United States Air Force Academy: Identifying Areas at Risk for the Persistence of Plague using the Bioagent Transport and Environmental Modeling System (BioTEMS)

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Abstract

Introduction: *Yersinia pestis*, the etiologic agent of plague, has caused major pandemics in human history and continues to be both a natural and bioterrorist threat to human populations. Plague exists in nature in either an epidemic or enzootic state. Geographic models of the epidemic state have primarily been developed using flea and reservoir species, however little is known of the enzootic state and potential cryptic reservoir species and few endemic models have been produced.

Methods: Flora, fauna, soil data were analyzed using geographic information systems and the Bio agent and Environmental Transport System Model (*BioTEMS*). BioTEMS has been used to evaluate and model several pathogens globally.

Objective: BioTEMS is used in the present study to identify likely sites for enzootic transmission and cryptic species of *Y. pestis* to enhance surveillance and control of plague by public health professionals at the United States Air Force Military Academy.

Results: One hundred fifty-five sites were identified as being at risk of high persistence of plague. Eight sites were within 250 meters of base housing and could serve as sources for infecting fleas, rodents and human infection. A significant number of black-tailed prairie dog mounds were within 250 meters of HPP sites, 52 of 67, X^2=40.9, p<0.01.

Conclusion: Areas at risk of persistence of *Yersinia pestis*, the etiologic agent of plague were identified at the United States Air Force Academy using the Bio agent Transport and Environmental Modeling System. Several of these sites were near base family housing and near prairie dog mounds. This information can be used by public health officials to optimize vector/rodent control and to conduct environmental surveillance to reduce the risk of outbreaks of plague on the academy property.

Keywords: *Yersinia pestis;* Epidemiology; Terrorism GIS; Infectious disease; Microbial ecology; Free-living pathogenic amoeba

Introduction

Yersinia pestis, the etiologic agent of plague, has caused three pandemics, and continues to be a threat to human populations across the globe as a naturally occurring organism and as a potential biological weapon. The most common methods of humans becoming infected is through the bite of a flea infected by feeding upon a rodent reservoir or by the person handling an infected carcass. Currently, more than 200 species of animals and 80 species of fleas have been implicated in maintaining *Y. pestis* endemic foci throughout the world [1]. Plague was first introduced to North America in the 19th century and is now endemic from California eastward to the eastern slope of the United States [2]. *Yersinia pestis* exists as either an enzootic in a resistant host population or in an epizootic state in susceptible hosts [3].

Both plague infected animals and human cases have been reported on the United States Air Force Academy Base (AFA), located in Colorado [4]. The AFA is composed of nearly 8,000 ha located in El Paso County on the eastern slope of the Rocky Mountains. Children have died in family housing, where infected rodents and their associated fleas have been found [4]. Determining where plague is present on the AFA is important not only in preventing plague in cadets and staff at the academy, but also military personnel and their families occupying family housing at the installation. Current models have low spatial accuracy for identifying epizootic activity prior to human plague cases suggesting other mammalian reservoirs or their fleas may be more important sources in high risk areas, e.g. chipmunks, however several models have been used with increasing resolution to within 30 to 100 m [5]. In addition to mammalian reservoirs and flea species, microbial communities and environmental factors may play a role in identifying high risk areas for plague at the AFA. The objective of this study was to identify high risk areas of persistence of *Y. pestis*

at the AFA to assist in plague surveillance and prevention, and identify if enzootic persistence may be located near base housing utilizing the Bioagent Transport and Environmental modeling system (BioTEMS).

