Large Bowel Diarrhea in Dogs: What's New?

Dogs with large bowel diarrhea usually have small amounts of feces with mucous and/or fresh blood, frequent defecation with urgency, and tenesmus. The term *canine idiopathic large bowel diarrhea* (CILBD) was coined to describe this syndrome. Previously, many cases were called *irritable bowel syndrome*, but CILBD is more appropriate because studies of GI motility and visceral sensitivity in affected dogs are lacking. Two different groups of canine patients with CILBD have been defined: dogs that are fiber-responsive and those with suspected stress-associated large bowel diarrhea. Diagnostic criteria for CILBD include chronic or chronic recurring diarrhea for at least 4 weeks, diarrhea of large bowel origin, a lack of identifiable cause (such as *Trichuris vulpis* infestation or dietary indiscretion), and minimal or no changes observed during colonoscopy. Most dogs respond to fiber supplementation, but not all—some require behavior modification.

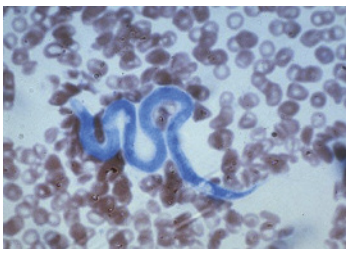
Commentary: CILBD is a diagnosis of exclusion that applies to dogs with chronic or chronic recurring large bowel diarrhea in the absence of any other identifiable disorder. Disorders to be excluded include whipworm infestation, clostridial infection, diet-responsive colitis, inflammatory bowel disease, and granulomatous colitis associated with mucosa adherent-invasive *Escherichia coli* in specific breeds. Dogs affected by CILBD lack evidence of colonic inflammation.

This article reviews the limited published studies on CILBD and presents information on 18 new cases that accounted for 22% of dogs referred for chronic large bowel diarrhea. Most dogs respond to fiber supplementation; other treatment options (eg, motility modifiers, antispasmodics, behavior-modifying drugs) are systematically discussed in this informative article.—*P. Jane Armstrong, DVM, MS, MBA, Diplomate ACVIM*

Chronic idiopathic large bowel diarrhea in the dog. Lecoindre P, Gaschen FP. ***VET CLIN NORTH AM SMALL ANIM PRACT*** 41:447-456, 2011.

Research Note

Population Structure & Gene Flow for Canine Heartworm



In an effort to examine the population genetic structure of *Dirofilaria immitis*, 192 nematode samples were collected from 9 geographic regions throughout the United States and Mexico. Analysis and comparison of genome sequences demonstrated that the population clusters into 4 genetic groups strongly influenced by geography. Populations are divided east-to-west by the Rocky Mountains but connected north-to-south by the Mississippi River. There is a significant amount of gene flow in the eastern United States and Gulf Coast regions, and the authors warn that should drug resistance alleles arise they would rapidly spread along the East Coast. This study provides the necessary information to create a predictive model of gene flow in canine heartworm that will inform future disease control strategies.

Inference of population structure and patterns of gene flow in canine heartworm (*Dirofilaria immitis*). Belanger DH, Perkins SL, Rockwell RF. ***J PARASITOL*** 97:602-609, 2011.