first observations suggest that villages with a high plague incidence are connected through typical fertile valley bottoms, i.e. Gleysols and Fluviosols, and that hamlets (part of a village) in this valley bottom have had more human plague cases. Soil and plant samples are being analyzed to test if factors that define the microclimate (in this study, bulk density, soil texture, pH, and organic carbon, and concentrations of chemical elements in soil and plant) are linked with plague occurrence in Lushoto. Our results give an indication that a landscape ecological study approach can provide insights into the persistence of plague and how its distribution can be affected by landscape features, and therefore in this case, might open the track towards a better understanding of the underlying ecology of plague’s distribution in Lushoto.

References:


P9 PRELIMINARY STUDY OF FLEAS ON RODENTS IN THREE COLORADO COUNTIES

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Some species of fleas are found on multiple species of rodents, thus increasing the likelihood of spreading disease from one host to another. As part of a preliminary study, fleas were collected off live-trapped and killed-trapped rodents from October 2003 through August 2005 in El Paso, Pueblo Counties, Colorado. Twelve species of fleas representing three families were collected off nine species of rodents. The two most common species of fleas, Aethesagenus and Orchopeas leacopus were found on four species of mice (Peromyscus spp.), Mexican woodrats (Neotoma mexicana), and rock squirrels (Spermophilus variegatus). Oropsylla montana was found in high numbers on rock squirrels and, because of its high incidence, is an important vector in plague transmission (Lewis 2002). In addition, we found small numbers of Hoplospylas anomala, a known plague vector, on rock squirrels. We also found high numbers of Fossella ignota, a primary parasite of northern pocket gophers (Thomomys talpoides), which is a minor vector of plague (Pigage et al. 2005). Although pocket gophers are frequently found in the same areas as other rodents, we did not collect F. ignota from any other host. Our current goal is to investigate rodent populations that live in or near black-tailed prairie dog (Cynomys ludovicianus) colonies and their fleas as well as some predators of the prairie dogs in order to examine flea exchange.

References:


P11 SOCIO-ECONOMIC RISK FACTORS ASSOCIATED WITH HUMAN PLAGUE CASES IN NEW MEXICO


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Plague, caused by the bacterium Yersinia pestis, is a zoonotic disease that is rare in the United States, but can be highly fatal in humans, when left untreated. The majority of human cases in recent decades have been acquired in New Mexico. A recently developed habitat suitability model for the disease identified areas which support a diverse assemblage of rodent hosts for plague as those most at risk for human infections in this state (Eisen et al. 2007). Here, we combine known environmental risk factors with socio-economic features of U.S. census block groups in a Geographic Information Systems (GIS) model to further refine the area within New Mexico which poses the highest plague risk for humans. The socio-economic risk factors identified included proportion of housing units with incomplete plumbing, proportion of housing units built 40 or more years prior to a census, and poverty rate. The overall accuracy of our model was about 82%, and reduced the area considered at highest risk from about 17% to between 2 and 7% of New Mexico. This reduction in the area identified as high-risk highlights the potential importance that human behavioral or lifestyle factors play in Y. pestis infection risk, particularly when these factors are ones that might influence the likelihood of native rodent species invading peri-domestic habitats. Moreover, such integration of environmental and socio-economic risk factors may aid in the targeting of limited public health resources to areas where prevention and control efforts may be most effective.

Reference:


P10 DETERMINATION OF THE BLOOD TITER LEVELS OF IMIDACLOPRID AND EFFECTIVENESS AGAINST XENOPSyllA CHEOPS FLEAS ON LABORATORY RATS (RATTUS NORVEGICUS)

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Rats have been long considered a reservoir host of flea-borne diseases, especially plague. Systemic insecticides commonly used for flea control in veterinary medicine could also be applied to control flea populations on rats. Imidacloprid [1-(6-chloro-3-pyridylmethyl)-N-nitroimidazolidin-2-ylideneamine] is a versatile and effective insecticide that could be used to control flea populations on rats. Imidacloprid [1-(6-chloro-3-pyridylmethyl)-N-nitroimidazolidin-2-ylideneamine] is a versatile and effective insecticide and systemically control Xenopsylla cheops fleas on laboratory rats and thus to mitigate flea-borne diseases. A high performance liquid chromatography (HPLC) method with reverse phase separation for determining imidacloprid level in blood of rats was developed. Imidacloprid was detected by UV at 270 nm with the Limit of Detection at 0.018 µg/mL, Limit of Quantification at 0.051 µg/mL, and mean recovery of 97.6%. The method was validated for imidacloprid concentration range from 0.02 to 0.82 µg/mL. For testing imidacloprid as an insecticide, single doses of 0.2 mg (group 1) and 0.4 mg (group 2) were orally delivered to two treatment groups (n = 5) of rats. The control group (n = 3) was given an aliquot of pure solvent. After 3 hours of delivery ~ 20 fleas were applied to each rodent using flea chambers placed on animals. Fleas were allowed to feed for 3 hours and then removed. Blood was collected into 3 mL EDTA tubes. Liquid samples for HPLC were prepared by liquid-liquid extraction of imidacloprid from blood by dichloromethane. The imidacloprid level was found to be 0.47 ± 0.049 µg/mL and 0.89 ± 0.188 µg/mL for group 1 and group 2, respectively. No traces of imidacloprid were found in the control group. Flea mortality in group 1 was 78.0% and 80.5% after 24 hours and 48 hours of imidacloprid exposure, respectively. Flea mortality in group 2 was 72.2% and 77.8% after 24 hours and 48 hours of imidacloprid exposure, respectively. Mortalities of fleas in the control group were 10.5% and 12.6% respectively. The reported HPLC/feather application method allows determination of the effective imidacloprid doses that need to be delivered to host rats to reach effective imidacloprid concentrations in host blood and lethally control Xenopsylla cheops fleas.

