Spatial Analysis Studies Wildlife's Role in Bovine TB

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In 2005, Veterinary Services (VS) completed a 7-year study to determine if wildlife on Molokai Island, Hawaii, serve as a potential reservoir for *Mycobacterium bovis.* Collaborators in this study were from the Alaska/Hawaii/Washington/Pacific Trust Territories Area Office, the VS Western Regional Office, and the VS Centers for Epidemiology and Animal Health (CEAH). This study incorporated novel methods for obtaining sample collection data and using a place-based method for reporting test results.

Periodic *M. bovis* infections in cattle on Molokai Island have been detected since the 1940s. Between 1983 and 1987, some 9,000 animals were depopulated to eradicate this disease from the island. Molokai was later restocked with cattle. In 1997, bovine tuberculosis was detected in a herd located on a farm in southeastern Molokai. Because earlier studies suggested that a wildlife reservoir may be maintaining this pathogen, VS initiated a study to identify which wildlife species might be involved in *M. bovis* maintenance and transmission.

Hunter survey

Axis deer, feral goats, feral swine, and mongooses were selected as potential species that could serve as reservoir hosts for *M.bovis.* The selection of these species was based on previous field studies and published reports. Between 1998 and 2004, analysts collected and processed 1,048 lymph node tissue samples from hunter-killed animals at a central collection site. The proportion of samples included: axis deer, 42.2 percent; feral goats, 6.9 percent; mongooses, 4.9 percent; and feral swine, 46 percent.

The tissue samples were sent to USDA's National Veterinary Services Laboratory for analysis by culture and histopathology.

Hunters marked the geographic location of each animal killed on a detailed map of Molokai. The location of each animal sampled was then digitized from the hunter survey maps and combined with other information to create a spatial database for analysis. The distribution of wildlife populations was examined relative to terrain, vegetation, and land use. From the distribution of hunter samples, population centers and home ranges were calculated to estimate population densities for each species. Sample densities, adjusted spatially and temporally, were compared with existing cattle densities to evaluate population proximities and possible wildlife-cattle interaction dynamics.

Results

This study of wildlife species on Molokai Island found evidence of *M.bovis* infection in feral swine only. While similar quantities of feral swine and axis deer were sampled, low sample numbers for the other species tested means that the role of feral goats and mongooses remains inconclusive. Although feral swine were the only test-positive species found, the results also show that the frequency of infection is low and that the geographic distribution is limited to a small area in southeastern Molokai (Figure 1).

As shown in Table 1, analysis results suggest that control and eradication of bovine tuberculosis from Molokai Island may be possible using a systematic zonal strategy for surveillance (Figure 2).

This study has shown that feral swine are the only wildlife species found infected with *M. bovis* on Molokai Island; however, the low level of infection raises the question of whether feral swine are actually serving as a pathogen reservoir. The low level of

infection in a small geographic area does suggest that implementation of one or more control strategies might be successful in reducing transmission risk even further. Finally, this study highlighted the value of incorporating geospatial methods in a surveillance design and then combining data collection with an ongoing system of spatial analysis to understand the ecology of this disease and the possible role of wildlife.

Acknowledgements

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Figure 1. Density estimates of all feral swine samples relative to terrain features.

