ANTHROPOGENIC HABITAT DISTURBANCE AND THE DYNAMICS OF HANTAVIRUS USING REMOTE SENSING, GIS, AND A SPATIALLY EXPLICIT AGENT-BASED MODEL

by

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ABSTRACT

Sin Nombre virus (SNV), a strain of hantavirus, causes hantavirus pulmonary syndrome (HPS) in humans, a deadly disease with high mortality rate (>50%). The primary virus host is deer mice, and greater deer mice abundance has been shown to increase the human risk of HPS. There is a great need in understanding the nature of the virus host, its temporal and spatial dynamics, and its relation to the human population with the purpose of predicting human risk of the disease.

This research studies SNV dynamics in deer mice in the Great Basin Desert of central Utah, USA using multiyear field data and integrated geospatial approaches including remote sensing, Geographic Information System (GIS), and a spatially explicit agent-based model. The goal is to advance our understanding of the important ecological and demographic factors that affect the dynamics of deer mouse population and SNV prevalence. The primary research question is how climate, habitat disturbance, and deer mouse demographics affect deer mouse population density, its movement, and SNV prevalence in the sagebrush habitat.

The results show that the normalized difference vegetation index (NDVI) and the enhanced vegetation index (EVI) can be good predictors of deer mouse density and the number of infected deer mice with a time lag of 1.0 to 1.3 years. This information can be very useful in predicting mouse abundance and SNV risk.

The results also showed that climate, mouse density, sex, mass, and SNV infection had significant effects on deer mouse movement. The effect of habitat disturbance on mouse movement varies according to climate conditions with positive relationship in predrought condition and negative association in postdrought condition. The heavier infected deer mice moved the most. Season and disturbance alone had no significant effects.

The spatial agent-based model (SABM) simulation results show that prevalence was negatively related to the disturbance levels and the sensitivity analysis showed that population density was one of the most important parameters affecting the SNV dynamics. The results also indicated that habitat disturbance could increase hantavirus transmission likely by increasing the movement and consequently contact rates. However, the model suggested that habitat disturbance had a much stronger effect on prevalence by decreasing population density than by increasing mice movement. Therefore, overall habitat disturbance reduces SNV prevalence.

TABLE OF CONTENTS

Chapter

LIST OF FIGURES

Figure **Page**

LIST OF TABLES

Table **Page**

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CHAPTER 1

INTRODUCTION

Problem Statement

Animal populations and the diseases they carry are strongly affected by environmental change, which can enhance or control the development of certain diseases (IES, 2005a). The progression of human society in the past several centuries has dramatically changed the ecological landscape. Human population growth and related landscape modification threaten to reduce biological capital and disrupt ecological processes (Myers, 1998). From large-scale land transformation to the global movement of people, animals, and plants, very few ecosystems can be considered remote or pristine (IES, 2005a). These are a few factors that have led to a dramatic increase in new and emerging zoonotic diseases (i.e. diseases spread from animals to people), such as hantavirus, Avian Flu, and West Nile Virus.

Traditionally, infectious diseases have been addressed through the use of vaccines or drugs. However, an understanding of how ecological systems influence disease dynamics could help advance our ability to both manage and predict infectious diseases in humans, wildlife, and natural habitat. Karl Johnson, a world-famous virologist, noted at the 2005 Ecology of Infectious Diseases Conference, "Successfully addressing the infectious diseases of the future will require building a bridge between both sides of the disease equation: epidemiology and ecology". Sharon Deem, a veterinarian at the Smithsonian Institution, commented, "Incorporating ecological approaches into the infectious disease framework will strengthen our ability to respond to emerging pathogens" (IES, 2005b).

One example of a zoonotic disease that has occurred in North America is hantavirus pulmonary syndrome (HPS). HPS is characterized by acute respiratory distress with a high mortality rate (>50%) (Glass et al., 2000; Nichol et al., 1993). HPS has been traced to the infection with Sin Nombre virus (SNV), a strain of hantavirus of which the deer mouse *(Peromyscus maniculatus)* is the primary reservoir (CDC, 1993; Childs et al., 1994; Hjelle et al., 1996). So far there is no vaccine or effective drug to prevent or treat HPS (Buceta et al., 2004; Custer et al., 2003). Therefore, there is a need to understand the nature of the virus host, its temporal and spatial dynamics, and its relation to the human population in order to predict the risk of the disease and design effective prevention policies.

The goal of this research is to advance our understanding of the effects of anthropogenic habitat disturbance on deer mouse movement and the prevalence of SNV using remote sensing, Geographic Information System (GIS) and agent-based modeling (ABM). This research will help us understand the important ecological parameters of hantavirus infections in the deer mouse population, and expand our understanding of the risk factors of developing HPS in humans as a consequence of SNV infection.

Research Objectives

The objectives of this research are to increase the understanding of the ecology of the primary virus host of SNV and the dynamics of SNV in a desert sagebrush habitat in the Great Basin, Utah. The specific objectives are as follows:

1. Identifying the factors potentially affecting deer mouse movement in the desert sagebrush habitat by: (1) measuring deer mouse movement using GIS and recapture data, and (2) examining the relationships between deer mouse movement and various factors, including climate, season, habitat disturbance, population density, sex, mass, and SNV infection status. The results can help increase our understanding of the important factors that may affect hantavirus dynamics.
2. Investigating the value of Moderate Resolution Imaging Spectroradiometer (MODIS) time-series data for estimating rodent abundance and SNV prevalence with the goal of predicting hantavirus risk. We examine the relationships between environmental conditions (vegetation greenness and moisture), deer mouse density, and SNV prevalence using high temporal resolution (16 day) MODIS satellite imagery and multiyear field survey data. The central hypothesis is that vegetation indices can serve as proxies for deer mouse food availability that affects deer mouse abundance and SNV prevalence.
3. Identifying the relationships between habitat disturbance, deer mouse density, movement, and SNV prevalence using a spatially explicit agent-based model at microlevels. In recent years, agent-based modeling (ABM) has emerged as a very promising bottom-up modeling approach to simulate individual behaviors and their interactions at a microlevel, which results in emergent phenomena at a macrolevel. It is a great exploratory tool to test hypotheses as well as to experiment with a range of “what-if” scenarios.

Research Questions

The primary research questions are the following:

1. How do climate condition, deer mouse demographics (e.g. mass and sex), and anthropogenic habitat disturbance affect deer mouse movement in desert sagebrush habitats?

It has been suggested that deer mouse movement through the landscape affects the rate and pattern of disease transmission (Langlois et al., 2001). Escutenaire et al. (2002) found that hantavirus infection was associated with higher mobility in juvenile and subadult males. However, much research still needs to be done to further understand the relationship between the movement and the disease transmission rate and pattern and how the environmental and demographic factors affect deer mouse movement.

2. How do environmental conditions affect deer mouse population densities and SNV prevalence?

Environmental conditions, such as climate (Glass et al., 2000; Langlois et al., 2001), seasonality (Cantoni et al., 2001; Dearing et al., 2009), and vegetation type have been associated with the geographic distribution of SNV in deer mouse populations in past studies. One of the main drivers for the interannual changes in HPS cases is thought to be fluctuation in precipitation and temperature. The El Niño of 1991 - 1992 is believed to be the major climatic factor leading to the outbreak of HPS in 1993 in the southwestern U.S. The dramatically increased rainfall is thought to have brought more food and thus increased local rodent populations (Engelthaler et al., 1999; Parmenter et al., 1993). This affects the abundance of deer mice and subsequently, the human risk of HPS.

3. How might changes in habitat disturbance, mouse density, and deer mouse movement in this system affect hantavirus prevalence? Does disturbance hinder or increase the hantavirus transmission in deer mice?

There exist two contrasting hypotheses on how habitat disturbance affects hantavirus prevalence. Langlois et al. (2001) suggested that fragmented habitat increased mouse movement and thus contact rates, and consequently increased hantavirus transmission. In contrast, Calisher et al. (2000) proposed that habitat disturbance reduced rodents' habitat and thus virus host, and therefore decreased hantavirus prevalence.

Hantavirus Dynamics

In May 1993, an outbreak of HPS characterized by acute respiratory distress with high mortality rate (>50%) (Glass et al., 2000; Nichol et al., 1993) among previously healthy young people occurred in the Four Corners region of the southwestern United States, where the borders of Colorado, New Mexico, Arizona, and Utah meet. Hantaviruses are rodent-borne zoonotic agents that produce mild to severe hemorrhagic fevers in victims (Mills et al., 1999). There have been about 30 different types of hantaviruses identified throughout most of Europe, Asia, and the Americas (Schmaljohn & Hjelle, 1997). Sin Nombre virus (SNV), one of the hantaviruses, was not isolated until the 1993 outbreak in the Four Corners region. SNV causes HPS which has emerged as a significant public health problem throughout the Americas (Schmaljohn & Hjelle, 1997).

The primary host of SNV is the deer mouse (Childs et al., 1994; Hjelle et al., 1996), *Peromyscus maniculatus*, one of the most common mammals in North America. The virus establishes a chronic infection in the mouse population, but it is not lethal to them. The principal means of the virus transmission in the mice population is believed to be aggressive fighting (Calisher et al., 1999; Glass et al., 1988; Mills et al., 1997). Many studies have found that scars or wounds in the rodents are positively related to SNV infection (Calisher et al., 2002; Root et al., 1999). Humans are frequently infected by inhaling the infectious aerosols of the urine, feces, and saliva shed by the rodents (Tsai, 1987).

A number of factors have been related to the dynamics of hantaviruses in mouse populations, including environmental conditions (e.g. precipitation, vegetation type and structure, elevation), the demographics of rodent population (e.g. sex, reproductive status, age, mass, species richness, host density), and movement. The El Niño of 1991 - 1992 is believed to be the major climatic factor leading to the outbreak of HPS in 1993 in the Four Corners region. The dramatically increased rainfall is thought to have brought more food and thus increased local rodent populations (Engelthaler et al., 1999; Parmenter et al., 1993). Glass et al. (2000) found an association between environmental conditions and HPS risk using rainfall pattern data at weather stations combined with remotely sensed data. Boone et al. (2000) used remote sensing and GIS to characterize vegetation type and density, elevation, slope, and hydrologic features to predict SNV infection of deer mice with up to 80% accuracy. Many studies have found that there is a higher prevalence of SNV in male than female rodents (Calisher et al., 2002; Escutenaire et al., 2002)). Escutenaire et al. (2002) found that sexually active animals were significantly more often wounded and this was positively related with infection. Calisher et al. (2002) found a negative association between rodent species diversity and prevalence of SNV infection in deer mice. This was believed to be because higher species diversity reduces the primary disease reservoir (deer mice).

A few studies have suggested that landscape structure may have significant effects on disease dynamics. Langlois et al. (2001) found that virus transmission increased with habitat disturbance. They present two possible explanations for the positive effect of habitat disturbance on hantavirus transmission. First, if deer mice move further in a more disturbed habitat or fragmented landscape, which was found to be the case in Diffendorder et al. (1995), they may have a wider range of contact and therefore increase virus transmission probability. Second, habitat disturbance may confine deer mice in small habitat patches and therefore increase deer mouse local population density, contact, and thus virus transmission rates. Mackelprang et al. (2001) suggested that a high level of SNV prevalence at one site in Utah may be due to disturbance by humans, primarily the intensive use of all-terrain vehicles (ATVs) at a recreation area. Heavy recreation use produces numerous dirt roads, campsites, and large open spaces. Open space caused by this disturbance reduces preferred habitat for species such as deer mice, and may cause animal density to increase within a microhabitat. Increased interactions may lead to a higher rate of SNV transmission. From the opposite point of view, Calisher et al. (2001) suggested that habitat disturbance, primarily by grazing, decreased prevalence, in that a high rate of turnover could not maintain the virus as there were fewer good virus hosts in the disturbed habitat.

The potential effect of landscape pattern on disease transmission is becoming increasingly recognized (Kitron, 1998; Ostfeld et al., 2002; Taylor & Merriam, 1996). A few recent studies have suggested that anthropogenic habitat disturbance may have significant effects on hantavirus dynamics (Calisher et al., 2001; Langlois et al., 2001; Mackalprang et al., 2001). However, the findings have been contradictory. Langlois et al.

(2001) found that virus transmission increased with habitat disturbance. They present two possible explanations for the positive effect of habitat disturbance on hantavirus transmission. First, if deer mice move further in a more disturbed habitat or fragmented landscape, which was found to be the case in Diffendorder et al. (1995), they may have a wider range of contact and therefore increase virus transmission probability. Second, habitat disturbance may confine deer mice in small habitat patches and therefore increase deer mouse local population density, contact, and thus virus transmission rates. Mackelprang et al. (2001) suggested that a high level of SNV prevalence at one site in Utah may be due to disturbance by humans, primarily the intensive use of all-terrain vehicles (ATVs) at a recreation area. Heavy recreation use produces numerous dirt roads, campsites and large open spaces. Open space caused by this disturbance reduces preferred habitat for species such as deer mice, and may cause animal density to increase within a microhabitat. Increased interactions may lead to a higher rate of SNV transmission. From the opposite point of view, Calisher et al. (2001) suggested that habitat disturbance, primarily by grazing, decreased prevalence, in that a high rate of turnover could not maintain the virus as there were fewer good virus hosts in the disturbed habitat. Calisher et al. (2001) also suggested that long-lived infected deer mice served as transseasonal, over-winter reservoirs for the virus, providing the mechanism for its survival. Whether disturbance hinders or increases hantavirus prevalence is still in question.

Methodology Framework

This section provides an overview of three major components of this research and their connections shown in Figure 1.1: 1) GIS movement mapping and analysis (in green), 2) MODIS satellite data analysis (in cyan), and 3) the spatially explicit agent-based model (in blue). The red lines represent interactions between the major components. GIS is used to visualize movement vectors and calculate movement distances to examine the effects of climate, season, habitat disturbance, mass, and sex on deer mice movement with a statistical testing approach. The GIS movement vectors are overlaid on the high resolution remote sensing imagery for a visual and qualitative evaluation of how habitat disturbance affects deer mice movement. Environmental indices derived from MODIS satellite imagery are examined for the relationships with deer mice density and hantavirus prevalence. The environmental indices may be used to specify the food resource level, which affects deer mice density in the spatial agent-based model (SABM). The SABM is fed with a GIS categorical habitat map derived from high resolution imagery, and mouse densities are calculated from the field data. Deer mouse population dynamics, their movement and contacts, and hantavirus transmission are simulated with various adjustable parameters, and the process is visualized with graphical displays.

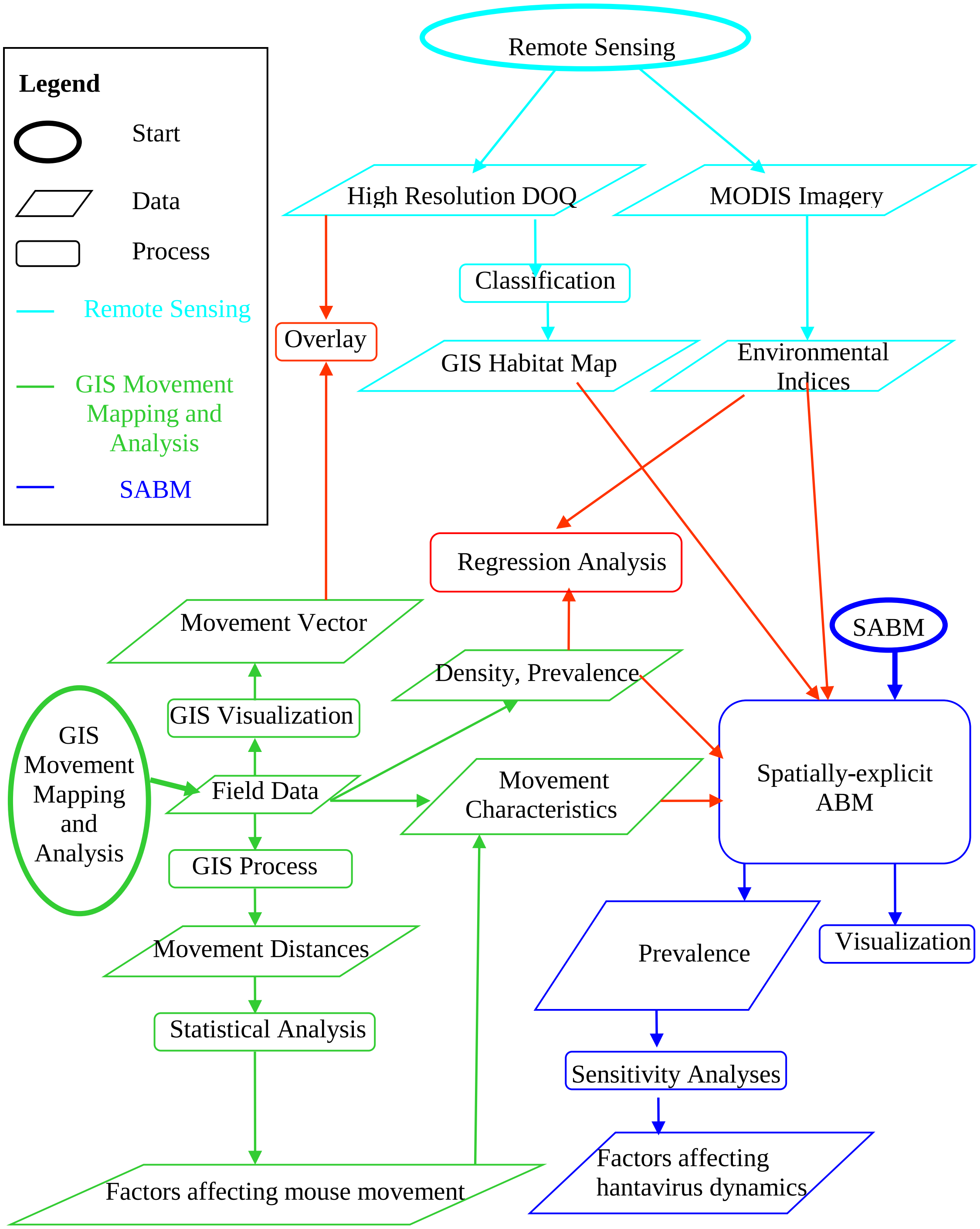

Figure 1.1 Methodology Framework.

