Journal of Animal and Veterinary Advances 11 (11): 1939-1945, 2012
ISSN: 1680-5593

Mapping Quantitative Trait Loci Associated with Growth Quality Traits in a Chicken Population on Chromosome 8, 9, 10, 11, 13

Sun Gui-Rong, Zhang Yan-Fang, Li GuoXi, Han RuiLi, Tian Ya-Dong,
Sun YiMei and Kang XiangTao
Henan Innovative Engineering Research Center of Poultry Germplasm Resource,
College of Livestock Husbandry and Veterinary Engineering,
Henan Agricultural University, 450002 Zhengzhou, P.R. China

Abstract: The objective of the current study was to identify QTL associated with growth trait. An F_2 resource population of Gushi chicken crossing with Anka broiler was used in the current study. Thirty two growth traits at different weeks in this study were measured in the F_2 population which included body weight (measured every 2 weeks from hatch) and body size index measured every 4 weeks containing shank length, shank circle, chest depth chest width, chest angle, pelvis width, breast bone length and body slanting length. A total of 860 F_2 individuals produced from 7 F_1 families their parents and the grandparents F_0 birds were genotyped by 19 microsatellite markers on Chromosome 8, 9, 10, 11 and 13. Interval mapping was conducted to identify putative QTL. For the 32 growth traits, the QTL significant at the genome wide level that affected bodyweight at all ages were identified on Chromosomes 8. The QTL related to BW at early ages were identified on Chromosome 10 and 11 and only one QTL affected body weight were located on Chromosome 13. The QTL for body size index were first in detail reported on all the five chromosomes.

Key words: Chicken, growth trait, quantitative trait loci, microsatellite marker, chromosomes, genome

INTRODUCTION

The majority of economic traits in domestic animals exhibit quantitative variation that is controlled by many Quantitative Trait Loci (QTLs) with relatively small effects and is modified by environment. The identification and utilization of QTL provide the potential for more rapid genetic improvement in selection programs, especially for traits that are difficult to improve with traditional selection (Ikeobi *et al*., 2002; Torkamanzehi and Kuhnlein, 2007; Gholizadeh *et al*., 2008; Cai *et al*., 2011). Besides of increased genetic improvement, the detection of a QTL is the first step toward cloning genes underlying quantitative traits and studying their physiology. This would greatly promote our understanding of quantitative genetic variation and its physiological background (Atzmon *et al*., 2008). Because of the microsatellite's larger numbers, broadly distributed, richer polymorphism and the ability to automate the genotyping along with the high likelihood of finding a DNA polymorphism which have made microsatellite markers the primary genetic marker to map and use in genome-wide QTL searches (Goldstein *et al*., 1995; Takezaki and Nei, 1996). Although, the chicken breeds are rich in China, the performance trait is not perfect and lower productive efficiency comparing to the foreign commercial breeds. The improved breeds become the bottleneck and limitation for highly effective chicken productive industry. Growth traits have high heritability which could be effectively improved through genetic selection and breeding. However, before attempting to identify potential genes and exploiting them in animal breeding programs by Marker Assisted Selection (MAS), confirmation is necessary to verify the existence of QTL observed in an initial genome scan, preferably by using independent populations (Marklund *et al*., 1999).

Several reports have showed that chicken genome's micro chromosome (chr 11-39) has the very big difference with the macro chromosome (chr 1-10) in the hereditary feature (McQueen *et al*., 1996; Smith *et al*., 2000). At present, 206 QTL (relate to growth, the quality of meat, slaughter, egg productive and behavior) have been reported on Chromosome 8, 9, 10, 11 and 13 in chicken. As parental breeds with different phenotypes is thought to result in efficient finding of distinguished QTLs so, a slow-growing Chinese native line and a fast-growing

Corresponding Author: Xiangtao Kang, Henan Innovative Engineering Research Center of Poultry Germplasm Resource, College of Livestock Husbandry and Veterinary Engineering, Henan Agricultural University, 450002 Zhengzhou, P.R. China

broiler parent stock were selected for crossing to produce an unique F_2 population that was characterized for a large number of traits to facilitate the search for the QTL affecting them. The purpose of the current experiment was to describe the crosses involved and genotyping of the F_2 and to study the association of a number of markers on Chromosome 8, 9, 10, 11 and 13 with growth traits including Body Weight (BW) and body size index.

