

Identification Of Quantitative Trait Loci For Shank Length And Its Growth Curve At Rearing Period In Chickens

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Introduction

Traditionally, genetic improvement in growth of chickens has proceeded with selection for body weight and/or shank length (as bone developments) at a fixed age. On the other hand, as early as 1926, Write appeared to have first suggested the use of the Gompertz curve for biological growth, then in 1928, Davidson used the Gompertz curve to represent the growth in body weight of Jersey Cows (Winsor (1932)). Since then, in poultry, there were many reports for growth curve analyses (e.g. Grossman and Bohren (1985); Grossman and Koops (1988); Anthony, N. B., Emmerson, D. A., Nestor, K. E. et al. (1991); Barbato (1991); Mignon-Grasteau, S., Piles, M., Varona, L. et al. (2000)).

So far, many number of quantitative trait locus (QTL) analyses have been performed on growth of body weight, shank length, and its related traits. However, these phenotypic traits were at a fixed age (point) and/or the differences between two points. QTLs affecting growth curve, as it is entire growth, were unavailable.

The purpose of this study was to identify QTLs for growth of Shank length on both at a fixed age (point) and the growth curve.

Material and methods

Animals. An Oh-Shamo male and three White Leghorn females were mated to built a resource family. Subsequently, four F₁ males and twenty-two F₁ females were mated in full-sib matings. As F₂ birds, 224 males and 215 females were obtained.

Trait measurements. Shank length was measured at hatch (SH00) and every week until 16 weeks of age (SH01 – SH16). Then the Gompertz curve (Gompertz (1825); Winsor (1932)) was applied to estimate shank length's growth curve parameters on each bird. To calculate the curve parameters, NLIN procedure of SAS 9.01 (SAS Institute Inc., Cray, NC, USA) was used. The estimated parameters were also considered as phenotypic traits, and they are: growth rate (GR), curve position (CP), and upper asymptote (UA).

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Marker genotyping and linkage map construction. Two hundreds and seventy-five micro-satellite markers were placed on 28 chromosomes including sex chromosome (chromosome Z). The details for genotyping have been described in our earlier paper (Takahashi, H., Tsudzuki, M., Sasaki, O. et al. (2005)). A linkage map was constructed with Map Manager QTXb20 (Manly, K. F., Cudmore, R. H. Jr., and Meer, J. M. (2001)) with Kosambi map function.

QTL analyses. Prior to QTL analyses, the phenotypic records were revised with the hatch date and sex by using JMP 5.01 (SAS Institute Inc., Cray, NC, USA). To detect QTLs, simple interval mapping based on the Extended Haley-Knott regression (Haley and Knott (1992); Borman and Sen (2009)) was implemented with R/qtl 1.13 (Borman and Sen (2009)). Since segregation pattern for marker genotypes was different between autosomes and chromosome Z in the F₂ mapping population, the intercross model was applied to autosomes and the back cross model was applied to Z chromosome for analyses. Experiment-wise significance thresholds were established with 1000 permutations.

Results and discussion

Thirteen main effect QTLs for the shank length and its growth curve parameters were found on chromosomes 1, 3, 4, 28, and Z (Table 1). QTLs 1, 3, 9, 11, and 12 were continuously appeared with age of weeks. QTL 9 on chromosome 4 increased the level of phenotypic variance with age developments. The percent variance at SH10 was estimated to 5.13 %, and then it increased to 22.77 % at SH16.

QTLs for the growth curve parameters were consistent with QTLs for shank length. A QTL for GR and UA were detected on chromosome 4 as the same as the QTL for SH00-01 and SH10-16. A QTL for CP were found on chromosome 3 as the same as the QTL for SH07 and SH09. In addition, a QTL for CP were identified on chromosome Z as the same as the QTL for SH09.

Since the growth parameters of GR and CP explain growth rate itself and the growth speed positioning, QTLs of 6, 9, and 13 may be affecting growth speed. Moreover, since the parameter UA gives the maximum growth point, QTL 9 may be acting as one of major QTLs for maturity of shank length. Evidentially, the percent of variance on QTL 9 rose from 5.13 % to 22.77 % as it was explained at above.

In comparison with similar study of QTLs for shank length (Gao, Y., Du, Z.-Q., Feng, C.-G. et al. (2009)), some of detected QTLs in this study are close. Their reported QTL on chromosome 3 for shank length at 2 weeks of age is close to QTL 6 in this study. And, their identified QTLs on chromosome 4 for shank length at 9 and 2 weeks of age are near to QTL 8 and QTL 9 in this study, respectively.

On the other hand, there are some other QTLs' reports for shank length related traits. In comparison between other reports and this study, some of QTLs in other reports are also

close to QTLs in this detection. For example, a QTL for shank weight to length ratio on chromosome 1 (Zhou, H., Deeb, N., Evock-Clover, C. M. et al. (2007)) is close to QTL 1, and a QTL for shank weight on chromosome Z (Zhou, H., Deeb, N., Evock-Clover, C. M. et al. (2007)) is near to QTL 12 in this study. Also, a QTL for shank length on chromosome 4 (Tsudzuki, M., Onitsuka, S., Akiyama, et al. (2007); Sharman, P. W. A., Morrice, D. R., Law, A. W. et al. (2007)) is near to QTL 9 in this report.

Table 1: Identified QTLs and their chromosomes, close markers, and affecting traits

QTL	Chromosome	Close Marker	Trait ^a
1	1	<i>ABR0379</i>	SH15-16
2	3	<i>ABR0472</i>	SH01
3	3	<i>ABR0253</i>	SH02-06
4	3	<i>ABR0353</i>	SH10
5	3	<i>ABR0507</i>	SH12
6	3	<i>ABR0255</i>	SH07, SH09, CP
7	3	<i>ABR0161</i>	SH08
8	4	<i>ADL0317</i>	SH02
9	4	<i>ABR0628</i>	SH00-01, SH10-16, GR, UA
10	28	<i>LEI0135</i>	SH00
11	Z	<i>ABR0633</i>	SH14-16
12	Z	<i>ABR0620</i>	SH03-04
13	Z	<i>ABR0621</i>	SH09, CP

^aSH00 = shank length at hatch, SH01 = shank length at one week of age, SH02 = shank length at two weeks of age, and so on, GR = growth rate, CP = curve position, UA = upper asymptote.

Conclusion

This study revealed thirteen main-effect QTLs controlling shank length growth. One of them was highly related with traits at rearing period in chickens. In addition, three of QTLs for growth curve of shank length were consistent with QTLs for shank length. Therefore, these QTLs may contain some genes working for shank development in chickens.

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