INTISARI

Kajian Ankilostomiasis: Klinis dan Molekuler Berdasarkan *Sekuen Internal Transcribed Spacer* (ITS1) Pada Anjing

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Ankilostomiasis merupakan infeksi parasit yang disebabkan *Ancylostoma* spp. *Ancylostoma caninum, A. ceylanicum* dan *A. brazilienze* dapat menginfeksi anjing sehingga menyebabkan kaheksia, rambut rontok dan kusam serta anemia pada kasus kronis. Kejadian ankilostomiasis pada anjing sering bersifat sub klinis. Persebaran cacing *Ancylostoma* spp. tersebar luas di beberapa negara, namun kajian spesies *Acylostoma* di Indonesia, termasuk di Yogyakarta masih terbatas dan identifikasi morfologi spesies *Ancylostoma* melalui pemeriksaan telur dan larva secara mikroskopis masih sulit dibedakan, sehingga metode *Polymerase Chain Reaction (PCR)* dapat lebih akurat mengamplifikasi DNA target. Penelitian ini bertujuan untuk mengetahui gejala klinis dan spesies *Ancylostoma* yang meginfeksi anjing. Penelitian dilakukan dalam beberapa tahapan, yaitu koleksi dan pemeriksaan feses segar, koleksi dan pemeriksaan darah pada sampel yang positif *Ancylostoma* spp., pembiakan larva untuk uji molekuler dengan menggunakan primer *Internal Transcribed Spacer* (ITS). Hasil amplifikasi *Polymerase Chain Reaction* (PCR) dari larva *Ancylostoma* spp. disekuensing dan dianalisis menggunakan program MEGA 11. Pohon filogenetik dikerjakan dengan metode *Negihbor-Joining* dengan nilai Bootstrap 1000 kali. Anjing yang mengalami ankilostomiasis sebanyak 30 dari 53 ekor (56,6%). Gejala klinis berupa mukosa anemis 6,6% (2/30), rambut kusam dan rontok 33,3% (10/30), feses disertai darah 63,3% (19/30). Pemeriksaan hematologi menunjukkan anemia, leukositosis, eosinophilia, dan trombositopenia. Hasil amplifikasi PCR menunjukkan *band* sebesar 690bp untuk sekuen ITS dan sekuen dari kedelapan sampel tidak memiliki perbedaan jumlah nukleotida yaitu nol terhadap *A. ceylanicum* Australia, China dan Jepang. Dua sampel memiliki perbedaan jumlah nukleotida sebanyak nol hingga satu terhadap *A. caninum* China. Kesepuluh sampel memiliki kekerabatan genetik dekat dengan kemiripan dengan spesies *A. ceylanicum* (Australia, China dan Jepang) dan *A. caninum* (China) dari GenBank berdasarkan jarak genetik sebesar 0% – 0,3%. Konstruksi pohon filogenetik menggambarkan bahwa *A. ceylanicum* isolat sampel penelitian homolog dengan isolat Australia, China dan Jepang. *A. caninum* isolat sampel penelitian homolog dengan isolat China.

Kata Kunci: ***Ancylostoma ceylanicum*, *Ancylostoma caninum*, anjing, hematologi, ITS, PCR**

ABSTRACT

Study of Ancylostomiasis: Clinical and Molecular based Sequence of Internal Transcribed Spacer (ITS 1) of Dogs

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Ancylostomiasis is a parasitic infection caused by *Ancylostoma* spp. *Ancylostoma caninum, A. ceylanicum* and *A. brazilienze* can infect dogs, causing cachexia, hair loss and dullness and anemia in chronic cases. The incidence of ancylostomiasis in dogs is often sub-clinical. The distribution of *Ancylostoma* spp. is widespread in several countries, however research on *Acylostoma* species in Indonesia, including in Yogyakarta is still limited and identification of the morphology of *Ancylostoma* species through microscopic examination of eggs and larvae is still difficult to differentiate, so the Polymerase Chain Reaction (PCR) method can more accurately amplify target DNA.. This study aims to determine the clinical symptoms and species of *Ancylostoma* that infect dogs. The research was carried out in several stages, namely collection and examination of fresh feces, collection and examination of blood on samples that were positive for *Ancylostoma* spp., cultivating larvae for molecular testing using Internal Transcribed Spacer (ITS) primers. Polymerase Chain Reaction (PCR) amplification results from *Ancylostoma* spp. sequenced and analyzed using the MEGA 11 program. The phylogenetic tree was carried out using the Negihbor-Joining method with a Bootstrap value of 1000 times. Dogs suffering from ancylostomiasis were 30 out of 53 dogs (56.6%). Clinical symptoms include anemic mucosa 6.6% (2/30), dull hair and loss 33.3% (10/30), feces with blood 63.3% (19/30). Hematological examination revealed anemia, leukocytosis, eosinophilia, and thrombocytopenia. The PCR amplification results showed a band of 690bp for the ITS sequence and the sequences from the eight samples had no difference in the number of nucleotides, namely zero for *A. ceylanicum* from Australia, China and Japan. Two samples had differences in the number of nucleotides of zero to one against *A. caninum* from China. The ten samples have a close genetic relationship with similarities to the species *A. ceylanicum* (Australia, China and Japan) and *A. caninum* (China) from GenBank based on a genetic distance of 0% – 0.3%. Construction of a phylogenetic tree illustrates that *A. ceylanicum* isolates from research samples are homologous to isolates from Australia, China and Japan. *A. caninum* isolates from research samples were homologous to China isolates.

Keywords : ***Ancylostoma ceylanicum*, *Ancylostoma caninum*, dog, hematology, ITS, PCR,**