Materials and Methods

Flora, fauna, soil data were obtained from the Natural Resources Department (AFA) and the United States Geological Service (USGS). Soil samples and observations of ground squirrels and prairie dog communities were recorded and GPS referenced. Neural network analysis of microbial density, measured by Luminultra test kits, from soil samples sampled in Colorado and Montana were utilized for characterization of microbial microhabitat (Figure 1). ArcGIS geospatial analysis software, Statistica software and the BioTEMS were used to analyze geographic information and conduct data analysis to identify likely areas of persistence of *Y. pestis*. The BioTEMS has previously been used for biological weapons defense modeling and infectious disease modeling in several countries, including plague [6]. The BioTEMS utilizes up to several hundred abiotic and biotic factors to produce risk and vulnerability assessments for biological agents and infectious diseases. Examples of biotic and abiotic factors include; pathogen strain, vector/host relationship, vectorial capacity, host/vector physiology, colonization ability, population dynamics of hosts and vectors, microbial density, soil, shade, and weather conditions, such as wind, temperature, and precipitation. Analytical methods within BioTEMS include; artificial intelligence, fuzzy logic, and niche analysis.
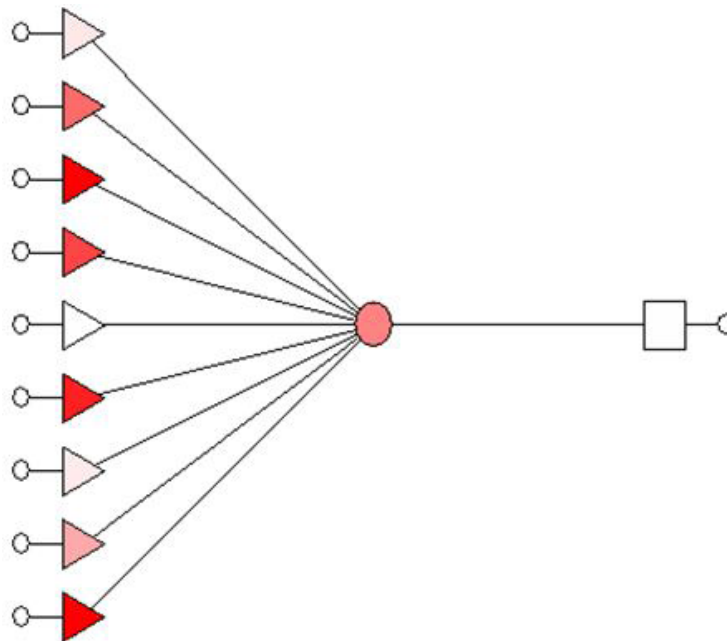

Figure 1: Radial Basis Function Neural Network of predicted microbial density in microhabitats of soils within the US Air Force Military Academy; Profile: RBF 9:9-1-1:1, Index=20 Train Perf.=0.99, Select Perf.=1.03, Test Perf.=0.90

Results and Discussion

One hundred fifty-five sites were identified as being at risk of high persistence of plague (HPP) (Figure 2). Eight HPP were within 250 meters of base housing and could serve as sources for infecting fleas, rodents and human infection. A significant number of black-tailed prairie dog mounds were within 250 meters of HPP sites, 52 of 67, X^2=40.9, p<0.01. This is within the range of dispersion by other rodents, e.g. spotted ground squirrels [7] and could be a source of infection for prairie dogs. Black-tailed prairie dogs are an important species for plague surveillance; however resources should also be directed towards other possible hosts and evaluating human risk by incorporating fluctuations in levels of endemic and epidemic risk [5]. Adding potential interactions with microbial hosts and microhabitats can increase the resolution of the model and provide a preventive model with reduced cost.

Enzootic models have been used to identify probable reservoir and flea species where enzootic and non-peridomestic plague continues between epizootic outbreaks [5]. The potential distribution of flea vectors of *Y. pestis* in California has provided assistance in focusing sampling of plague vectors [8]. In addition to flea vectors and mammalian reservoirs, soil and microbial communities appear to play a role in enzootic maintenance of *Y. pestis*, including free-living amoeba [9-14]. Models of human associated plague using environmental and host factors have been used to assist in prevention of plague from epizootics in four southwest states, including Colorado [15-17]. However, these models do not include potential *Y. pestis* interactions in the microbial environment.

Free-living amoeba, provide a macrophage-like environment and serve as suitable hosts for several human pathogens. Pathogenic bacteria interact with the amoebae, residing in both trophozoite and cyst forms, protected from deleterious environmental factors and even gaining pathogenicity [18]. *Yersinia pestis* is associated with and can persist in free-living pathogenic amoeba, e.g.

