*Journal of Livestock Science and Technologies*, **2014, 2 (1): 49-55** **http://lst.uk.ac.ir**

# Quantitative trait loci for body weight and carcass traits in Japanese quail

E. Rezvannejad1*, M. Yaghoobi[1], M. Rashki[2]

[1]Department of Biotechnology, Institute of Science and High Technology and Environmental Science, Graduate University of Advanced Technology, Kerman, Iran

[2] Department of Ecology, Institute of Science and High Technology and Environmental Science, Graduate University of Advanced Technology, Kerman, Iran

* Corresponding author, E-mail address: rezvannejad2002@yahoo.com

**Abstract** Body weight (BW) and carcass traits are complex and important economic traits that may benefit from the implementation of MAS. The objective of the current study was to identify QTL associated with BW and carcass traits in an experimental half-sib cross of Japanese quails selected for BW at 4 weeks of age. Body weight and carcass traits were measured in the F2 population. Total F2 individuals and their parents were genotyped by 6 informative microsatellite markers on chromosomes 1, 2 and 9. Interval mapping was conducted to identify putative QTL. Two QTL for BW at hatch were detected on chromosomes CJA02 and CJA01 at the 1% chromosome wide and the suggestive levels, the significant QTL explained 1.24% of the phenotypic variance. For BW at 4 wk of age three QTL were identified on chromosomes CJA01, CJA02 and CJA09 at the 1% chromosome wide and the suggestive levels, the significant QTL explained 1.21% of the phenotypic variance. A QTL for carcass weight (CW) at 4 wk of age was identified on chromosome CJA01 at the suggestive level. Three QTL for breast weight (BRW) at 4 wk of age were identified on chromosomes CJA02, CJA01 and CJA09 at the 5% chromosome wide and the suggestive levels, the significant QTL explained 1.08% of the phenotypic variance. A QTL for breast percentage (BRP) at 4 wk of age was identified on chromosome CJA02 at the 5% chromosome wide; the significant QTL explained 1.10% of the phenotypic variance. The present study identified chromosome regions harboring significant QTL effecting BW and carcass traits. The results provide a useful reference for further candidate gene research and MAS for BW and carcass traits.

**Keywords**: breast weight, carcass weight, microsatellite marker, Japanese quail, quantitative trait loci

*Received:* 8 Jan. 2014, *accepted:* 27 Apr. 2014, *published online:* 7 May. 2014

## Introduction

The Japonica quail belongs to the Phasianidae family. It is wildly reared for egg and meat production in several countries of Asia, Europe and America (Minvielle, 2004).

Despite the large variety of traits that have been studied in the Japanese quail, until recently, only few linkage groups have been identified, and few genes have been mapped (Tsudzuki, 2008).

In 2000, an integrated comprehensive linkage map was constructed in chickens (Groenen et al., 2000; Schmid et al., 2000) on the basis of modern molecular techniques, including 51 linkage groups. Until 2005, over 900 microsatellite loci had been mapped in the integrated map with 31 chromosomes and 22 linkage groups in chicken (Schmid et al., 2005). On the other hand, in 2000, only 4 linkage groups (3 autosoms and Z chromosomes) were known in Japanese quail, with a few loci in each linkage group, due to the absence of DNA markers (Tsudzuki, 2008).

In chickens, the first report for QTL mapping appeared in 1998 on the basis of microsatellite DNA markers (Vallejo et al., 1998; Van Kaam et al., 1998). Science then, about 200 QTLs have been discovered for economic traits in chickens (Roussot et al., 2003).

There are at present only a few reports concerning QTLs in Japanese quails, although QTL mapping is possible with DNA markers in addition to the mapping of traits. Beaumont et al. (2005) tried to identify QTLs for body weight and 11 kinds of fear fullness-related traits with AFLP markers developed by Roussot et al. (2003). Furthermore, Minvielle et al. (2005) carried out QTL analysis using microsatellite markers developed by Kayang et al. (2004). Until now no report has been published on QTL for carcass traits in Japanese quails.

The objective of the present work was to produce the first set of QTL detected in Japanese quail for body weight and carcass traits at 4 week of age.

