

Abstract

The aim of this study was to identify local growth control genes on chromosome 1 in Japanese quail (*Coturnix japonica*). For this purpose, the quail population from a four-generation cross pattern was used. To create the first generation, four Japanese quail (*Coturnix japonica*) strains, including A and M Texas, Wild, Italian Speckled and Tuxedo, were crossed in *diallel cross* and backcross. Then, from the hybrid bird cross, a mapping population was created, including the second, third and fourth generation. Blood samples of all these birds were collected from the vein under the wings in tubes containing 0.5% EDTA for DNA extraction and genotyping of microsatellite markers on chromosome 1. Observations included weight records from birth to 45 days (every 5 days). Data analysis was performed with three models including additive, dominance and additive-dominance with multiple regression model with GVCBLUP software. Significance of QTLs was performed by *the Bonferroni correction method* ($P < 0.05$) and also for estimating QTL location, bootstrap method with ten thousand series of replications was used. *Analysis of QTL for weight traits including 10, 15, 40 and 45 days old in additive and dominance models showed that QTL was effective in the middle of chromosome 1. The results of QTL analysis for 20 and 25 days old weight traits showed that the effective QTL is in the middle in the additive model and at the end of chromosome 1 in the dominance model. For the 30-day-old weight trait, the results of additive and dominance models indicated a QTL affecting the growth trait at the end of chromosome 1. Finally, QTL analysis for 35-day-old weight trait in the additive model and QTL dominance affecting the mentioned trait were identified in the middle of chromosome 1. Therefore, the results of this Thesis confirm the existence of at least one influential position on growth traits in Japanese quail (Coturnix japonica).*

Keywords: Japanese quail, Diallel cross, genomic scan, body weight traits



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