Variability in sequences of mitochondrial cox1 and nadh1 genes in Toxocara canis, Toxocara cati, and Toxascaris leonina (Nematoda: Toxocaridae) from different hosts

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Sequences of two mitochondrial genes, cox1 and nadh1 were analysed in T. canis, T. cati, and T. leonina from foxes (T. canis, T. leonina) and cats (T. cati) from north-western Poland. The DNA was isolated with Genomic Mini kit from A & A Biotechnology. The primers (JB3, JB 4.5 for cox1 and ND1F, ND1R for nadh1) and PCR conditions were set according to Li et al. (2008). The products of amplification were sequenced. No intraspecific variability in cox1 and nadh1 was found in any of the three species of nematodes for all individuals examined. However, when our amplicons were compared with sequences available in the gene bank (using BLAST), in all species examined some polymorphic variability was noticed. In T. canis from foxes in Poland, the sequence of cox1 differed from sequences of that gene in nematodes obtained from dogs, jackals, and polar foxes from different parts of the world in the range of 0.5%–2.7%. Nadh1 in T. canis from foxes in Poland and from dogs, wolves, and polar foxes from other regions revealed polymorphism in the range of 0.4%–2.3%. Cox1 in T. cati from cats in Poland showed variability in comparison with the nematodes from cats in other regions of the world at the level of 0.3%–1.7%. This species has shown a much higher polymorphism in cox1, when our sequences were compared with sequences of nematodes from jungle cats and Bengal cats – the differences reached 5.7% and 6.6%, respectively. Nadh1 in T. cati from cats in Poland differed from the gene from cats in other regions of the world at the level 0.3%–3% while, if compared with the same gene from T. cati found in catopuma, the difference was 10.4%. The highest polymorphism was noted in cox1 and nadh1 in T. leonina. Comparing sequences of cox1 in nematodes from foxes in Poland with sequences obtained from dogs, wolves, lynx, and tigers living in different regions of the world, variability was at the level of 4.5%–5.3% and for nadh1 the differences were higher: 8.4%–10%. All the polymorphic changes in the analysed sequences were classified as transitions. The interspecific divergences of cox1 gene sequences between T. canis and T. cati was 10.4%, T. canis and T. leonina – 8.4%, and T. cati and T. leonina – 10.6%. The differences for nadh1 were 13.8%, 16.6%, and 17.7%, respectively.