CHAPTER 2

USING MODIS SATELLITE IMAGERY TO PREDICT HANTAVIRUS RISK

Abstract

Sin Nombre virus (SNV), a strain of hantavirus, causes hantavirus pulmonary syndrome (HPS) in humans, a deadly disease with high mortality rate (>50%). The primary virus host is deer mice, and greater deer mice abundance has been shown to increase the human risk of HPS. Our aim is to identify and compare vegetation indices and associated time lags for predicting hantavirus risk using remotely sensed imagery.

A five-year time-series of Moderate Resolution Imaging Spectroradiometer (MODIS) satellite imagery and corresponding field data was utilized to compare various vegetation indices that measure productivity with the goal of indirectly estimating mice abundance and SNV prevalence. Relationships between the vegetation indices and deer mouse density, SNV prevalence, and the number of infected deer mice at various time lags were examined to assess which indices and associated time lags might be valuable in predicting SNV outbreaks.

The results reveal varying levels of positive correlation between the vegetation indices and deer mouse density as well as the number of infected deer mice. Among the vegetation indices, the normalized difference vegetation index (NDVI) and the enhanced vegetation index (EVI) produced the highest correlations with deer mouse density and the

number of infected deer mice using a time lag of 1.0 to 1.3 years for May and June imagery.

This study demonstrates the potential for using MODIS time-series satellite imagery in estimating deer mouse abundance and predicting hantavirus risk. The one-year time lag provides a great opportunity to apply satellite imagery to predict upcoming SNV outbreaks, allowing preventive strategies to be adopted. Analysis of different predictive indices and lags could also be valuable in identifying the time windows for data collection for practical uses in monitoring rodent abundance and subsequent disease risk to humans.

Introduction

In May 1993, an outbreak of hantavirus pulmonary syndrome (HPS) occurred among previously healthy young people in the Four Corners region of the southwestern United States. HPS has a relatively high mortality rate (>50%) and is characterized by acute respiratory distress (Glass et al., 2000; Nichol et al., 1993). HPS was traced to the infection with Sin Nombre virus (SNV), a strain of hantavirus of which the deer mouse *(Peromyscus maniculatus)* is the primary reservoir (CDC, 1993; Childs et al., 1994; Hjelle et al., 1996). There is currently no vaccine or effective drug to prevent or treat HPS (Buceta et al., 2004; Custer et al., 2003), and for this reason there is a need to understand the nature of the virus as well as its spatial and temporal dynamics in order to predict the risk of the disease and design effective prevention policies.

Environmental conditions, such as climate (Glass et al., 2000; Yates et al., 2002), seasonality (Cantoni et al., 2001; Dearing et al., 2009), and vegetation type (Boone et al., 2000) have been associated with the geographic distribution of SNV in deer mouse populations in past studies. One of the main drivers for the interannual changes in HPS cases is thought to be fluctuation in precipitation and temperature. The El Niño of 1991 - 1992 is believed to be the major climatic factor leading to the outbreak of HPS in 1993 in the southwestern U.S. The dramatic increase in rainfall is believed to have resulted in more food and thus increased local rodent populations such as deer mice (Engelthaler et al., 1999; Parmenter et al., 1993). This increase in deer mice abundances enhances the human risk of HPS (Parmenter et al., 1993). Child et al. (1995) conducted a household-based, case-control study of environmental factors associated with HPS and found that a higher number of captured, infected deer mice is associated with HPS occurrence.

Yates et al. (2002) outlined the effects of climate change on the abundance of rodent populations in the Trophic Cascade Hypothesis. As precipitation increases and temperature is more tolerable, net primary productivity increases and subsequently results in a larger deer mouse population. Increased mouse density increases viral transmission among mice and results in a larger number of dispersing mice. This leads to increased disease transmission to humans who come into contact with these mice. When environmental conditions become more severe, mouse populations decline, but the environmental conditions at some locations allow survival of a sufficiently large rodent population for the virus to persist. Thus, it is important to identify the environmental conditions needed to maintain host populations of sufficient sizes to sustain the virus. Hantaviruses are horizontally transmitted among members of the rodent population but are not vertically transmitted to offspring. They need a large host population to avoid local extinction (Glass et al., 2007).

Satellite imagery has demonstrated value in linking environmental conditions to disease distribution and dynamics. For example, Linthicum et al. (1999) found that Rift Valley Fever outbreaks could be predicted up to 5 months in advance in Kenya using the normalized difference vegetation index (NDVI) and Pacific and Indian Ocean sea-surface temperature anomalies. Thomson et al. (1997) used meteorological satellite data to model the spatial and seasonal dynamics of infectious disease transmission and developed affordable early warning systems for malaria. A study of malaria prevalence in the children of Gambia used NDVI to measure changes in vegetation growth as proxy ecological variables representing changes in rainfall and humidity to predict length and intensity of malaria transmission (Thomson et al., 1999).

A few previous studies have utilized Landsat Thematic Mapper (TM) satellite imagery to study hantavirus dynamics. Glass et al. (2002) developed logistic regression models to predict human risk of HPS using Landsat TM imagery. They found that heavy rainfall associated with El Niño/Southern Oscillation increased the rodent population and preceded HPS cases in the southwestern U.S. (Glass et al., 2000). Goodin et al. (2006) evaluated the relationship between land-cover and hantavirus prevalence in rodents. Their land-cover map was derived from a variety of coarse resolution satellite imagery depending on the type of land cover being mapped (e.g. Along Track Scanning Radiometer (ATSR) and SPOT-VGT). A positive relationship was found between agricultural land cover disturbance and hantavirus in rodents in Paraguay. However, single-date satellite imagery can be limited in capturing the vegetation dynamics that impact rodent population dynamics.

The Moderate Resolution Imaging Spectroradiometer (MODIS) launched on the NASA satellites *Terra* (December 1999) and *Aqua* (May 2002) significantly improved data availability for epidemiological studies. There have been a few studies that utilized MODIS time-series data in modeling rodent pathogen transmission and predicting disease risk to humans. Glass et al. (2007) applied MODIS NDVI data to compare vegetation growth patterns in years of severe drought from 2002 to 2004 and found high risk HPS areas had higher levels of green vegetation and longer durations of greenness. Marston et al. (2007) modeled the spatial distribution of the rodent species that were the hosts of a parasitic tapeworm. The rodent distribution was modeled with landscape characteristics using four different types of remotely sensed data. Their results showed that the MODIS time-series image data provided the strongest relationships and explained the highest percentage deviance of the relationships present (up to 41.4%). These results support the idea that using time-series NDVI data can offer improved results over single date imagery.

In this study, we investigated the value of MODIS data for estimating rodent abundance and SNV prevalence with the goal of predicting hantavirus risk. We examined relationships between environmental conditions (vegetation greenness and moisture), deer mouse density, and SNV prevalence using high temporal resolution (16 days) MODIS satellite imagery and multiyear field survey data. The central hypothesis is that vegetation indices can serve as proxies for deer mouse food availability that affects deer mouse abundance and SNV prevalence. We applied MODIS time-series imagery to measure vegetation productivity and to indirectly estimate mice abundance and SNV prevalence in deer mouse population.

Methods

Study Area

The study area is located in proximity to the Little Sahara Recreation area in Juab County, Utah (39°40´ N, 112° 15´ W). The elevation in this area ranges from 1600 to 1900 m. Dominant vegetation species in the area include Great Basin sagebrush (*Artemisia tridentata*) and Utah juniper (*Juniperus osteosperma*). Areas with high sagebrush cover are positively correlated with deer mouse abundance (Pearce et al., 2008). The preferred habitat for deer mice is sagebrush. This particular area has experienced heavy recreation use, mainly by all-terrain vehicles (ATVs) (Lehmer et al., 2008). Landscape disturbance due to ATV recreation use has created new roads, trails, and open space. Trapping webs at the study area were selected based on low and high levels of disturbance. Low disturbance refers to those areas where ATVs have had little or no effect, and high disturbance refers to the areas with trails and vast bare ground caused by camping and the heavy use of recreational vehicles.

Field Data

Rodents were live-trapped in the spring and fall of 2004, 2005, and 2006. Twelve 3.14-ha trapping sites using a web-based approach (Anderson et al., 1983) were established for spring and fall seasons of 2004, 2005, and 2006. There have been two general field sampling designs for estimating small-mammal population: grid-based regimes and web-based approaches (typically transect lines or trapping webs) (Anderson et al., 1983; Buckland et al., 1993, 2001; Burnham et al., 1980). Web-based trapping has been utilized in a number of studies, including small-mammal studies at a number of sites within the U.S. Long Term Ecological Research network, monitoring programs for rodent-borne zoonotic diseases conducted by public health agencies in the United States (Parmenter et al. 1999), and global-change/biodiversity programs around the world. The trapping web design in this study is the most commonly used trapping arrangement in longitudinal studies of hantavirus (Abbott, 1999; Calisher et al., 1999; Kuenzi et al., 1999; Mills et al., 1999a, b; Root et al., 1999;).

Trapping webs are centered on a reference location with traps emanating from this point. The trapping web contains twelve 100-m trap-transects radiated from the center trap at 30° angles from one another. Transects were numbered from 1 to 12 with the first transect facing south and other transects incremented in a clock-wise direction. Twelve traps are placed on each trap-transect. For each trap-transect, the first four traps are spaced 5 m apart, and the other eight traps are 10 m apart. Each trap is coded and marked by the transect number and its location along each transect labeled by letters from A to L with A for the closest trap to the center and L for the furthest.

In each sampling period, traps were set for each trapping web for three consecutive nights. Small mammal processing was conducted according to protocols and methods for trapping and sampling small mammals for virological testing (Mills et al., 1995). Ear tags with individual numbers were attached to newly captured mice. Captured mice were weighed and recorded for trap code, sex, reproductive status, weight, ear tag number, wounds, scars, etc. Blood was drawn from deer mice for testing the presence of SNV. Rodents were released where they were captured.

Enzyme-Linked Immunosorbent Assay for detection of Sin Nombre virus antibody was performed on all blood samples (Feldman et al., 1993; Lehmer et al., 2008).

Prevalence is reported as the percentage of infected deer mice at each sampling site. For this reason, an estimate of prevalence increases in accuracy with the sample size.

MODIS Satellite Imagery

This study utilized MODIS surface reflectance 16-day composite data with 500 m spatial resolution to derive environmental conditions of the study sites across multiple years (2003 to 2006). MODIS instruments capture data in 36 spectral bands ranging in wavelength from 0.4 to 14.4 µm and at varying spatial resolutions (2 bands at 250 m, 5 bands at 500 m, and 29 bands at 1 km). They provide twice-a-day global coverage at 250m (Red, NIR), 500m (MIR), and 1000m resolution (TIR). The data sets are available to the public approximately one week after acquisition, and they are designed to provide measurements in large-scale global dynamics and processes occurring on the land, and in the oceans and lower atmosphere. MODIS imagery has been successfully used for a variety of applications, including quantifying vegetation cycles, assessing land cover change, and mapping the spatial distribution of habitats (Beck et al., 2006; Jinet et al., 2005; Lunetta et al., 2006; Xiao et al., 2006).

Temporal Compositing Methods

Temporal compositing of remote sensing time-series data is a common practice to compress data and reduce the impacts of cloud effects and changing view geometry (Qi & Kerr, 1997). Temporal compositing algorithms analyze the pixel values across time and select the single best pixel value to represent the entire time period (Dennison et al., 2007).

Many temporal compositing algorithms have been developed for moderate-to-coarse resolution remote sensing systems. Dennison et al. (2007) introduced a new class of compositing algorithms based on two measures of spectral similarity, endmember average root mean square error (EAR) and minimum average spectral angle (MASA). Their research demonstrated that these novel algorithms reduce short-term variability in spectral indices across several land cover types (Dennison et al., 2007). A set of 16-day MODIS compositing data across March to July of five years (2002 ~ 2006) using MASA and EAR methods were created and used to derive several vegetation indices.

Vegetation Indices from MODIS

The correlations between a set of vegetation indices calculated from five years of MODIS data and deer mouse density, hantavirus prevalence, and the number of infected mice for each site across four years (2003 to 2006) were examined using linear regression. The sample sizes varied from 36 for spring to 43 for fall because a few additional sites were added in fall 2003 and 2004. Four commonly used vegetation indices were calculated, including normalized difference vegetation index (NDVI; Rouse et al., 1973), the enhanced vegetation index (EVI; Huete et al., 2002), normalized difference water index (NDWI; Gao et al., 1996), and visible atmospherically resistant index (VARI; Gitelson et al., 2002). NDVI, EVI, and VARI are greenness indices based on chlorophyll absorption and near infrared reflectance and/or visible reflectance, while NDWI is a moisture index based on near infrared water absorption.

NDVI is a very simple, well-known, and widely used remote sensing vegetation index. It is calculated from the individual measurements as follows:

$$NDVI = (\rho_{NIR} - \rho_{RED}) / (\rho_{NIR} + \rho_{RED}) \qquad (1)$$

where ρ_{RED} and ρ_{NIR} stand for the red and near-infrared reflectance. The resulting values range from -1.0 to + 1.0.

EVI was developed to improve the NDVI by accounting for soil and atmospheric interference (Huete et al., 1997, 2002; Justice et al., 1998). EVI normalizes the red band reflectance by the blue band reflectance (Huete et al., 1997). EVI is more sensitive in high Leaf Area Index (LAI) vegetation, where NDVI saturates quickly and shows very little dynamic range for high LAI canopies in crop fields (Boegh et al., 2002). EVI is formulated as:

$$EVI = G\,(\rho_{NIR} - \rho_{Red}) / (\rho_{NIR} + C1 * \rho_{Red} - C2 * \rho_{Blue} + L) \qquad (2)$$

where G = 2.5, C1 = 6, C2 = 7.5, and L =1. VARI is a vegetation index based entirely on visible reflectance (Gitelson et al., 2002). VARI is calculated as:

$$VARI = (\rho_{Green} - \rho_{Red}) / (\rho_{Green} + \rho_{Red} - \rho_{Blue}) \qquad (3)$$

NDWI was introduced by Gao (1996) to assess water content using near infrared water absorption. NDWI increases with vegetation water content. It is defined as follows:

$$NDWI = (\rho_{0.86\,\mu m} - \rho_{1.24\,\mu m}) / (\rho_{0.86\,\mu m} + \rho_{1.24\,\mu m}) \qquad (4)$$

The 0.86 µm and 1.24 µm channels of MODIS are band 2 and band 5, respectively.

Time Lags

Glass et al. (2002) found that there was an apparent one-year lag between the end of the 1997–1998 El Niño and the increase in hantavirus prevalence in high-risk areas, which was also the case in the 1993 HPS outbreak preceded by the 1991–1992 El Niño event. This time lag is also in line with the trophic cascade hypothesis (Yates et al., 2002).

Vegetation indices were calculated for MODIS composites from March through July, 2002-2006. This time period coincides with vegetation green-up in the study area, and the index values during this time period should indicate vegetation productivity. Time lag effects between the spring vegetation indices (2002-2006) and deer mouse density and hantavirus prevalence (2003-2006) were explored with lags of 0, 0.3, 1.0, and 1.3 years. A 0-year lag examined the correlation between spring vegetation indices and the same-year spring field data. The 0.3-year lag examined the correlation between spring vegetation indices and fall field data in the same year. The 1.0-year time lag examined the correlation between spring vegetation indices and field data from the following spring. The 1.3-year time lag examined correlations between spring vegetation indices and fall field data in the following year. Linear regression was used and r^2 was calculated and compared.

Results

Deer Mouse Density and Vegetation Indices

Correlations between vegetation indices and deer mouse density typically peaked in May or June for NDVI and EVI and in March for NDWI. For VARI, the correlation with density peaked in March at 0-year and 0.3-year time lag and was highest in May at 1.0-year and 1.3-year lag. Figure 2.1 shows an example of changing correlations between EVI and deer mouse density for each composite period, and at the four different lag times. At peak r^2, linear correlations between deer mouse density and NDVI/EVI at 1.3-

year lag were mostly significant. Figure 2.2 shows an example of the relationship between June 10th EVI and density at a 1.0-year time lag.

The maximum r^2 for each vegetation index and lag are shown in Table 2.1. Linear regression showed that all vegetation indices had significant ($P < 0.01$) correlations with deer mouse density at various time lags. For correlations between deer mouse density and NDVI/EVI over various time lags, the 1.0-year and 1.3-year lags yielded higher r^2 than the 0-year and 0.3-year lags, where the 1.3-year lag had the highest r^2. Correlations were highest for NDVI at a 1.3-year lag, with an r^2 of 0.50 and significance greater than 99.9%. The intercept and slope coefficients of the linear regression were -99.39 and 527.26. Correlations were also high for EVI at 1.0-year and 1.3-year lag, with r^2 of 0.46 and 0.47 and significance greater than 99.9%. The intercepts and slope coefficients of the regression lines were -77.68 and 772.30 for 1.0-year lag, and -100.15 and 893.44 for 1.3-year lag, respectively. Significant correlations were also found between VARI and deer mouse density at all time lags, with r^2 ranging from 0.21 to 0.29. There were significant correlations between NDWI at 0-year and 0.3-year lag and deer mouse density, with r^2 of 0.35 and 0.23.

Average May 9th NDVI and mouse density in the fall across 12 study sites were computed and plotted in Figure 2.3. The average May 9th NDVI increased 19% in 2005 from 2004, while mouse density doubled in the fall of 2006 over the fall of 2005. When average NDVI varied little between 2002 and 2003, there was little change in mouse density from 2003 to 2004.

Total Number of Infected Mice and Vegetation Indices

Correlations between the number of infected mice and the vegetation indices across the time lags (0, 0.3, 1.0, 1.3 years) were also examined. Table 2.2 lists the maximum r^2 and the dates of the maximum r^2 for the number of infected mice and the vegetation indices. The results were very similar to those of mouse density. This may indicate that density and the number of infected mice are correlated.

