Abstract

Immune traits are very important because of their direct relationship with the growth traits and the economic value of quail breeding, but a little genomic research has been done to find quantitative trait loci (QTLs), especially immunity trait. Therefore, the purpose of this study was to investigate the part of the Japanese quail genome in order to detect QTL affecting on immunity traits in quail using a four-generation crossover design. For this purpose, four strains of A and M Texas, Wild, Italian Speckled and Tuxedo Japanese quails were mated as reciprocal crossed for creating the first generation. Then, another generation, including the second, third and fourth generations were created from the crossing of the first generation hybrid birds, . Phenotypic data included traits related to the innate and acquired immunity of birds, including T, M and Y immunoglobulins. The third and fourth generation parents and all birds from the fourth generation parents were genotyped for three microsatellite markers located on the chromosome 5. QTL analysis was performed by interval mapping based on regression with GridQTL software. Three adjacent QTLs in the middle of chromosome 5 for the three IgT, IgM, and IgY was identified at the positions 13.5, 8.9, and 14.7 cm near the marker GUJ0049, respectively. Therefore, the results showed there is at least one gene locus with a major effect on immunity traits that adjacent to the marker GUJ0049, and adding the information of the mentioned marker genotypes to the statistical models can improve the accuracy of prediction breeding values of immunity traits in quail.

Key words: Genome scan, Immunity traits, Bootstraping, Permutation test.

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