Iranian Journal of Animal Science Research
Vol. 9, No. 1, Spring 2017, p. 125-134

نشریه پژوهشهای علوم دامی ایران
جلد ۹، شماره ۱، بهار ۱۳۹۶، ص. ۱۳۴-۱۲۵

Analysis of Additive, Dominance and Imprinting QTL Effects by Sex and Hatch Interactions on Some Traits of Japanese Quail on Chromosome 5

M. Ahmadi[1]- A.K. Esmailizadeh[2]*- E. Nasirifar[3]

Received: 07-01-2016
Accepted: 04-04-2016

Introduction The purpose of breeding is to rear animals which are biologically and economically important. Among the domestic species, the poultry, due to the large number of offspring per parent and short generation interval, enable researchers to run breeding programs even on small farms. In this regard, quail because of certain characteristics: short generation interval, large numbers of eggs, disease resistance, and low cost farming is of great interest to biologists and commercial growers. Japanese quail (*Coturnix coturnix* japonica) has been grown for the production of meat and eggs in Asia and for its meat in Europe and America during the recent years. Despite the great diversity of traits in Japanese quail, only a limited number of genes and linkage groups related to the bird have been identified. Japanese quail belongs to the order Galliformes and the Phasianidae family. The considerable phylogenetic similarity between quail and chickens in the number of chromosomes and the genome size makes the quail qualified enough as a model for studies on poultry. Furthermore, the similarities between 9 chromosomes and chromosome Z in quail and chicken have been confirmed and following the divergence, only small numbers of chromosomes of the two species have changed. In recent years, the attempts at mapping of quail genome based on the segregation and identification of microsatellite markers has begun and 50 microsatellite markers were identified in quail. This study examined F2 population of Japanese quail to find the loci for carcass traits on chromosome 5 using microsatellite markers. The population included crosses of two strains of Japanese quail (white and wild strains) and the traits examined included weights of hot and cold carcasses, internal organs and carcass parts.

Materials and Methods Polymerase chain reaction (PCR) amplifications of each marker for 472 birds were carried out on a Thermal Cycler (Eppendorf, UK). Afterward, the population was genotyped using AlphaEaseFC 4.0 software for each marker. Parental (P0), F1 and F2 individuals were genotyped with 3 microsatellite markers. A genetic model, line-cross, was applied for QTL interval mapping analyses using the regression method in the GridQTL software. Data analysis was performed with least squares regression interval mapping method. The line-cross analysis employed the models including joint effects of additive, dominance and imprinting. The QTL by sex interaction was assessed to determine whether the effect did differ between the two sexes. The additive QTL effect by hatch interaction was also analyzed.

Results and Discussion Significant QTLs were identified for carcass efficiency, breast percentage and breast weight, liver percentage and liver weight, back weight and back percentage, spleen weight and spleen percentage, gizzard and head on chromosome 5. The QTL for breast weight and percentage were identified at 19 cM (in position marker GUJ0100) on chromosome 5. The QTL for head weight and percentage and weight of back were identified at 12 cM (in position marker GUJ049) on chromosome 5. Other QTLs were mapped at 10 cM for carcass efficiency and spleen weight, at 0 cM for Gizzard weight, at 17 cM for head weight, at 15 cM for weight of liver, at 16 cM for liver percentage and at 11 cM for spleen percentage. The proportion of the F2 phenotypic variation explained by the significant additive, dominance and imprinting QTL effects ranged from 2.22 to 11.11%. In the current study, QTL affecting different traits were mapped to similar chromosomal regions. These evidence are indicative of genetic correlation among traits and correlated response to selection. If these traits are really controlled by the same pleiotropic QTL or by closely linked QTL, therefore they are in linkage disequilibrium (LD). However, higher resolution analysis is required to distinguish LD from pleiotropic.

Conclusion The present study identified informative QTL regions that may form a useful resource as part of our advance on developing DNA tests for carcass quality and internal organs in Japanese quail. However, it should be noted that to identify candidate genes and informative markers in linkage disequilibrium with QTL

1- Former MSc. Student, Department of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman, Iran,
2- Professor of Animal Sciences Department, Faculty of Agriculture, Shahid Bahonar University of Kerman, Iran,
3- Former PhD Student, Department of Animal Science, Science and Research Branch of Islamic Azad University, Tehran, Iran.
(*- Corresponding Author Email: aliesmaili@mail.uk.ac.ir)

affecting carcass and internal organs traits, association studies using SNP markers may be needed for the significant QTL regions detected in this study. The results showed that the identified positions for some carcass and internal organs traits on chromosome 5 were similar to the characteristics of quantitative traits (including pleiotropic and epistasis effects) and can be effective in phenotypic differences of trait. Such results are indicative of genetic correlation among traits and correlated response to selection.

Keywords: Carcass traits, Chromosome 5, F2 population, Japanese quail, QTL.