All vegetation indices had significant ($P < 0.01$) correlations with the number of infected mice at various time lags. For correlations between the number of infected deer mice and NDVI/EVI over various time lags, the 1.0-year and 1.3-year lags yielded higher r^2 than the 0 and 0.3 lags. Correlations were highest for EVI at 1.0-year lag, with an r^2 of 0.53 and significance greater than 99.9%. Correlations were also high for NDVI at 1.0-year and 1.3-year lag, with r^2 of 0.36 and 0.43, and significance greater than 99.9%. There were significant correlations between NDWI at 0-year, 0.3-year, and 1.0-year lag and the number of infected deer mice, with r^2 of 0.25, 0.16, and 0.20. Similar to the results for density, the maximum r^2 for NDWI and the number of infected mice were in March, while for NDVI and EVI, the high significant maximum r^2 were in May and June.

SNV Prevalence and Vegetation Indices

Correlations between SNV prevalence and the vegetation indices across the time lags (0, 0.3, 1.0, 1.3 years) were examined. Table 2.3 lists the maximum r^2 and the dates of the maximum r^2 of SNV prevalence and the vegetation indices.

Most of the r^2 of prevalence and vegetation indices were not significant. The highest significant r^2 (0.40) was of VARI in June at 1.0-year lag. The next highest r^2 was for NDVI with an r^2 of 0.28 at a 0-year lag. The next highest r^2 were of NDVI and EVI in

June at 1.0-year lag, with values of 0.27 and 0.25, respectively. NDWI did not have significant correlations with SNV prevalence at any time lag.

Discussion and Conclusions

This study examined the relationships between vegetation indices (NDVI, EVI, VARI, and NDWI), deer mouse density, SNV prevalence, and the number of infected deer mice (potential risk to humans) at various time lags with the goal of identifying useful vegetation indices and time lags for predicting the risk of hantavirus outbreaks. The results revealed reasonably good correlations between vegetation indices and deer mouse density, and the number of infected deer mice. In contrast, correlations between vegetation indices and SNV prevalence were much weaker. Prevalence is calculated as the ratio of the number of infected mice and the overall number of mice and but may not be necessarily correlated to either the number of infected mice or the overall number of mice. For example, the prevalence on a study site with a low number of infected mice and low overall number of mice may be the same to the prevalence on a study site with a high number of infected mice and high overall number of mice.

Among four tested vegetation indices, NDVI and EVI yielded higher significant r^2 while NDWI had lower significant values. VARI produced the lowest r^2. The 1.0-year and 1.3-year lags for NDVI and EVI provided the best correlations overall, which suggests that spring NDVI and EVI are better correlated with next year's deer mice abundance and the number of infected deer mice than the current year's. This finding corresponds to the study by Glass et al. (2002), which found that there was an apparent 1.0-year lag between the 1997–1998 El Niño and the increase in SNV prevalence in high-risk areas in the subsequent year. This was also the case in the 1993 hantavirus pulmonary syndrome outbreak in the southwestern U.S., which indicated that the previous 1991–1992 El Niño event was the major climatic factor leading to the outbreak. The dramatically increased rainfall is believed to result in greater food resources that permitted increases in deer mouse population sizes and subsequently the human risk of hantavirus pulmonary syndrome (Engelthaler et al., 1999; Parmenter et al., 1993). This time lag is also consistent with the findings of the trophic cascade hypothesis (Yates et al., 2002). The 1.0-year time lag provides great opportunities in applying satellite imagery to predict upcoming SNV outbreaks, allowing preventive strategies to be deployed in a timely manner.

While NDVI and EVI had the most significant r^2 at 1.0-year and 1.3-year lags, NDWI had most significant r^2 at 0-year and 0.3-year lags. The significant correlation between NDWI and deer mouse density occurred on March 6th. The most significant correlation between NDWI and the number of infected mice was also on March 6th. This indicates that early spring vegetation moisture may be a predictor of deer mouse density and the number of infected mice in the same spring and following fall. Combinations of different indices and lags could be valuable for identifying the time windows for data collection for practical uses in monitoring rodent abundance and subsequent disease risk to humans.

Although there have been a few studies applying remotely sensed data in predicting hantavirus risk (Boone et al., 2000; Glass et al., 2000), most of them used single-date TM imagery. However, single-date image data makes it difficult to capture the vegetation dynamics and their effect on disease dynamics. The high temporal resolution compositing satellite data eliminates the cloud cover and bad imagery, providing more reliable data. Glass et al. (2007) explored the use of January 2002 to April 2004 MODIS NDVI data to compare the seasonal patterns of vegetation growth at low-risk and high-risk hantavirus areas. The study showed that vegetation growth at high-risk sites started earlier and last longer than that at comparable lower risk sites regardless of land cover. Marston et al. (2007) showed the advantages and associated potential of using time-series MODIS NDVI datasets to model rodent distributions over single-time NDVI datasets. The use of high temporal resolution MODIS imagery in epidemiologic studies has been limited. This study demonstrated that using MODIS in estimating rodent abundance and predicting disease risk to humans has potential. While our study area is in Utah, USA, MODIS data is available for free with worldwide coverage. It is suitable to be extended to other rodent-borne diseases around the globe. A few examples are leptospirosis and the Argentine hemorrhagic fever**.** Herbreteau et al. (2006) explored the use of land use map and vegetation indices derived from the Advanced Spaceborne Thermal Emission and Reflection Radiometer satellite imagery in studying leptospirosis dynamics in the rice fields in Thialand. Porcasi et al. (2005) incorporated the Advanced Very High Resolution Radiometer NDVI as an environmental variable in a simple numerical model of rodent population dynamics and viral infection for Junin virus. These studies have shown the usefulness of satellite-derived vegetation indices in predicting rodent-borne diseases. MODIS data may improve predictive models for many of the 11 types of rodent-borne diseases listed in Table 2.4 (CDC, 2009).

A predictive model utilizing NDVI or EVI and NDWI could be built to predict deer mice abundance and hantavirus risk to humans. Other factors should be built into the model, such as temperature and the length of vegetation greenness. Tersago et al. (2009) found high summer and autumn temperatures in the previous 1 and 2 years were related to high hantavirus disease incidences in Belgium. Clement et al. (2009) reported the increase in bank vole populations may be because that the mild autumn in the previous year provides more food resources and therefore increases the survival rate in the winter. Longer vegetation greenness has been associated with high HPS risk areas. Glass et al. (2007) found the NDVI in high HPS risk areas had an early onset, with significantly higher levels of green vegetation that lasted longer than at lower risk sites. In a large extent of area, other variables have been found useful in relating environmental conditions with rodent borne diseases, such as land use (Goodin et al., 2006), vegetation types (Boone et al., 2000) and elevation (Jay et al., 1997).

While the results were promising, further study with more years of data would help to prove the long-term efficacy. Long-term studies are crucial for understanding the temporal patterns of virus host population and identifying characteristics of reservoir ecology associated with outbreaks of human disease. In spite of their importance and utility, long-term studies of reservoir populations of zoonotic diseases are rare. They require continuous funding for many years, they are labor intensive, expensive, and may not produce significant results in the short term (Mills et al., 1999). Our study collected a rich amount of field mice trapping data that has not been seen in past hantavirus studies. During six field seasons from 2004 to 2006, over 8000 mice at twelve study sites were captured, recorded, and released. This valuable field data provides great opportunities in understanding mice population ecology and hantavirus dynamics.

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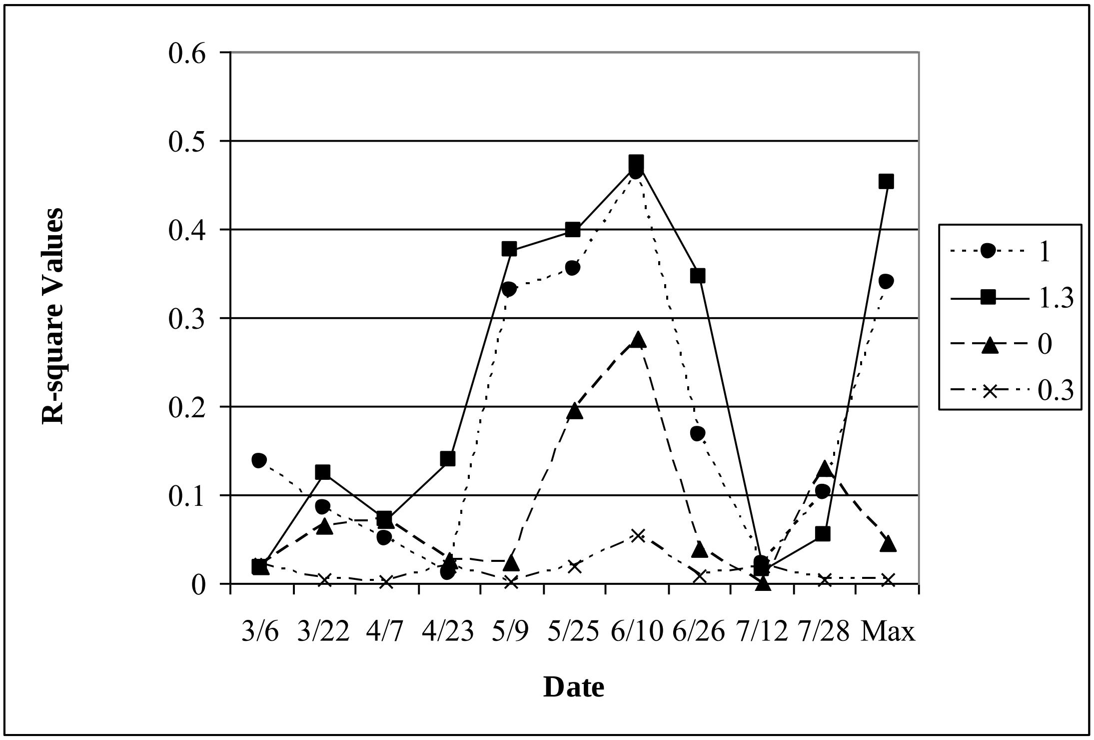


Figure 2.1 The r^2 of deer mouse density and the enhanced vegetation index (EVI) between March and July at 0, 0.3, 1.0, and 1.3-year lags. The correlation peaked in June, and the 1.0 and 1.3-year lag yielded highest significant r^2 (0.46 and 0.47, respectively).

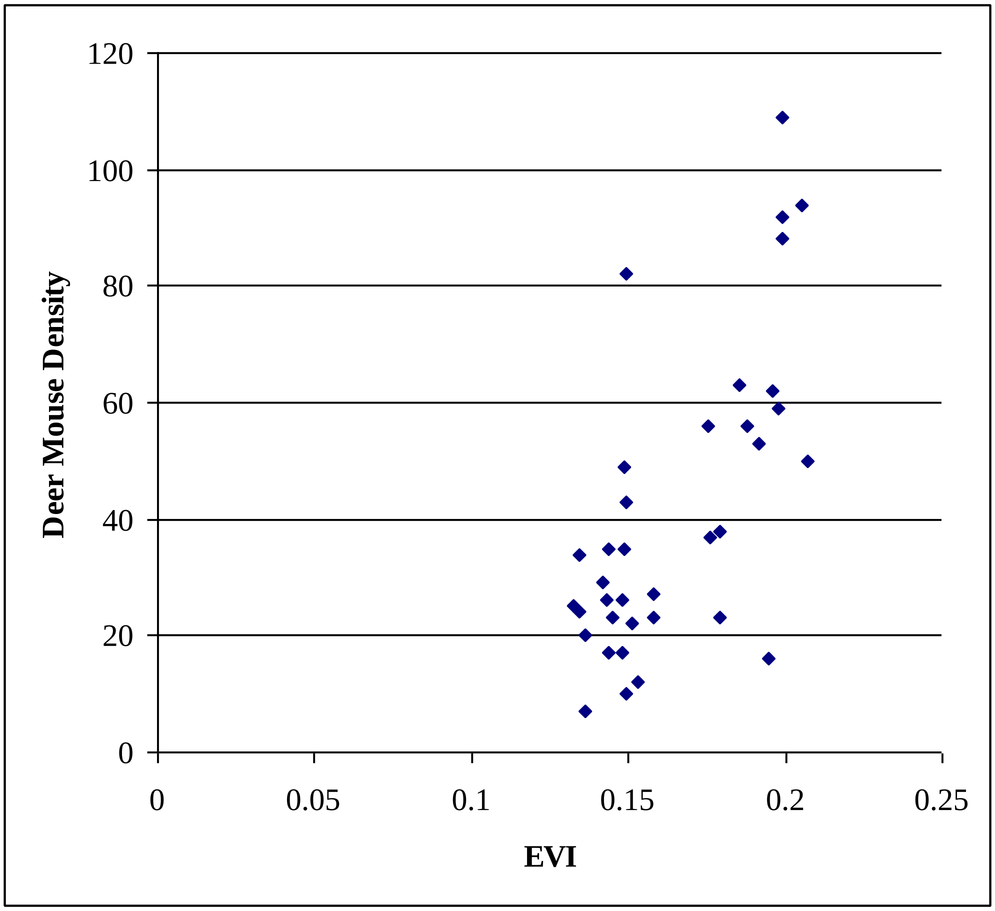
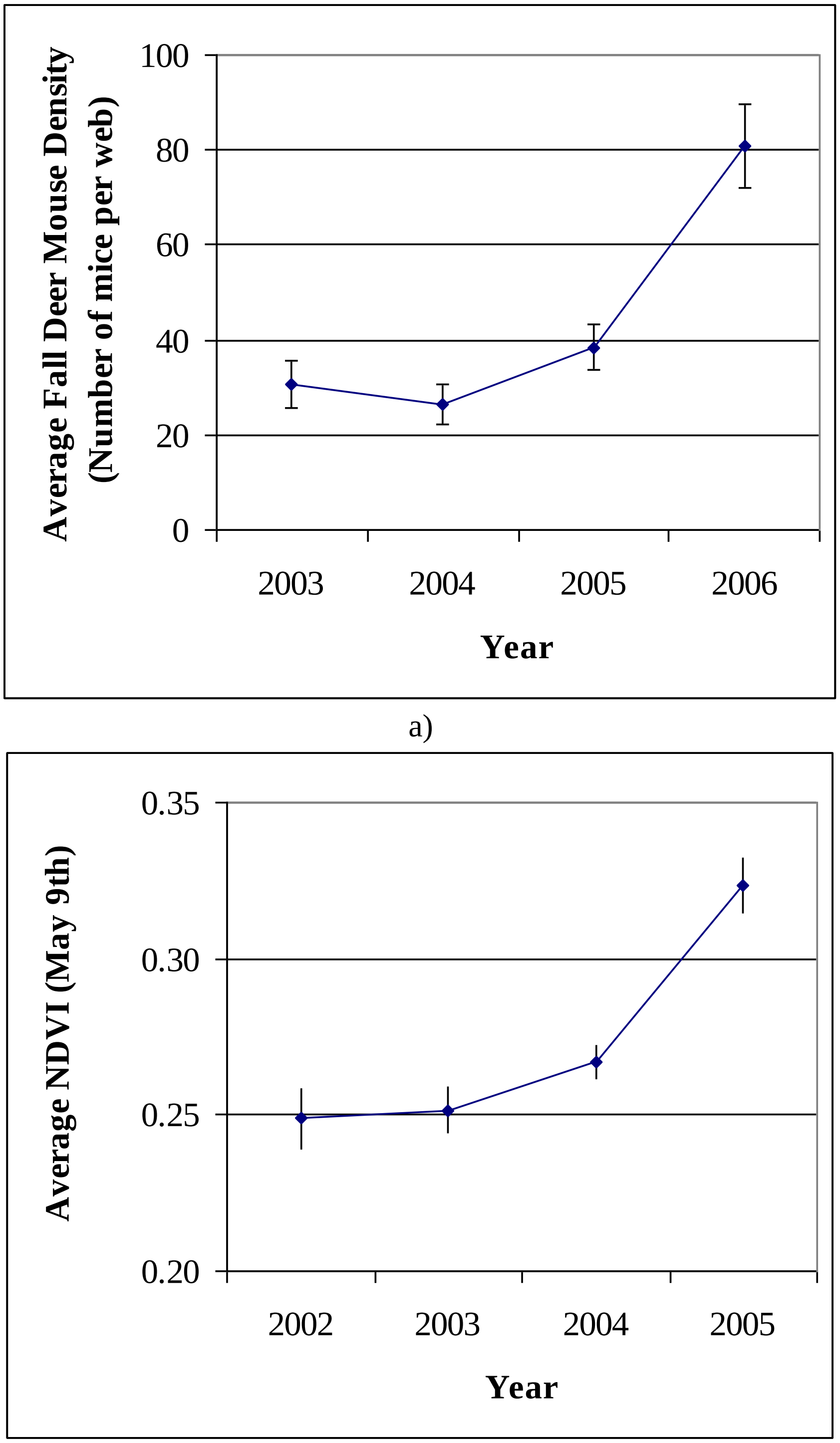


Figure 2.2 Deer mouse densities vs. EVI on June 10th at 1.0-year lag. The r^2 is 0.46 and significant at level of 0.001.



a)

b)

Figure 2.3 Deer mouse density and NDVI. a) Average fall deer mouse density (number of mice per web) from 2003 to 2006; b) Average NDVI on May 9th across 2002 ~ 2005.

Table 2.1 Maximum r^2 values and dates of maximum r^2 values between March and July for normalized difference vegetation index (NDVI), enhanced vegetation index (EVI), visible atmospherically resistant index (VARI), and normalized difference water index (NDWI) regressed against the deer mouse density at 0, 0.3, 1.0, 1.3-year lags.

Time Lag (Year)	*Maximum NDVI r^2*	*Date of Maximum NDVI r^2*	*Maximum EVI r^2*	*Date of Maximum EVI r^2*	*Maximum VARI r^2*	*Date of Maximum VARI r^2*	*Maximum NDWI r^2*	*Date of Maximum NDWI r^2*
0	0.31*	March 6	0.28*	June 10	0.29*	March 6	0.35*	March 6
0.3	0.18	March 6	0.05	June 10	0.21*	March 6	0.23*	March 6
1	0.32*	May 9	0.46*	June 10	0.24*	May 9	0.11	May 25
1.3	0.50*	May 9	0.47*	June 10	0.27*	May 9	0.07	May 25

* Significance ($P < 0.01$)

Table 2.2 Maximum r^2 values and dates of maximum r^2 values between March and July for normalized difference vegetation index (NDVI), enhanced vegetation index (EVI), visible atmospherically resistant index (VARI), and normalized difference water index (NDWI) regressed against the number of infected deer mice at 0, 0.3, 1.0, 1.3-year lags.