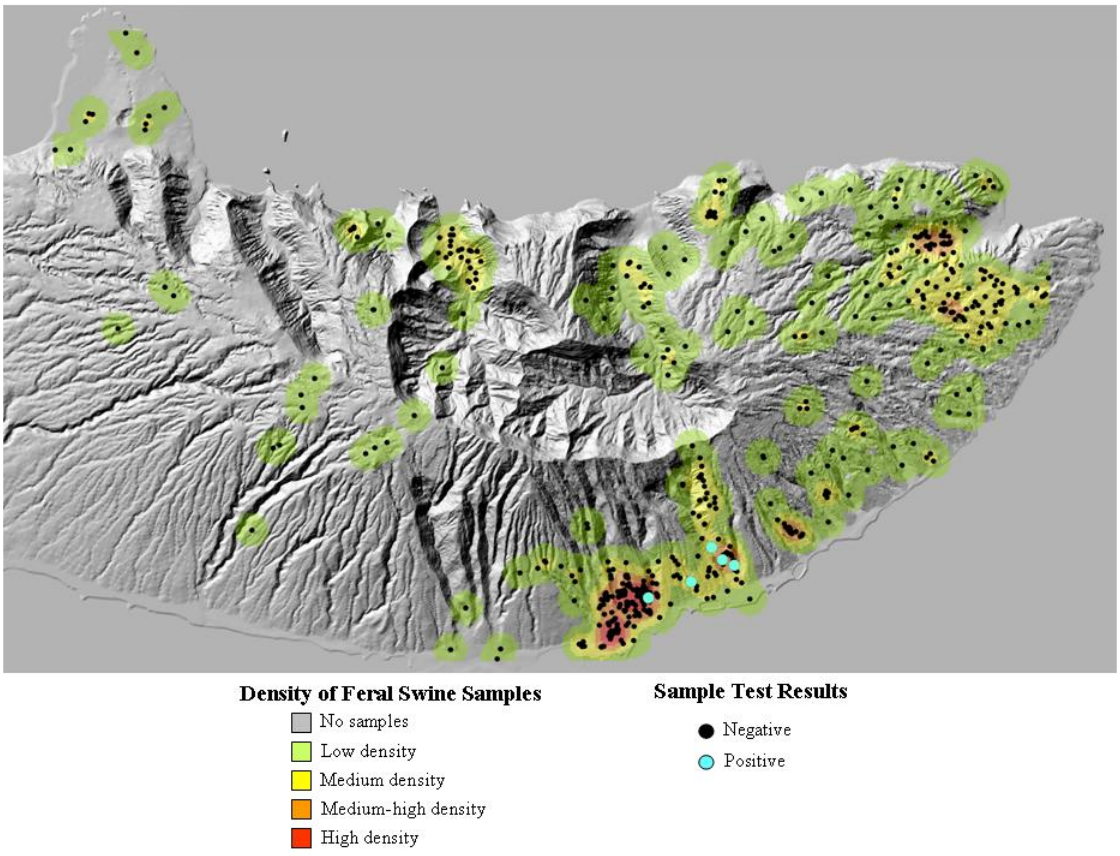

Figure 2. Proposed disease control zones

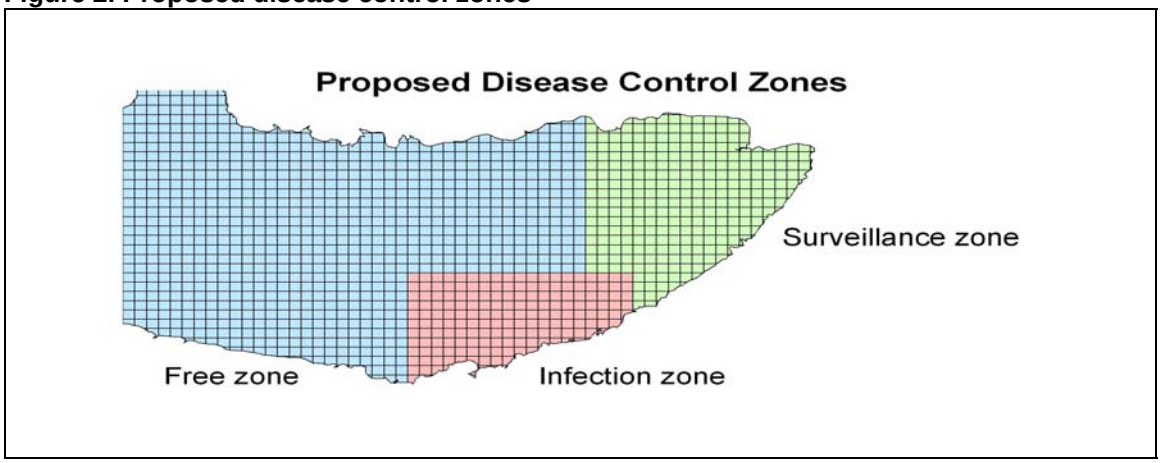

Table 1. Infection prevalence expressed as the proportion of samples testing positive from all feral swine samples collected within each zone.

Zone	No. samples	Percentage of total samples	No. positive samples	Percentage prevalence
Free	102	21.2	0	0.0
Surveillance	161	33.4	0	0.0
Infection	219	45.4	5	2.3
Infection + Surveillance	380	78.8	5	1.3
Infection + Surveillance + Free	482	100.0	5	1.0