

Finding and identifying QTLs in Japanese quail (*Coturnix japonica*)

Summary

The Japanese quail genome has received relatively little study. Despite significant interest in the search for QTL in poultry, particularly chickens, there has been little research devoted to the identification of QTL regions in Japanese quail. Studies by various researchers have led to the identification of QTLs for laying capacity, body weight, feed efficiency and growth in Japanese quail. Molecular monitoring has been conducted since 2004 in an experimental herd of Japanese quail selected for increased body weight, belonging to the Department of Genetics and Animal Breeding, Faculty of Animal Sciences, SGGW. Analysis of relationships between quantitative traits and genotype with regard to microsatellite sequences confirmed that a given allelic form usually occurred in birds with higher or lower values for these traits. In the 10th generation, carriers of some alleles of ADL0024, ADL0106, ADL0134, ADL0142, ADL0143, ADL0255, ADL0272, GUJ0001, GUJ0014, GUJ0052 and GUJ0087 had higher values for the traits analysed than birds which did not have these alleles in their genotype. Analysis of marker genotypes demonstrated that some alleles of ADL0024, ADL0134, ADL0142, ADL0143, ADL0255 and GUJ0001 were associated with increased body weight at 28 days of age, which was the basis for selection in the population investigated. These findings have enabled the genome of the Japanese quail to become better known and in the near future may lead to sequencing of its genome, thus contributing to a more comprehensive use of this species as an animal model in research.

KEY WORDS: Japanese quail, QTL, microsatellite sequences