Acanthamoeba castellani [13,14]. *Yersinia pestis* also persists in free-living pathogenic amoeba, providing prolonged survival and subversion of intracellular digestion of *Y. pestis* within a soil free-living amoeba. This suggests the potential role for protozoa as a protective soil reservoir for *Y. pestis* [19]. Mammals often come into contact with free-living amoebae but vary in susceptibility to free-living pathogenic amoeba, such as *Naegleria* species, can depending on species, age and sex of the host [20]. Susceptible mammals may become infected by *Y. pestis* when they come into contact with free-living amoeba [18].
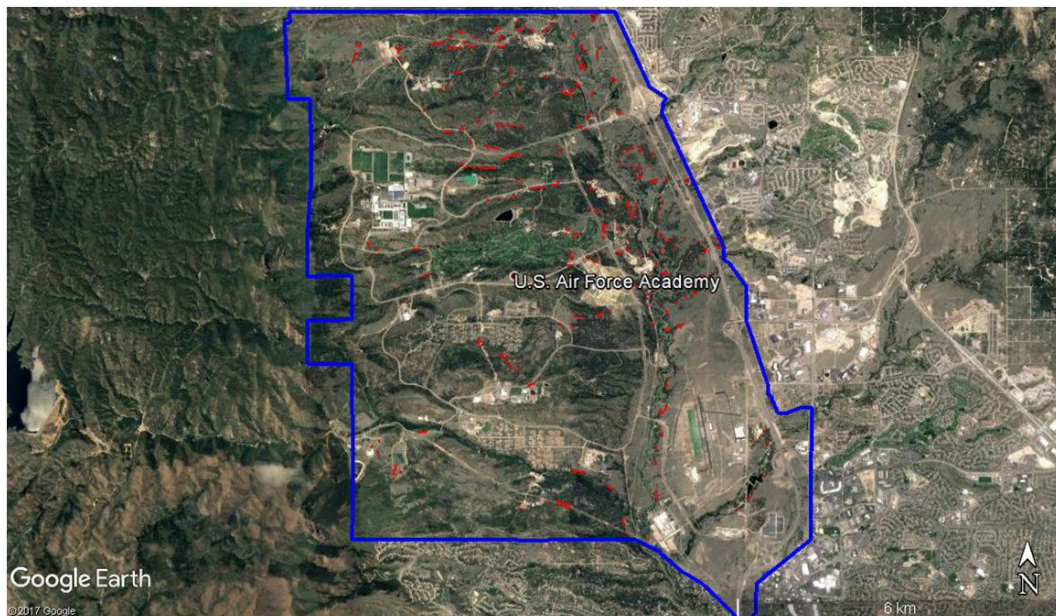

Figure2: High risk areas of *Yersinia pestis* persistence identified using the Bio agent Transport and Environmental Modeling System

Human cases of plague have occurred in military housing at the AFA [4]. Even though peridomestic rodent control is conducted in military housing, the death of a child in base housing at the AAF emphasizes the need to develop new strategies of surveillance and control methods in family housing in order to reduce risk to military personnel and their families. Housing areas on military bases are sometimes at high risk from vector-borne diseases, e.g. enlisted housing at Edgewood Army Base, MD was identified as being at high risk for *Ixodes scapularis* the tick vector of *Borrelia burgdorferi*, the etiologic agent of Lyme borreliosis (Kollars, unpublished). In the present study, several high risk areas for plague were identified near base housing using BioTEMS. Having the ability to prioritize likely areas and identify sites for sampling for endemic persistence of plague can reduce the manpower and logistics spent in surveillance while enhancing prevention. Current methods of plague surveillance focus on rodent and flea testing for prevention and control of plague outbreaks. Adding the testing of the soil microbial community, e.g. free-living amoebae into surveillance operations may provide valuable insight into sites identified as high persistence areas for *Y. pestis* and other pathogens. Niche analysis is a useful tool when identifying the potential distribution of pathogenic species and should incorporate factors in addition to geographic locality and habitat, e.g. genotypic/phenotypic diversity, host susceptibility, and potential microbial reservoirs. Strain variation of *Y. pestis* plays a role in host invasion and environmental survival and behavioral and physiologic condition of individuals affects susceptibility to *Y. pestis* [21-23].

Conclusion

Areas at risk of persistence of *Yersinia pestis*, the etiologic agent of plague were identified at the United States Air Force Academy using the Bio agent Transport and Environmental Modeling System. Several of these sites were near base family housing and near prairie dog mounds. This information can be used by public health officials to optimize vector/rodent control and to conduct environmental surveillance to reduce the risk of outbreaks of plague on the academy property.

Acknowledgment

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