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Wild Boars as Hosts of Human-Pathogenic *Anaplasma phagocytophilum* Variants

To the Editor: Michalik et al. (*1*) reported a 12% prevalence of *Anaplasma phagocytophilum*, the causative agent of human granulocytic anaplasmosis and tick-borne fever of ruminants, in wild boars in Poland. *A. phagocytophilum* has been reported with low prevalence among wild boar in the Czech Republic, Slovenia (*2*), and Japan (*3*). In Spain and Mississippi, United States, *A. phagocytophilum* in wild boars or feral pigs, respectively, has not been reported (*4*,*5*). Furthermore, in Slovenia and Poland, the *A. phagocytophilum* gene sequences found in samples from wild boars were identical to those found in samples from humans and the tick vector *Ixodes ricinus* (*1*). These results suggested, as pointed out by Michalik et al. (*1*), that wild boar might play a role in the epizootiology of *A. phagocytophilum* by serving as a natural reservoir host, at least in some regions.

To test this hypothesis, we conducted transcriptomics studies to characterize host response to *A. phagocytophilum* infection in naturally and experimentally infected boars (*6*,*7*). The results suggested that boars are susceptible to *A. phagocytophilum*, but are able to control infection, mainly through activation of innate immune responses and cytoskeleton rearrangement to promote phagocytosis and autophagy. Control of *A. phagocytophilum* infection in boars might result in infection levels below PCR detection or infection clearance, contributing to the low percentage of infection prevalence detected for this species in most regions.

The low detection levels suggest that boars have a low or no impact as a reservoir host for *A. phagocytophilum*. Even if boars remain persistently infected with *A. phagocytophilum* at low levels by downregulating some adaptive immune genes and delaying the apoptotic death of neutrophils through activation of the Jak-STAT pathway, among other mechanisms (*6*), their role as a source of infection for ticks remains to be demonstrated.

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Migratory Birds, Ticks, and Crimean-Congo Hemorrhagic Fever Virus

To the Editor: In a recently published study, Estrada-Peña et al. reported the finding of Crimean-Congo hemorrhagic fever virus (CCHFV) in adult *Hyalomma lusitanicum* ticks from red deer (*Cervus elaphus*) in Spain during 2010 (*1*). Phylogenetic analysis showed that the virus was most likely of African origin. Here, we present a model for the transfer of CCHFV-infected ticks by migratory birds from Africa to Europe.

CCHFV is an RNA virus in the genus *Nairovirus*, family *Bunyaviridae*. It is transmitted to humans through tick bites or by contact with blood or tissues from infected ticks, livestock, or humans. Manifestations of severe cases are internal and external hemorrhages and multiorgan failure; the case-fatality rate is ≈30% (*2*,*3*). CCHFV has the widest geographic distribution of any tick-borne virus, encompassing ≈30 countries from eastern China through Asia, the Middle East, and southeastern Europe to Africa (*3*,*4*). During the past decade, the virus has emerged in new areas of Europe, Africa, the Middle East, and Asia and has increased in disease-endemic areas (*5*) (online Technical Appendix, wwwnc.cdc.gov/EID/pdfs/12-0718-Techapp.pdf).

In response to the emergence of CCHFV in Europe, during spring 2009 and 2010, we screened migratory birds for ticks as they traveled from Africa to Europe. At 2 bird observatories on the Mediterranean Sea (Capri, Italy, and Antikythira, Greece), 14,824 birds of 78 different species were caught and examined for ticks. Most (88%) of the 747 collected ticks were identified as members of the *Hyalomma marginatum* complex, most probably *H. rufipes* and *H. marginatum* sensu stricto (s.s.), i.e., the principal vectors of CCHFV (*2*). Of 10 morphologically representative ticks, 9 were identified by molecular methods as *H. rufipes* and 1 as *H. marginatum* s.s. (*6*).

Ticks belonging to the *H. marginatum* complex are common in large parts of the African and Eurasian continents. The immature ticks feed mainly on birds and, to a lesser extent, on small mammals, whereas the adults actively seek larger mammals, including hares, wild and domesticated ungulates, or humans (*4*). In accordance with this pattern, 99% of the collected ticks in our study were larvae and nymphs.

On April 23, 2009, a woodchat shrike (*Lanius senator senator*) was caught at the Antikythira Bird Observatory in the Greek archipelago. The bird was a female in her second calendar year and harbored 19 *H. marginatum* complex ticks (3 larvae and 16 nymphs, most likely *H. rufipes*). Three of the nymphs, 1 half-fed and 2 fully engorged, were found positive by real-time PCR for the CCHFV small (S) segment by using methods previously described (*7*), amplifying a 127-bp product. The 3 positive samples were sequenced and found to be identical. Previous studies, based on the S segments, have identified 7 phylogenetically distinct genotypes: Africa 1–3, Asia 1–2, and Europe 1–2 (*8*). Europe 1 has been reported from Russia, Turkey, Greece, Bulgaria, and the Balkans, and Europe 2 is the nonpathogenic strain AP92 found in Greece. Alignment of the Antikythira strain with CCHFV S segment sequences deposited in GenBank showed that it had the greatest similarity with strains belonging to the genotype Africa 3 (*8*). In addition, a phylogenetic tree clearly places the Antikythira sequence within the Africa 3 clade (Figure).

The woodchat shrike winters in a belt from Senegal to Somalia and breeds in southern Europe and northern Africa (*9*). The Antikythira