Research Journal of Poultry Sciences 3 (1): 5-10, 2010
ISSN: 1993-5285

Correlations Between Microsatellite Loci and Growth and Carcass Traits in Chinese Silkies

[1]Yao Dong Hu, [1, 2]Y. Zhou, [2]Xin Hua Liu and [1]Qing Zhu
[1]Laboratory of Animal Genetics and Breeding, College of Animal Science and Technology,
Sichuan Agricultural University, Ya'an, Sichuan, 625014, China
[2]Poultry Institute of Shandong Academy of Agricultural Science, Jinan, 250023, China

Abstract: In this study, we investigated the correlations between microsatellite DNA polymorphic loci and growth and carcass traits in Chinese Silkies (*Gallus gallus*) to find possible candidate loci for marker-assisted selection. A total of 240 birds were scored for allele size at 18 microsatellite loci which were offspring of a dam line of Silkies specialized for production performances and a sire line of Silkies for growth performances. Totally, 123 alleles were detected from these polymorphic loci, with a range of 5-8 alleles and an average of 6.83 per locus. The frequencies of the 123 alleles ranged from 0.0532-0.4035. The average value of Polymorphism Information Content (PIC) was 0.805, ranging from 0.707-0.855. The average observed heterozygosity and the average expected heterozygosity of 18 markers was 0.244 and 0.833, respectively. Seven microsatellite loci were found to be correlated with seven growth traits and four carcass traits ($p<0.01$ or $p<0.05$). Allele 113 in MCW0254, allele 270 in LEI0146 and allele 172 in MCW0154 may be regarded as three candidate-loci for growth and carcass traits of Silkies.

Key words: Chicken, carcass and growth traits, correlation, microsatellite loci, polymorphism

INTRODUCTION

With traditional selection, great progress has been made in many economically important traits of animals including growth, body composition and feed efficiency over the last 50 years. But some traits such as carcass traits were not routinely directly measured on living body and that blocked the selective advance of them. The development of molecular genetics made it possible to uncovering the genetic basis of these traits. Previous studies have indicated that genetic markers affecting quantitative traits can increase the selection response of animal breeding programs, especially for traits that are difficult to improve when using traditional selection (Lande and Thompson, 1990; Sewalem *et al*., 2002). So, the marker-assisted selection based on microsatellite DNA polymorphism, RAPD, RFLP, AFLP benefited the animal breeding program.

Silkies (*Gallus gallus*) is one of the standard poultry varieties in China and is characterized by the global distribution of melanin in the skin, muscle and entrails, so they are also, named Black-bone Chicken in China. One special trait of Silkies is its unique medical property, which was recorded in Chinese traditional medical dictionary about 700 years ago. It was reported that the meat quality traits of Silkies are better than both broiler and other Chinese local chicken populations (Zhang *et al*., 1997; Li and Chen, 2004).

Unfortunately, Silkies grow rather slowly and have a poor production performance, so many breeders were marking efforts in improving the growth and production performances of this valuable poultry breed. The identification of DNA molecular markers and the development of marker-assisted selection would provide an effective approach.

QTLs for growth and carcass traits have been found on chromosomes one and Z (Van Kaam *et al*., 1999a, b; Sewalem *et al*., 2002; Liu *et al*., 2007). In this study, we were interested in identifying and confirming microsatellite DNA markers affecting growth and carcass traits in these two chromosomes in Silkies. We investigated the genetic diversity and distribution of microsatellite marker alleles and analyzed the correlations of these molecular markers with growth and carcass traits.

This study may provide valuable theoretical basis for marker-assisted selection to improve the growth and carcass performances in Silkies.

Corresponding Author: Qing Zhu, Laboratory of Animal Genetic and Breeding, College of Animal Science and Technology, Sichuan Agricultural University, Ya'an, Sichuan, 625014, China