Time Lag (Year)	*Maximum NDVI r^2*	*Date of Maximum NDVI r^2*	*Maximum EVI r^2*	*Date of Maximum EVI r^2*	*Maximum VARI r^2*	*Date of Maximum VARI r^2*	*Maximum NDWI r^2*	*Date of Maximum NDWI r^2*
0	0.18	March 6	0.11	June 10	0.23*	March 6	0.25*	March 6
0.3	0.09	March 6	0.03	April 10	0.12	March 6	0.16*	June 26
1	0.35*	June 10	0.53*	June 10	0.40*	June 10	0.20*	May 25
1.3	0.43*	June 10	0.36*	May 9	0.21*	May 9	0.04	May 9

* Significance ($P < 0.01$)

Table 2.3 Maximum r^2 values and dates of maximum r^2 values between March and July for normalized difference vegetation index (NDVI), enhanced vegetation index (EVI), visible atmospherically resistant index (VARI), and normalized difference water index (NDWI) regressed against the Sin Nombre virus (SNV) prevalence at 0, 0.3, 1.0, 1.3-year lags.

Time Lag (Year)	*Maximum NDVI r^2*	*Date of Maximum NDVI r^2*	*Maximum EVI r^2*	*Date of Maximum EVI r^2*	*Maximum VARI r^2*	*Date of Maximum VARI r^2*	*Maximum NDWI r^2*	*Date of Maximum NDWI r^2*
0	0.12	April 7	0.05	May 9	0.28*	April 7	0.11	May 25
0.3	0.11	June 26	0.11	April 7	0.07	April 7	0.02	April 7
1	0.27*	June 26	0.25*	June 10	0.40*	April 7	0.19	April 7
1.3	0.06	July 28	0.03	July 28	0.05	April 7	0.03	March 6

* Significance ($P < 0.01$)

Table 2.4 The diseases directly transmitted by rodents and their locations in the world.

Disease	Where the Disease Occurs
Hantavirus pulmonary syndrome	Throughout most of North and South America
Hemorrhagic fever with renal syndrome	Primarily in eastern Asia, Russia, Korea, Scandinavia, western Europe, and the Balkans.
Lassa fever	West Africa
Leptospirosis	Worldwide
Lymphocytic Chorio-meningitis (LCM)	Worldwide
Omsk hemorrhagic fever	Western Siberia
Plague	Western US, S. America, Africa, Asia
Rat-Bite fever	Worldwide; *Strepto-bacillus moniliformis* in North America and Europe; *Spirillum minus* in Asia and Africa.
Salmonellosis	Worldwide
South American Arenaviruses (Argentine hemorrhagic fever, Bolivian hemorrhagic fever, Sabiá-associated hemorrhagic fever, Venezuelan hemorrhagic fever)	South America: parts of Argentina, Bolivia, Venezuela and Brazil
Tularemia	Worldwide

CHAPTER 3

DEER MOUSE (*PEROMYSCUS MANICULATUS*) MOVEMENT IN DESERT SAGEBRUSH HABITAT

Abstract

Deer mouse (*Peromyscus maniculatus*) is the primary reservoir for Sin Nombre virus (SNV), a North American hantavirus that causes hantavirus pulmonary syndrome with high mortality in humans. Understanding deer mouse movement is critical for understanding disease transmission. Greater movement leads to greater potential for encounters and increases transmission probability. Our objective was to investigate the factors potentially affecting deer mouse movement in the desert sagebrush habitat of the Great Basin, Utah by: (1) measuring deer mouse movement using GIS and recapture data, and (2) examining the effects of climate, season, habitat disturbance, population density, sex, mass, and SNV infection on deer mouse movement. The results show that climate, mouse density, sex, mass, and SNV infection had a significant effect on deer mouse movement. There were also significant interaction effects between climate and disturbance, as well as mass and SNV infection. In predrought conditions, deer mouse movement at more disturbed sites was greater than the movement at less disturbed sites, whereas in postdrought conditions the movement at more disturbed sites was less than the movement at less disturbed sites. This suggests that the effect of habitat disturbance on mouse movement varies according to climate conditions. The larger infected deer mice

moved the most, and this may be because they are more territorial and aggressive. These infected aggressive mice could greatly increase SNV transmission in deer mouse populations. Season and disturbance alone had no significant effects.

Introduction

The deer mouse (*Peromyscus maniculatus*) is the most common small mammal in North America (Baker, 1968; Mills et al., 1998). It is the principal reservoir for Sin Nombre virus (SNV), which causes hantavirus pulmonary syndrome (HPS) with high mortality in humans. While there are few cases of HPS in humans, studying SNV dynamics in deer mouse populations may help us to better understand its spread. There is currently no vaccine or effective drug to prevent or treat HPS (Buceta et al., 2004; Custer et al., 2003), and for this reason, there is a need to understand the nature of the virus host in order to predict the risk of the disease and design effective prevention policies.

The principal mode of hantavirus transmission in deer mice is through direct interactions such as aggressive fighting and mating (Calisher et al., 1999; Glass et al., 1988; Mills et al., 1997). Previous studies have found that scars or wounds in the rodents are positively related to SNV infection (Calisher et al., 2002; Root et al., 1999). For this reason, understanding deer mice movement is critical in understanding their interactions and thus the disease transmission. Increased movement increases the contact rates in a population, which in turn may lead to increased disease transmission. Escutenaire et al. (2002) found that hantavirus infection was associated with higher mobility in juvenile and subadult males. Langlois et al. (2001) suggested deer mouse movement through the landscape affected the rate and pattern of disease transmission.

An increased prevalence of infection of the Junin virus in male rodents may be due to their greater movement and a greater level of agonistic behavior, when compared to that of females (Mills et al., 1992). Junin virus is a rodent-born virus occurred in Argentina and is a strain of Arenavirus causing Argentine hemorrhagic fever with a mortality rate of between 20 and 30%. Further, differences in movement across habitat types may contribute to increased SNV prevalence among different deer mouse communities because movements of greater distances, relative to areas where movements are short, should increase the number of encounters and interactions. Longer movement distances may increase the probability that mice become infected with SNV. The average range of deer mice during a 1-month period in a Nevada desert was 159 m for males and 101 m for females (Allred & Beck 1963).

Although deer mouse movement is critical in understanding animal ecology, population dynamics, and hantavirus dynamics, information on deer mouse movement is limited. Data on deer mouse movement in sagebrush habitat has been especially inadequate. This lack of data is due to the difficulties in estimating mouse movement (e.g. limitations of collecting locational data, limitations of estimating mouse space use, and equipment costs).

Our objective was to investigate the factors potentially affecting deer mouse movement in the desert sagebrush habitat of the Great Basin, Utah by: (1) measuring deer mouse movement using GIS and recapturing data, and (2) examining the relationships between deer mouse movement and various factors, including climate, season, habitat disturbance, population density, sex, mass, and SNV infection status. The results can help increase our understanding of the important factors that may affect hantavirus dynamics. They also can provide knowledge in building hantavirus transmission simulation models.

Methods

Study Area

The study area is located in proximity to the Little Sahara Recreation area in Juab County in Utah (39°40´ N, 112° 15´ W). The elevation ranges from 1600 to 1900 m. The dominant vegetation in the area primarily consists of the Great Basin Sagebrush (*Artemisia tridentata*), followed by Utah Juniper (*Juniperus osteosperma*). The preferred habitat of deer mice is sagebrush, which provides them with food and cover. This particular area has experienced heavy recreation use, mainly by all terrain vehicles (ATVs). Landscape disturbance due to ATV recreation use has created new roads, trails, and exposed landscape. Trapping webs at the study area were selected based on low and high levels of disturbance. Low disturbance refers to those areas where ATVs have had little or no effect, and high disturbance refers to the areas with trails and vast bare ground induced by camping and the heavy use of recreational vehicles.

Trapping Webs

There have been two general field sampling designs for estimating small-mammal population: grid-based regimes and web-based approaches (typically transect lines or trapping webs) (Anderson et al., 1983; Buckland et al., 1993, 2001; Burnham et al., 1980). The most commonly used trapping arrangement in longitudinal studies of hantavirus (Abbott, K.D., 1999; Calisher et al., 1999; Kuenzi, et al, 1999; Mills et al., 1999) is web-based. It has also been utilized in a number of other studies, including small-mammal studies at sites within the U.S. Long Term Ecological Research network, monitoring programs for rodent-borne zoonotic diseases conducted by public health agencies in the United States (Parmenter et al., 1999), and global-change/biodiversity programs around the world.

The web-based trapping was used at all study sites analyzed in this paper. The size and configuration of these webs have been described elsewhere (Mills et al., 1999b). For spatial analyses, it was assumed that: (1) trap stations included in the trapping webs were sufficient to describe the general space use of the rodents captured, and (2) biasness in captures of rodents were equal between the groups that we analyzed.

Twelve 3.14-ha trapping webs (Anderson et al., 1983; Root et al., 1999) were established for spring and fall seasons in 2004, 2005, and 2006. Trapping webs are centered on a reference location with traps emanating from this point. The trapping web contains twelve 100-m trap-transects radiated from the center trap at 30° angles from one another. Transects were numbered from 1 to 12 with the first transect facing south and other transects incremented in a clock-wise direction. Twelve traps are placed on each trap-transect. For each trap-transect, the first four traps are spaced 5 m apart, and the other eight traps are 10 m apart. Each trap is coded and marked by the transect number and its location along each transect labeled by letters from A to L with A for the closest trap to the center and L for the furthest (Figure 3.1).

Sampling Periods and ELISA

Rodents were live-trapped in spring and fall of 2004, 2005, and 2006. In each sampling period, traps were set for each trapping web for three consecutive nights. Small mammal processing was conducted according to protocols and methods for trapping and sampling small mammals for virological testing (Mills et al., 1995). Ear tags with individual numbers were attached to newly captured mice. Captured mice were weighed and recorded for trap code, sex, reproductive status, mass, ear tag number, wounds, scars, etc. Blood was also drawn from deer mice for testing the presence of hantavirus. Rodents were released where they were captured.

Enzyme-Linked Immunosorbent Assay for detection of Sin Nombre virus antibody was performed on all blood samples. Prevalence is simply reported as the percentage of infected deer mice in a sample. For this reason, estimated prevalence increases in accuracy with the sample size and the number of infected mice.

GIS Movement Mapping

GIS provides a valuable tool to map and visualize the movement of mice, as well as to analyze movement data from the field sampling data. The field data recorded the trap code where each mouse was caught. Movement distances across recaptures can be utilized to examine the effects of disturbance, year, season, sex, and mass on deer mouse movement. A recapture is when a mouse is caught again in another trap (or the same trap).

The movement distance for a given mouse recapture was measured by the straight-line distance from the first capture trap to the recapture trap. This underestimates the actual distance that deer mice move, but allows relative comparison between webs as well as mouse characteristics (e.g. male versus female) under the assumption that the error is uniform across sites. GIS is a valuable tool for efficiently measuring the movement distance and also in visualizing the movement vectors of deer mice. With digital aerial photos as a backdrop, it is possible to infer whether deer mouse movement vectors are affected by habitat disturbance.

The coordinates of the center points of the trapping webs were recorded using a global positioning system (GPS) unit in the field. They were then mapped in GIS, and 12 concentric buffers with distance 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, and 100 m from the center point were created. Twelve 100 m transects that radiate from the center point with 30° angles were delineated in GIS. The 144 traps where the buffers and transects intersect were represented as points, and each were recorded with the individual trap code described above. The attributes such as sex, age, and reproductive status of deer mice were geo-linked to the traps using the common field of trap code initially recorded in a spreadsheet.

The movement vectors were delineated by drawing a straight line from the trap where a deer mouse was initially captured to where the mouse was recaptured. This movement distance was calculated and associated with the individual deer mouse. The movement distances for each recapture were calculated using ArcGIS 9.1 and the associated attributes such as the climate condition (predrought/postdrought), season (spring/fall), disturbance level (low/high), sex (female/male), mass, and SNV infection status(yes/no) were geo-linked to each movement vector. Figure 3.2 shows an example of GIS mapping of the movement of recaptured deer mice. The movement vectors are displayed with different colors to represent various characteristics of the recaptured deer mice (e.g. sex, infection status). The aerial photo is used as a backdrop to illustrate the disturbance at the study area.

Statistical Analysis

The dataset was then analyzed to examine the effects of climate, season, disturbance level, density, sex, mass, SNV infection, and all possible interactions of the factors on the deer mouse movement using a generalized linear mixed model (GLMM) in SAS 9.1. GLMM does not require balanced sampling of longitudinal repeated data (Cnaan et al., 1997), and thus was appropriate considering our unbalanced study design (i.e. sites repeatedly sampled, but not equally). Deer mouse movement distances were nonnormal and were categorized into 10 m intervals that followed a Poisson distribution. The transformed movement distances were used as the dependent variable. The fixed factors were climate condition (predrought/postdrought), season (spring/fall), disturbance level (low/high), density (number of mice per site), sex (female/male), mass, and SNV infection status (yes/no). Spring 2004, 2005, and fall 2004 sampling periods were labeled as a predrought condition and fall 2005, 2006, and spring 2006 were labeled as a postdrought condition. The site is the random factor.

A portion of the recaptures occurred in the same trap, which implied a movement distance of zero because the deer mice returned to the same trap. The recaptures with zero movement distance were excluded from further analysis, as they should not be considered movement. The deer mouse movement least square means and associated stand errors were also calculated and compared.

Results

GIS Mouse Movement Vectors

A total number of 886 deer mouse recaptures over six sampling periods from 2004 to 2006 were processed to create GIS movement vectors. The mouse movement vectors were generated and visualized in GIS with high resolution remote sensing imagery/digital air photo as a backdrop showing the habitat conditions. Figure 3.2 reveals an inverse relationship between the number of recaptured deer mice and the disturbance level. We can see relatively longer movement vectors in high disturbance sites, and this may be due to the further distances that mice had to move to acquire the same amount of resources in these environments.

Deer Mouse Movement, Climate, Season, and Disturbance

The generalized linear mixed model revealed that climate had significant effect on deer mouse movement ($F = 13.75$, $P < 0.01$). Deer mice move greater distances in predrought conditions than in postdrought conditions. There was no significant difference in deer mouse movement between seasons. There was no effect of disturbance on deer mouse movement; however, the interaction of climate and disturbance ($F = 4.59$, $P = 0.03$) was significant. Site was not a significant random effect.

Figure 3.3 shows the disturbance and climate condition interaction effect on deer mouse movement. The mean deer mouse movement was highest at high disturbance sites in predrought conditions (33.3 m) and lowest at high disturbance sites in postdrought conditions (24 m). The mean deer mouse movement was 28.3 m in predrought conditions and 26.1 m in postdrought conditions at low disturbance sites. In predrought conditions, the mean movement at high disturbance sites was 18% greater than that at low disturbance sites. In contrast, in postdrought conditions, the mean movement at high disturbance sites was 9% less than that at low disturbance sites. There was less variation in movement at low disturbance sites but greater change at high disturbance sites.

Deer Mouse Movement, Population Density, Sex, Mass, SNV Infection Status

The generalized linear mixed model showed that there was a negative relationship between density and deer mouse movement (estimate = - 0.00268, $F = 9.63$, $P < 0.01$). The deer mice moved shorter distances as deer mouse density increased. Mass was found to be positively related to deer mouse movement (estimate = - 0.047, $F= 24.36$, $P < 0.01$), with heavier mice moving greater distances. Sex ($F = 5.49$, $P = 0.02$), SNV infection status ($F = 13.77$, $P < 0.01$), and mass against SNV infection status ($F = 13.73$, $P < 0.01$) have significant effects on deer mouse movement. The least square means of the deer mouse movement were 29 m for males and 26.5 m for females (Figure 3.4). The standard errors were 1.26 m for males and 1.17 m for females. Infected deer mice moved less than uninfected, with the mean movement of 26 m for infected deer mice and 29 m for uninfected deer mice (Figure 3.5). The standard errors were 1.2 m for infected deer mice and 1.25 m for uninfected mice. Figure 3.6 shows the interaction effect of mass and SNV infection status on deer mouse movement. The mean deer mouse movement was highest for heavier, infected mice. For infected mice heavier than 28g, the mean mouse movement rapidly increased to 45 m from 28 m for 24 ~ 26g mice. The mean movement for lighter infected mice (24 ~ 20g) was less than that of the uninfected deer mice with comparable mass.

Discussion

The objective of this study was to investigate and identify the potential factors that affect deer mouse movement in the desert sagebrush habitat. The effects of climate, season, habitat disturbance, population density, sex, mass, SNV infection, and all possible interactions on the deer mouse movement were examined. The results showed that climate, mouse density, sex, mass, and SNV infection have a significant effect on deer mouse movement. There were also significant interaction effects of climate against disturbance and mass against SNV infection. Season and disturbance alone had no significant effects.

Improving our understanding of the factors that affect mice movement increases our understanding of SNV dynamics in host populations. This would help health officials to predict the risk of the disease and design effective prevention policies. This study also contributed to the limited number of studies of deer mouse movement in the sagebrush habitat. The use of GIS in studying deer mouse movement is unique and demonstrated usefulness in measuring and visualizing deer mouse movement. Further spatial analysis could be performed to study the spatial relationships of deer mouse movement.

Climate and Habitat Disturbance Effects on Deer Mouse Movement

The results show that deer mice move more in predrought climate conditions than in postdrought conditions. This could be due to the limited food resources in predrought conditions forcing deer mice to search for food more intensively. The interaction effect of climate against disturbance was also significant. In predrought conditions, deer mouse movement at high disturbance sites was greater than that at low disturbance sites, whereas in postdrought conditions, the movement at high disturbance sites was less than that at low disturbance sites. This suggests that the effect of habitat disturbance on mouse movement varies according to climate conditions. In predrought conditions, areas with high disturbance have fewer food resources than areas with low disturbance, which forces mice to move greater distances to obtain enough food to survive. In postdrought conditions, when there is enough food, the open spaces at high disturbance sites become barriers for mice to move across because of the high exposure risk to predators. Deer mice use the vegetation cover to reduce exposure to predators (Kotler & Brown, 1988). Falkenberg and Clarke (1998) found deer mice were more active and consume more seeds in areas with vegetation cover than in open areas. This may explain why deer mice move less at high disturbance sites when the food resources are relatively rich.

