Zoonotic Bacteria in Fleas Parasitizing Common Voles, Northwestern Spain

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We detected Francisella tularensis and Bartonella spp. in fleas parasitizing common voles (Microtus arvalis) from northwestern Spain; mean prevalence was 6.1% for F. tularensis and 51% for Bartonella spp. Contrasted vector–host associations in the prevalence of these bacteria suggest that fleas have distinct roles in the transmission cycle of each pathogen in nature.

A dynamic prevalence of Francisella tularensis and Bartonella spp. was reported in irruptive common vole (Microtus arvalis) populations during 2013–2015 from agricultural landscapes of northwestern Spain (1,2). In that area, notifiable tularemia has been endemic since 1997, and human cases periodically occur during outbreaks in voles (3,4). Prevalence of F. tularensis and Bartonella spp. in voles increases with vole density (1,2), highlighting the key role of fluctuating rodents in shaping zoonoses dynamics (1–4). Rodent ectoparasites often play a major role in transmitting zoonotic pathogens. In the population studied, ticks rarely infest voles (2% prevalence), whereas fleas are much more prevalent (68%) (2). Nevertheless, any potential role for vole fleas in the circulation of F. tularensis or Bartonella spp. in natural environments remains unknown. To elucidate realistic transmission route scenarios in host–dynamnic environments (5–8), we investigated whether zoonotic bacteria occur concomitantly in voles and fleas.

Our main goal was to study the prevalence of F. tularensis in fleas collected from voles previously tested for tularemia (1). We screened flea DNA in search of 6 main zoonotic bacteria simultaneously (Anaplasma phagocytophilum, Bartonella spp., Borrelia spp., Coxiella burnetii, F. tularensis, and Rickettsia spp.), following the same molecular procedure (multiplex PCR) (9) previously used to screen vole pathogens (1,2). Voles and fleas were live-trapped in northwestern Spain during March 2013–March 2015 (Appendix, https://wwwnc.cdc.gov/EID/article/25/7/18-1646-App1.pdf). We collected fleas from each individual vole and identified and grouped them in pools (pool = total fleas/vole). Three flea species parasitize common voles in the area: Ctenophthalmus apertus, Nosopsyllus fasciatus, and Lepotysylla taschenbergi (2). We screened monospecific pools (all fleas in a pool belonged to the same species and came from the same vole host), for a sample size of 90 vole hosts (pools) and 191 fleas. We screened 78 C. apertus fleas (39 pools) and 113 N. fasciatus fleas (51 pools). Among the 90 voles providing fleas, 27 were F. tularensis PCR-positive; the remaining 63 were negative (1). Of these same 90 voles, 45 were Bartonella PCR-positive and 45 were negative. Seventeen were positive for both F. tularensis and Bartonella spp. (2).

Flea pools had an average of 2.12 fleas (range 1–9); however, most (>70%) contained 1 (51%) or 2 (22%) fleas (Table). We did not detect DNA from pathogens other than F. tularensis and Bartonella spp. in fleas. Three (3%) flea pools harbored F. tularensis DNA; we estimated the overall prevalence at 6%. F. tularensis prevalence in both flea species was low (1 positive pool of 51 in N. fasciatus and 2 of 39 in C. apertus). All F. tularensis PCR-positive flea pools came from F. tularensis PCR-positive vole, and prevalence of F. tularensis in fleas was significantly associated with its prevalence in voles (analysis of variance [ANOVA], $R^2 = 0.072$, $F_{0.05, 1, 88} = 6.81$; $p = 0.011$). Of note, all fleas containing F. tularensis DNA were collected during July 2014, when vole populations reached top densities and tularemia prevalence peaked among them (33%) (1). The low prevalence of F. tularensis detected in fleas carried by infected hosts (3 of 27 pools) and the detection of infected flea pools only when abundance of the bacterium in the environment was highest (during vole peaks) (1,4) suggest that the quantitative role of fleas in the circulation of F. tularensis might be modest.

