QTL Mapping of Chicken Carcass Traits on GGA27

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Introduction

Chicken autosomes are sorted by size into five large macro chromosomes, five intermediate chromosomes and 28 micro chromosomes. Micro chromosomes are characterized as higher G+C content, CpG content, and density of genes compared with macro chromosomes (ICGSC, 2004). More economically important genes were referred to exist on micro chromosomes than on macro chromosomes (Axelsson et al, 2005). However, the numbers of QTL previously identified on micro chromosomes using linkage analysis are relatively fewer due to poor density of microsatellite markers and uncompleted linkage map. Therefore, we expect to construct completed genetic map and identify more QTL at GGA27 by combining highly polymorphic microsatellite markers and dense SNP markers.

Material and methods

Experimental population. A total of 502 F2 chickens in 17 Xinghua and White recessive Rock full-sib families from six hatches were obtained at two-weekly intervals, and the birds were reared for trait measurement (described in detail by Rao et al. (2007)).

Linkage map. Marker information is showed in Table 1. Microsatellites and SNP are genotyped by ABI 3730 sequencer and PCR-RFLP, respectively. A genetic map (See Figure 1) was obtained using the CRI-MAP 2.4 program (Green et al, 1990).

Statistical analyses. The QTL mapping method proposed by Haley et al. (1994) was implemented using QTL Express software (Seaton et al. 2001). The linear model included family, sex, batch and a covariate-carcass weight as fixed effects. Significance threshold analyses were conducted using a permutation test (1000 times) (Churchill et al, 1994). An approximate confidence interval for significant QTL was obtained using the bootstrap technique (1000 times) (Lander et al, 1995; Visscher et al, 1996).

Results and discussion

The length of genetic map obtained was 103.6 cM, which was longer than the consensus genetic map (71cM). Ikeobi et al (2004) identified QTL of wing weight at marker ROS0071 (between MCW0328 and ADL0376). This QTL (See Figure 2) was confirmed in our population and was mapped at 99 cM ($F=5.22$, $P<0.05$), and two novel QTL for leg muscle weight and fat thickness under skin were mapped at 102 cM ($F=4.89$, $P<0.05$) and 103 cM ($F=5.03$, $P<0.05$) (See Figure 2), respectively. However, the confidence intervals are wider (See Table 2). The QTL for wing weight, leg muscle weight and fat thickness under skin explain 0.4%, 0.8% and 3% phenotypic variance respectively.

Table 1: Marker information[α]

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Marker name	M1	Mcw0233	Mcw0328	ADL0376	M2
Physical distance (bp)	4,259	1,905,347	3,493,381	3,872,706	4,840,951
Genetic distance (cM)	0	24.8	57.0	78.6	103.6

[α] Physcial distance information obtained from NCBI. Genetic distance information comes from the result of Figure1.

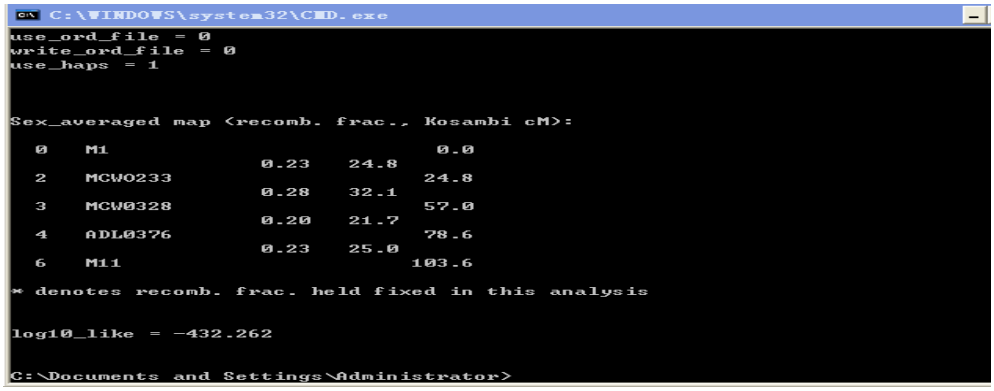

Figure1. Genetic map was constructed by CRI-MAP 2.4 program.

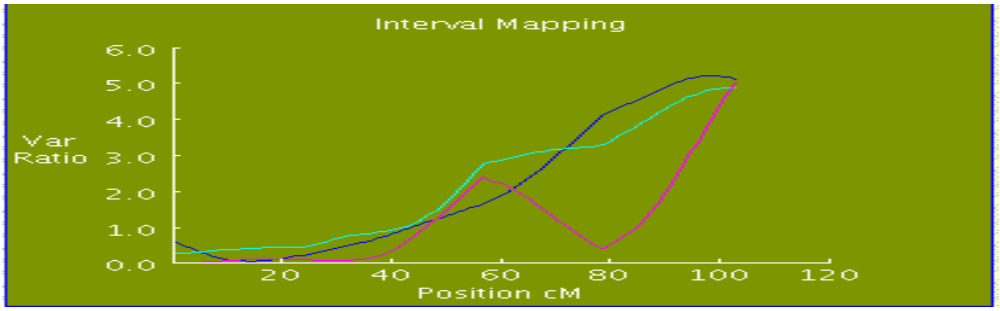

Figure2. QTL analysis for wing weight (WW) (blue line), leg muscle weight (LMW) (green line) and fat thickness under skin (FTS) (red line).

Table2: Significance thresholds and confidence intervals

Trait	F value [a]		95%C.I.of QTL Position(cM)[b]
	P=0.05	P=0.01	
WW	4.82	6.93	0-103
LMW	4.57	6.41	32-103
FTS	4.95	6.67	14-103

[a] F value obtained from permutation test. [b] Confidence intervals(C.I.) obtained from bootstrap test.

Conclusion

These results showed that more QTL were probably present on GGA27 (about 4.8 Mb). The QTL for wing weight was surely identified on GGA27, and it can be fine mapped by LD methods and LDLA methods (Meuwissen et al, 2001; Meuwissen et al, 2002; McClurg et al, 2006), which could be implemented in future animal breeding production.

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