CLINICAL HISTORY AND HEMATOLOGICAL FINDINGS AMONG CANINES WITH MONOCYTIC EHRLICHIOSIS

Walasinee Moonarmart¹, Sivapong Sungpradit², Thanakorn Rawangchue², Karuna Suphaphiphat², Sineenart Suksusieng² and Charoonluk Jirapattharasate²

¹Department of Clinical Science and Public Health, ²Department of Pre-clinic and Applied Animal Science, Faculty of Veterinary Science, Mahidol University, Bangkok, Thailand

Abstract. Canine monocytic ehrlichiosis is a tick borne disease caused by Ehrlichia canis, an obligate intracellular rickettsial organism belonging to the family Anaplasmataceae. Canine ehrlichiosis causes hematological changes among infected animals which could be used as a potential predictor for diagnosing canine monocytic ehrlichiosis (CME). Ninety-four blood samples were obtained from canines that either presented for a routine health check-up or for clinical illness. A history, physical and laboratory test were conducted on each animal. All samples were examined for E. canis using a 16S rDNA polymerase chain reaction (PCR) amplification to confirm CME infection. Thirty-six of the samples were positive for E. canis using PCR and the rest were negative. The Mann-Whitney and chi-square test were used to compare the differences between the PCR-positive and negative animals. PCR-positive animals had a higher mean body temperature than PCR-negative animals. The following were significantly lower in PCR-positive animals: white blood cell count, eosinophil count, red blood cell count, hemoglobin, hematocrit, platelet count, and the random distribution of width (RDW) of the red blood cells. We evaluated complete blood cell count findings to determine factors associated with CME using multivariable logistic regression analysis and found thrombocytopenia was significantly associated with CME (OR=0.085; 95%CI: 0.78-0.92, p<0.001). For every decrease in the platelet count of 10,000 there was a 15% increase in the likelihood of having CME.

Keywords: canine monocytic ehrlichiosis, hematological profiles, thrombocytopenia, platelet count, predictor, 16S rDNA