MICROSATELLITE POLYMORPHISM SELECTING LOCI IN A JAPANESE QUAIL (*COTURNIX JAPONICA*) POPULATION

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The Japanese quail (*Coturnix japonica*), a species of poultry, is both a meat and egg producer and a laboratory animal. Work on the quail genome is recently initiated. Here we described the analysis of microsatellite DNA polymorphism in a Japanese quail population. The study included both males and females. Genomic DNA was extracted from their blood by phenol-chloroform extraction. Then molecular analysis was performed by using the polymerase chain reaction (PCR) for the following microsatellite markers, isolated from chickens microsatellite DNA-enriched library: ADL0206 (number of birds - n = 24), ADL0037 (n = 43), ADL 0315 (n = 43) and HUJ0006 (n = 31). The PCR was performed at various annealing temperatures for the various markers: 47°C (ADL0037), 50°C (ADL0315) and 61°C (ADL0206, HUJ0006), each for thirty cycles, preceded and followed by 30 cycles at 95°C and 72°C, respectively. The PCR amplification products were separated in 10% nondenaturing polyacrylamide gel. Then, the gel was silver-stained and scanned (Epson GT - 9000). The length of alleles was determined using a Scan Pack 3.0 program (Biometra). Thirty five alleles ADL0037 (length 148bp – 224bp), 19 alleles HUJ0006 (81bp – 127bp), 14 alleles ADL0206 (87bp – 127bp) and 12 alleles ADL0315 (244bp – 268bp) were detected. Microsatellite polymorphism was detected in all of the tested loci. The highest frequency was observed in: alleles ADL0037, 178bp length (0.081); HUJ0006 – 103bp and 105bp (0.18), ADL0206 - 103bp (0.21) and ADL0315 - 254bp and 258bp (0.19). The data allowed to calculate the following percentage of homozygotes in quail population: 16.3% for ADL0037; 12.9% - HUJ0006; 100% -ADL0315; 37.5% - ADL0206. Heterosigosity was as follows: 97.1% for ADL0037; 89.5% - HUJ0006; 87.8% - ADL0315 and 91.4% - ADL0206. The high heterosigosity calculated for the loci analysed suggests that there is a possibility to use these microsatellites as genetic markers.