Langlois et al. (2001) reported SNV prevalence was higher at fragmented habitats than less fragmented habitats. They proposed that increased deer mouse movement at fragmented sites increases contact rates and subsequently SNV prevalence. However, Lehmer et al. (2008) found a negative relationship between habitat disturbance and SNV prevalence. They suggested that when the food becomes limiting (in predrought conditions), deer mice are required to travel across open spaces more frequently, which leads them to emigrate to more favorable habitats compared to low disturbance site. The greater use of the open space could increase predation rates of deer mice, resulting in reduced virus hosts and thereby decreased SNV prevalence. These contrasting findings demonstrate the complex mechanisms that affect deer mouse movement and SNV dynamics. Thus, the role of deer mouse movement at disturbed habitats in SNV transmission warrants further investigation (e.g. relationship of movement and SNV prevalence in postdrought conditions).

Population Density, Sex, Mass, and SNV Infection Effects

Deer mouse density was negatively related to deer mouse movement. Increased mouse density may result from increased food availability, which does not require deer mice to move as far to obtain food. Additionally, while density increased, the home range for each mouse becomes more constrained, which reduces mouse movement. This finding corresponded with previous home range studies of rodent populations that suggest that average home range size decreases as the density increases (Abramsky & Tracy, 1980; Erlinge et al., 1990).

Our results also showed that male deer mice move more than female mice. Mills et al. (1999) suggested males are more often infected with SNV than females because males usually had larger home ranges and thus had greater chances in contacting with infected mice. The results also indicated that heavier deer mice move greater distances, and infected mice move more than uninfected mice. There was also significant interaction effect of mass and SNV infection. The heavy infected deer mice moved the greatest distances and had much greater movement than others. One interpretation is that these heavier infected deer mice are the territorial resident mice that move around a lot and often have aggressive encounters with other mice. These infected aggressive mice could greatly increase SNV transmission in deer mouse populations. We called these mice “super spreaders” as they are the primary virus hosts of SNV transmission. Fairbairn (1978) found that resident males were more aggressive than subordinate males and the level of aggression was positively related to mass. There has been very limited literature that suggests SNV infection affects deer mice behavior (e.g. aggression, movement). Further study would be helpful.

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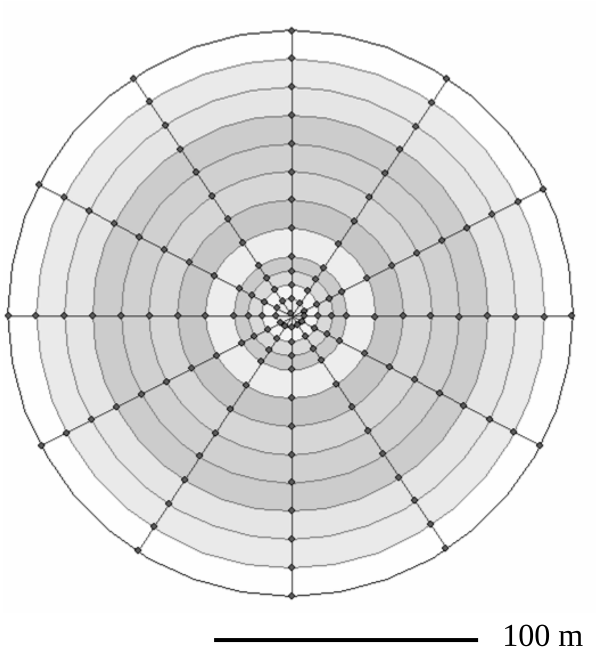
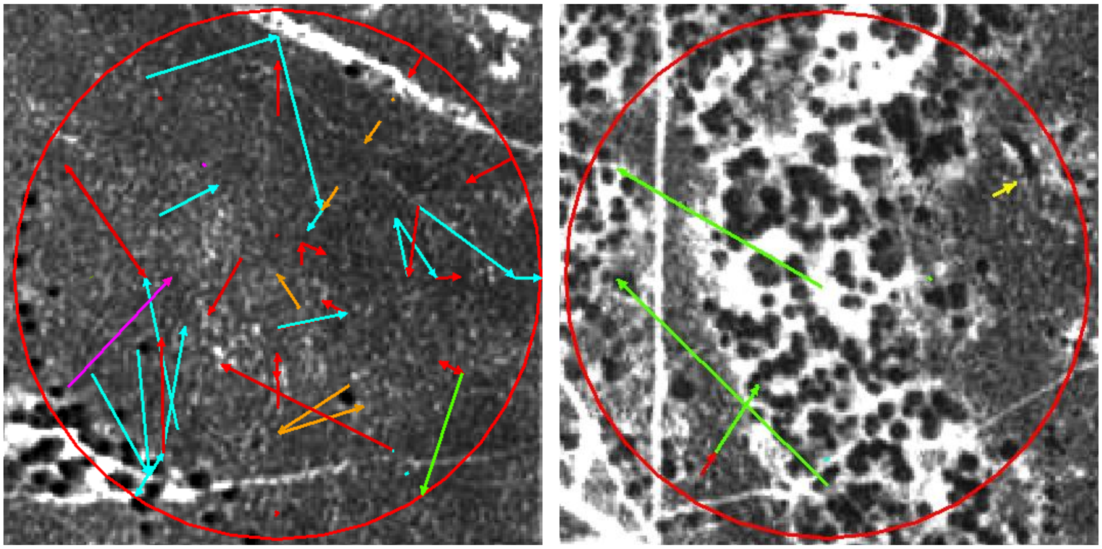


Figure 3.1 Trapping web.



(a) (b)

Figure 3.2 Deer mouse movement vectors (a) at a low disturbed site; (b) at a highly disturbed site. There are more recaptures at low disturbance sites. Various colors represent various sex and reproductive status.

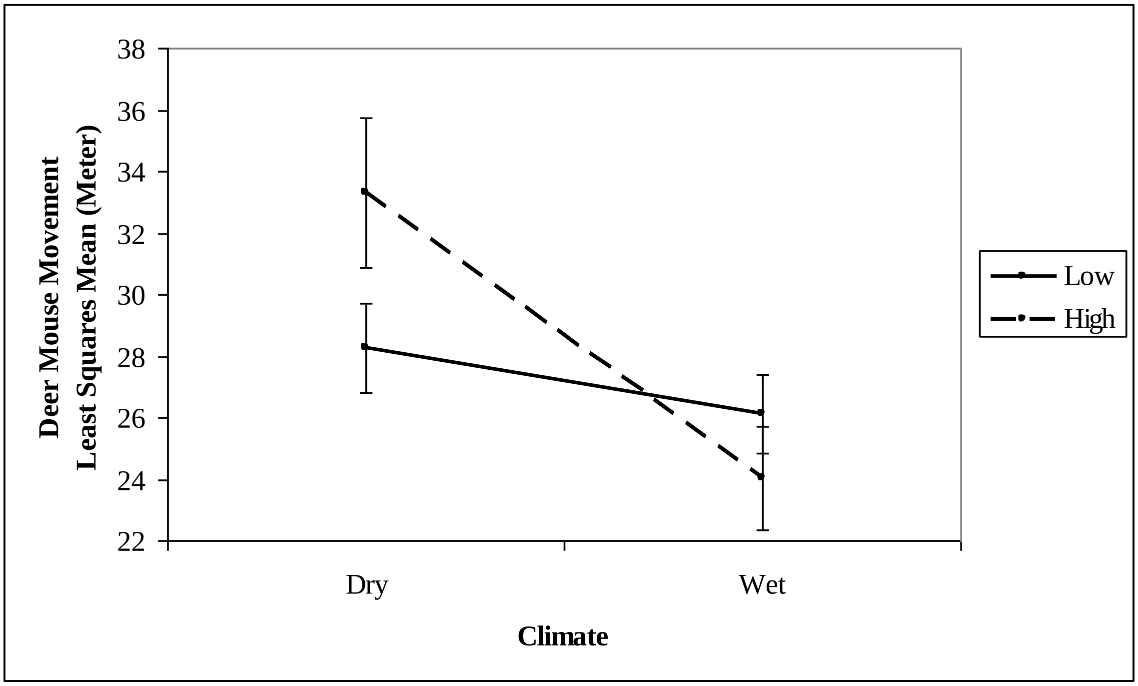


Figure 3.3 Disturbance and climate condition interaction effect on deer mouse movement. The mean deer mouse movement was highest at high disturbance sites in predrought condition and lowest at high disturbance sites in postdrought condition. In predrought condition, the mean movement at high disturbance sites is 18% greater than that at low disturbance sites. In contrast, in postdrought condition, the mean movement at high disturbance sites is 9% less than that at low disturbance sites.

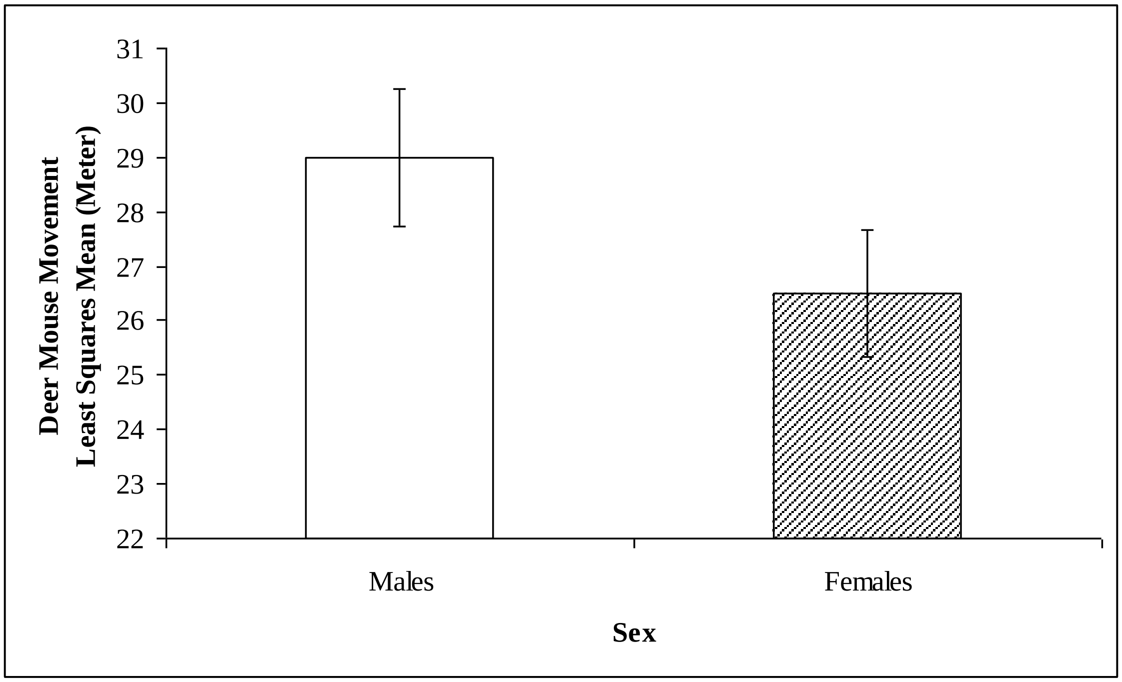


Figure 3.4 Female and male deer mouse movement. The least squares means of the deer mouse movement were 29 m for males and 26.5 m for females.

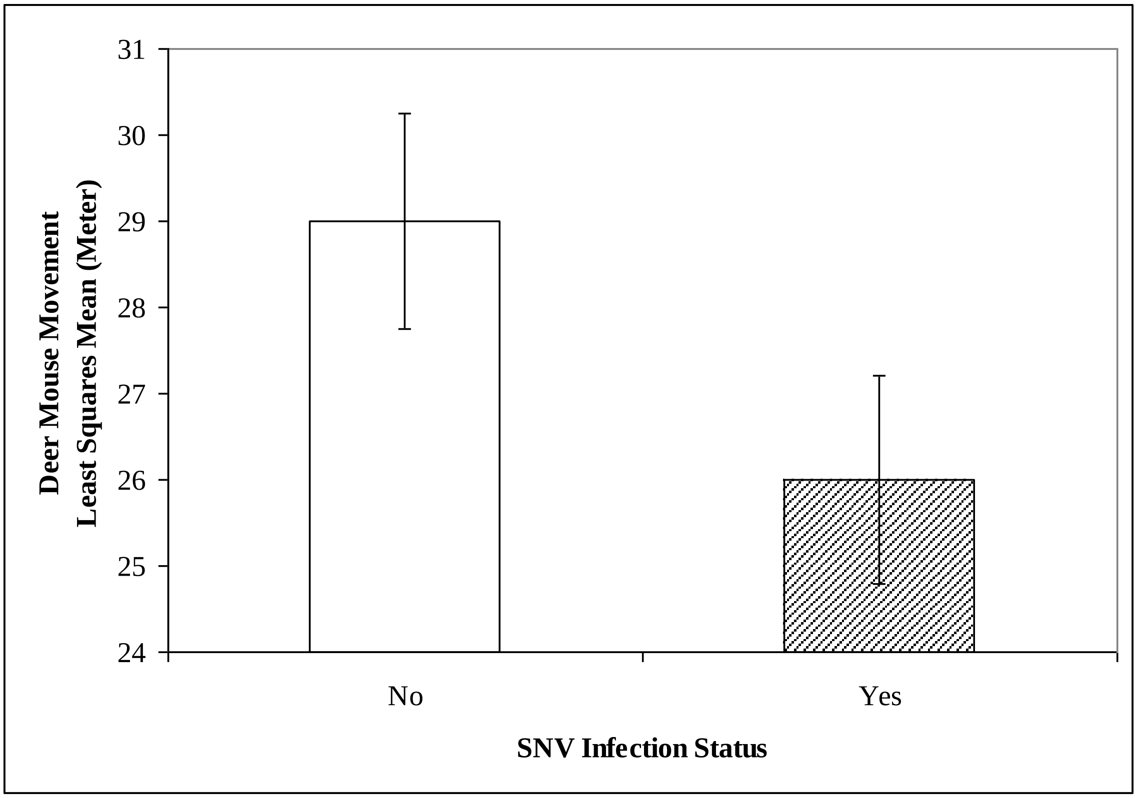


Figure 3.5 Infected and uninfected deer mouse movement. The least squares means of the deer mouse movement were 26 m for infected deer mice and 29 m for uninfected deer mice.

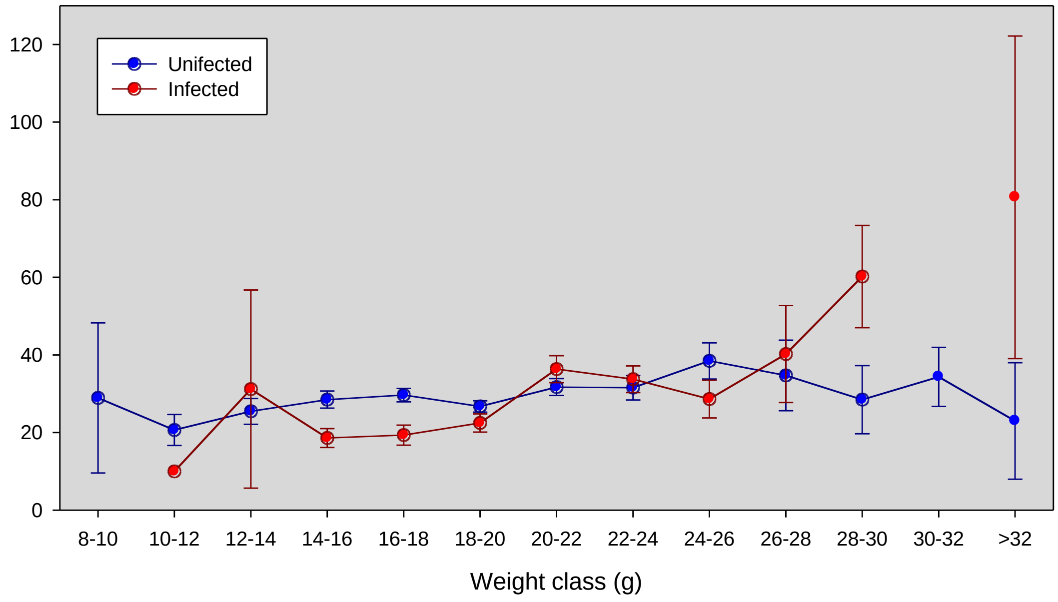


Figure 3.6 The interaction effect of mass and SNV infection status on deer mouse movement. The mean deer mouse movement was highest for heavy infected mice.

CHAPTER 4

SIMULATING HANTAVIRUS DYNAMICS IN DEER MICE USING A SPATIALLY EXPLICIT AGENT-BASED MODEL

Abstract

Hantavirus pulmonary syndrome (HPS) in humans is characterized by acute respiratory distress with a high mortality rate (>50%). HPS was traced to infection with Sin Nombre virus (SNV), a strain of hantavirus of which deer mice are the primary reservoir. This research helps us understand the important ecological parameters of hantavirus infections in deer mouse populations, and expand our understanding of the risk factors of developing HPS in humans as a consequence of SNV infection.

A spatial agent-based model was developed to simulate deer mouse population dynamics, their movement, contacts, and subsequent hantavirus transmission using Repast Java 3.1. The model integrated GIS habitat maps where deer mice could interact to take into account the spatial dynamics of landscape effects on hantavirus dynamics. We used empirical data from a multiyear field survey and a habitat map derived from remotely sensed imagery as inputs. Four simulation experiments were performed with varying levels of population density and disturbance. Each simulation scenario was run 1000 times to overcome the stochastic effects of the model. The averages at each time step were computed and recorded.

The simulation results consistently showed that prevalence was lower at high disturbance sites where deer mouse density was lower. These findings supported the hypothesis of Calisher et al. (2000) -- that habitat disturbance decreases prevalence because it reduces rodent habitat and thus the virus host population. The simulation also suggested that the prevalence is positively related to population density. The sensitivity analysis showed that population density was one of the most important parameters affecting the prevalence dynamics. The sensitivity analysis indicated that habitat disturbance could increase hantavirus transmission likely by increasing the movement and consequently contact rates. However, the results suggested that habitat disturbance had a much stronger effect on prevalence by decreasing population density than by increasing mice movement.