MATERIALS AND METHODS

Experiment birds: Totally, 240 birds were used, which were offspring of a dam line of Silkies specialized for production performances and a sire line of Silkies specialized for growth performances in Huangzhong Breeding Farm, Chengdu, China. All the experiment chickens had free access to feed and water. Data were collected from the offspring only. The body weight was measured biweekly from birth (BW0) to 14 weekss of age. A blood sample of 2.5-5 mL was collected from the wing vein of each bird at 14 weeks. DNA was extracted from these blood samples by standard phenol/chloroform method and then Live body Weight (LW) was measured on live birds after 12 h with no access to feed. After slaughter at the same day of age, the carcass traits were measured, including Eviscerated Weight (EW), Semi-Eviscerated Weight (SEW), Breast Muscle Weight (BMW), Leg Muscle Weight (LMW). Semi-eviscerated weight was measured on the carcass after removal of the trachea, oesophagus, gastrointestinal tract, spleen, pancreas and gonad. Eviscerated weight was measured on the semi-eviscerated weight after removal of the head, claws, heart, liver, gizzard, glandular stomach and abdominal fat. All the experiments complied with the requirements of the Directory Proposals on the Ethical Treatment of Experimental Animals of China.

PCR primers: According to the genetic linkage maps of the three chicken reference populations (www.thearkdb.org), 18 microsatellite markers were selected from chromosomes 1 and Z. The 5'-terminus of each locus was labeled with either 6-FAM or 6-HEX fluorescent dye (Shanghai Sangon Biological Engineering Technology and Services Co., Shanghai, China). The details of the 18 microsatellite loci are presented in Table 1.

Table 1: The details of 18 microsatellite loci in chicken

Locus	Chromosome	Position (cM)	5'-terminal labeling
LEI0106	1	Unknown	6-HEX
MCW0168	1	0	6-FAM
MCW0208	1	38	6-FAM
MCW0254	1	57	6-FAM
MCW0289E	1	119	6-HEX
LEI0146	1	136	6-HEX
MCW0112	1	172	6-FAM
MCW0068	1	256	6-FAM
MCW0313	1	271	6-HEX
MCW0200	1	300	6-HEX
MCW0036	1	356	6-FAM
MCW0177	1	415.6	6-HEX
LEI0134	1	504.9	6-FAM
MCW0331	Z	19.6	6-FAM
MCW0258	Z	42	6-HEX
MCW0154	Z	101.9	6-FAM
MCW0294	Z	108.3	6-FAM
MCW0128	Z	164.1	6-HEX

Detection of PCR products: The PCR reactions for all microsatellite markers were performed separately in a total reaction volume of 20 μL, containing 3.0 μM MgCl$_2$, 200 μM dNTP, 1U Taq polymerase and 5 pmol of each primer and 100 ng Silkies genomic DNA. The PCR was performed at 94°C for 10 min, then 35 cycles of 30 sec at 94°C, 45 sec at 55°C and 90 sec at 72°C, followed by a final elongation step of 10 min at 72°C.

The mixture composed by 3 μL PCR product, 11.4 μL Hi-Di formamide and 0.6 μL Genescan-500 ROXTM internal size standard (Applied Biosystems, CA, USA) was analyzed using an ABI 3100-Avant Genetic Analyzer (Applied Biosystems). Fragment sizes were calculated relative to the Genescan-500 ROXTM internal size standard by using the Genescan 3.7 fragment analysis software (Applied Biosystems) and Genotype 3.7 software (Applied Biosystems). The polymorphism of every microsatellite locus, polymorphism information content (Botstein *et al.*, 1980) and heterozygosity (Nei and Roychoudhury, 1974) were analyzed using Cervus 2.0 software (University of Edinburgh, UK).

Statistical analysis: The General Linear Models (GLM) procedure of SAS software package was used to evaluate the correlation between the polymorphic markers and growth and carcass traits. The following is the linear model:

$$Y = \mu + G + S +(S\times G) + bX +e$$

Where:

Y = The phenotypic value
μ = The population mean
G = The fixed effect of genotype
S = The fixed effect of sex
$S\times G$ = The interaction between the genotype or sex
X = Carcass weight (covariance)
b = Coefficient of regression
e = Random error

The interaction G by S was included in the model if its effect was ($p<0.05$) for a given trait, otherwise, they were excluded from the final model. Finally, Duncan's Multiple Range Test was used to analyze the difference between different genotypes of each locus which had a significant correlation with the trait ($p<0.01$ or $p<0.05$).

The data of some carcass traits were not normally distributed. The Body weight of Hatch, 2, 4, 6, 8, 10, 12 and 14 weeks, SEW, EW, BMW and LMW were analyzed as the linear model with parameters estimated on the Square Root scale.

