Gender, Breed, and Age Distributions in Horses With Cervical Vertebral Compressive Myelopathy

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Various gender, breed, and age predilections are present in horses with cervical vertebral compressive myelopathy. Improved understanding of these signalment distributions will aid clinical recognition of the disease and stimulate future studies to further delineate etiopathogenesis, such as breed-related genetic causality. Authors' addresses: Departments of Small Animal Clinical Sciences (Levine, Nghiem, Levine) and Large Animal Clinical Sciences (Cohen), College of Veterinary Medicine, Texas A&M University, College Station, TX 77843-4475; e-mail: ncohen@cvm.tamu.edu. © 2008 AAEP. *Presenting author.

1. Introduction
The objective of this study was to determine gender, breed, and age distributions in a population of horses diagnosed with cervical vertebral compressive myelopathy (CVCM) compared with contemporaneous control horses.

2. Materials and Methods
The Veterinary Medical Database was searched to identify horses diagnosed with CVCM and contemporaneous control horses between July 1974 and August 2007. Admission date, admitting institution, gender, breed, age at diagnosis, weight, and discharge status (alive, died, euthanized) were recorded for each case and control horse. Cases and controls were compared using bivariate and multivariate random effects logistic regression. The study included 811 horses with presumed or confirmed CVCM and 805 control horses.

3. Results
Geldings and intact males had a significantly higher likelihood of being diagnosed with CVCM than females. Thoroughbreds (p = 0.005), Tennessee Walking Horses (p = 0.019), and Warmbloods (p = 0.020) were over-represented in the CVCM group relative to Quarter Horses. Horses that ranged from <6 mo of age to 4 to <7 yr of age all had significantly higher odds of being diagnosed with CVCM compared to horses ≥10 yr of age.

4. Discussion
Improved understanding of the observed signalment factors associated with CVCM will aid clinical recognition of the disease and stimulate future studies to further delineate etiopathogenesis, such as breed-related genetic causality.

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