## Materials and methods

### *Experimental design*

The current F2 population was produced by crossing 2 short-term divergently selected lines for high weight (H line) and low weight (L line) at 4 wk of age ($P < 0.01$). They were maintained at in the Animal Science Research Center of the University of Tehran in Iran. Ten H males and twelve L females, and ten L males and twelve H females were crossed to produce F1 quails (HL and LH). F1 males were mated to two or three unrelated control females to create F2 individuals. The 4 largest half-sib families were chosen for QTL analysis. Each bird was identified with a leg- band. The birds were reared and slaughtered at 28 days of age. The F2 chicks were reared on floor pens. During the experimental period, feed (26% CP and 2900 kcal/kg ME) and water were supplied *ad libitum*.

### *Phenotyping*

Body weight (BW) was measured at hatch, 2 and 4 wk of age. Carcass weight (CW) and breast weight (BRW) were recorded at 4 wk of age. The BRW was also expressed as a percentage of BW at 4wk of age (BRP). Measurements were carried out on 650 individuals at hatch, 640 individuals at 2 wk of age and 635 individuals at 4 wk of age, carcass weight and breast weight.

### *Genetic analysis*

To estimate the heritability and genetic and phenotypic correlations among BW at different ages and carcass traits, bivariate analyses were performed using an animal model and the ASREML software package (Gilmour et al., 2002), using the following mixed model:

$$\begin{pmatrix} y1 \\ y2 \end{pmatrix} = \begin{pmatrix} X1 & 0 \\ 0 & X2 \end{pmatrix} \begin{pmatrix} b1 \\ b2 \end{pmatrix} + \begin{pmatrix} Z1 & 0 \\ 0 & Z2 \end{pmatrix} \begin{pmatrix} a1 \\ a2 \end{pmatrix} + \begin{pmatrix} e1 \\ e2 \end{pmatrix}$$

Where, $Y_1$ and $Y_2$ represent different traits. The vectors of fixed effects for trait1 and trait 2 are $b_1$, $b_2$. The vectors $a_1$ and $a_2$ are random additive genetic effects; $e_1$ and $e_2$ are the residual effects for trait 1 and trait 2, respectively. The incidence matrices $X_1$ and $X_2$ associate elements $b_1$ and $b_2$ with the records in $Y_1$ and $Y_2$. The expectation of $Y_1$ is $X_1b_1$, and that of $Y_2$ is $X_2b_2$. The fixed effects for the BW and carcass traits were sex and hatch with 2 levels.

### *Genotyping*

In this study, the three candidate regions on three chromosomes 1, 2 and 9 were selected for identify QTLs for measured traits. These candidate regions were selected from recent study (Minvielle et al., 2005) that QTL was detected for BW at 5 wk of age in these positions. Genomic DNA was isolated from blood samples using the salting out method (Helms, 1990). Polymerase chain reactions for each marker were carried out separately in a reaction volume of 25 µl including 2 µl template DNA, 2.5 µl 1x PCR reaction buffer, 1 µl primer, 1 µl deoxynacleotide triphosphate (dNTP), 1.5 µl magnesium Chloride (MgCl2), 0.25 µl Taq polymerase and deionized water. The PCR products were electrophoresed in 6% polyacrylamide gels. Fragment sizes were analyzed with TOTAL LAB analysis software (*http*:// www.totallab.com). All genotypes were checked twice. However, genotyping of birds from generations F1 (4 sires), F2 (635 individuals) were needed for half sib model analysis QTLs.

### *QTL analysis*

Phenotypic data were analyzed by using SAS software (SAS Institute Inc, 2000), and the mean, standard deviation and coefficient of variation were calculated.

