<0.05

Table 6. Pearson's correlation analysis between different biochemical parameters and body weight and fatness traits in F1generation

Parameter	Liver TG	Liver TC	Serum TG	Serum TC	Serum HDL	Serum GLU
BW 0	0.00	0.00	0.00	0.00	0.00	0.00
BW 7d	0.34	0.26	0.40	-0.09	0.33	-0.44
BW 14d	0.00	0.43	-0.03	-0.33	-0.58	-0.84*
BW 21d	-0.52	0.08	-0.20	-0.23	-0.82*	-0.60
BW 28d	-0.35	-0.04	-0.39	-0.07	-0.66	-0.44
WG1	0.00	0.00	0.00	0.00	0.00	0.00
WG2	-0.21	0.40	-0.25	-0.33	-0.85*	-0.72
WG3	-0.33	-0.02	-0.23	-0.16	-0.77*	-0.41
WG4	-0.28	0.34	-0.18	-0.54	-0.75	-0.60
WG total	0.00	0.00	0.00	0.00	0.00	0.00
Feed Intake 3-4 week	-0.75	0.34	-0.62	-0.11	-0.55	-0.54
FCR 3-4 w	-0.01	0.11	0.15	0.02	-0.09	-0.11
Liver	-0.33	-0.13	-0.50	0.06	-0.48	-0.26
Gizzard	0.01	-0.60	0.41	-0.11	0.21	-0.33
AF	-0.91**	0.15	-0.61	-0.12	-0.64	-0.55
VF	-0.92**	0.08	-0.59	-0.33	-0.70	-0.41
SF	-0.89**	0.02	-0.70	-0.27	-0.74	-0.16
Total fat	-0.76*	-0.13	-0.71	0.02	-0.40	-0.14
Total PM minor	-0.46	-0.11	-0.63	-0.03	-0.42	0.46
Total PM major	-0.48	0.56	0.01	-0.43	-0.51	-0.89
Total breast muscles	-0.29	-0.05	-0.45	-0.04	-0.62	-0.20
Liver TG	1.00	-0.19	0.50	0.73	0.78	0.50
Liver TC	-0.19	1.00	-0.13	-0.26	-0.37	-0.43
Serum TG	0.50	-0.13	1.00	-0.45	0.33	-0.21
Serum TC	0.73	-0.26	-0.45	1.00	0.56	0.57
Serum HDL	0.78	-0.37	0.33	0.56	1.00	0.59
Serum GLU	0.50	-0.43	-0.21	0.57	0.59	1.00

** P< 0.01 * P<0.05

Table 7. Pearson's correlation analysis between the different biochemical parameters and body weight and fatness traits in F2 generation

Parameter	Liver TG	Liver TC	Serum TG	Serum TC	Serum HDL	Serum GLU
BW 0	-0.21	0.04	-0.07	-0.02	0.09	-0.04
BW 7d	0.05	0.13*	0.05	0.05	0.00	-0.01
BW 14d	0.05	0.20**	0.00	0.03	-0.04	0.04
BW 21d	0.08	0.06	-0.03	0.04	-0.03	-0.01
BW 28d	-0.04	0.04	-0.08	-0.05	-0.10	-0.09
WG1	0.11	0.11	0.07	0.05	-0.03	0.00
WG2	0.04	0.15*	0.01	0.04	-0.04	0.06
WG3	0.03	-0.03	-0.08	0.02	-0.04	-0.06
WG4	-0.11	-0.01	-0.07	-0.15*	-0.10	-0.08
WG total	-0.06	0.06	-0.04	-0.03	-0.10	-0.08
Feed Intake 3-4 week	-0.05	0.00	0.02	-0.02	-0.04	-0.18
FCR 3-4 w	-0.02	0.05	-0.05	0.06	0.12	0.07
Liver	0.17	-0.09	0.18	0.14	0.04	0.03
Gizzard	-0.01	0.01	-0.05	-0.01	0.00	0.07
AF	0.01	0.15*	-0.16*	-0.01	0.00	-0.03
VF	-0.06	0.05	-0.06	0.01	0.00	-0.04
SF	0.00	0.00	-0.07	-0.02	0.01	-0.12
Total fat	-0.01	0.07	-0.10	0.00	0.00	-0.10
Total PM minor	-0.07	0.08	-0.17	-0.04	-0.10	-0.11
Total PM major	-0.05	0.10	-0.14	-0.08	-0.12	-0.12
Total breast muscles	-0.03	0.12	-0.13	-0.06	-0.11	-0.11
Liver TG	1.00	-0.17	0.29	0.10	-0.04	0.12
Liver TC	-0.17	1.00	-0.09	-0.14	0.05	-0.06
Serum TG	0.29	-0.09	1.00	0.16	-0.03	0.09
Serum TC	0.10	-0.14	0.16	1.00	0.34	0.04
Serum HDL	-0.04	0.05	-0.03	0.34	1.00	0.01
Serum GLU	0.12	-0.06	0.09	0.04	0.01	1.00