Introduction

Hantavirus pulmonary syndrome (HPS) is characterized by acute respiratory distress with a high mortality rate (>50%) (Glass et al., 2000; Nichol et al., 1993). HPS was traced to the infection with Sin Nombre virus (SNV), a strain of hantavirus of which deer mice are the primary reservoir (CDC, 1993; Childs et al., 1994; Hjelle et al., 1996). So far, there is no vaccine or effective drug to prevent or treat HPS (Buceta et al., 2004). Therefore, there is a need to understand the nature of the virus host, its temporal and spatial dynamics, and its relation to the human population in order to predict the risk of the disease and design effective prevention strategies. An understanding of how ecological systems influence disease dynamics could help advance our ability to both manage and predict infectious diseases in humans, wildlife, and natural habitat.

In recent years, agent-based modeling (ABM) has emerged as a very promising bottom-up modeling approach to simulate individual behaviors and their interactions at a microlevel, which results in emergent phenomena at a macrolevel. It provides virtual laboratories to replicate real or potential behaviors of the complex system and test various hypotheses as well as to experiment with a range of "what-if" scenarios. The spatially explicit dimension of the model takes account of the spatial variations of each individual, and their interactions among the agents and with the environment.

This study built a spatially explicit agent-based model to simulate deer mouse population dynamics and movement, their interactions, and hantavirus transmission in the deer mice population. This research helps us understand the important ecological parameters of hantavirus transmission in the deer mouse population, and expand our understanding of the risk factors of developing HPS in humans as a consequence of SNV infection. The construction of a spatially explicit agent-based simulation model for virus dynamics in an animal population can facilitate the examination of the potential impacts of landscape patterns on disease transmission in deer mouse populations. The parameterization of mouse behaviors and coupling of geo-spatial data of a spatially explicit agent-based model in this research may inform other studies concerning disease dynamics in animal populations in a heterogeneous environment.

The focus of this research is the question of whether disturbance hinders or increases hantavirus transmission in deer mouse populations. There exist two contrasting hypotheses on how habitat disturbance affects hantavirus prevalence. Langlois et al. (2001) suggested that fragmented habitat increased mouse movement and thus contact rates, and consequently increased hantavirus transmission. In contrast, Calisher et al.

(2000) proposed that habitat disturbance reduced rodent habitat and thus the virus host, and therefore decreased prevalence.

Background

Hantavirus

In May 1993, an outbreak of hantavirus pulmonary syndrome (HPS) characterized by acute respiratory distress with high mortality rate (>50%) (Glass et al., 2000; Nichol et al., 1993) among previously healthy young people occurred in the Four Corners region of the southwestern United States, where the borders of Colorado, New Mexico, Arizona, and Utah meet. HPS was later traced to the infection with Sin Nombre virus (SNV), a strain of hantavirus of which deer mice are the primary reservoir or host (CDC, 1993, Childs et al., 1994; Hjelle et al., 1996). Whether the SNV infection affects deer mouse fitness is still unclear. Douglass et al. (2007) suggested that SNV infection may negatively impact the health of infected deer mice. Adler et al. (2008) found the infected deer mice had a significant higher mortality rate in their preliminary analysis. However, Previtali et al. (2010) found no effect of SNV infection on deer mouse survival rate. Infection is chronic, and deer mice maintain SNV infection for life (Botten et al., 2000; Yamada et al., 1995). The SNV is believed to be horizontally transmitted between rodents and transmission is hypothesized to occur through intraspecific aggressive behaviors, such as biting and perhaps through social behaviors such as communal nesting (Boone et al., 1998; Calisher et al., 1999; Mills et al., 1997). The primary mode of SNV infection in humans is through inhalation of the aerosolized virus particles contained in mouse urine, feces, and saliva (Mills et al., 1998).

Environmental conditions, such as climate (Glass et al., 2000), seasonality (Cantoni et al., 2001; Dearing et al., 2009), and vegetation type have been associated with the distribution of SNV in the past studies. However, few studies have investigated the effects of habitat disturbance on the dynamics of SNV in deer mice. Langlois et al. (2001) found that hantavirus transmission increased with habitat disturbance. Mackelprang et al. (2001) suggested that a high level of SNV prevalence at one site in Utah may be due to anthropogenic disturbance. There exist two possible explanations for the positive effect of habitat disturbance on hantavirus transmission. First, if deer mice move further in a more disturbed habitat/fragmented landscape (Diffendorfer et al., 1995), deer mice may have a wider range of contact, which increases virus transmission probability. Escutenaire et al. (2002) also found that hantavirus infection was associated with higher mobility in juvenile and subadult males.

Alternatively, habitat disturbance may confine deer mice in small habitat patches and therefore increase the local population density and thus contact and virus transmission rates. Mackelprang et al. (2001) suggested that a high level of SNV prevalence at one site in Utah may be due to disturbance by humans, primarily intensive use of all-terrain vehicles (ATVs) at a recreation area. The heavy recreation use can produce numerous dirt roads, campsites, and barren spaces. Barren space caused by this disturbance reduces preferred habitat for species such as deer mice and may cause animal density to increase within a microhabitat. Increased interaction within the microhabitat may lead to a higher rate of SNV transmission. Other demographics of deer mice such as sex, reproductive status, and mass are also believed to affect pathogen transmission.

Agent-based Modeling

ABM has emerged as a very valuable tool in modeling space-time dynamics within complex environmental and urban systems in recent years (Batty and Jiang, 1999; Benenson et al., 2002; Jiang & Gimblett, 2002; Kohler & Gummerman, 2000). The basic idea of ABM is to specify the behavioral rules of individual agents and the rules of their interactions to explore the macrolevel consequences stemming from individual-level interactions. ABM is able to capture individual and collective behaviors in a complex and dynamic environment and has thus received significant attention (Bonabeau, 2002; Gilbert & Bankes, 2002). It helps researchers study the relationship between microlevel individual actions and the emergent macrolevel phenomena (Jiang, 2001). ABM has been widely applied in the areas of ecology (DeAngelis et al., 1996; Grimm, 1999; Grimm & Railsback, 2005; Judson, 1994; Uchmanski & Grimm, 1996), geography (An et al., 2005; Cederman et al., 2001; Parker et al., 2003;), epidemiology (Barrett et al., 2005; Carpenter, 2004; Hotchkiss et al., 2005; Joshua et al., 2002; Teweldemedhin et al., 2004), economics (Holland & Miller, 1991), business (Robertson, 2003), social science (Dean et al., 2000; Epstein & Axtell, 1996; Gotts et al., 2003), and political policy (Bernard, 1999).

ABM has two essential components: agents and their environment. Franklin and Graesser (1997) defined the autonomous agent as “a system situated within and a part of an environment that senses that environment and acts on it, over time, in pursuit of its own agenda so as to effect what it senses in the future.” An agent is environment-dependent and able to sense and act autonomously. It has the ability to satisfy internal goals through actions based on a set of internal rules (Iglesias et al., 1999). It has to be situated in an environment. Once it leaves the environment, it is no longer considered an agent. Responding to what is sensed, agents take actions autonomously. The environment has a degree of autonomy but can also be influenced by the behaviors of agents. Agent dynamics are most naturally implemented in an ABM by a set of behaviors that can include conditional decision making and other (nonlinear) rules that distinguish them from mathematically continuous models (Parunak et al., 1998).

ABM in Animal Movement and Disease Transmission

While many studies have been conducted on pedestrian movement using ABM (Batty, 2001; Batty et al., 2003; Jiang, 1999), relatively few researchers have investigated animal movement in the context of ecosystems. Railsback et al. (1999) studied the movements of fish in a stream using an agent-based model. Goodwin et al. (2001) modeled the detailed movement of juvenile salmon at a hydroelectric dam. Harper et al. (2002) simulated the movement of cowbirds and cattle herds at the landscape scale. Cater et al. (1999) developed a simulation model of animal behavior (MOAB) that can create spatially explicit, individual-based animal foraging models. MOAB can be used to explore hypotheses concerning the influence of landscape pattern on animal movement and foraging behaviors. Users can create heterogeneous landscape patterns and place various resources and individual animals of a given species on that landscape to simultaneously simulate the foraging behavior of multiple species. The heuristic rules for animal behavior are maintained in a user-modifiable expert system. The animal consults the expert system, which asks the animal questions regarding its hunger level and time of day. The expert system tells the animal what it should do based on the user-supplied rules of behavior. For example, if the hunger level is greater than a threshold, move to a neighboring cell and look for food; if there is food, stay and eat; if there is no food, move to another neighboring cell. As animals forage, they build up a memory of where they have been and what they last saw at any particular spot. Beecham et al. (2002) developed an agent-based system, Hierarchical Object Orientated Foraging Simulator (HOOFS), to examine the interactions between foraging animals and a spatially explicit description of the environment. The model used direct walking towards a food source rather than a simple random walk. At this point, agent-based models of animal behavior are often not realistic in terms of the animal's bioenergetics (Beer & Anderson, 2000), and there is still much research and development to be done.

Directly transmitted pathogens are transmitted from individual to individual following the network of contact between them through space and time. Epidemiological models are needed to represent spatially varying, temporally dynamic, and individual-based epidemiological phenomena. Traditional epidemiological models represent the dynamics of infectious diseases with a nonspatial and population-based approach (Bian, 2004). There has been increased interest in using ABM to model epidemics in recent years because of its ability to capture the essence of epidemiological phenomena – individuals, space, and time. ABM have been applied to modeling epidemics of small pox (Barrett et al., 2005; Joshua et al., 2002), anthrax, flu (Carpenter, 2004), pathogen dissemination (Hotchkiss et al., 2005), and AIDS (Callaghan, 2005; Heuveline et al., 2003; Teweldemedhin et al., 2004). Bian (2004) proposed a conceptual framework to formalize a spatially explicit agent-based model for the epidemiology of infectious diseases. The conceptual spatial agent-based model assumes that individuals are different, mobile, and interact with each other locally in an environment that is heterogeneous. The agent-based model uses a stochastic computation approach to simulate the population instead of a deterministic approach, which is often used by traditional population-based epidemiological models. The model also takes into account the spatial distribution of individuals.

Barrett et al. (2005) at Los Alamos National Laboratory (LANL) developed the largest agent-based epidemiological simulation model to date called EpiSims. It provides a virtual laboratory where health officials can test the effectiveness of various responses at time of diseases outbreaks. It helps officials to alter social networks through measures such as school closings and quarantines by knowing the paths by which diseases are transmitted. EpiSims was used to test several response strategies that are to contain the spread of small pox. It was found that response time was the most critical factor in limiting deaths and mass vaccination of the population would be unnecessary. Carpenter (2004) used ABM to simulate the influenza epidemic of a small community in Manitoba, Canada. The community was dispersed in small, family hunting groups, leaving a small group of people running the fort in winter. Hunters would return to the fort periodically for trade. In the summer, the entire community would gather near the fort. The simulation was used to investigate the impact of seasonal travel pattern on the spread of the flu epidemic. It was found that in the summer, when people are gathered around the fort, the epidemic is short and intense and in the winter, when people are dispersed, the epidemic is long and less intense. Tweldemedhin et al. (2004) used ABM to estimate and predict the spread of the Human Immunodeficiency Virus (HIV). Callaghan (2005) applied ABM not only to model the spread of HIV/AIDS but also to investigate the aspects of the immune responses to HIV infection.

Most of the models in human epidemics are based on social networks whereas models in animal epidemics more often use geographic landscapes. Bagni et al. (2002) used an agent-based model implemented with Swarm to study Bovine Leukemia epidemic, a viral pathology sustained by a retrovirus from the same family as HIV that exclusively strikes cattle within dairy farms. The simulation model they implemented exhibited the emergence of a complex behavior although with quite simple behaviors of the agents. The overall dynamic of the system appeared very complex and sensitive to the initial conditions. This characteristic led to a great opportunity to evaluate the effect of changes at the microlevel on the entire system. Eisinger et al. (2005) developed a spatially explicit agent-based simulation model to contrast two strategies for emergency rabies vaccination in fox populations. The spatial explicit model is based on fox group home-ranges, which facilitates the simulation of rabies spread to larger areas relevant to management. The model helped to determine what the best spatial design is for an emergency vaccination program, especially when resources are limited.

ABM Development Platforms

Building agent-based models from scratch requires extensive programming efforts; thus, many toolkits and platforms have been developed to facilitate their implementation. These include Swarm (Santa Fe Institute, 2000), Recursive Porous Agent Simulation Toolkit (RePAST) (Collier et al., 2003), NetLogo (NetLogo, 2005) and ASCAPE (Parker, 1999; Parker, 2000). These tools allow researchers with limited computer-programming background to construct relatively complex simulations. Swarm is one of the first software platforms for agent-based simulation of complex systems. It consists of a set of object-oriented libraries that facilitates the implementation of agent-based models and helps to build user interfaces easily. RePAST borrows many concepts from Swarm. It has multiple pure implementations in several languages and built-in adaptive features such as genetic algorithms and regression. It has been evaluated rigorously and is considered to be a leader in terms of ease of use, user documentation, and support for modeling and simulation control (Tobias & Hofmann, 2004).

These libraries require modelers to have a good working knowledge of the programming language (e.g. Java for RePAST). Some software packages exist that allow building of simple agent-based models without much programming experience. A good example is Netlogo. However, these tools can have limited functionality. Gilbert and Bankes (2002) and Tobias and Hofmann (2004) provide valuable reviews of Swarm, RePAST and other agent-modeling toolkits.

In recent years, interest in integrating GIS with agent-based modeling has grown in Geography and Ecology. GIS data can provide “real-world” representation of the environment with which the agents interact. A few GIS extensions to ABM have been developed such as the Kenge libraries, a Swarm GIS extension (Box, 2001), and Agent Analyst, a RePAST GIS extension (North, 2004). Agent Analyst is an open source ArcGIS extension that provides full integration of ABM into ArcGIS. Users can create agents directly from spatial objects in ArcGIS and include the rules for agent behaviors in the language Python. Agent Analyst is graphical and allows the user to create agents, schedule simulations, produce maps in ArcGIS, and specify the behaviors and interaction of the agents (North, 2004). Dibble and Feldman (2004) developed the GeoGraph extension to the RePAST agent-based simulation platform support models in which mobile agents interact on network and other interesting geographic landscapes.

Interactive GeoGraph 3D visualizations allow researchers to zoom and pan within the simulation landscape as the model runs. GeoGraphs support building and testing simulation models on geographic scale-free networks, or GIS representations of real-world landscapes.

Methods

Study Area and Field Data

The study area was located in proximity to the Little Sahara Recreation area in Juab County in Utah (39°40´ N, 112° 15´ W). Vegetation in the area primarily consists of sagebrush (*Artemisia tridendata*) and juniper (*Juniperus osteosperma*). This particular area had experienced heavy recreation use, mainly by all terrain vehicles (ATV). ATV have created large amounts of pronounced trails throughout the area and made a substantial disturbance in desert habitats. We mainly studied the disturbance caused by ATV use as it is the predominant type of the disturbance in the study area (Lehmer et al., 2008). The lowest disturbance sites were restricted to ATV access and had 10 ~ 17% bare ground, whereas the high disturbance sites experienced varying levels of ATV recreation use with the highest disturbance site having more than 40% bare ground (Previtali et al., 2010)

Rodents were sampled at twelve sites with low and high levels of disturbance in the spring and fall of 2004, 2005, and 2006. Low disturbance sites referred to those areas where ATVs have had little or no effect. High disturbance sites referred to the areas with trails and vast bare ground introduced by camping and the heavy use of recreational vehicles and ATVs.

Over 2000 mice were captured and released from 2004 to 2006. The ear tag identification number, trap location, sex, reproductive status, mass, wounds, and scars were recorded for each captured mouse. Blood was drawn from deer mice for testing SNV presence. Prevalence was calculated as the ratio of infected mice to the total number of mice.

Spatially Explicit ABM Overview

A spatial ABM model was developed to simulate deer mouse population dynamics, their movement, contacts, and subsequent hantavirus transmission using Repast Java 3.1. This model integrates GIS habitat maps where deer mice interact to take into account spatial dynamics of landscape effect on hantavirus dynamics. We used empirical data from a multiyear field survey and remotely sensed GIS habitat maps as input. The model was designed to answer various research questions on hantavirus dynamics in deer mouse populations. For example, how does habitat disturbance affect hantavirus prevalence? How does population density affect hantavirus? How does mouse movement affect hantavirus dynamics? The model itself is as a finite state machine describing how agents move, interact, are exposed to hantavirus, and become infected.

The implementation of how deer mice move was one of the most critical components to the simulation. It determined the contact rates in the population and thus affected the prevalence.

The mouse agents had the following properties:

1) Home range. Wood et al. (2010) estimated that deer mouse home range in the desert sage brush habitat varied from 360 m^2 to 5868 m^2. We applied an approximate home range of 2835 m^2 with 30 m radius from the initial

location. Wood et al. (2010) reported that deer mice had high site fidelity across a three-month period. We assumed that the mice would stay in their established territories and had no probability of moving out of their home range area. Their initial locations were considered as the center of their territory.

2) Infection status. The infection status is either susceptible or infected. The infection is chronic and does not cause death. The mice carry hantavirus for their entire life once infected.
3) Sex. There were male and female mouse agents. Their movement parameters could be varied for various experiments.
4) Movement. This was represented by a vector with length and direction.

In the simulation, the initial locations of the mice were considered as their home. They move around foraging for food on the landscape within their home range (e.g. 30 m radius from their home). The time step unit in this model represents one hour in the real-world. It is assumed that during one time period, mice move from an origin to a food destination. The food destination will only be on a sagebrush or juniper cell. If it occurs on a bare cell, a new selection would be made until a sagebrush/juniper cell is chosen. The mouse is counted to have contacts and probability of SNV transmission when it has neighbors at the food destination and also along the movement vector.

Mouse agent actions include the following:

1) Move. The movement rules were explained in the above paragraph.
2) Contact. When two mice were in neighboring habitat cells, a contact is recorded, either at the destination or on the movement vector.

3) Infect. Whenever a susceptible mouse encounters an infected mouse, an infection probability can be defined by the simulation user that determines the transmission likelihood.