For QTL analyses was been used the QTL express software under a half-sib model (*http*:// qtl.cap.ed.ac.ukl). Data subjected to a model with sex and hatch as fixed effects in the model. The percentage difference in the residual sums of squares between the full and reduced model was calculated as the phenotypic variance which that QTL could explain. Significant thresholds for analy-

**Table 1.** Descriptive statistics for various traits in the Japanese quail[1]

| Trait | N | Mean (g) | SD (g) | CV | Minimum (g) | Maximum (g) |
|---|---|---|---|---|---|---|
| BW0 | 650 | 8.83 | 0.95 | 9.87 | 7 | 11 |
| BW2 | 640 | 59.53 | 9.43 | 13.85 | 21.9 | 84.9 |
| BW4 | 635 | 149.48 | 22.5 | 12.73 | 67 | 200 |
| CW | 635 | 114.04 | 20.96 | 15.22 | 45 | 166 |
| BRW | 635 | 29.25 | 6.33 | 16.86 | 10.6 | 46.8 |
| BRP | 635 | 19.34 | 2.59 | 10.83 | 12.37 | 30.03 |

[1] Numbers following BW indicates the age in weeks;

CW= carcass weight; BRW=breast weight; BRP=BRW expressed as percentage of BW4

**Table 2.** Heritabilities (on diagonal), and genetic (above diagonal) and phenotypic (below diagonal) correlations of BW and carcass traits in Japanese quails[1]

| Variable | W0 | W2 | W4 | CW | BRW | BRP |
|---|---|---|---|---|---|---|
| W0 | **0.29±0.08** | 0.36±0.09 | 0.34±0.05 | 0.30±0.08 | 0.30±0.08 | 0.28±0.07 |
| W2 | 0.49±0.19 | **0.23±0.10** | 0.79±0.02 | 0.56±0.03 | 0.50±0.04 | 0.44±0.10 |
| W4 | 0.58±0.10 | 0.88±0.05 | **0.40±0.06** | 0.89±0.06 | 0.86±0.07 | 0.73±0.08 |
| CW | 0.32±0.08 | 0.69±0.04 | 0.97±0.06 | **0.33±0.09** | 0.94±0.05 | 0.88±0.12 |
| BRW | 0.32±0.08 | 0.64±0.04 | 0.93±0.07 | 0.99±0.08 | **0.39±0.07** | 0.92±0.09 |
| BRP | 0.31±0.03 | 0.51±0.07 | 0.77±0.10 | 0.89±0.14 | 0.98±0.12 | **0.37±0.10** |

[1]Numbers following BW indicates age in weeks,
CW= carcass weight; BRW=breast weight; BRP=BRW expressed as percentage of BW4

ses were calculated using a permutation test (Churchill and Doerge, 2000). A total of 1000 permutations were computed to determine the empirical distribution of the statistical test under the null hypothesis of no QTL associated with the part of genome under study. Three significance levels were used: suggestive, 5% and 1% chromosome-wide (Lander and Kruglyak, 1995).

## Results

### *Phenotypic data*

The mean and standard deviation of traits are shown in Table 1. The coefficient of variations of BW were from 9.87 (for BW at hatch) to 13.85 (for BW at 2 wk of age), and the carcass traits CV were higher (15.22 for CW and 16.86 for BRW) than for BW. The mean of body weight at 4 wk of age in H line (171.12± 12.31 g) was significantly higher than L line (137.5± 13.01 g) ($P < 0.01$).

### *Estimation of genetic parameters*

Estimated heritability of the BW at different ages as well as the genetic and phenotypic correlations among BW at different ages and carcass traits are presented in Table 2. Estimated heritabilities for BW at different ages and carcass traits were between 0.40(0.06) and 0.23 (0.10) (the heritability for BW at hatch and 2 wk of age was estimated with maternal effect). A positive phenotypic correlation was observed among all of traits. The highest phenotypic correlation (0.99±0.08) was recorded between carcass weight and breast weight. The lowest phenotypic correlation (0.31±0.03) was found between BW at hatch and breast percent. Moderate to high positive genetic correlations among different traits were found. The largest genetic correlation was (0.94±0.05) between breast weight and carcass weight, whereas the lowest correlation (0.28±0.07) was between breast percent and BW at hatch.