RESULTS AND DISCUSSION

Genetic variation: The genetic parameters of 18 microsatellite loci including total allele number, observed

Table 2: Genetic polymorphism of 18 microsatellite loci in silkies

Loci	Alleles (bp) and frequencies	K[1]	H(O)[2]	H(E)[3]	PIC[4]
LEI0106	285(0.1000) 289(0.0867) 291(0.1867) 293(0.1000) 295(0.1400) 297(0.1600) 301(0.1200) 309(0.1066)	8	0.347	0.872	0.852
MCW0168	101(0.1882) 107(0.2941) 109(0.2176) 111(0.1118) 113(0.1118) 119(0.0765)	6	0.094	0.805	0.771
MCW0208	202(0.1436) 210(0.1436) 216(0.0798) 218(0.1223) 220(0.1649) 222(0.1117) 224(0.1330) 228(0.1011)	8	0.362	0.875	0.855
MCW0254	103(0.1333) 107(0.1278) 109(0.1278) 111(0.3056) 113(0.1167) 115(0.0944) 117(0.0944)	7	0.111	0.829	0.804
MCW0289E	210(0.0532) 212(0.2074) 214(0.1702) 218(0.1011) 220(0.0958) 222(0.0638) 224(0.0904) 226(0.2181)	8	0.511	0.850	0.827
LEI0146	252(0.3493) 254(0.0685) 256(0.1712) 262(0.1644) 270(0.0685) 288(0.1781)	6	0.178	0.786	0.750
MCW0112	267(0.2900) 269(0.1500) 271(0.1600) 273(0.2000) 277(0.2000)	5	0.140	0.796	0.754
MCW0068	164(0.1818) 168(0.1875) 174(0.1648) 176(0.1023) 182(0.1761) 184(0.0795) 192(0.1080)	7	0.352	0.850	0.826
MCW0313	200(0.0690) 226(0.1379) 234(0.2241) 236(0.1121) 246(0.2155) 250(0.1293) 256(0.1121)	7	0.138	0.845	0.817
MCW0200	229(0.1037) 233(0.1463) 235(0.0976) 237(0.1341) 241(0.1768) 247(0.1159) 249(0.0854) 253(0.1402)	8	0.268	0.874	0.854
MCW0036	155(0.1220) 159(0.1098) 161(0.2195) 165(0.2805) 167(0.2683)	5	0.037	0.779	0.737
MCW0177	290(0.1908) 292(0.0724) 294(0.0855) 298(0.1776) 304(0.1645) 310(0.1184) 314(0.1908)	7	0.211	0.848	0.822
LEI0134	292(0.0571) 294(0.2000) 296(0.1071) 298(0.2214) 300(0.1571) 310(0.1357)314(0.1214)	7	0.271	0.844	0.818
MCW0331	200(0.1061) 202(0.1061) 206(0.0859) 210(0.1414) 212(0.2677) 214(0.1414) 218(0.1515)	7	0.313	0.840	0.815
MCW0258	135(0.0728) 141(0.1505) 145(0.1456) 149(0.0680) 151(0.1699) 157(0.0720) 161(0.0971) 163(0.1748)	8	0.369	0.867	0.847
MCW0154	160(0.2222) 162(0.1056) 166(0.1722) 168(0.1333) 172(0.1056) 176(0.2611)	6	0.300	0.817	0.786
MCW0294	294(0.1228) 300(0.1579) 310(0.4035) 314(0.1140) 316(0.2018)	5	0.105	0.750	0.707
MCW0128	158(0.0691) 164(0.0851) 166(0.1330) 168(0.1383) 170(0.1117) 172(0.1702) 174(0.1277) 176(0.1649)	8	0.287	0.871	0.851
Average		6.83	0.244	0.833	0.805

[1]K: Total allele number; [2]H (O): Observed Heterozygosity; [3]H (E): Expected Heterozygosity, [4] PIC: Polymorphism Information Content

Table 3: Correlations among microsatellite loci and growth traits and carcass traits in silkies