Basic Mouse Population Model

We adapted a basic stochastic population model to simulate deer mouse population dynamics (Renshaw, 1991). The model assumes each time step interval was short enough that there would be only three scenarios: 1) one mouse was born; 2) one mouse died; 3) nothing happened. Renshaw (1991) defined the probabilities for each case as follows:

1) one mouse was born: $N\lambda h$
2) one mouse died: $N\mu h$
3) nothing happened: $1-N(\lambda+\mu)h$

Here N is the number of deer mice at current time step; λ is the birth rate and μ is the death rate; h is the time interval of each simulation step. At each time step, the probability was independent with other time steps.

This basic mouse population model assumed that hantavirus was transmitted within a relatively stable population level within the simulation time. It assumed no sudden decrease or increase in the population, which may be caused by severe weather or in the breading season. Seasonal variability was not considered. We assumed there was a consistent food resource to support the input population level. During the simulation, there were newly uninfected mouse agents coming in the system and part of the mouse agents would die; however, the overall population level was relatively stable. The total number of births and deaths was determined by the birth and death rate. Only adult mice were considered in the simulation. There was no mouse growth simulated in the model.

Heterogeneous Environment

The environment consists of a two-dimensional cellular lattice. Each cell contains a value which represents the habitat type. Real-world geographic data was integrated into this agent-based simulation model. The habitat maps were derived from 1 meter panchromatic digital air photos provided by Utah Automated Geographic Reference Center. The imagery was classified into three categories: sagebrush, juniper, and bare ground using ArcGIS 9.2 slice tool. Sagebrush habitat is the most preferred habitat for deer mice, which provided deer mice with food and cover (Pearce-Duvet et al., 2006). Juniper habitat is less preferred habitat. Bare ground contains no food resource and high exposure to predators. Thus, it is nonpreferred habitat.

Two sets of habitat maps (Figure 4.1) at the study area derived from the digital air photos with low and high disturbance levels were selected to examine the effect of habitat disturbance on hantavirus transmission. The low disturbance site had roughly 10% bare ground, whereas the high disturbance site had more than 50% bare ground. Dark green represents sagebrush habitat. Bright green cells correspond to juniper trees. White is bare ground. The geographic area that each habitat map covered was approximately 30,000 square meters. GIS habitat raster maps were converted to ASCII files and used by the simulation model to represent the environment. When the mouse agents moved around, they utilized the habitat information to select a foraging destination. They are also assumed to stay on the preferred sagebrush and juniper habitat and avoid bare ground.

Simulation Experiments

Simulation experiments were performed with varying levels of population and habitat disturbance (low and high). Each simulation scenario was run 1000 times to overcome the stochastic effects of the model. The averages of the prevalence at each time step were computed and recorded.

Figure 4.2 shows the interface of the simulation model. We assume mouse movement occurs 5 hours per day during the night. The model was run for 500 steps with each time step representing an hour, and therefore, it simulates approximately three months of mouse movement and hantavirus transmission. The model was initialized with a number of mice (in blue) with 10% population infected (in red).

The purpose of these experiments was to see how prevalence responds to changes in density and habitat disturbance, with real-world field surveyed population density data and GIS habitat maps as model inputs. The field data showed that the population levels varied significantly during the predrought and postdrought years. For example, in the predrought years of 2004, there were 51 deer mice at the lowest disturbance sites and there were 23 mice correspondingly at the highest disturbance site. In the postdrought year of 2006, the population density more than doubled from the predrought year mouse density with 134 mice at the lowest disturbance sites and 62 mice at the highest disturbance site. The year 2005 is the transition year from drought to postdrought weather. Regardless of precipitation, mouse population density at the highest disturbance site was approximately half of the density at the lowest disturbance sites in 2004 and 2006.

Four simulation experiments were performed with varying levels of population and disturbance levels. Table 4.1 shows the specific input values for each simulation scenario. The first and second experiments used a low population density for predrought years at the lowest and highest disturbance sites as the input. The third and fourth experiments applied a higher population density for postdrought years at the lowest and highest disturbance sites as the model input.

The simulation applied 40% for the birth and death rates over the whole simulation period based on rodent's high population turnover rate. They were held the same for all four simulation experiments in order to compare the population density and disturbance effects alone. For other experiments, they could be adjusted according to the past studies or field observations. Transmission probability was artificially set to 10%, which meant whenever an infected mouse came into contact with a noninfected mouse, there was a 10% probability of transmitting the infection. At each time step, a random number was generated to determine how many cells the mouse would move. The minimum or maximum movement size sets the movement range that a mouse could move.

Sensitivity Analyses

Sensitivity analysis was performed by examining the proportional change in hantavirus prevalence, which resulted from a given proportional change in parameter values. The tested parameters were population density, birth, death rates, transmission probability, maximum movement per time step, and initial infection rate. Disturbance levels were also tested for model sensitivity by altering disturbance level from low to high. We used +/-10% change in the parameter values, which was also used for the sensitivity analysis of other rodent disease transmission models (Holt et al., 2006; Sauvage et al., 2003). The final prevalence at the end of the simulation was then compared.

Simulation Results

Population Density, Disturbance, and Prevalence

The total population levels were very stable for all four experiments while approximately 40% of the initial number of deer mice moved out of the system (through death) and approximately 40% of the initial number of deer mice were added in the simulation (through birth) during the simulation period. All newly added deer mice were initially uninfected. For the example of the simulation of the low disturbance in the predrought year, the initial number of deer mice was 51. At the end of the simulation, 24 deer mice were dead and 3 out of 24 dead deer mice were infected. The population dynamics from all simulations matched our assumption that population level was held relatively steady over the simulation period.

In the predrought year, the population density for the low disturbance simulation (51 mice per site) was more than twice that for high disturbance simulation (23 mice per site). In the postdrought year, the population density for low disturbance simulation (134 mice per site) was more than twice of the population density for high disturbance simulation (62 mice per site).

Figure 4.3 shows the prevalence changes over 500 time steps for the four simulation experiments. The prevalence was the average prevalence from the 1,000 simulation runs at each given time step. All simulations resulted in increasing prevalence over time. All simulations were initiated with 10% prevalence, and the prevalence trended higher as population densities increased for the four simulation scenarios. In both the predrought and postdrought year simulations, the prevalence at low disturbance was higher than the prevalence at high disturbance. The prevalence in the postdrought year was higher than the prevalence in the predrought year.

Table 4.2 lists the prevalence at the end of each simulation experiment. The low disturbance in the postdrought year simulation yielded the highest final prevalence of 0.57. The final prevalence for the high disturbance in the predrought year simulation was the lowest at 0.10 and remained almost unchanged from the initial infection rate. In the predrought year, the final prevalence for the low disturbance simulation (0.19) was almost twice the final prevalence for the high disturbance simulation (0.10). In the postdrought year, the final prevalence for the low disturbance simulation (0.57) was more than twice the final prevalence for the high disturbance simulation (0.26).

Sensitivity Analyses

Figure 4.4 shows the impacts of a 10% increase and decrease in parameter values on the changes in the final prevalence. The most sensitive parameters were the population density and initial infection rate when increased by 10%. The corresponding final prevalence increased 17% and 19%, respectively. When population density and initial infection rate were decreased by 10%, there was not much of a change in the final prevalence. A 10% increase and decrease in maximum movement and transmission probability yielded similar results. The final prevalence increased and decreased in the range of 6% ~ 9%. The birth and death rate were the least sensitive parameters. There was less than a 2.6% change in the final prevalence level when the birth and death rates were varied by 10%. When altering the disturbance levels alone and holding population densities the same, the final prevalence for the high disturbance simulation increased 13% from that of the low disturbance simulation, which suggested that habitat disturbance increases prevalence because of the changing landscape that may lead to the increased movement, whereas in reality, increased habitat disturbance would decrease population density, which would decrease the prevalence. These counter effects and the results showing negative effect of habitat disturbance using the field input data suggested that population had much greater effect than the movement, which supported the hypothesis of Calisher et al. (2001) that habitat disturbance decreases prevalence because of reducing virus host population.

Discussion

The focus of this study was to construct a spatially explicit agent-based model to simulate hantavirus dynamics in the deer mouse population utilizing field surveyed population data and a GIS habitat maps as model input. The main question was whether habitat disturbance decreases or increases hantavirus transmission. Four simulation experiments were performed using varying levels of population densities and disturbance. Sensitivity analysis was conducted by examining the change in the final prevalence resulting from a 10% increase or decrease in population density, birth, death rates, transmission probability, maximum movement per time step, and initial infection rate. Sensitivity for disturbance levels was also analyzed by altering the disturbance level from low to high. The sensitivity analysis also provides an indication of the importance of the different parameters (Holt et al., 2006).

The simulations consistently showed that prevalence was lower at high disturbance site where deer mouse density was lower regardless of predrought or postdrought climate conditions. These findings support the hypothesis of Calisher et al. (2000) that habitat disturbance decreases prevalence because it reduces rodent habitat and thus the virus host. The model results also correspond to the findings in Lehmer et al. (2008) and now Previtali et al. (2010) which suggest that habitat disturbance is negatively related to prevalence, and habitat disturbance has a strong effect on deer mouse population densities.

The simulations also show that prevalence increases as population density increases, as mice that reside in a more crowded space have a higher encounter rate. The sensitivity analysis showed that population density is one of the most sensitive parameters in terms of affecting prevalence. These model results support the findings in the “El Niño” model of hantavirus studies that suggests prevalence is positively related to virus host density (Calisher et al., 2002) and predicts that hantavirus prevalence or the number of infected animals are highest during seasons or years when deer mouse density is greatest (Glass et al., 2000; Parmenter et al., 1999). Increased precipitation in the southwestern United States associated with an El Niño event is often accompanied by a subsequent boom in rodent populations (Parmenter et al., 1999). Some have proposed a ‘‘delayed density-dependence’’ mechanism, in which hantavirus prevalence in a particular season is positively correlated to the density of hosts in a previous season (Adler et al., 2008; Calsiher et al., 1999; Mills et al., 1999; Niklasson et al.,1995;).

When altering the disturbance levels in the simulation, the final prevalence of the high disturbance simulation increased 13% from that of the low disturbance simulation. This indicated that habitat disturbance could actually increase hantavirus transmission. This may be because the open space and limited food resources force deer mice to move greater distances to forage, and therefore increase the encounter rate. However, the sensitivity analysis showed that population density is the most critical factor that affects prevalence dynamics. A 10% increase in population density resulted in a 17% increase in prevalence. Our field data showed that mouse population density at the highest disturbance site could be about half of the density at the least disturbed sites in either a predrought or postdrought year. This suggests that habitat disturbance has a much stronger effect on prevalence by decreasing population density than by increasing movement. However, this may suggest that in some situations, habitat disturbance may not be a significant contributing factor. For example, severe environmental conditions (e.g. drought, early frost, sudden temperature drop) could result in dramatic population dynamics that could lead to chaotic hantavirus dynamics within a site.

Sensitivity analysis also showed that the initial infection rate, which determined initial number of infected mice was another sensitive parameter in addition to population density. This may suggest that the transseasonal survival rate is critical in affecting prevalence dynamics. The virus needs a sufficient number of virus hosts to persist the virus transmission. Lehmer et al. (2008) also suggested that prevalence is higher during periods of increased deer mouse survival.

A 10% increase and decrease in maximum movement and transmission probability yielded similar results. The final prevalence increased and decreased in the range of 6% ~ 8% when the maximum movement varied by +/- 10%. This implied that increased movement may lead to increased prevalence because of the increased contact probability.

The positive relationship between deer mouse density and prevalence leads to the possibility of using remote sensing imagery in predicting hantavirus risk to humans over large geographic areas. Pearce-Duvet et al. (2006) related a high percentage of sagebrush within a habitat to high mouse density. This simulation model suggested a positive relationship between mouse density and hantavirus. Therefore, the coverage of sagebrush within a habitat could be utilized to predict hantavirus prevalence.

This study is one of very few studies on rodent pathogen transmission using an agent-based modeling approach. Our spatially explicit agent-based model of hantavirus dynamics has demonstrated the utility of SABM in identifying important ecological factors that affect prevalence. The use of real-world GIS data provided realistic representations of the environment and greatly enhances a model's representation of the real world. SABM helped us obtain a better understanding of hantavirus dynamics in the complex ecosystem.

This spatially explicit agent-based model provides ecologists a virtual laboratory to experiment with numerous "what-if" scenarios, identify relationships, and test various hypotheses, which may be impossible or too expensive to test in the field. This type of modeling can also be used to guide the planning of field work with better resource utilization because field data collection is very expensive and labor extensive.

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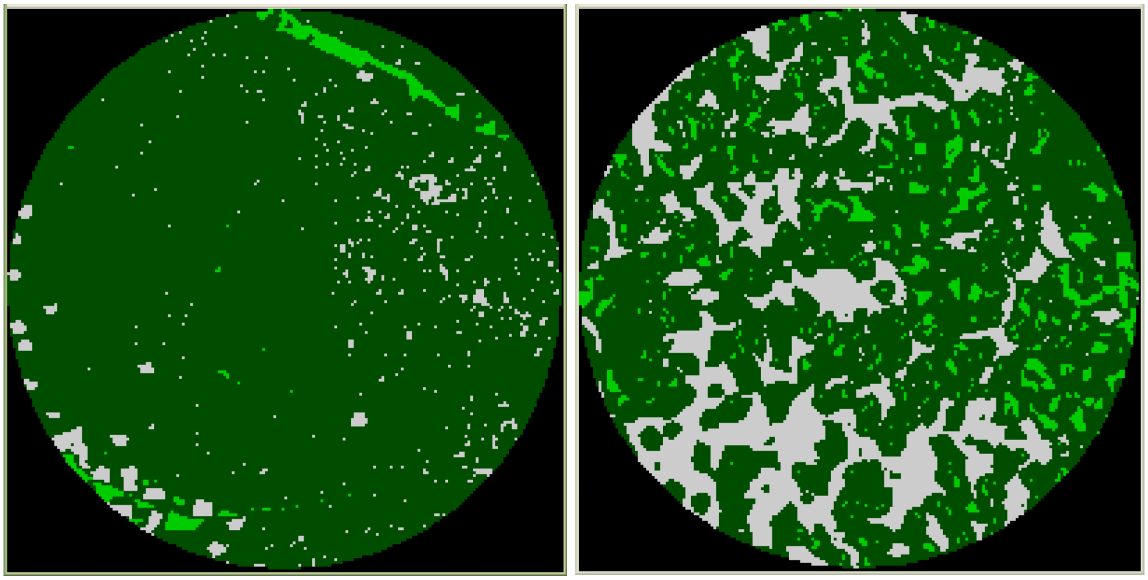
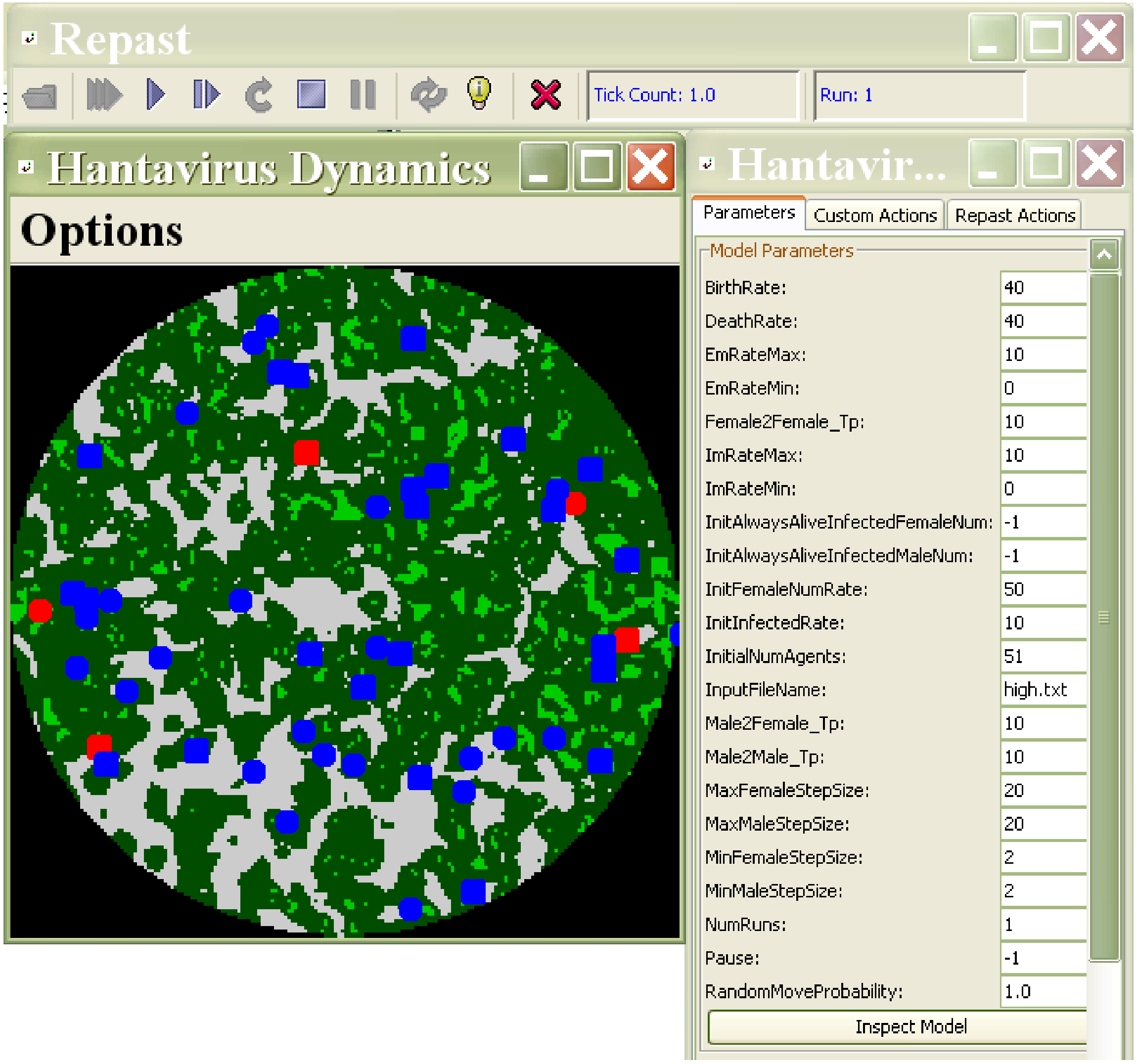


a) b)

Figure 4.1 Habitat maps derived from a digital air photo. Dark green represents deer mice preferred sagebrush habitat. Bright green is juniper habitat. White cells are bare ground. a) the low disturbance study site; b) the high disturbance study site.