### *Half-sib Analysis*

The QTL for BW at hatch, 2 and 4 wk of age and CW, BRW and BRP, using the half-sib analysis model are presented in Table 3. Two QTL were found for BW at hatch. A very significant QTL was detected on CJA02, between marker brackets CUJ0063 and CUJ0027 with an F-ratio=7.51 and one suggestive QTL was detected on CJA01 between marker brackets CUJ0055 and CUJ0052 with an F-ratio=2.38. Three QTL were found for BW at 4 wk of age. A very significant QTL was detected on CJA01, between marker brackets CUJ0055 and

**Table 3.** Quantitative trait loci for BW and carcass traits in Japanese quails using the half-sib analysis model[1]

| BW | Chromosome | Marker bracket | Position (cM) | F-ratio[2] | QTL variance%[3] |
|---|---|---|---|---|---|
| BW0 | CJA01 | CUJ0055,CUJ0052 | 12 | 2.38† | 1.07 |
| BW0 | CJA02 | CUJ0063,CUJ0027 | 60 | 7.51** | 1.24 |
| BW4 | CJA01 | CUJ0055,CUJ0052 | 13 | 6.2** | 1.21 |
| BW4 | CJA02 | CUJ0063,CUJ0027 | 60 | 2.30† | 1.05 |
| BW4 | CJA09 | CUJ0071,CUJ0074 | 4 | 2.91† | 1.06 |
| CW | CJA01 | CUJ0055,CUJ0052 | 19 | 2.09† | 1.07 |
| BRW | CJA01 | CUJ0055,CUJ0052 | 7 | 2.96† | 1.07 |
| BRW | CJA02 | CUJ0063,CUJ0027 | 60 | 3.37* | 1.08 |
| BRW | CJA09 | CUJ0071,CUJ0074 | 1 | 2.65† | 1.06 |
| BRP | CJA02 | CUJ0063,CUJ0027 | 60 | 4.06* | 1.10 |

[1]Numbers following BW indicates age in weeks;
CW= carcass weight; BRW=breast weight; BRP=BRW expressed as percentage of BW4

[2]†Denotes suggestive linkage; *denotes chromosome wide significant at the 5% level; **denotes chromosome wide significant at the 1% level

[3]Proportion of total variance explained by the QTL

CUJ0052 with an F-ratio=6.20. Two suggestive QTL were detected, one on CJA02 between marker brackets CUJ0063 and CUJ0027 with an F-ratio=2.30 the second one on CJA09 between marker brackets CUJ0071 and CUJ0074 with an F-ratio=2.91. One suggestive QTL was found for CW at 4 wk of age on CJA01 between marker brackets GUJ0055 and CUJ0052 with an F-ratio=2.09 Three QTL were found for BRW at 4 wk of age. A significant QTL was detected on CJA02, between marker brackets CUJ0063 and CUJ0027 with an F-ratio=3.37. Two suggestive QTL were detected, one on CJA01 between marker brackets CUJ0055 and CUJ0052 with an F-ratio=2.96, and the second one on CJA09 between marker brackets CUJ0071 and CUJ0074 with an F-ratio=2.65. One significant QTL was found for BRP at 4 wk of age on CJA02, between marker brackets CUJ0063 and CUJ0027 with an F-ratio=4.06.

In Figure 1 shows the detected QTLs for studied traits with interval mapping model on 3 chromosomes 1, 2 and 9. Significant thresholds of QTLs on chromosome are significant ($P < 0.05$) and very significant ($P < 0.01$).

## Discussion

In general, the line-cross analysis model is claimed to be more powerful than half-sib analysis, but only if the alleles in founder lines are fixed (Weller, 2001). The founder lines of the present experimental population were short-term divergently selected for BW at 4 wk of age. Therefore, it is unlikely that the QTL alleles for BW were fixed in the founder population and therefore, half-sib model were perfect to line-cross model.