MATERIALS AND METHODS

Resource populations: The F_2 resource population was described by Han *et al.* (2010, 2011). In detail, the F_2 resource population was generated from Gushi (G) chickens (24 hens and 2 roosters) which represented a slow-growing native Chinese chicken breed and Anka (A) broilers (12 hens and 4 roosters), representing a fast-growing broiler type. The F_2 population consisted of four cross-bred families (A-roosters mated with G-hens) and two reciprocal families (G-roosters mated with A-hens). To build the F_2 population, 9 F_1 females were selected from each of 7 families (6 unrelated rooster families and 1 half sib); the 63 F_1 females were mated by 7 F_1 males from 7 families. Over two hatches that occurred at 2 weeks intervals, the resource population was established. It comprised 42 grandparents, 70 F_1 parents and 860 F_2 chickens. All the chickens were managed in cages and were fed the same corn-soybean diet which contained 11.90 MJ kg^{-1} of ME and 190 g kg^{-1} CP from 0-8 weeks then 12.13 MJ kg^{-1} of ME and 170 g kg^{-1} of CP after 8 weeks.

Measurement of phenotypes: Thirty two growth traits in this study were measured in total which included Body Weight (BW) and body size index containing Shank Length (SL), Shank Circle (SC), Chest Depth (CD), Chest Width (CW), Chest Angle (CA), Pelvis Width (PW), Breast Bone Length (BBL) and Body Slanting Length (BSL). The body weight was individually measured every 2 weeks from birth to slaughter while the traits of the body size index were measured every 4 weeks. The 860 F_2 chickens were slaughtered at the age of 84 days and samples of fresh blood were collected by superficial venipuncture of a wing vein then stored in -40°C.

Marker selection and genotyping: Twenty six microsatellite markers were selected on chr 8, 9, 10, 11 and 13 space interval 15~20 cM (Kerje *et al.*, 2003) from the consensus map 2000 cM of the three resource populations (Compton, East Lansing and Wageningen) supplied by the Poultry Genome Coordinators (http://poultry.mph.msu.edu). The primer sequences used are shown in Table 1. Genomic DNA samples were extracted from the stored blood in -40°C of 849 F_2 chickens and 70 F_1 and 42 grandparents by the Phenol-Chloroform Method (Wang *et al.*, 2006). The PCR reactions for all

Table 1: Information of microsatellite markers

Loci	Chr	Position (cm)	Forward primers	Reverse primers
MCW0275	8	6	TTTTTTTCGAGTTTCTGCAG	AAACCGACTTCGATACC
MCW0095	8	26	GATCAAAACATGAGAGACGAAG	TTCATAGCTTGAATTGCATAGC
ADL0154	8	46	GCTGCCACCTTCAAAACCTG	CTCACCATCTCATTCTTCAT
MCW0147	8	66	GATCCATTTATAAAGACCCCA	CCTGGTTTGCCAATACACTTG
ADL0286	8	80	GAAGTGAAGAGTTGGAGACG	GCTAGATGCTGGCTGAATAA
MCW0351	8	105	GTAAAGGCTCTTTACAAACGG	GAGTAGGGCTTAGGAAGTAAG
ROS0078	9	0	AGGGCTTGCACTGTACTTAGC	CAGAACGTGAGCAAATTCATG
ADL0021	9	53	GCTGGTCGCTTTGCTCTGAA	GCTTAGCCTCATCTCTTGTA
MCW0017	9	72	CAATAGGGTTTCCATGTAACCAGC	CAGCTACTTAGAGGAAGCCAAACC
ADL0136	9	107	TGTCAAGCCCATCGTATCAC	CCACCTCCTTCTCCTGTTCA
MCW0149	9	127	ACTCCTACAACAGCATACAT	TGCAATTAAAGGAGTAACCT
MCW0228	10	0	GATCTCTGCATTACAAGCATG	TTGCTGACCTGCTCATGCAAG
ADL0209	10	45	GGTTAGCTCCCTCCTTCCAG	TCACTCCAGCTTGAGACAGG
ADL0231	10	62	ACTATTAGCCTGGGGAGAGC	AAGGAAACAAAGAGAAATCC
ADL0102	10	88	TTCCACCTTTCTTTTTTATT	GCTCCACTCCCTTCTAACCC
MCW0003	10	105	CCTAAACATAGCAATGAGGATAAC	ATTCAGTTCCTTAAAGTTCTTGGG
LEI0143	11	0	GATCAATGAGTGCCGGGAGAG	CGGAGGTGATACGGATGGAG
MCW0097	11	18	GGAGAGCATCTGCCTTCCTAG	TGGTCTTCCAGTCTATGGTAG
LEI0072	11	32	TAAGCTGACATTCACCACCAG	GACTCTTTCAGTACATACTGG
ADL0210	11	54	ACAGGAGGATAGTCACACAT	GCCAAAAAGATGAATGAGTA
MCW0066	11	69	CTGGAATCACTGTTGTGGACTT	GGCCTTGAGATTTCATTCAGAGAC
MCW0230	11	88	GATCCTCTGATGGCTGCCG	TGCACAGAGCCAAGCTGCTTC
MCW0213	13	22	CTGTTCACTTTAAGGACATGG	GACAAGTCAACAACTTGCCAG
MCW0197	13	39	GTGCTGCTGGGTTTAACCTA	CTCACACGCGCACATACTTA
MCW0110	13	59	CATCTGTGTTACTGTCACAG	TCAGAGCAGTACGCCGTGGT
MCW0104	13	74	TAGCACAACTCAAGCTGTGAG	AGACTTGCACAGCTGTGACC