	BW[1] (week of age)								Carcass traits[5] (g)			
Loci	0	2	4	6	8	10	12	14	SEW	EW	BMW	LMW
MCW0254	**[2]	-[3]	**	*[4]	-	-	-	-	-	-	*	**
MCW0154	-	-	-	-	-	-	*	*	-	*	-	-
LEI0134	-	-	-	-	-	-	*	*	*	*	*	*
LEI0106	**	-	-	-	-	*	-	-	-	-	-	-
LEI0146	-	-	-	-	**	-	-	-	**	**	-	-
MCW0177	-	-	**	-	*	-	-	-	-	-	-	-
MCW0112	*	-	*	-	-	-	-	-	-	-	-	-

[1]BW: Body Weight, [2]**: A very significant correlation ($p<0.01$), [3]-: No significant correlation ($p>0.05$), [4]*: A significant correlation ($p<0.05$), [5]SEW = Semi-Eviscerated Weight, EW = Eviscerated Weight, BMW = Breast Muscle Weight, LMW = Leg Muscle Weight

heterozygosity, expected heterozygosity, PIC, alleles and allele frequencies were presented in Table 2. A total of 123 alleles were observed in these loci in 240 birds, with a range of 5-8 alleles and an average of 6.83 alleles per locus. The average PIC was 0.805, the highest PIC was 0.855 of MCW0208 and the lowest PIC was 0.707 of MCW0294. The average expected population heterozygosity and the observed heterozygosity were 0.833 and 0.244, respectively. The results indicated that this Silkies population had a high genetic variation level and a great potential for further selection.

Correlations among microsatellite loci and growth and carcass traits: Significant or very significant correlations were observed among 7 microsatellite loci and 7 growth traits and 4 carcass traits by the GLM procedure (Table 3). Only 2 traits, BW of 6 and 10 weeks had significant correlation with MCW0254 and LEI0106, respectively. The other nine traits had significant correlations with 2 or 3 microsatellite loci. MCW0254 showed multiple significant correlations with BW at Hatch (BW0), 4 and 6 weeks, BMW and LMW. LEI0134 showed multiple significant correlations with BW at 12 and 14 weeks, SEW, EW, BMW and LMW.

Effects of different genotypes within microsatellite loci: The effects of different genotypes within one microsatellite locus which showed significant correlation with a growth or carcass trait were analyzed using Duncan's multiple range test (Table 4 and 5). If no significant differences were observed in some trait between genotypes at one locus, they would not be presented in Table 4 and 5.

From Table 4 and 5, we found that BW at Hatch, 4 and 6 weeks, BMW and LMW of genotypes 113/113 and 107/113 in MCW0254 were higher than that of genotype 107/107 and 107/111. So, allele 113 presented positive effects on growth and carcass traits, while allele 107 presented negative effects on them. About LEI0146, BW at 8 weeks of genotypes 270/270 and 262/270 were higher than that of genotypes 262/262 and 256/262 ($p<0.05$). Allele 270 may have a positive correlation with growth traits, while allele 262 may have a negative correlation with them. As for MCW0154, EW of genotypes 166/172 and 172/172 were higher than that of genotypes 162/162, 160/162 and 162/176. These results of genotype effects indicate that allele 113 in MCW0254, allele 270 in LEI0146 and allele 172 in MCW0154 may be regarded as 3 candidate-loci for growth and carcass traits of Silkies.

Table 4: Effects of different genotypes within each microsatellite locus on growth traits in Silkies