** P< 0.01 * P<0.05

in addition to its feed intake and FCR excess fat disposition at various areas of the body and larger breast muscle weight compared to *Nagoya* breed, (Sae et al., 2018) also, reported differences related to body weight at 49 days of age between *Nagoya*, *White Plymouth Rock* and *White Cornish*. Van Kaam et al. (1998, 1999a, b) used a population derived from a cross of two broiler dam lines which showed characteristic differences in growth for scanning the whole chicken genome for QTL controlling body weight, feed intake, growth, and other carcass related traits.

Similarly, (Tatsuda and Fujinaka, 2001a; Tatsuda & Fujinaka, 2001b) used two breeds, *Satsumadori*, native Japanese breed with inferior body weight and low fat content and WPR which showed liability for abdominal fat deposition with significant body weight gain as Parental breeds for QTL analysis affecting body weight and abdominal fat deposition. Nevertheless, since broilers are heavier and fatter than layer at the same age with 3 times increase in the abdominal fat content.

Concerning the carcass traits and fat deposition, *White Plymouth Rock* breed showed marked growth and higher percentage of pectoral muscles which came in agreement to results obtained by Sae et al., (2018). Nagoya breed was the lower in liver and gizzard weights and their percentage of the slaughter weight compared with WPR chicken these results were not agreed with that obtained by Sae et al., (2018). This variation may be caused by the differences in the rearing seasons and the complex nature of fatness which difficult to be dissected and mainly caused by interaction between genetic factors with environment and knowledge about it is still incomplete (Arner, 2000; Jennen, 2004).

Concerning the biochemical analyses, the levels of different biochemical indices results showed no significant differences regarding to serum TG which came in agreement with results obtained by Sae et al., 2018. On the other side, serum TC was higher in NAG than WPR while SAE et al., 2018 reported no differences between them. Obesity associated with higher levels of TG, lower HDL levels and lower TC levels (Musa et al., 2007).

Regarding to relationship between different biochemical levels and fat content our results showed that, in NAG breed AF correlated negatively with liver TC while there was positive correlation between total fat and liver TG while, Musa et al., (2007) found that in leaner chickens the abdominal fat correlated positively with different biochemical parameters in serum as TC and TG. Nevertheless, Musa et al., (2006) also reported that in lean chicken abdominal fat positively correlated with cholesterol. This variation may be attributed to the fact that fatness is complex trait difficult to be dissected and mainly caused by interaction between genetic factors with environment and knowledge about it is still incomplete (Arner, 2000; Jennen, 2004).

5. Conclusion

These results showed marked differences between the two breeds NAG and WPR and tracking the depletion of these traits in two generations concerning growth and fat deposition. In addition to the relationship between increasing body weight and fat deposition was established. Thus, future QTL analysis can be performed for identification of chromosomal regions controlling growth and fatness traits and subsequently candidate gene influencing these traits could be revealed in further investigations.

Competing Interests

The authors have no conflict of interest.

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