reaction volume of 10 μL contained 30 ng genomic DNA, 1× buffer (including 1.5 mM $MgCl_2$), 100 μM of each microsatellite markers were performed separately in a total deoxynucleotide triphosphate and 0.5 units of TaqDNA polymerase (Dongsheng Biotechnology Co., Guangzhou, China).Touch-down PCR procedure was performed at a hot start of 5 min at 94°C then 3 cycles of 1 min at 94°C, 1 min at 65°C and 2 min at 72°C then 3 cycles of 1 min at 94°C, 1 min at 60°C and 1 min at 72°C then 3 cycles of 1 min at 94°C, 1 min at 55°C and 2 min at 72°C followed by 30 cycles of 1 min at 94°C, 1 min at 65°C and 2 min at 72°C with a final elongation step of 10 min at 72°C.

A 3.5 μL PCR product were electrophoresed in 12% denaturing Polyacrylamide Gel Electrophoresis patterns (PAGE) in 1× TBE buffer and constant voltage (200 V) for 3~4 h. The gel was stained with 0.1% silver nitrate and photograph. In case of existing polymorphism, the PCR products showed different electrophoresis patterns which were sequenced by ABI 310 DNA sequencer and genotyped data was collected using Genescan (Version 3.1) and Genotyper (Version 2.5) Software (Applied Biosystems).

Statistical and QTL mapping: Phenotypic data were analyzed by using JMP software (SAS Institute, Cary, NC). Means, standard deviation and coefficient of variation of traits were calculated.

QTL detection by using QTL Express Software (http://qtl.cap.ed.ac.uk/. The parameter estimates of detected QTLs such as map position, F-value and test threshold value, additive effect (half the difference between two homozygotes) and dominance effect (deviation of a heterozygote from the mean of the two homozygotes). The least square regression model was used for QTL analysis as follows:

$$Y = \mu + Sex + Family + Covariate + e$$

Where:

Y = Phenotype of trait
μ = The average least square
Sex, family = The fixed effects on trait
Covariate = The correct variance (shank length at birth as the covariate for shank length at other weeks)
e = The residual effect

Percentage of F_2 phenotypic variance explained by model was calculated as:

$$\text{Variance percentage} = 100\times(RMS-FMS)/RMS$$

Where:

RMS = The Residual Mean Square from the reduced model, omitting QTL but including all fixed effects
FMS = The residual mean square from the full model including QTL and all fixed effects

Significance thresholds and confidence intervals: Significance thresholds were derived at the chromosome by the Permutation test (Churchill and Doerge, 1994). Average thresholds across the 32 traits in F_2 cross were used for significance testing to determine the empirical distribution of the statistical test under the null hypothesis of no QTL associated with the part of the genome under study. Two significance levels were used: 5 and 1% genome-wide (Lander and Kruglyak, 1995).

An approximate 95% confidence interval for the localization of each of the significant QTL was obtained using the bootstrap technique (Visscher *et al*., 1996; Knott *et al*., 1998) with a total of 1000 samples.

RESULTS AND DISCUSSION

Phenotypic data of F_2 resource population: The mean values and standard deviations of the traits were shown in Table 2. The CV of BW were from 9.23 (for BW0)-19.18% (for BW6), the CV for the other body size index have different ranges; the CV of SL were from 4.24 (SL0)-14.65% (SL4); the CV of SC, CD, CW, BBL, CA, BSL and PW were from 7.49~8.11, 13.10~9.72, 10.31~11.59, 7.27~8.29, 5.01~5.86, 6.28~7.28 and 9.15~9.83%, respectively. All the growth traits we measured were perfectly separated in Gushi and Anka resource population so it can be further studied for QTL.

QTL analysis for body weight and body size index: The QTL with estimated significant levels (F-value) for BW and body size index are shown in Table 3 and 4 with map positions, details of the additive and dominance effects, confidence interval and percentage of F_2 variance explained by each QTL.