P12 SEASONAL AND SPATIAL CHANGES IN FLEA COMMUNITIES OF BLACK-TAILED PRAIRIE DOGS OF NORTHERN WESTERN MEXICO

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Host population structure and density, and changes in flea community structure and composition, are considered to be important in the dynamics of vector borne diseases in prairie dogs, including plague and tularemia. In Mexico, neither tularemia nor plague is recognized despite the presence of environmental conditions similar to those
found in the southern USA where these diseases are frequently reported. We carried out a survey of fleas parasitizing black-tailed prairie dogs at 8 160 x 160 m quadrants in 4 prairie dog colonies in northwestern Chihuahua, Mexico during the dry and rainy seasons of 2006. The colonies of the survey are included at the core of one of the largest black-tailed prairie dog colony complexes in North America, and differ in size, isolation degree of isolation and host density. Fleas were collected directly from the pelage of the trapped prairie dogs, along with some blood samples to search for evidence of plague or tularemia infection. All captured animals were measured and released at the site of capture. We trapped 51 prairie dogs and collected 119 fleas belonging to 5 flea species, including Echinophaga gallinacean, Pulex simulans, Pulex sp., Thraissia fousa, and Oropsylla hirsuta. Pulex was the dominant genus among the prairie dog colonies surveyed, comprising 37% of the total fleas, followed by Oropsylla hirsuta with 38%. Seasonal changes in flea community structure were recorded. During the dry season, Oropsylla hirsuta was the dominant flea, comprising 42% of all fleas collected, followed by Pulex spp. (31%) and Pulex simulans (24%). During the wet season, Pulex simulans dominated the flea community with 79% occurrence, followed by Pulex spp. with 24%. The smallest and most isolated colony of prairie dogs exhibited the lowest diversity of flea species. Changes in flea community structure due to changes in host densities, degree of isolation and changes in flea communities due to seasonal changes may produce changes in vector competence for infectious agents. These changes also may create a different pattern of disease occurrence between prairie dogs colonies from northern Mexico and southern USA. Recognizing the role of flea communities, vector competence and host population structure is the key to understanding and predicting disease outbreaks. Further analyses are needed, including molecular and serologic tests for plague and tularemia in fleas and prairie dogs of northern Mexico. In future studies, we will assess the relationship of flea community dynamics and disease prevalence in both fleas and hosts with different spatial and temporal scales. The results of this research will contribute to the development of predictive models for prairie dogs colonies in northern Mexico.

**References**


**P14**

**FLEA LOADS ON BLACK-TAILED PRAIRIE DOGS (CYNOMYS LUDOVICIANS) DURING PLAGUE EPIZOOTICS IN COLORADO**

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Plague, caused by the bacterium Yersinia pestis, is primarily a disease of wild rodents and their fleas. Black-tailed prairie dog colonies (Cynomys ludovicianus) are highly susceptible and mortality on individual towns often reaches 100%. Flea load, or the number of fleas per host, fluctuates seasonally and transmission of the pathogen during epizootics is likely to become more efficient as flea load increases. Fleas were collected from live-trapped black-tailed prairie dog colonies before and during plague epizootics and tested by PCR for the presence of Y. pestis DNA. The predominant fleas infesting Black-tailed prairie dog colonies were Oropsylla hirsuta, Oropsylla tuberculata cynomuris, and Pulex simulans, with greatest flea abundance occurring in March and October. Flea load and infestation intensity increased during epizootics and was highest on prairie dogs with Y. pestis-infected fleas. The seasonal occurrence of epizootics among black-tailed prairie dogs was found to coincide with seasonal peaks in mean flea load.

**P15**

**PLAGUE ACTIVITY IN CALIFORNIA: A SUMMARY OF STATEWIDE PUBLIC HEALTH SURVEILLANCE, 1984–2007**

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Yersinia pestis, the causative bacterial agent of plague, entered California by way of infected rats and humans who disembarked at the major port cities during the early 1900s. Over the succeeding decades, plague rapidly adapted to indigenous wildlife and spread throughout the western United States. Since 1930 the California Department of Public Health (CDPH) has maintained an integrated statewide plague surveillance program that encompasses investigations of clinical plague in humans and domestic felids, evaluation of epizootic activity in rodents, and serologic monitoring of wild carnivores. This poster provides a 24-year summary of surveillance data collected in California from 1984 through 2007: Twenty-four human cases of plague occurred from 14 counties, two of which were fatal. Y. pestis was isolated from 82 domestic pets in 12 counties. We recorded at least 68 epizootic events among wild rodents in 21 counties. Rodent species most frequently involved in plague maintenance and transmission were California ground squirrels (Spermophilus beecheyi), Douglas’ squirrels (Tamiasciurus douglasii), shadow chipmunks (Tamias senex), and yellow-pine chipmunks (Tamias amoenus). Carnivores frequently detected with serum antibodies to Y. pestis were black bears (Ursus americanus), bobcats (Lynx rufus), and coyotes (Canis latrans). Animals evaluated for plague activity totaled 34,537 and provided 2,555 positive results. Through the use of this cooperative statewide plague surveillance program, CDPH has been able to respond effectively to human cases and epizootic activity when they occur. The program has also enabled CDPH to gain a greater understanding of the epidemiology of the disease.