

## **Analysis of 18S rRNA, ITS2 and cox1 sequences of *Dictyocaulus* spp. (Trichostrongyloidea: Dictyocaulidae) from the European bison, roe deer and red deer in Poland: molecular evidence for a new species**

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Lungworms from the genus *Dictyocaulus* cause parasitic bronchitis (dictyocaulosis) characterized by coughing and severe lung pathology in both domestic and wild ruminants. In this study we investigated the phylogeny of *Dictyocaulus* spp. from European bison (*Bison bonasus* L.), roe deer (*Capreolus capreolus*) and red deer (*Cervus elaphus*) by nucleotide sequence analysis spanning the 18S RNA gene (SSU) and internal transcribed spacer 2 (ITS2) regions of the ribosomal gene array as well as the mitochondrial cytochrome *c* oxidase subunit 1 (*cox1*). Phylogenetic analyses of sequence data obtained, partly with novel primers, from between 10 and 50 specimens from each host were carried out. The Bayesian inference (BI) and the maximum parsimony (MP) analyses showed that each host species was mono-infected with different genotypes. Data from lungworms of European bison revealed a distinct genotype of *D. viviparus*, whereas *D. capreolus* was only found in roe deer. Red deer were infected with a taxon with unique SSU, ITS2 and *cox1* sequences. These results indicate the occurrence of a novel genotype from red deer, which represents a new species with a distribution limited to European countries. The molecular evidence was supported by morphological study with description and figuration of *Dictyocaulus cervi* n.sp. recovered from red deer. *Dictyocaulus cervi* n.sp. can be distinguished from *D. eckerti* on the basis of the absence of cervical papillae, length of a tail in females, morphometry of female reproductive system and measurements of gubernaculum in males. In conclusion, our findings further strengthen the idea that the genetic complexity in *Dictyocaulus* lungworms of wildlife ruminants is larger than previously believed and warrants further investigation.