For BW, the QTL at all the stages were located on Chromosome 8 and 5 QTL were at the 1% genome-wide level. The additive effect of all the QTL on chr 8 were positive. On Chromosome 10, QTL for BW4, BW6 and BW8 were located at the same position 23 cM then the QTL for BW0, BW2 were detected at 0 and 1 cM, respectively. The 4 QTL were detected on Chromosome 11. Only one QTL for BW0 on chr 13 were detected at 0 cM with negative additive and positive dominance effect. Details of the QTL relate to body size index such as Shank Length (SL), Shank Circle (SC), Chest Depth (CD), Chest Width (CW), Chest Angle (CA), Breast Bone

Table 2: Statistical table phenotyped for body measurement trait

Traits (unit)	Samples	Min.	Max.	Mean	SE	CV (%)
SL0 (cm)	843	2.26	3.00	2.58	0.00	4.24
SL4 (cm)	784	3.00	7.25	5.50	0.03	14.65
SL4 (cm)	784	3.00	7.25	5.50	0.03	14.65
SL8 (cm)	779	5.60	10.30	7.93	0.03	10.92
SL12 (cm)	812	7.30	12.20	9.39	0.03	8.85
SC4 (cm)	780	2.00	3.50	2.69	0.01	7.49
SC4 (cm)	780	2.00	3.50	2.69	0.01	7.49
SC8 (cm)	767	2.90	4.40	3.42	0.01	7.80
SC12 (cm)	806	3.00	4.90	3.84	0.01	8.11
CD4 (cm)	783	3.00	7.00	4.85	0.02	13.10
CD8 (cm)	783	4.00	10.00	6.54	0.03	13.66
CD12 (cm)	835	5.00	10.00	7.88	0.03	9.72
CW4 (cm)	783	2.80	6.00	4.09	0.02	11.59
CW8 (cm)	783	4.00	9.00	5.68	0.02	10.31
CW12 (cm)	835	4.50	10.00	6.33	0.02	10.54
BBL4 (cm)	783	4.40	7.80	6.21	0.02	8.29
BBL8 (cm)	783	5.50	11.10	8.92	0.03	8.14
BBL12 (cm)	835	7.80	13.20	11.00	0.03	7.27
CA4 (°C)	783	60.00	90.00	74.17	0.13	5.01
CA8 (°C)	783	8.30	90.00	76.44	0.16	5.86
CA12 (°C)	835	70.00	92.00	79.00	0.14	5.16
BSL4 (cm)	783	7.50	13.50	11.39	0.03	6.98
BSL8 (cm)	783	10.10	19.60	16.23	0.04	7.28
BSL12 (cm)	835	14.00	23.50	19.78	0.04	6.28
PW4 (cm)	783	4.00	6.50	5.16	0.02	9.15
PW8 (cm)	783	5.00	8.50	6.87	0.02	9.83
PW12 (cm)	835	5.50	11.50	8.66	0.03	9.73
BW0 (g)	843	22.80	39.00	30.59	0.10	9.23
BW2 (g)	781	41.60	185.50	122.18	0.67	15.23
BW4 (g)	785	156.00	464.00	321.35	1.72	15.02
BW6 (g)	813	274.00	915.00	566.10	3.81	19.18
BW8 (g)	784	451.50	1285.00	816.26	5.15	17.68
BW10 (g)	817	447.00	1691.00	1113.30	6.39	16.42
BW12 (g)	830	471.00	2102.00	1351.90	7.73	16.46

SL = Shank Length; SC = Shank Circle; CD = Chest Depth; CW = Chest Width; BBL = Breast Bone Length; CA = Chest Angle; BSL = Breast Slanting Length; PW = Pelvis Width; BW = Body Weight; All traits were measured at the different time (such as 0 2, 4, 6, 8, 10 and 12 weeks)

Table 3: The QTL significant at the 5 and 1% genome-wide level for body weight on each chromosome

