glycoprotein–specific antibodies are present at high levels concurrent with the longitudinal detection of genomic RNA. A large-scale seroprevalence and cross-neutralization study is ongoing.

We used complete genome and H gene sequences in a comprehensive phylogenetic analysis. FeMV^{US1} is closely related to viruses from Asia, highlighting the global distribution of FeMV (Figure, panel A). Compared with the sequence for the FeMV^{776U} H gene, sequences for FeMV^{US1} and FeMV^{US5} were 98% and 81% similar, and the glycoproteins were 98% and 86% identical. The complete H gene of the most divergent US strain (FeMV^{US5}) clustered phylogenetically in a basal sister relationship with all other viruses from Asia and the United States (Figure, panel B), suggesting a long evolutionary association of FeMV in feline hosts.

Ecologic surveys continue to identify novel viruses that are homologous to known paramyxoviruses in many wildlife species, including bats and rodents (*6*). Investigating closely related viruses in domestic species is warranted, given the substantial number of animals that cohabitate with humans. Switches from natural to unnatural host species can result in enhanced pathogenicity (e.g., receptor switching has caused feline panleukopenia virus to infect dogs as canine parvovirus) (*7*). Given the high degree of antigenic relatedness of morbilliviruses, understanding evolutionary origins and trajectories and conferring cross-protection through immunization are critical. Although no evidence for FeMV transmission to humans or other animals exists, the propensity for noncanonical use of signaling lymphocytic activation molecule 1 F1 (CD150) should be investigated because epizootic transmission of morbilliviruses can occur (*8*).

The detection of FeMV sequences in a clinically healthy animal after 15 months is a novel and surprising observation but is consistent with the known propensity for morbilliviruses to persist in vivo (*9*). All known morbilliviruses cause acute infections, and the typical long-term clinical manifestations occur in the central nervous system, not the urinary system (*1*). These observations should prompt additional research because the prevalence of CKD in cats is high and because CKD decreases the quality of life of affected animals and is the ultimate cause of death for approximately one third of cats (*10*).

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Difficulties in Schistosomiasis Assessment, Corsica, France

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To the Editor: We would like to add some specification and clarification to the discussion regarding the diagnostics and case definitions for urinary schistosomiasis in travelers to Corsica, France (*1–3*). Evidence for a *Schistosoma*

haematobium infection typically depends on the detection of viable ova in the urine. However, in regard to *S. haematobium* infections acquired in Corsica, several ova excreted by the first 2 published case-patients (i.e., the 12-year-old boy and his father) exhibited atypical morphology (*4*). Therefore, we supplemented our morphologic study with a molecular study of miracidia by using cytochrome c oxydase mitochondrial DNA barcoding and the internal transcribed spacer 2 gene.

The results indicated that the schistosome responsible for the infection of the first case-patient reported in Corsica was *S. haematobium* that had been introgressed by genes of zoonotic *S. bovis* through a hybridization process. *S. bovis* is the cause of bovine intestinal schistosomiasis and uses the same intermediate host (*Bulinus truncatus* snails) that *S. haematobium* uses (*5*). Such interactions between *S. haematobium* and *S. bovis* have also been reported in Benin (*5*). These findings imply that the clinical course of case-patients and diagnostic test results might be affected by atypical schistosomiasis. Whereas the boy in our study experienced a clinically typical schistosomal infection of the bladder, his father and his siblings, who had identical histories of exposure, were seropositive for *S. haematobium* but were asymptomatic (*4*).

We recommend that clinicians treat any suspected case of *S. haematobium* infection, whether or not the patient excretes ova, given that the disease is potentially serious and the indicated drug for treatment (praziquantel) is safe. Epidemiologic analyses should take into account the role of zoonotic *S. bovis* infection and supplement parasitological investigations with molecular analyses (*5*,*6*).

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Cryptococcus was misspelled in the title of Climatic Influences on *Cryptococcus gattii* Populations, Vancouver Island, Canada, 2002–2004 (C.K. Uejio al.). The article has been corrected online (http://wwwnc.cdc.gov/eid/article/21/11/14-1161_article).