

## 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.