Conversely, the role of fleas in the circulation of Bartonella spp. seems much more relevant. We detected Bartonella spp. in 28 (37%) flea pools and in both flea species (37% of N. fasciatus and 23% of C. apertus) (Table). We detected Bartonella spp. in fleas collected from Bartonella PCR-positive and Bartonella PCR-negative vole in nearly equal proportions (51% vs. 44%) (Table). The average prevalence of Bartonella spp. in fleas was not associated with its prevalence in voles (ANOVA, $R^2 = 0.006$, $F_{0.05, 1, 88} = 0.53$; $p = 0.467$). We found a higher Bartonella spp. prevalence in N. fasciatus (65%) than in C. apertus (33%).
We identified 3 Bartonella species among fleas (B. taylorii [17%], B. grahamii [14%], and B. rochalimae [3%]), as well as mixed infections (Appendix). These findings are in accordance with other research showing fleas as a main vector of Bartonella spp. (5). Although F. tularensis and Bartonella spp. have been simultaneously detected in ≥13% of voles during population density peaks (2), we identified no co-infection among flea pools (ANOVA, $R^2 = 0.011$, $F_{0.05,1.88} = 0.97; p = 0.328$).

Our data show that F. tularensis and Bartonella spp. occur in the fleas infesting wild common voles in northwestern Spain, with notable differences in prevalence (6% and 51%, respectively) and associations with prevalence in vole hosts. Future studies are needed to determine the role of fleas in the circulation of these pathogens in nature and in particular to ascertain any effective vectoring of F. tularensis.

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**Mycobacterium bovis**

Infection in African Wild Dogs, Kruger National Park, South Africa


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We screened African wild dogs (*Lycaon pictus*) in Kruger National Park, South Africa, for *Mycobacterium bovis* infection using an interferon-gamma release assay. We detected *M. bovis* sensitization in 20 of 21 packs; overall apparent infection prevalence was 83%. These animals experience high infection pressure, which may affect long-term survival and conservation strategies.

The African wild dog (*Lycaon pictus*) is an endangered carnivore occurring in fragmented, small populations (in South Africa, <500 animals). These factors make them susceptible to adverse factors, such as infectious diseases, that may threaten their long-term survival (1,2). Of particular concern are diseases caused by multihost pathogens that are capable of persisting in reservoir host species, such as *Mycobacterium bovis*, the causative agent of bovine tuberculosis (bTB). This pathogen may pose a major threat to the conservation of endangered host populations (3).

Since 2012, sporadic cases of wild dogs with macroscopic and histological lesions consistent with tuberculosis (TB) have been recorded in South Africa, specifically in Kruger National Park (KNP; n = 8), uMkuze Game Reserve (n = 1), and Hluhluwe-iMfolozi Park (HiP; n = 2). *M. bovis* infection is endemic in these parks and occurs in multiple species that are preyed upon by wild dogs, such as warthogs, which have an estimated *M. bovis* seroprevalence up to 38% in KNP (4,5). In 2 cases from KNP, acid-fast bacilli were associated with granulomatous lymphadenitis, and spoligotype analysis of *M. bovis* isolates from lesions in affected wild dogs from KNP (strain type SB0121) and HiP (strain type SB0130) were the same as those found in local prey (6).

*M. bovis* is a novel pathogen of wild dogs; understanding the impact of bTB disease in wild dogs is imperative to making informed management decisions regarding these animals’ conservation. Estimation of prevalence would provide a starting point for this investigation but requires diagnostic tools for accurate detection of *M. bovis* infection. To estimate prevalence in the KNP wild dog population, we assessed sensitization to TB antigens ESAT-6 and CFP-10.

During July 2016–January 2018, we tested blood samples from 77 wild dogs from KNP using an interferon-gamma release assay (IGRA) developed by our group (7). We tested animals from 21 wild dog packs; 20 of these included ≥1 IGRA-positive animal, indicating widespread exposure to *M. bovis* throughout KNP (Figure). We observed no significant difference in IGRA results based on sex (p = 0.79 by 2-tailed Mann-Whitney test). Overall, the apparent prevalence of *M. bovis* infection was 82% (63/77; 95% CI 72%–89% by modified Wald test).

Few reports of active bTB disease and related deaths have been documented in wild dogs, so the high apparent...