

The use of the chicken microsatellite markers in the study of genetic variability of Japanese quail (*Coturnix japonica*) experimental population

S u m m a r y

The study was conducted on 98 birds originated from the experimental population of Japanese quail (*Coturnix japonica*). Genomic DNA was extracted from their blood by phenol-chloroform extraction. The molecular analysis was performed by using the polymerase chain reaction (PCR) for the microsatellite markers, isolated from the chicken microsatellite DNA-enriched library. The PCR products were analysed using Sequencer ALF Express II (Pharmacia LKB). Microsatellite polymorphism was detected in all of the tested loci. We detected 6 alleles in locus ADL0142; 7 in ADL0143; 9 in ADL0272 and 6 alleles in locus MCW0088. The result was quite different from those obtained by Pang et al. [16] and Inoue-Murayama et al. [8] who found only 3 and 1 alleles in two first mentioned loci. For the first time it was proved that chicken markers ADL0272 and MCW0088 can be amplified also in quails and there are microsatellite sequences too. Significant differences in the allele frequency distribution depending on the sex for the ADL0142 and ADL0272 were stated. The high heterozygosity (H_e) 0.82 (ADL0142); 0.72 (ADL0143); 0.88 (ADL0272); 0.73 (MCW0088) and polymorphism information content (PIC) 0.79; 0.7; 0.87; 0.7, respectively, suggests that there is a possibility to use these microsatellites as genetic markers.