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Preliminary results of application of chosen DNA sequence primers of *Canis familiaris* in amplification of *Nyctereutes procyonoides* genom parallel loci

The purpose of the study was to evaluate usefulness of primer sequences designed for amplification of genes' fragments and microsatellite loci of *Canis familiaris* to analyze analogous loci in genom of *Nyctereutes procyonoides*. After isolation of DNA from raccoon dogs blood, its quantitative and qualitative evaluation, the amplification of DNA by the PCR method was conducted. Fragments of 4 genes as well as 20 microsatellite sequences were taken into consideration. Primers of *Canis familiaris* DNA sequences were used for amplification of analogous loci of raccoon dog genom. Qualitative and quantitative control of PCR reaction as well as analysis in UV was performed. PCR products of 24 examined DNA sequences were obtained. They showed homology of flank sequences of DNA individual fragments of both studied species of *Canidae* family (*Canis familiaris*, *Nyctereutes procyonoides*). Results obtained from the research proved the possibility of estimating the raccoon dog genetic variability on the basis of polymorphism of genes as well as the second class genetic markers i.e. DNA microsatellite sequences and allowed to conduct the evaluation of usefulness of studied DNA sequences to control the quality of raccoon dog functional and performance traits.