Traits	Chr	Location (cM)	F-value[2]	Additive effect±SE	Dominance effect±SE	95% CI (cM)	Variation
BW0	8	40	12.33**	-0.0109±0.16750	-1.2446±0.25520	3-51.0	3.4
BW4	8	57	11.37**	3.4050±4.07880	-35.7931±8.33410	0-76.5	3.2
BW6	8	67	6.13*	6.7938±10.9506	-71.2586±23.3783	0-98.5	1.6
BW8	8	63	5.80*	13.3464±13.0496	-77.0765±27.4019	0-99.0	1.3
BW1	8	81	10.31**	24.0380±19.1442	-128.4578±35.7837	20-99.0	2.6
BW1	8	79	11.13**	31.7432±23.2467	-165.4163±44.6340	20-99.0	2.6
BW0	10	1	7.85**	0.0064±0.21920	-1.4524±0.36930	0-55.0	2.1
BW2	10	0	6.83**	0.0339±1.42430	-8.6843±2.36470	0-55.0	1.8
BW4	10	23	7.69**	-3.1673±3.60450	-22.7488±5.97630	0-29.0	2.1
BW6	10	23	7.48**	-14.5030±8.05110	-45.6943±13.2624	0-28.0	2.0
BW8	10	23	6.53*	-17.6009±10.0856	-53.3931±16.7015	0-60.0	1.5
BW0	11	0	7.12**	-0.0618±0.21430	-0.9435±0.25070	0-37.0	1.9
BW2	11	4	7.90**	-3.5253±1.59720	-6.7646±2.11630	0-37.0	2.1
BW4	11	37	9.17**	1.5877±3.69770	-20.8131±4.91280	0-37.0	2.5
BW6	11	37	6.63**	4.1183±8.28920	-39.4456±11.0129	0-37.0	1.7
BW0	13	0	7.79**	-0.6483±0.19680	0.8944±0.34040	0-52.0	2.1

F-value: *Significant linkage at $p<0.05$; **Significant linkage at $p<0.01$; BW = Body Weight. All traits were measured at the different time (such as 0, 2, 4, 6, 8, 10 and 12 weeks)

Length (BBL) and Body Slanting Length (BSL) at 4, 8 and 12 weeks were first reported in the research shown in Table 3. On Chromosome 8, the QTL for BSL, BBL and CW at the 3 stages of age (4, 8 and 12 weeks) as well as CA12 were detected at 20-93 cM, especially concentrated at 84-88 cM. On Chromosome 9, three significant QTL relate to CA at 3 age stages at 5% genome wide and one for CD4 at 1% genome wide were located. Beside of a QTL affecting BBL on Chromosome 10 at 3 age stages. One QTL for SL8 was significant located on Chromosome 10.

On Chromosome 11, 5 QTL for PW4, SC4, BSL4, BBL4 and SC8 were detected at two positions. On Chromosome 13, 3 QTL for BSL4, BBL4 and BSL8 were located at the same position 52 cM and one at 9 cM for CW12.

Body weight is under complex genetic control. Uncovering the molecular mechanism of growth will contribute to more efficient selection for growth in broiler chickens (Deeb and Lamont, 2002). Considering many Chinese native breeds with good meat and egg quality but

Table 4: The QTL significant at the 5 and 1% genome-wide level for body size index on each chromosome

Traits	Chr	Location (cM)	F-value	Additive effect±SE	Dominance effect±SE	95% CI (cM)	Variation
BSL4	8	84	11.12**	0.0367±0.0858	-0.6407±0.15450	3.0-99	8.05
BBL4	8	88	10.00**	0.0649±0.0554	-0.3236±0.09260	0-99	3.05
CW4	8	93	8.45**	-0.0204±0.0481	-0.2843±0.07240	6.0-99	1.91
PW8	8	85	4.61*	0.073±0.0739	-0.2939±0.13090	14.5-99	1.88
SC8	8	87	5.62*	0.0254±0.0292	-0.1307±0.04980	0-99	1.40
BBL8	8	79	5.87*	0.0667±0.0793	-0.4217±0.15230	20-99	0.87
BSL8	8	92	5.87*	0.0554±0.1163	-0.5318±0.17870	3.0-99	0.52
CW8	8	20	7.49**	0.0578±0.0293	0.1939±0.05520	15-95	8.26
BSL12	8	85	9.21**	0.0757±0.1266	-0.826±0.222300	36-99	8.88
BBL12	8	86	5.90*	0.0368±0.0829	-0.4278±0.14310	2.5-99	4.37
CA12	8	76	5.28*	1,1232±0.4369	2.4052±0.86830	4.87-71	1.25
CW12	8	54	7.46**	0.0619±0.0508	-0.3246±0.09930	20-99	4.19
CA4	9	127	6.07*	0.345±0.2095	0.9879±0.30400	0-127	3.67
CD4	9	100	9.21**	-0.0080±0.0417	-0.3617±0.08430	5.5-113	5.25
CA8	9	125	5.56*	-0.0919±0.2703	1.3537±0.41730	0-127	1.27
CA12	9	53	7.30**	0.4729±0.3113	1.1209±0.33280	0-127	1.80
BSL4	10	0	6.65*	-0.0169±0.0579	-0.3418±0.09620	0-43.5	6.79
BBL4	10	0	9.71**	-0.0299±0.0384	-0.2656±0.06370	0-30	2.97
SL8	10	10	6.01*	-0.2227±0.0703	-0.1484±0.10890	0-44	4.28
BSL8	10	49	6.06*	-0.2992±0.0859	0.0572±0.14790	0-57.5	0.29
BBL8	10	22	7.57**	-0.1149±0.0507	-0.2657±0.08190	0-60	1.82
CD8	10	3	5.00*	-0.0092±0.0679	-0.3609±0.11520	0-60	3.02
BBL2	10	22	4.93*	-0.0868±0.0546	-0.2442±0.08830	0-60	4.12
PW4	11	9	5.50*	0.013±0.0438	-0.2168±0.06538	0-37	2.73
SC4	11	37	6.85**	-0.0054±0.0163	-0.0822±0.02224	0-37	2.21
BSL4	11	37	5.75*	-0.0092±0.0600	-0.2705±0.07975	6-37	6.52
BBL4	11	37	6.77**	-4.0E-4±0.0398	-0.1946±0.05293	1-37	2.11
SC8	11	37	4.69*	-0.0043±0.0207	-0.0844±0.02755	0-37	1.12
BSL4	13	52	7.48**	-0.0863±0.0535	-0.03391±0.1065	2.0-52	5.12
BBL4	13	52	9.02**	-0.0499±0.0355	-0.2615±0.07064	25-52	2.78
BSL8	13	52	5.42*	-0.1067±0.0778	-0.4987±0.15590	0-52	0.81
CW12	13	9	6.89**	-0.0371±0.0458	0.288±0.079080	0-37	4.03