The QTL affecting BW at hatch to 4 wk of age and carcass traits were located in the regions 1 to 20 cM on chromosome 1, 44 to 60 cM on chromosome 2 and 1 to 20 cM on chromosome 9. Kerje et al. (2003) indicated that when the 2 QTL positions differed by a recombination distance of <30 cM in a chromosomal region, a single QTL for the given traits was assumed on that chromosome. Therefore, it is likely that the detected QTLs for BW at 4 wk of age, CW and BRW located at 13, 19 and 7 cM on CJA01 and also, detected QTLs for BW at 4 wk of age, BRW and BRP located at 60 cM on CJA02, represented a single gene or linked genes. The current results were also supported by high genetic correlations between BW at 4 wk of age and carcass traits. Indeed, body weight and carcass weight are known to be highly correlated genetically (0.50 to 0.90) in poultry (Chambers, 1990). In this study, correlations between these traits were 0.30 to 0.94 in the F2 population. No QTL for BW at 2 wk of age was detected, suggesting that distinct sets of genes are involved at this age and later ages. A very significant QTL detected on CJA01 for 4 wk of age in the studied population was located in the same marker bracket as the one detected by Minvielle et al. (2005) for BW at 5 wk of age. This finding confirmed the region on CJA01 as related to growth traits.

Significant QTL for body weight in the chicken were only reported repeatedly on GGA01 (Van Kaam et al., 1999; Kerje et al., 2001; Tatsuda and Fujinaka, 2001; Sewalem et al., 2002; Jennen et al., 2005). Moreover, in three chicken studies where both BW and body composition were measured, QTL were found at the same position for body weight, carcass weight and breast weight on GGA01 (Nones et al., 2005; Park et al., 2006; Liu et al., 2007) as found on CJA01 in the present work. Overall, the largest chicken and quail chromosomes might contain important and homologous QTL for growth. It is unlikely that these converging results obtained independently in two species from the family phasianidae were coincidental. Consequently, they should raise interests in looking further for this type of effect in the avian species (where reciprocal effects are common).

Another interesting observation was that 10 growth QTLs detected in this intercross explained only 1.05-1.24% of the residual phenotypic variance for body weight or carcass traits. Growth is a highly complex trait affected by many loci influencing the appetite, feed intake, nutrient utilization, body composition, physical activity and so forth. This means that any individual locus affecting growth in this cross explains only a rather small fraction of the genetic variance.

In summary, commercial breeding programs of Japanese quails have become more complex and challenging because many objectives need to be simultaneously considered to reduce production costs, maintain health and improve product quality. Breeding goals must include increased growth rate, increased % breast weight, maintenance of good development and growth of the skeletal system and overall fitness. The relationships of these traits are complex and some traits are very difficult to measure. Therefore, molecular MAS may be required to improve genetic selection programs. The current study found that there exit significant QTL affecting BW and carcass traits on chromosome 1, 2 and 9. This is the first step toward the fine mapping QTL affecting BW and carcass traits. With focus on the QTL identified on chromosome 1 (in the chicken, the gene for the insulin-like growth factor-IA is associated with growth (Vasilatos-Younken et al., 2000), valuable candidate genes may be found by combining results of fine mapping and the Japanese quail genome sequence, and further function study of the genetic background of growth and carcass traits of Japanese quail.

