Abstract

Growth traits related to animal domestic are important because of their direct economic benefit. A little genomic research has been done to find quantitative trait loci (QTLs), especially for growth traits in Japanese quail. Therefore, the aim of this study was to investigate a partial genome scan of Japanese quail to detect of QTL affecting quail growth traits based on a four-generation cross-sectional design. For this purpose, four strains A and M of Texas, Wild, Italian Speckled and Tuxedo Japanese quails crossed in two strains reciprocal and were created first generation. Then, due to the intersection of the first-generation hybrid birds, subsequent generations, including the second, third and fourth generations were created. The phenotypic data, including birth weight measurements up to 45 days old were collected in 5 day intervals on this population. The estimated heritability of weight traits, including the weight of the hatch, 5, 10, 15, 20, 25, 30, 35, 40 and 45 days of age were 0.378, 0.199, 0.468, 0.137, 0.148, 0.123, 0.134, 0.44, 0.47, 0.25, respectively. Grandparents and parents and all of birds of fourth generation were genotyped for a three microsatellite markers. The QTL analysis was carried out using a regression-based interval mapping method and by using Gridqtl software. The results showed the three different QTLs for hatch weight, weight 15 and 20 days of age in 4.65, 16.03 and 15.63 cM, respectively. Therefore, if the adjacent marker information is entered in the equation of estimate breeding values, it can lead to improved prediction breeding value and ultimately genetic progress.

Keywords: Genomic Scan, Traits, Bootstrapping

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Genetic diversity and interpolation of loci controlling growth traits in Japanese quail

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