F-value: *Significant linkage at $p<0.05$; **Significant linkage at $p<0.01$; SL = Shank Length; SC = Shank Circle; CD = Chest Depth; CW = Chest Width; BBL = Breast Bone Length; CA = Chest Angle; BSL = Breast Slanting Length; PW = Pelvis Width; BW = Body Weight; All traits were measured at the different time (such as 0 2, 4, 6, 8, 10, 12 weeks)

lower growth rate. Because of the higher heritability for growth traits, researchers hope find the QTL for bodyweight and body size index applying in breeding. In order not to change the quality of native breeds' meat and egg quality and to have the growth rate improved. The QTL affecting BW on GGA8 were located at different positions which was close to the region reported by Rabie *et al.* (2005) and inconsistent with other reports (Atzmon *et al.*, 2008; Carborg *et al.*, 2003; Zhou *et al.*, 2006; Kerje *et al.*, 2003) indicated that when the 2 estimated QTL positions differed by a recombination distance of 30 cM in a chromosome region, a single QTL for the given trait was assumed on that chromosome. Because BW at 2-12 weeks of age were highly correlated and the QTL positions were close, it was reasonable to assume that three QTLs affected BW at different stages on Chromosome 8. The additive effect of the QTLs are all positive indicating that the allele conferring the higher trait value was inherited form the broiler line.

The three significant QTL for BW on Chromosome 10 must be the same QTL relate to BW at early ages because of locating at the same position 23 cM.

Atzmon *et al.* (2008) found a QTL for BW at 45 cM on Chromosome 11, inconsistent with the result. Only one QTL for BW0 on GGA13 were detected at 0 cM. Zhou *et al.* (2006) found the QTL for BW6 at 0 cM on GGA13 in Broiler-Fayoumi cross which was different from the result. At present, more QTL on Chr13 relate to BW were reported at 34, 58 (Zhou *et al.*, 2006), 22 (Atzmon *et al.*, 2008) and 68 cM (Jacobsson *et al.*, 2005). Also some reports didn't found any QTL on the micro Chromosome 10, 11 and 13 in some resource population (Zhou *et al.*, 2006; Tsudzuki *et al.*, 2007). All the studies suggested that a different set of genes may be involved in different life stages of chicken growth and development and the QTL found may vary with the markers and population used, choice of statistical models and most importantly the use of a different resource population (McElroy *et al.*, 2006). Therefore, it is essential to define marker-QTL phase and its effect in the specific populations for application. No QTL for BW was detected on Chromosome 9 and the confidence intervel for BW on each chromosome were longer so, more markers needed to apply in the resource population in order to precise