BirthRate:	40
DeathRate:	40
EmRateMax:	10
EmRateMin:	0
Female2Female_Tp:	10
ImRateMax:	10
ImRateMin:	0
InitAlwaysAliveInfectedFemaleNum:	-1
InitAlwaysAliveInfectedMaleNum:	-1
InitFemaleNumRate:	50
InitInfectedRate:	10
InitialNumAgents:	51
InputFileName:	high.txt
Male2Female_Tp:	10
Male2Male_Tp:	10
MaxFemaleStepSize:	20
MaxMaleStepSize:	20
MinFemaleStepSize:	2
MinMaleStepSize:	2
NumRuns:	1
Pause:	-1
RandomMoveProbability:	1.0

Figure 4.2 Simulation model interface.

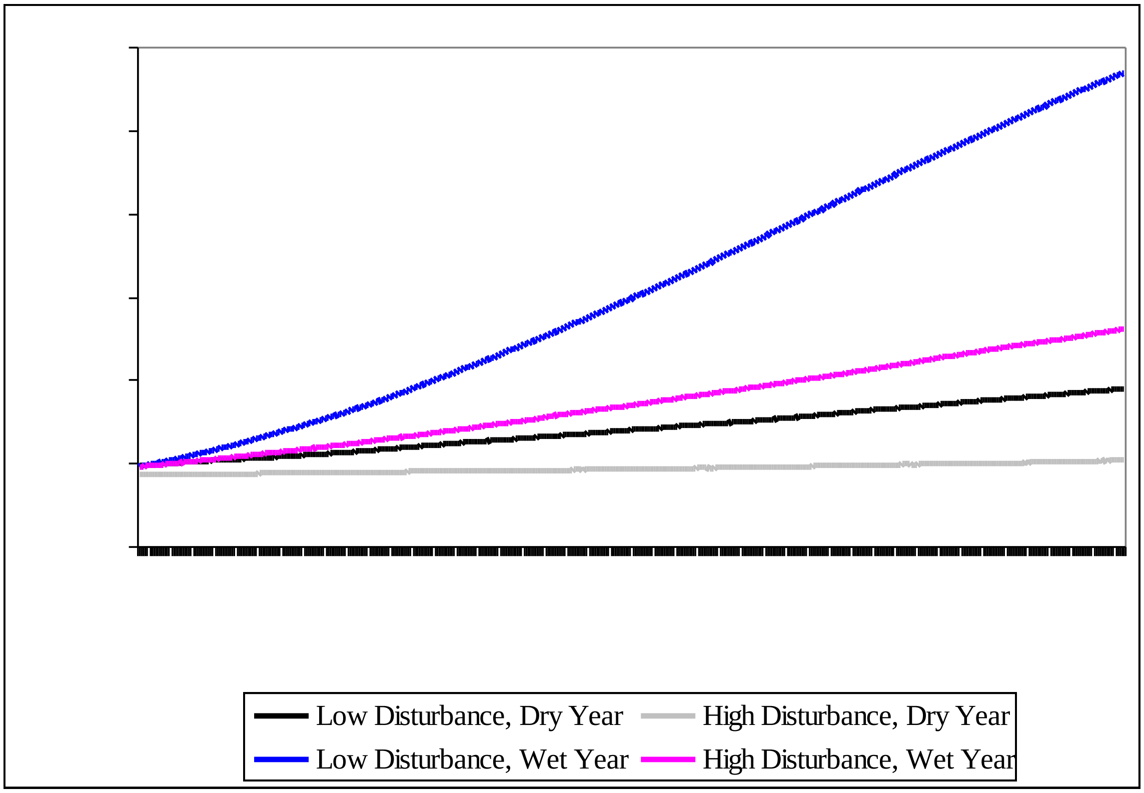


Figure 4.3 The prevalence changes over 500 time steps for four simulation experiments that used field-surveyed population densities. The four sets of population densities were of the study sites that have low and high disturbance in the predrought and postdrought year.

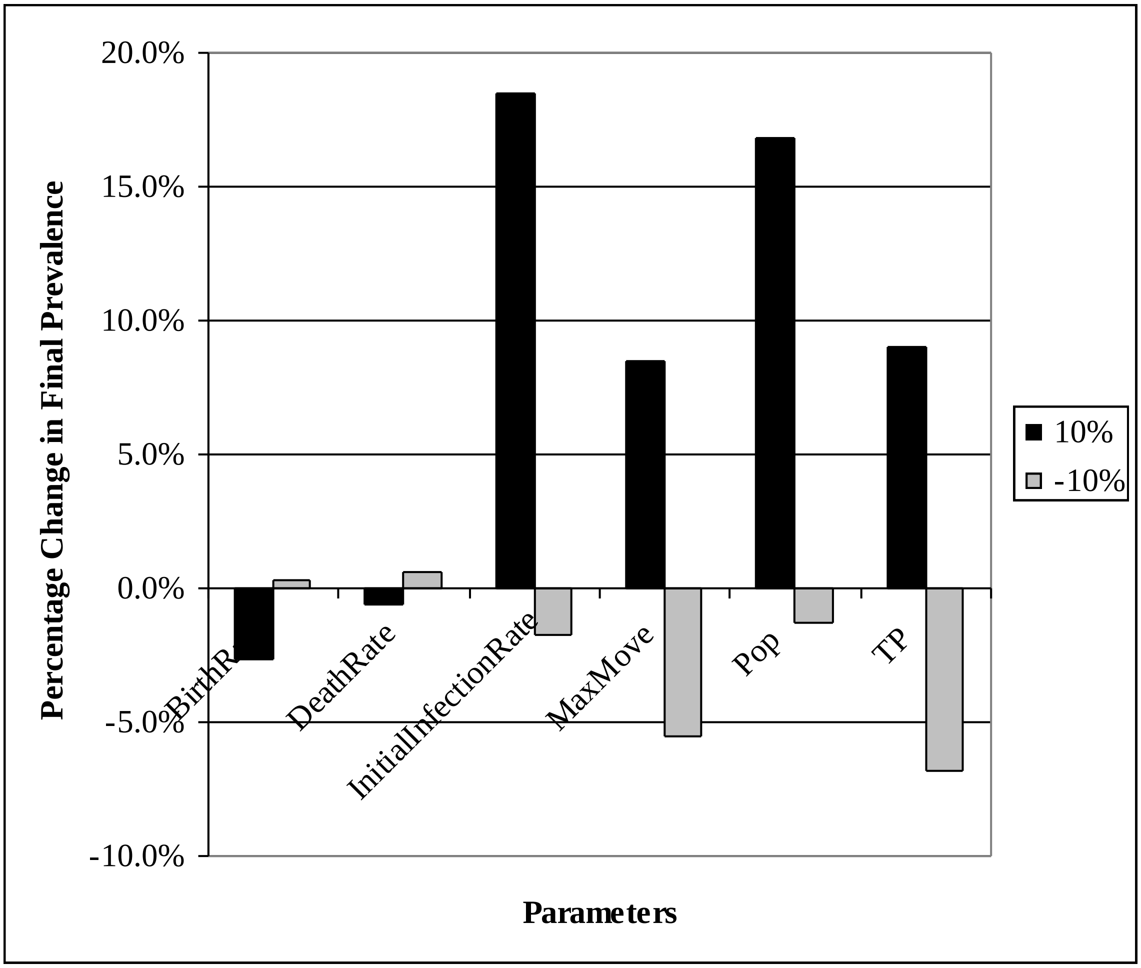


Figure 4.4 Sensitivity analyses of birth rate, death rate, initial infection rate, maximum movement, population density, and transmission probability.

Table 4.1 Parameter values used for the four simulation scenarios.

Parameters	Predrought Years		Postdrought Years	
	Low Disturbance	High Disturbance	Low Disturbance	High Disturbance
Initial Number of Mice	51	23	134	62
Birth Rate	40	40	40	40
Death Rate	40	40	40	40
Transmission Probability	0.1	0.1	0.1	0.1
Minimum Movement (meter)	2	2	2	2
Maximum Movement (meter)	20	20	20	20

Table 4.2 Final prevalence for each simulation.

Prevalence	Low Disturbance	High Disturbance
Predrought Year	0.19	0.10
Postdrought Year	0.57	0.26

CHAPTER 5

CONCLUSION

Environmental changes (e.g. climate, habitat disturbance) can have large impacts on the dynamics of population density and behaviors of a species. Consequently, these changes could greatly affect the dynamics of the pathogen they carry, threatening human health. In the past few decades, there has been a dramatic increase in zoonotic diseases such as HPS, SARS, and the West Nile Virus. There is a great need to understand the nature of the virus host, its temporal and spatial dynamics, and its relation to the human population with the purpose of predicting human risk of the disease and deploying effective prevention strategies and policies.

The focus of this research is hantavirus dynamics in deer mice in the Great Basin Desert of Central Utah, USA using multiyear field data and integrated geospatial approaches, including remote sensing, GIS, and a spatially explicit agent-based model. The goal is to advance our understanding of the important ecological and demographic factors that affect the dynamics of deer mouse population and SNV prevalence, as well as expand our knowledge of the risk factors of developing HPS in humans as a consequence of SNV infection. The primary research question is how climate, habitat disturbance, and deer mouse demographics affect deer mouse population density, movement, and SNV prevalence in the sagebrush habitat.

To address the main research question, this research design includes three major components. The first component uses high temporal resolution (16-day) MODIS satellite time-series data (2002 ~ 2006) to estimate rodent abundance and SNV prevalence with the purpose of predicting SNV risk. The relationships between four MODIS vegetation indices and deer mouse density, SNV prevalence, and the number of infected deer mice at various time lags are examined and compared. The central hypothesis is that vegetation indices can serve as proxies for deer mouse food availability, which affects deer mouse abundance and SNV prevalence. The results reveal varying levels of positive correlation between the vegetation indices and deer mouse density, as well as the number of infected deer mice. Among the vegetation indices, the NDVI and EVI produce the highest correlations with deer mouse density and the number of infected deer mice using a time lag of 1 to 1.3 years for May and June data. This information can be very useful in predicting mouse abundance and SNV risk. The NDVI and EVI can be used to estimate population density that is one of the main input variables for the SABM.

The second component is mapping the deer mouse movement from the recapture field data and identifying the potential environmental and demographic factors that can affect deer mouse movement. Understanding deer mouse movement is critical for understanding disease transmission. Greater movement leads to greater potential for encounters and increases transmission probability. The research investigates the roles of climate, seasonality, habitat disturbance due to ATV recreation use, deer mouse demographics, and infection with Sin Nombre virus on deer mouse movement. Generalized linear mixed models are used to estimate the effects of these factors and their interactions by fitting movement data collected seasonally from 2003 to 2006 at twelve sites in the Great Basin Desert of central Utah, USA. The results show that climate, mouse density, sex, mass, and SNV infection have significant effects on deer mouse movement. There are also significant interaction effects between climate and disturbance, as well as mass and SNV infection. The effect of habitat disturbance on mouse movement varies according to climate conditions with a positive relationship in predrought conditions and negative association in postdrought conditions. The heavier infected deer mice move the most. Season and disturbance alone have no significant effects.

Lastly a spatially explicit agent-based model is built upon the knowledge gained from the first and second components to further test the hypotheses and understand the mechanism of SNV dynamics. It is a great exploratory tool to test hypotheses as well as to experiment with a range of “what-if?” scenarios. The model simulates how SNV changes with deer mouse movement, population density, and demographics. There are two contrasting hypotheses on how habitat disturbance affects hantavirus prevalence. Langlois et al. (2001) suggests that fragmented habitat increases mouse movement and thus contact rates, and consequently increases hantavirus transmission. In contrast, Calisher et al. (2000) proposes that habitat disturbance reduces rodents’ habitat and thus the virus host population, and in turn, hantavirus prevalence. This model tests these opposing hypotheses by including these variables. The simulation results consistently show that prevalence is lower at high disturbance sites where deer mouse density is lower, which supports the hypothesis of Calisher et al. (2000). The sensitivity analysis shows that population density is one of the most important parameters affecting prevalence dynamics and also indicates that habitat disturbance could increase hantavirus transmission by increasing the movement of deer mice and consequently contact rates. However, the results suggest that habitat disturbance had a much stronger effect on prevalence by decreasing population density than by increasing mice movement. Therefore, overall habitat disturbance reduces prevalence mainly by reducing the size of the virus host population.

Figure 5.1 shows the structure of the three main components and their interactions. The solid lines represent the data-flow in and out from the SABM model. The dashed lines correspond to the simulation results that explain how population density, movement, and habitat disturbance affect SNV infection. MODIS data can provide a means for population estimation that can serve as one of the important parameters in the SABM. Deer mouse movement measurements from mapping recapture field data can guide the settings of the movement parameters. SABM tests two contrasting hypotheses on the mechanisms of how various factors could affect hantavirus dynamics. The model results suggest that population density has much greater effects than the mouse movement. It also suggests that habitat reduces SNV infection by reducing the virus host population. The simulated prevalence is compared with the field surveyed prevalence and is found to be within the reasonable range.

This research contributes to the fields of geography, ecology, and epidemiology in the following aspects: 1) it provides an example of studying ecology of animal hosts of zoonotic diseases in an arid environment. Zoonotic diseases are the diseases transmitted from animal to humans; examples are hantavirus, anthrax, and Avian Flu. The results will help us to identify important ecological parameters that affect disease dynamics in animal populations, and therefore enhance our ability to manage and predict disease risk to humans. The results may also be applicable to other animal disease studies elsewhere in an arid land which covers 47% of the world's land surface; 2) It applies both top-down and bottom-up approaches to study the disease dynamics. This not only helps researchers understand the macrolevel phenomena but also the underlying mechanisms. The agent-based modeling approach simulates individual movement, interactions, and hantavirus transmission as a probability of contacts. This simulation can increase the knowledge of pathogen transmission pattern and help public health officials make informed decisions. The incorporation of geospatial data in the simulation model provides a realistic simulation environment and good visualization capability. The model parameterization and coupling of geospatial data with a spatially explicit agent-based model may be illustrative for other studies concerning disease dynamics in animal populations in a heterogeneous environment.

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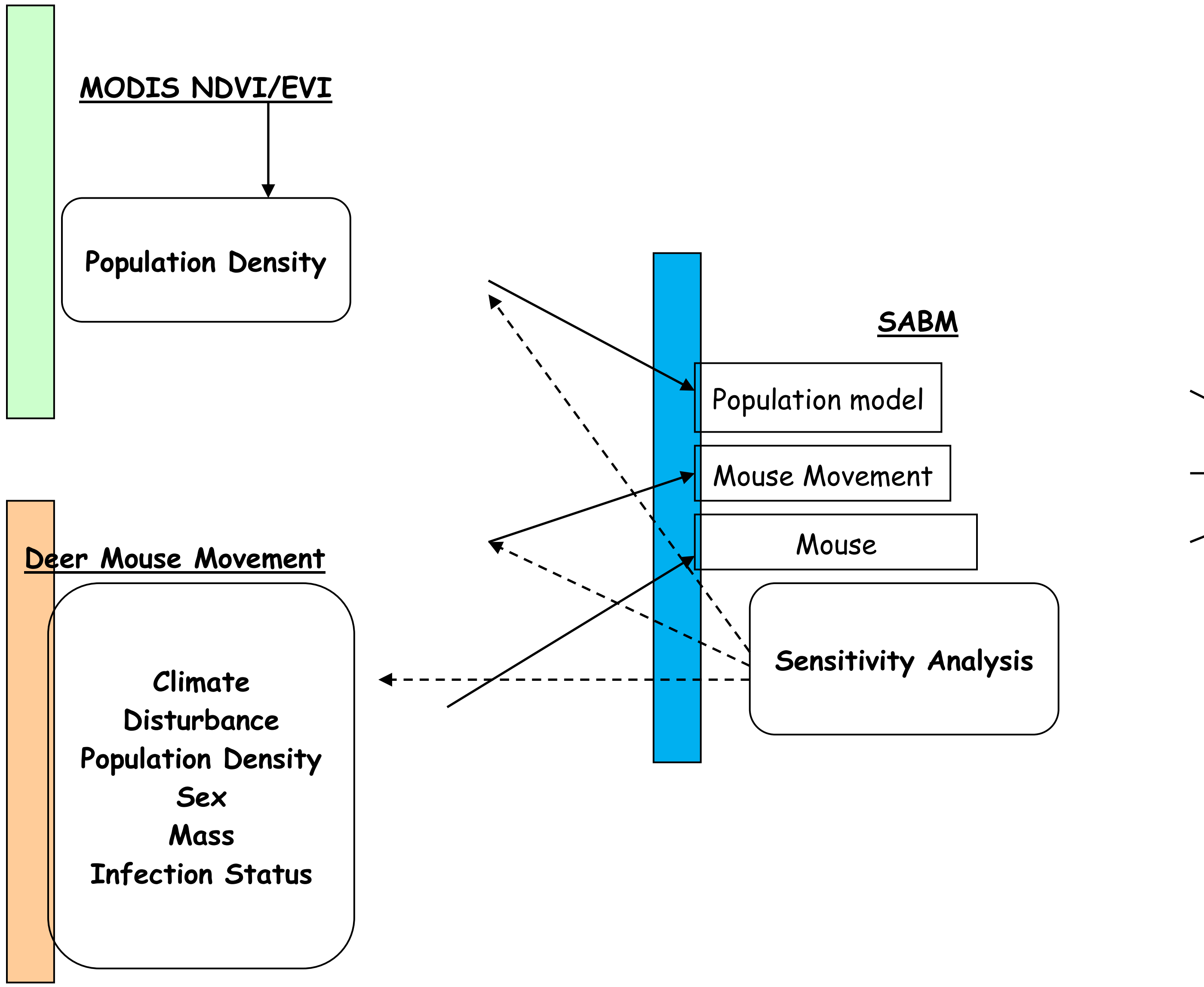

Figure 5.1 The relationships between the three major components.