

Abstract

Tick-borne spotted fever group (SFG) rickettsioses are emerging human diseases caused by obligate intracellular Gram-negative bacteria of the genus *Rickettsia*. Despite being important causes of systemic febrile illnesses in travelers returning from sub-Saharan Africa, little is known about the reservoir hosts of these pathogens. We conducted surveys for rickettsiae in domestic animals and ticks in a rural setting in western Kenya. Of the 100 serum specimens tested from each species of domestic ruminant 43% of goats, 23% of sheep, and 1% of cattle had immunoglobulin G (IgG) antibodies to the SFG rickettsiae. None of these sera were positive for IgG against typhus group rickettsiae. We detected *Rickettsia africae*-genotype DNA in 92.6% of adult *Amblyomma variegatum* ticks collected from domestic ruminants, but found no evidence of the pathogen in blood specimens from cattle, goats, or sheep. Sequencing of a subset of 21 rickettsia-positive ticks revealed *R. africae* variants in 95.2% (20/21) of ticks tested. Our findings show a high prevalence of *R. africae* variants in *A. variegatum* ticks in western Kenya, which may represent a low disease risk for humans. This may provide a possible explanation for the lack of African tick-bite fever cases among febrile patients in Kenya.