mapping the QTL linkage with BW. Although, body size index was ignored in chicken production, it is important for breeding to get a regular shape and perfect appearance which will be more cater to market and people requirement. In Gushi and Anka resource population, the QTL for body sixe index was first detailed reported on these chromosomes. Tsudzuki *et al.* (2007) found four shank length QTLs on GGA1, GGA4, GGA24 and GGA27 in the Silky Fowl and the White Plymouth Rock breeds; Schreiweis *et al.* (2005) identified significant QTLs affecting tibia and humerus lengths at 35 and 55 weeks of age on Chromosomes 4 and 27 in the resource family based on common layer and broiler lines. Schreiweis *et al.* (2005) detected QTLs affected different stages shank length at GGA2, GGA4, GGA7, GGA9 and GGA23. Ankra-Badu *et al.* (2010) detected the QTL for shank length and shank diameter at 9 weeks on GGA4 in an F_2 population and explained 7 and 10% of their phenotypic variances, respectively. Nadaf *et al.* (2009) had also identified the QTL for shank length and diameter on GGA4. In the experiment, only one QTL for shank length on Chromosome 10 was detected at 10 cM which explained 4.28% phenotypic variance. Three QTL for shank circle were located at GGA8 and GGA11, different reports showed shank length was a quantitative trait controlled by many genes with smaller effect and the major gene controlled the shank length need to be further studied. To some extent, body weight and body size index (BBL, BSL, SL and CD) show positive correlation. So, these traits can be improved through the selective of BW. For example, heavier birds tend to have stronger shank with longer shanks and shank circle (Chambers, 1990). Shank length affects chicken leg health and longer shanks are a source of leg problems in heavy-bodied chickens. There were also some QTLs affected body size index detected at the different locations with the body weight QTLs.

It seems to be possible to create birds that have short shank length and heavy body weight at the same time, especially with marker-assisted selection, the same to chest width. As shown in Table 3, individual QTLs detected accounted for 0.52-8.88% of the phenotypic variance which cannot explain major genes exist so, other chromosomes need to be scan to find the major genes relate to growth traits.

In conclusion using the special china native Gushi breed, several QTLs were preliminary mapped on Chromosome 8, 9, 10, 11 and 13 for bodyweight and body size index. The improving power need to be carried out to detect the true QTLs by using high-density molecular markers throughout the genome. All the results need further confirmation in other populations.

CONCLUSION

In the study, a total of 860 F_2 individuals produced from 7 F_1 families, their parents and the grandparents F_0 birds were genotyped by 26 microsatellite markers on Chromosome 8, 9, 10, 11 and 13. Interval mapping was conducted to identify putative QTL. For the 32 growth traits, the QTL significant at the genome wide level that affected bodyweight at all ages were identified on Chromosomes 8. The QTL related to BW at early ages were identified on Chromosome 10, 11 and only one QTL affected body weight were located on Chromosome 13. The QTL for body size index were first in detail reported on all the five chromosomes.

ACKNOWLEDGEMENTS

This research is supported by the National Natural Science Foundation of China (31072023) and the earmarked fund for Modern Agro-industry Technology Research System (CARS-41-k04).

REFERENCES

Ankra-Badu, G.A., E. Le Bihan-Duval, S. Mignon-Grasteau, F. Pitel and C. Beaumont *et al.*, 2010. Mapping QTL for growth and shank traits in chickens divergently selected for high or low body weight. Anim. Genet, 41: 400-405.

Atzmon, G., S. Blum, M. Feldman, A. Cahaner, U. Lavi and J. Hillel, 2008. QTLs detected in a multigenerational resource chicken population. J. Heredity, 99: 528-538.

Cai, S., Y. Liu, C. Zhang, W. Fu and Y. Gong *et al.*, 2011. Mapping of quantitative trait loci for hematological traits on pig chromosome 10. Asian J. Anim. Vet. Adv., 6: 469-475.

Carborg, O., S. Kerje, K. Schutz, L. Jacobsson, P. Jensen and L. Anderson, 2003. A global search reveals epistatic interaction between QTL for early growth in the chicken. Genome Res., 13: 413-421.

Chambers, G.K., 1990. The genetics of human alcohol metabolism. Gen. Pharmacol., 21: 267-272.

Churchill, G.A. and R.W. Doerge, 1994. Empirical threshold values for quantitative trait mapping. Genetics, 138: 963-971.

Deeb, N. and S.J. Lamont, 2002. Genetic architecture of growth and body composition in unique chicken populations. J. Heredity, 93: 107-118.

Gholizadeh, M., G.R. Mianji and H.S. Zadeh, 2008. Potential use of molecular markers in the genetic improvement of livestock. Am. J. Anim. Vet. Adv., 3: 120-128.

Goldstein, D.B., A.R. Linares, L.L. Cavalli-Sforza and M.W. Feldman, 1995. An evaluation of genetic distances for use with microsatellite loci. Genetics, 139: 463-471.

Han, R.L., X.Y. Lan, L.Z. Zhang, G. Ren and Y.J. Jing *et al*., 2010. A novel single-nucleotide polymorphism of the visfatin gene and its associations with performance traits in the chicken. J. Applied Genet., 51: 59-65.