Genotype	N	Mean	Genotype	N	Mean
LEI0106 (BW1 at Hatch)			**LEI0146 (BW at 8W)**		
301/301	21	32.3^{a}	270/270	14	570.7^{a}
285/285	16	29.7^{ab}	262/270	7	560.5^{a}
291/295	20	29.4^{ab}	254/254	14	526.0^{ab}
297/301	20	28.8^{ab}	288/288	43	517.8^{ab}
293/293	16	28.6^{ab}	252/252	78	496.5^{ab}
285/293	16	28.1^{ab}	256/256	27	485.8^{ab}
295/295	20	27.9^{ab}	252/256	20	480.1^{ab}
285/295	8	27.7^{ab}	262/262	30	458.1^{b}
309/309	33	27.5^{ab}	256/262	7	430.7^{b}
297/297	29	27.4^{ab}	**MCW0117 (BW at 4W)**		
289/289	25	27.0^{bc}	294/304	7	260.7^{a}
291/297	8	26.5c	292/298	7	225.2^{ab}
295/301	8	26.5c	314/314	37	214.5^{abc}
MCW0112 (BW at 4W)			310/310	23	212.9^{abc}
267/269	11	250.7^{a}	304/314	7	205.2^{abc}
277/277	48	206.7^{ab}	310/314	7	205.2^{abc}
273/273	48	204.1^{ab}	304/304	33	204.0^{abc}
267/267	64	190.8^{ab}	290/290	43	196.5^{abc}
271/271	37	188.6^{ab}	294/294	13	183.5^{bc}
269/269	32	170.3^{b}	292/292	13	183.1^{bc}
MCW0177 (BW at 8W)			294/298	7	177.2^{bc}
310/314	7	620.2a	298/298	37	173.5^{bc}
294/304	7	604.7^{ab}	290/314	6	151.7^{c}
292/298	7	582.7^{abc}	**MCW0254 (BW at 6W)**		
314/314	37	532.3^{abc}	107/113	6	401.2a
304/304	33	512.5^{abc}	113/113	25	376.6^{ab}
310/310	23	503.2^{abc}	117/117	22	364.0^{ab}
290/290	43	495.7^{abc}	109/111	6	344.2^{ab}
294/298	7	489.2^{abc}	103/103	33	343.0^{ab}
294/294	13	481.7^{bc}	107/111	8	337.1^{ab}
298/298	37	467.9^{c}	115/115	22	332.6^{ab}
304/314	7	467.5^{c}	109/109	27	328.8^{ab}
290/314	6	451.2^{c}	111/111	66	323.4^{ab}
292/292	13	448.8^{c}	107/107	25	303.6^{b}
MCW0254 (BW at Hatch)			**LEI0106 (BW at 10W)**		
115/115	22	30.1^{a}	295/301	8	823.7^{a}
113/113	25	29.7^{ab}	289/289	25	732.8^{ab}
117/117	22	29.6^{ab}	301/301	21	728.8^{ab}
107/113	6	29.5^{ab}	285/295	8	728.0^{ab}
103/103	33	29.4^{ab}	291/295	20	704.8^{ab}
109/109	27	28.6^{ab}	297/297	29	693.0^{ab}
109/111	6	28.6^{ab}	293/293	16	661.0^{ab}
111/111	66	27.1^{bc}	295/295	20	654.4^{ab}
107/111	8	25.1^{c}	297/301	20	645.7^{ab}
107/107	25	25.1^{c}	285/285	16	630.3^{ab}
MCW0254 (BW at 4W)			309/309	33	629.3^{ab}
117/117	22	223.1^{a}	291/297	8	619.7^{b}
113/113	25	221.3^{a}	285/293	16	553.6^{b}
107/113	6	217.5^{ab}			
103/103	33	204.7^{ab}			
109/109	27	202.5^{ab}			
115/115	22	198.0^{ab}			
109/111	6	194.5^{ab}			
111/111	66	191.4^{ab}			
107/111	8	179.3^{bc}			
107/107	25	160.5^{c}			

[1]BW= Body Weight, [2]Means within each microsatellite locus with different superscript differ significantly

Growth and meat yield traits in poultry were under complex genetic control. Uncovering the molecular mechanism of growth will contribute to more efficient selection for growth in broiler chickens.

Thus selecting individuals with additional information about their genotype for markers associated with QTLs for growth and carcass traits (Marker-Assisted Selection, MAS) is preferred (Deeb and Lamont, 2002). In marker-trait linkage analysis, comparing genotypes and phenotypic values, a significant level at 0.01 or 0.05 suggests that microsatellite loci have correlation with the traits. In this study, significant correlations were observed between seven microsatellite loci and eleven traits ($p<0.05$ or $p<0.01$).

Table 5: Effects of different genotypes within each microsatellite locus on carcass traits in silkies