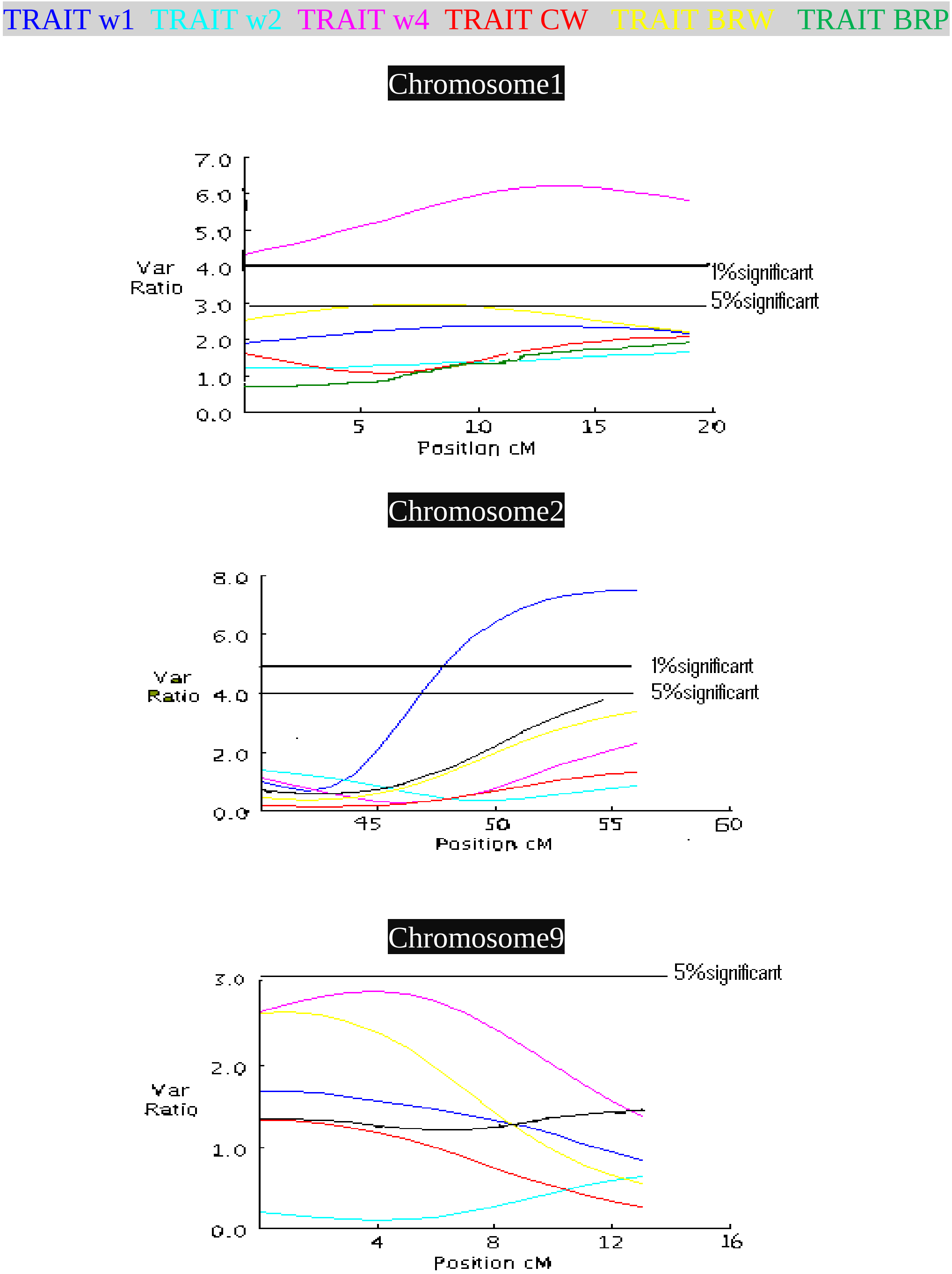

**Figure 1.** Interval mapping of QTL on chromosome 1, 2 and 9.

## Acknowledgments

The authors thank the International Center for Science, High Technology & Environmental Science for financial support and requirements of laboratory.

## References

Abasht, B., Dekkers, J.C.M., Lamont, S.J., 2006. Review of quantitative trait loci identified in the chicken. *Poultry Science* 85, 2079-2096.

Beaumont, C., Roussot, O., Fève, K., Plisson-Petit, F., Leroux, S., Pitel, F., Faure, J.M., Mills, A.D., Guémené, D., Leterrier, C., 2005. Genetic analysis of tonic immobility in Japanese quail with AFLP markers. *Animal Genetics* 36, 000-000.

Chambers, J.R., 1990. Genetics of growth and meat production in chicken. In Poultry Breeding and Genetics Edited by:

Crawford RD. Amsterdam: Elsevier, 599-643.

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

Gilmour, A.R., Cullis, B.R., Welham, S.J., Tompson, R., 2002. ASREML. NSW Agriculture, Orange, Australia

Groenen, M.A.M., Cheng, H.H., Bumstead, N., Benkel, B.F., Briles, W.E., Burke, T., Burt, D.W., Crittenden, L.B., Dodgson, J., Hillel, J., 2000. A consensus linkage map of the chicken genome. *Genetic Research* 10, 137-147.

Helms, C., 1990. Salting out procedure for human DNA extraction. In the doniskeller lab- lab manual home page. Protocol online. Available at http://hdkklab.Wustl.edu/lab manual/dna/dna2.html.