Han, R.L., Z.J. Li, M.J. Li, J.Q. Li and X.Y. Lan *et al*., 2011. Novel 9-bp indel in visfatin gene and its associations with chicken growth. Br. Poult. Sci., 52: 52-57.

Ikeobi, C.O., J.A. Woolliams, D.R. Morrice, A. Law, D. Windsor, D.W. Burt and P.M. Hocking. 2002. Quantitative trait loci affecting fatness in the chicken. Anim. Genet., 33: 428-435.

Jacobsson, L., H.B. Park, P. Wahlberg, R. Fredriksson, M. Perez-Enciso, P.B. Siegel and L. Andersson, 2005. Many QTLs with minor additive effects are associated with a large difference in growth between two selection lines in chickens. Genet. Res., 86: 115-125.

Kerje, S., O. Carlborg, L. Jacobsson, K. Schutz, C. Hartmann, P. Jensen and L. Andersson, 2003. The twofold difference in adult size between the red junglefowl and White Leghorn chickens is largely explained by a limited number of QTLs. Anim. Genet., 34: 264-274.

Knott, S.A., L. Marklund, C.S. Haley, K. Andersson and W. Davis *et al*., 1998. Multiple marker mapping of quantitative trait loci in a cross between outbred wild boar and large white pigs. Genetics, 149: 1069-1080.

Lander, E. and L. Kruglyak, 1995. Genetic dissection of complex traits: Guidelines for interpreting and reporting linkage results. Nat. Genet., 11: 241-247.

Marklund, L., P.E. Nystrom, S. Stern, L. Andersson-Eklund and L. Andersson, 1999. Confirmed quantitative trait loci for fatness and growth on pig chromosome 4. Heredity, 82: 134-141.

McElroy, J.P., J.J. Kim, D.E. Harry, S.R. Brown, J.C. Dekkers and S.J. Lamont, 2006. Identification of trait loci affecting white meat percentage and other growth and carcass traits in commercial broiler chickens. Poult. Sci., 85: 593-605.

McQueen, H.A., J. Fantes, S.H. Cross, V.H. Clark, A.L. Archibald and A.P. Bird, 1996. CpG islands of chicken are concentrated on microchromosomes. Nat. Genet., 12: 321-324.

Nadaf, J., F. Pitel, H. Gilbert, M.J. Duclos and F. Vignoles *et al*., 2009. QTL for several metabolic traits map to loci controlling growth and body composition in an F2 intercross between high-and low-growth chicken lines. Physiol. Genomics, 38: 241-249.

Rabie, T.S., R.P. Crooijmans, H. Bovenhuis, A.L. Vereijken and T. Veenendaal *et al*., 2005. Genetic mapping of quantitative trait loci affecting susceptibility in chicken to develop pulmonary hypertension syndrome. Anim. Genet., 36: 468-476.

Schreiweis, M.A., P.Y. Hester and D.E. Moody, 2005. Identification of quantitative trait loci associated with bone traits and body weight in an F2 resource population of chickens. Genet. Sel. Evol., 37: 677-698.

Smith, J., C.K. Bruley, I.R. Paton, I. Dunn and C.T. Jones *et al*., 2000. Differences in gene density on chicken macrochromosomes and microchromosomes. Anim. Genet., 31: 96-103.

Takezaki, N. and M. Nei, 1996. Genetic distances and reconstruction of phylogenetic trees from microsatellite DNA. Genetics, 144: 389-399.

Torkamanzehi, A. and U. Kuhnlein, 2007. Restriction fragment length and single strand conformational polymorphisms in chicken mitochondrial phosphoenol-pyruate carboxykinase gene and its association with egg production. Pak. J. Biol. Sci., 10: 4075-4080.

Tsudzuki, M., S. Onitsuka, R. Akiyama, M. Iwamizu and N. Goto *et al*., 2007. Identification of quantitative trait loci affecting shank length, body weight and carcass weight from the Japanese cockfighting chicken breed, Oh-Shamo (Japanese Large Game). Cytogenet. Genome. Res., 117: 288-295.

Visscher, P.M., R. Thompson and C.S. Haley, 1996. Confidence intervals in QTL mapping by bootstrapping. Genetics, 143: 1013-1020.

Wang, Q., H. Li, N. Li, L. Leng, Y. Wang and Z. Tang, 2006. Identification of single nucleotide polymorphism of adipocyte fatty acid-binding protein gene and its association with fatness traits in the chicken. Poult. Sci., 85: 429-434.

Zhou, H., N. Deeb, C.M. Evock-Clover, C.M. Ashwell and S.J. Lamont, 2006. Genome-wide linkage analysis to identify chromosomal regions affecting phenotypic traits in the chicken. II. Body composition. Poult. Sci., 85: 1712-1721.