Genotype	N	Mean	Genotype	N	Mean	Genotype	N	Mean
MCW0154 (EW[1])			**MCW0254 (BMW[2])**			**MCW0254 (LMW[3])**		
166/172	9	840.3^{a}	113/113	25	65.1^{a}	113/113	25	91.4^{a}
172/172	22	785.2^{ab}	109/111	6	63.0^{a}	107/113	6	83.7^{ab}
168/168	17	768.4^{ab}	107/113	6	62.7^{a}	109/111	6	76.0^{ab}
160/160	43	759.8^{ab}	109/109	27	57.0^{ab}	109/109	27	73.1^{b}
176/176	46	731.2^{ab}	111/111	66	55.5^{ab}	107/107	25	72.2^{b}
166/176	9	728.3^{ab}	115/115	22	55.1^{ab}	115/115	22	71.8^{b}
168/176	14	728.2^{ab}	103/103	33	54.5^{ab}	111/111	66	69.7^{b}
166/166	34	691.7^{ab}	117/117	22	53.6^{ab}	117/117	22	69.2^{b}
160/176	11	674.9^{ab}	107/107	25	53.1^{ab}	103/103	33	69.1^{b}
162/162	17	622.3^{b}	107/111	8	50.8^{b}	107/111	8	64.8^{b}
160/162	12	605.9^{b}						
162/176	6	602.8^{b}						

[1]EW = Eviscerated Weight, [2]BMW = Breast Muscle Weight, [3]LMW = Leg Muscle Weight, [4]Means within each microsatellite locus with different superscript differ significantly

Many previous studies reported that there were QTL affecting BW and carcass traits on chromosome 1. Van Kaam *et al.* (1999a) found a QTL for BW at 48 days at position 235 cM. Sewalem *et al.* (2002) found that 3 were at least three QTL for Body weight on chromosomes 1 in a Broiler Layer Cross. The first one was a QTL for BW at 3 and 6 weeks at positions 145 cM or 160 cM and the markers related to this QTL were LEI0068, LEI0146 and MCW0018.

In current study, LEI0146 was found significantly correlated with BW at 8 weeks, SEW and EW ($p<0.01$). Nones *et al.* (2006) also reported a QTL affecting BW at 35 and 42 days at 150 cM on the consensus map and the flanking markers were LEI0068 and MCW0097. The second one was a QTL for BW at 3 and 6 weeks at 466 cM or 481 cM (441-526 cM, ADL0183-ROS0025). LEI0134 (at position 504.9 cM) in this study was found correlated with BW at 12 and 14 weeks, SEW, EW, BMW and LMW ($p<0.05$). Van Kaam *et al.* (1999b) also found a QTL for carcass percentage at the same position. Liu *et al.* (2007) located a QTL affecting BW at 4-12 weeks of age near the region. The third one was a QTL for BW at 9 weeks at position 64 cM (MCW0010-ADL0188) or 404 cM (LEI0106-LEI0079). Marker MCW0254 (at position 57cM) located within the region (MCW0010-ADL0188) was found significant correlation with BW at Hatch, 4 and 6 weeks, BMW and LMW in this trial. And also MCW0112 (at position 172cM) was found significant correlations with BW at Hatch and 4 weeks ($p<0.05$) in the current study, one likely candidate genes in this region was insulin-like growth factor-I for its effect on animal growth (Zhou *et al.*, 2005).

About chromosome Z, Hamoen *et al.* (2001) reported that no significant indications were found for the presence of quantitative trait loci affecting growth traits on the Z-chromosome. But, Sewalem *et al.* (2002) detected a QTL affecting BW at 3 weeks at position 98-127 cM (LEI0111-LEI0075). In this trial, MCW0154 at position 101.9 cM was detected significant correlations with BW at 12 and 14 weeks and also EW ($p<0.05$). As a summary, the markers correlated with growth and carcass traits in this current study was in agreement with previous studies (Van Kaam *et al.*, 1999b; Sewalem *et al.*, 2002; Zhou *et al.*, 2005; Nones *et al.*, 2006; Liu *et al.*, 2007).

CONCLUSION

The results of this study indicated that the Silkies population used in this report had high genetic variation and broad diversity for further selection to improve the population's uniformity and growth performance.

The GLM and multiple range test showed that seven microsatellite loci were correlated with seven growth traits and four carcass traits, also, allele 113 in MCW0254, allele 270 in LEI0146 and allele 172 in MCW0154 may be regarded as three candidate-loci for marker-assisted selection for growth and carcass traits of Silkies. These findings would provide important theoretical basis for marker-assisted selection and breeding in the Silkies population. Further studies should be taken to check the possible existence of linkages between these microsatellite loci and their neighboring genes.

ACKNOWLEDGEMENTS

The research was financially supported by the Chinese national key technologies R and D program (Grant No: 2008BADB2B01); the Province Key Technologies R and D Program of Livestock and Poultry Breeding Programs of Sichuan Province (No. 2006-YZGG-19 and 2006-YZGG-25).