Jennen, D.G.J., Vereijken, A.L.J., Bovenhuis, H., Crooijmans, R.M.P.A., van der Poel J.J., Groenen, M.A.M., 2005. Confirmation of quantitative trait loci affecting fatness in chicken. *Genetic Selection Evolution* 37, 215-228.

Kayang, B.B., Vignal, A., Inoue-Murayama, M., Miwa, M., Monvoisin, J.L., Ito, S., Minvielle, F. 2004., A first generation micro satelite linkage map of the japaneas quail. *Animal Genetics* 35, 195-200.

Kerje, S., Carlborg, Ö., Jacobsson, L., Schütz, K., Hartmann, C., Jensen, P., Andersson, L., 2003. The twofold difference in adult size between the red jungle fowl and White Leghorn chickens is largely explained by a limited number of QTLs. *Animal Genetics* 34, 264-274.

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

Liu, X., Li, H., Wang, S., Hu, X., Gao, Y., Li, Q., Wang, N., Wang, Y., Zhang, H., 2007. Mapping quantitative trait loci affecting body weight and abdominal fat weight on chicken chromosome one. *Poultry Science* 86, 1084-1089.

Minvielle, F., 2004. The future of Japanese quail for research and production. *World's Poultry Science* 60, 500-507.

Minvielle, F., Kayang, B.B., Inoue-Murayama, M., Miwa, M., Vignal, A., Gourichon, D., Neau, A., Monvoisin, J.L., Ito, S., 2005. Microsatellite mapping of QTL affecting growth, feed consumption, egg production, tonic immobility and body temperature of Japanese quail. *BMC Genetics* 6, 87-96.

Nones, K., Ledur, M.C., Ruy, D.C., Baron, E.E., Melo, C.M.R., Moura, S.A.M.T., Zanella, E.L., Burt, D.W., Coutinho, L.L., 2005. Mapping QTLs on chicken chromosome one for performance and carcass traits in a broiler*layer cross. *Animal Genetics* 37, 95-100.

Park, H., Jacobsson, L., Wahlberg, P., Siegel, P.B., Andersson, L., 2006. QTL analysis of body composition and metabolic traits in an intercross between chicken lines divergently selected for growth. *Physiological Genomics* 3, 1-21.

Roussot, O., Fève, K., Plisson-Petit, F., Pitel, F., Faure, J.M., Beaumont, C., Vignal, A., 2003. AFLP linkage map of the Japanese quail *Coturnix japonica*. *Genetic Selection Evolution* 35, 559-572

SAS . 2000. SAS Release 8e. SAS, Institute Inc., Cary, NC.

Schmid, M., Nanda, I., Guttenbach, M., Steinlein, C., Hoehn, H., Schartl, M., Haaf, T., Weigend, S., Fries, R., Buerstedde, J.M., 2000. First report on chicken genes and chromosomes. *Cytogenetic and Genetic Research* 90, 169-218.

Schmid, M., Nanda, I., Hoehn, H., Schartl, M., Haaf, T., Buerstedde, J.M., Arakawa. H., Caldwell, R.B., Weigend, S., Burt, DW., 2005. Second report on chicken genes and chromosomes. *Cytogenetic and Genetic Research* 109, 415-479.

Sewalem, A., Morrice, D.M., Law, A., Windsor, D., Haley, C.S., Ikeobi, C.O., Burt, D.W., Hocking, P.M., 2002. Mapping of quantitative trait loci for body weight at three, six, and nine weeks of age in a broiler layer cross. *Poultry Science* 81, 1775-1781.

Tatsuda, K., Fujinaka, K., 2001. Genetic mapping of the QTL affecting body weight in chickens using a F2 family. *British Poultry Science* 42, 333-337.

Tsudzuki, M., 2008. Mutations of Japanese quail (coturnix japonica) and recent advances of molecular genetics for this species. *Journal of Poultry Science* 45, 159-179.

