

Genetic variation in the mitochondrial cytochrome c oxidase subunit 1 (cox1) gene of *Enterobius vermicularis* (Nematoda) in Poland: a preliminary study

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The pinworm, *Enterobius vermicularis* is one of the most common human intestinal parasites. The knowledge, however, of its genetic variability and epidemiology based on the molecular typing of pinworms in humans is fragmented.

The aim of this study was to investigate the genetic variation within *E. vermicularis* in the human population in Poland. The study material was DNA individually extracted from two adult females obtained from faecal samples, and from one female with eggs found on one cellophane tape sample collected from children in Olsztyn (north-eastern Poland). In the PCR method, primers (EVM1/EVM2) (Piperaki et al. 2011) targeting the region of the *E. vermicularis* mitochondrial cytochrome c oxidase subunit 1 (*cox1*) gene (Accession no. EU281143) were used. Three PCR products (390 bp) were successfully sequenced (Macrogen Europe, the Netherlands). Sequences were aligned and trimmed to a length of 333 bp according to previously published *cox1* alignments (Nakano et al. 2006, Piperaki et al. 2011, Ferrero et al. 2013). Phylogenetic analysis was performed using the neighbour-joining method in the Geneious 7.0 software created by Biomatters. A consensus tree was constructed using the bootstrap resampling method with 1000 replicates.

All three *E. vermicularis* isolates represented different haplotypes. Nucleotide variation among the sequences were found in two positions and located at the third position of codons. There were transitions (substitutions) and it did not change the amino acid sequences. All sequences clustered within type B (Nakano et al. 2006), together with human *E. vermicularis* isolates from Denmark, Germany, Greece, and Japan.

To the best of our knowledge, this is the first study of *E. vermicularis* genotypes from the human population in Poland.