REFERENCES

Botstein, D., R.L. White, M. Skolnick and R.W. Davis, 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am. J. Hum. Genet., 32: 314-331. PMID: 1686077. http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=6247908.

Deeb, N. and S.J. Lamont, 2002. Genetic architecture of growth and body composition in unique chicken population. J. Hered, 93: 107-118. PMID: 12140270, http://jhered.oxfordjournals.org/cgi/content/full/93/2/107.

Hamoen, F.F., J.B. Van Kaam, M.A. Groenen, A.L. Vereijken and H. Bovenhuis, 2001. Detection of genes on the Z-chromosome affecting growth and feathering in broilers. Poult. Sci., 80 (5): 527-534. PMID: 11372699. http://ps.fass.org/cgi/reprint/80/5/527.

Lande, R. and R. Thompson, 1990. Efficiency of marker-assisted selection in the improvement of quantitative traits. Genetics, 124 (3): 743-756. PMID: 1968875. http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=1968875.

Li, H.F. and K.W. Chen, 2004. Comparison of inosinic acid and fatty acid contents of muscle in different chicken. J. Yangzhou Univ. Agric. Life Sci. Edn., 25: 9-11 (in Chinese).

Liu, X., H. Li, S. Wang, X. Hu, Y. Gao, Q. Wang, N. Li, Y. Wang and H. Zhang, 2007. Mapping quantitative trait loci affecting body weight and abdominal fat weight on chicken chromosome 1. Poult. Sci., 86: 1084-1089. PMID: 17495077. http://ps.fass.org/cgi/content/full/86/6/1084.

Nei, M. and A.K. Roychoudhury, 1974. Sampling variances of heterozygosity and genetic distance. Genetics, 76: 379-390. PMID: 4822472. http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=4822472.

Nones, K., M.C. Ledur, D.C. Ruy, E.E. Baron, C.M.R. Melo, A.S.A.M.T. Moura, E.L. Zanella, D.W. Burt and L.L. Coutinho, 2006. Mapping QTLs on chicken chromosome 1 for performance and carcass traits in a broiler x layer cross. Anim. Genet., 37: 95-100. PMID: 16573522. http://www3.interscience.wiley.com/journal/118596162/abstract?CRETRY=1&SRETRY=0.

Sewalem, A., D.M. Morrice, A. Law, D. Windsor, C.S. Haley, C.O. Ikeobi, D.W. Burt and P.M. Hocking, 2002. Mapping of quantitative trait loci for body weight at 3, 6 and 9 weeks of age in a broiler layer cross. Poult. Sci., 81: 1775-1781. PMID: 12512565. http://ps.fass.org/cgi/reprint/81/12/1775.

Van Kaam, J.B., M.A. Groenen, H. Bovenhuis, A. Veenendaal, A.L. Vereijken and J.A. Van Arendonk, 1999a. Whole genome scan in chickens for quantitative trait loci affecting growth and feed efficiency. Poult. Sci., 78: 15-23. PMID: 10023741. http://ps.fass.org/cgi/reprint/78/1/15.

Van Kaam, J.B., M.A. Groenen, H. Bovenhuis, A. Veenendaal, A.L. Vereijken and J.A. Van Arendonk, 1999b. Whole genome scan in chickens for quantitative trait loci affecting carcass traits. Poult. Sci., 78: 1091-1099. PMID: 10472833. http://ps.fass.org/cgi/reprint/78/8/1091.

Zhang, Y.Y., L.S. Sun, Y.Q. Li, G.H. Chen, K.H. Wang, X.S. Wu, K.W. Chen, B.C. Li, H.B. Tong, Z.L. Wu and X.Y. Zhang, 1997. Comparison of chemical composition contents of breast muscle in native chicken breeds. Jiangsu Agric. Res., 18: 73-76 (in Chinese).

Zhou, H., A.D. Mitchell, J.P. McMurtry, C.M. Ashwell and S.J. Lamont, 2005. Insulin-like growth factor-I gene polymorphism associations with growth, body composition, skeleton integrity and metabolic traits in chickens. Poult. Sci., 84: 212-219. PMID: 15742956. http://ps.fass.org/cgi/reprint/84/2/212.