Vallejo, R.L., Bacon, L.D., Liu, H.C., Witter, R.L., Groenen, M.A.M., Hillel, J., Cheng, H.H., 1998. Genetic mapping of quantitative trait loci affecting susceptibility to Marek's disease virus induced tumors in F intercross chickens. *Genetics* 148, 349-360.

Van Kaam, J.B., Van Arendonk, J.A.M., Groenen, M.A.M., Bovenhuis, H., Vereijken, A.L.J., Crooijmans, R.P.M.A., Van der Poel, J.J., Veenendaal, A., 1998. Whole genome scan for quantitative trait loci affecting body weight in chickens using a three generation design. *Livestock Production Science* 54, 133-150.

Van Kaam, J.B., Groenen, M., Bovenhuis, H., Veenendaal, A., Vereijken AL, van Arendonk, J.A., 1999. Whole genome scan in chickens for quantitative trait loci affecting growth and feed efficiency. *Poultry Science* 78, 15-23.

Vasilatos-Younken, R., Zhou, Y., Wang, X., McMurtry, J.P., Rosebrough, R.W., Decuypere, E., Buys, N., Darras, V.M., der Geyten, S., Tomas, F., 2000. Altered chicken thyroid hormone metabolism with chronic growth hormone (GH) enhancement in vivo: consequences for skeletal muscle growth. *Journal of Endocrinology* 166, 609-620.

Weller, J.I., 2001. Quantitative trait loci analysis in animals. CABI Publishing, London.

---

***Communicating editor:** Mohammad Reza Mohammadabadi*

# نقشه یابی جایگاههای صفات کمی برای صفات وزن بدن و لاشه در بلدرچین ژاپنی

ا.رضوان نژاد

**نویسنده مسئول، پست الکترونیک:** rezvannejad2002@yahoo.com

**چکیده** وزن بدن و لاشه از صفات اقتصادی مهم و پیچیده هستند که انتخاب بر اساس مارکرها در مورد انها می تواند سودمند باشد. هدف از تحقیق حاضر تشخیص QTL مرتبط با صفات وزن بدن و لاشه در مدل آزمایشگاهی ناتنی ها در بلدرچین ژاپنی انتخاب شده بر اساس وزن بدن در چهار هفتگی از سن بود. صفات وزن بدن و لاشه در جمعیت F2 اندازه گیری شدند. کل افراد F2 و والدین آنها بر اساس ۶ مارکر ریزماهواره بر روی کروموزومهای ۱،۲ و ۹ ژنوتایپ شدند. نقشه یابی فاصله ای جهت تشخیص QTLهای موثر استفاده شد. دو QTL برای وزن در زمان تولد بر روی کروموزومهای CJA02 وCJA01 در سطح ۱٪معنی داری و پیشنهادی شناسایی گردید، که QTLمعنی دار ۱/۲۴٪ واریانس فنوتیپی را شرح می داد. برای وزن بدن در چهارهفتگی از سن، سه QTL بر روی کروموزومهای CJA01, CJA02وCJA09 در سطح ۱٪معنی داری و پیشنهادی شناسایی گردید، که QTLمعنی دار ۱/۲۱٪ واریانس فنوتیپی را شرح می داد. یک QTL برای وزن لاشه در چهار هفتگی از سن در سطح پیشنهادی بر روی کروموزوم CJA01 شناسایی شد. سه QTL برای وزن سینه در چهار هفتگی از سن بر روی کروموزومهای CJA01, CJA02 و CJA09در سطح۵٪ معنی داری و پیشنهادی شناسایی گردید که QTL معنی دار ۱/۰۸٪ واریانس فنوتیپی را شرح می داد. یک QTL برای درصد سینه در چهار هفتگی از سن در سطح ۵٪ معنی داری بر روی کروموزوم CJA01 شناسایی شد که QTL معنی دار ۱/۱۰٪ واریانس فنوتیپی را شرح می داد. تحقیق حاضر نواحی کروموزومی موثر بر صفات وزن بدن و لاشه را مورد بررسی قرار داد. این نتایج می تواند در آینده جهت مطالعات ژنهای کاندید در این نواحی از ژنوم و انتخاب بر اساس مارکرها در صفات وزن بدن و لاشه مورد استفاده قرار گیرند.