PRODUCTIVE PERFORMANCE AND MOLECULAR GENETIC CHARACTERIZATION OF BROWN AND WHITE JAPANESE QUAIL GENOTYPES USING RAPD AND ISSRs-PCR MARKERS

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The aims of the present study were to characterize the possible genetic and productive traits differences associated with the plumage colour in two genotypes of Japanese quail. Productive performance and DNA markers were used to identify these genotypes.

Genotype effect showed that the brown genotype had significantly heavier body weight (BW) at 7, 14 and 21 days of age and longer shank length (SL) at all studied ages, except for 1 and 14 days than the white genotype.

Sex effect on BW and SL was significant at all studied ages, except for one day old, females had significantly higher BW and SL than males. The interaction effect between genotype and sex on BW was significant at all studied ages except for one day old. The interaction effect between genotype and sex on SL was significant at all studied ages, except for 1 and 14 days.

Brown genotype had significantly heavier BW at first egg than the white genotype. The white genotype had significantly higher shape index than brown genotype. The brown genotype matured at earlier age ($P \leq 0.05$) than the white genotype and had shorter days ($P \leq 0.05$) to produce the first 30 eggs, and had shorter days ($P > 0.05$) to produce the first 10 eggs than the brown genotype. Brown genotype laid significantly more number of eggs during the first, the second and the first two months than the white genotype and had significant higher egg mass during the different study periods.

From the present results, it can be concluded that brown genotype had favored growth traits and most of egg production related traits during annual egg production.

The level of polymorphism among two Japanese quail genotypes brown and white, was estimated using two PCR-based marker techniques RAPD and ISSRs. Six RAPD and 6 ISSRs primers were employed to find out genetic variations and relationships among these genotypes of quail. RAPD and ISSRs analysis generated a total number of 442 and 467 amplicons representing a level of polymorphism of 74.24% and 72.86%, and an average number of polymorphic fragments/primer of 8.17 and 8.5, respectively. The genetic relationships among the 10 individuals of quail were estimated in terms of similarity using Dice coefficients. The genetic similarity ranged from 0.00-1.00 for RAPD, ISSRs, and RAPD and ISSRs combination. The inter-genotype relationships among the two quail genotypes based on RAPD, ISSRs, and RAPD and ISSRs combination revealed the highest genetic similarity between the genotype brown male (5) and brown female (2), white female (7) and brown female (1), and white female (6) and brown female (1), respectively. The inter-genotype relationships among the two quail genotypes based on RAPD, ISSRs, and RAPD and ISSRs combination revealed the lowest genetic similarity between the genotype brown female (2) and brown female (1), white female (7) and white female (6), and white female (7) and white female (6), respectively.

The RAPD based dendrogram clustered the brown genotype female and male, and white genotype females and males in the same group while, brown female and brown male genotypes were in separate clusters.