

11. Hunziker L, Recher M, Macpherson AJ, Ciurea A, Freigang S, Hengartner H, et al. Hypergammaglobulinemia and autoantibody induction mechanisms in viral infections. *Nat Immunol*. 2003;4:343–9. DOI: 10.1038/ni911
12. Poland AM, Vennema H, Foley JE, Pedersen NC. Two related strains of feline infectious peritonitis virus isolated from immunocompromised cats infected with a feline enteric coronavirus. *J Clin Microbiol*. 1996;34:3180–4.
13. Vennema H, Poland A, Foley J, Pedersen NC. Feline infectious peritonitis viruses arise by mutation from endemic feline enteric coronaviruses. *Virology*. 1998;243:150–7. DOI: 10.1006/viro.1998.9045
14. Rottier PJ, Nakamura K, Schellen P, Volders H, Haijema BJ. Acquisition of macrophage tropism during the pathogenesis of feline infectious peritonitis is determined by mutations in the feline coronavirus spike protein. *J Virol*. 2005;79:14122–30. DOI: 10.1128/JVI.79.22.14122-14130.2005
15. Stoddart CA, Scott FW. Intrinsic resistance of feline peritoneal macrophages to coronavirus infection correlates with in vivo virulence. *J Virol*. 1989;63:436–40.
16. Haijema BJ, Volders H, Rottier PJ. Switching species tropism: an effective way to manipulate the feline coronavirus genome. *J Virol*. 2003;77:4528–38. DOI: 10.1128/JVI.77.8.4528-4538.2003
17. Can-Sahna K, Soydal Ataseven V, Pinar D, Oguzoglu TC. The detection of feline coronaviruses in blood samples from cats by mRNA RT-PCR. *J Feline Med Surg*. 2007;9:369–72. DOI: 10.1016/j.jfms.2007.03.002
18. Dye C, Siddell SG. Genomic RNA sequence of feline coronavirus strain FCoV ClJe. *J Feline Med Surg*. 2007;9:202–13. DOI: 10.1016/j.jfms.2006.12.002
19. Hartley O, Klasse PJ, Sattentau QJ, Moore JP. V3: HIV's switch-hitter. *AIDS Res Hum Retroviruses*. 2005;21:171–89. DOI: 10.1089/aid.2005.21.171
20. Ballesteros ML, Sanchez CM, Enjuanes L. Two amino acid changes at the N-terminus of transmissible gastroenteritis coronavirus spike protein result in the loss of enteric tropism. *Virology*. 1997;227:378–88. DOI: 10.1006/viro.1996.8344
21. Saif LJA. K. Transmissible gastroenteritis virus and porcine respiratory coronavirus. In: Zimmerman JJ, editor. *Diseases of swine*. 9th ed. Ames (IA): Iowa State University Press; 2006. p. 489–516.
22. Sanchez CM, Izeta A, Sanchez-Morgado JM, Alonso S, Sola I, Balasch M, et al. Targeted recombination demonstrates that the spike gene of transmissible gastroenteritis coronavirus is a determinant of its enteric tropism and virulence. *J Virol*. 1999;73:7607–18.
23. Mongkolsapaya J, Dejnirattisai W, Xu XN, Vasana-wathana S, Tangthawornchaikul N, Chairunsri A, et al. Original antigenic sin and apoptosis in the pathogenesis of dengue hemorrhagic fever. *Nat Med*. 2003;9:921–7. DOI: 10.1038/nm887
24. Anishchenko M, Bowen RA, Paessler S, Austgen L, Greene IP, Weaver SC. Venezuelan encephalitis emergence mediated by a phylogenetically predicted viral mutation. *Proc Natl Acad Sci U S A*. 2006;103:4994–9. DOI: 10.1073/pnas.0509961103
25. Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. The CLUSTAL\_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res*. 1997;25:4876–82. DOI: 10.1093/nar/25.24.4876
26. Maddison DRaM. W.P. MacClade 3.05. Sunderland (MA): Sinauer; 1995.
27. Swofford DL. PAUP\*: Phylogenetic Analysis Using Parsimony (\*and other methods). Sunderland (MA): Sinauer; 2002.
28. Posada D, Crandall KA. MODELTEST: testing the model of DNA substitution. *Bioinformatics*. 1998;14:817–8. DOI: 10.1093/bioinformatics/14.9.817
29. Kumar S, Tamura K, Nei M. MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Brief Bioinform*. 2004;5:150–63. DOI: 10.1093/bib/5.2.150
30. Pearks Wilkerson AJ, Teeling EC, Troyer JL, Bar-Gal GK, Roelke M, Marker L, et al. Coronavirus outbreak in cheetahs: lessons for SARS. *Curr Biol*. 2004;14:R227–8. DOI: 10.1016/j.cub.2004.02.051
31. Rottier PJ. The coronavirus membrane glycoprotein. In: Siddell SG, editor. *The Coronaviridae*. New York: Plenum Press; 1995. p. 115–40.
32. He Y, Zhou Y, Siddiqui P, Niu J, Jiang S. Identification of immunodominant epitopes on the membrane protein of the severe acute respiratory syndrome-associated coronavirus. *J Clin Microbiol*. 2005;43:3718–26. DOI: 10.1128/JCM.43.8.3718-3726.2005
33. Heeney JL, Evermann JF, McKeirnan AJ, Marker-Kraus L, Roelke ME, Bush M, et al. Prevalence and implications of feline coronavirus infections of captive and free-ranging cheetahs (*Acinonyx jubatus*). *J Virol*. 1990;64:1964–72.
34. Pontius JU, Mullikin JC, Smith DR, Lindblad-Toh K, Gnerre S, Clamp M, et al. Initial sequence and comparative analysis of the cat genome. *Genome Res*. 2007;17:1675–89. DOI: 10.1101/gr.6380007

Address for correspondence: Meredith A. Brown, Laboratory of Genomic Diversity, National Cancer Institute, Frederick, MD 21702, USA; email: brownmer@gmail.com

The opinions expressed by authors contributing to this journal do not necessarily reflect the opinions of the Centers for Disease Control and Prevention or the institutions with which the authors are affiliated.

# etymologia

## *Borna disease virus*

[bor'nə]

Borna disease virus was named after the town of Borna in Saxony, southeastern Germany, where in 1885 many horses in a German cavalry regiment died of a fatal neurologic disease. The ill horses exhibited abnormal behavior—running about excitedly, walking into walls, being unable to chew food. A similar disease had been observed in horses, sheep, and cattle for more than 100 years. The causative agent was later found to be a negative-stranded RNA virus, which may also be a human pathogen.

**Source:** Carabone KM. Borna disease virus and its role in neurobehavioral disease. Washington: ASM Press; 2002.