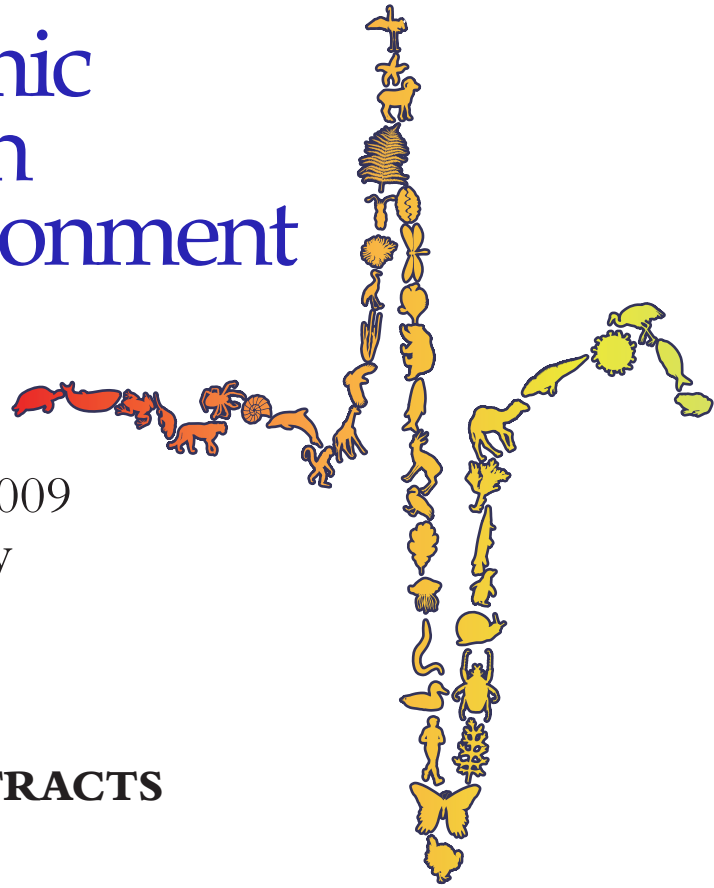


# Exploring the Dynamic Relationship Between Health and the Environment

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## POSTER ABSTRACTS



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Abstracts are listed alphabetically, by first author. Names appearing in all capitals are of the presenting author attending the symposium. Contact information appears after author affiliation in the byline.

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**HUMAN BEHAVIOR CAN INFLUENCE CANINE  
PATHOGEN EXPOSURE AND DISEASE MORTALITY  
IN THE ENDANGERED AFRICAN WILD DOG**

*Human modification of the environment has had important consequences on the emergence of infectious disease in both human, animal, and plant populations. Human behavior itself has had a powerful influence on pathogen invasion dynamics and infectious disease spread within human populations. This is particularly true for sexually transmitted diseases as seen in the emergence of human immunodeficiency virus. What role does human behavior and cultural practice play in pathogen transmission dynamics at the domestic animal - wildlife interface? We examined two systems (1991-1993) where humans, domestic dogs, and an endangered species, the African wild dog (Lycaon pictus) co-existed: Masai Mara, Kenya, and Okavango Delta, Botswana. The African wild dog is one of the most endangered large carnivore species in Africa. Domestic animal diseases and human conflict have been important in determining population distribution and have contributed to local extirpations. In both study localities, pastoral livestock production systems are practiced by rural communities. However, in Kenya, Maasai tribal people practice strong livestock husbandry with intensive herding of livestock accompanied by domestic dogs. In contrast, livestock farmers from Botswana (various tribal groups) rarely herd cattle and practice a more passive approach to livestock care. In the latter, domestic dog movement is primarily localized within villages. Through questionnaire-based interviews, canine pathogen serosurveys, and intensive ecological studies of African wild dogs in these two study sites, we identify a significant correlation between herding of cattle, increased domestic dog contact with African wild dogs, and disease related mortality in this endangered species. Human behavior and cultural practices can be an important determinant of contact between domestic animals and wildlife and can influence pathogen transmission dynamics*

*at this interface. Conservation planning would benefit from consideration of local community behavior in the development of disease control strategy and land use plans.*

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**LEMUR DISEASE ECOLOGY: LINKING HEALTH,  
ECOSYSTEM VIABILITY, AND CONSERVATION IN  
MADAGASCAR**

*Anthropogenic effects on ecosystems have reached unprecedented levels, with potentially disastrous consequences for global environmental, wildlife, and human health. Human encroachment into wildlife habitat leads to degradation and fragmentation, which in turn increases contact among wildlife, humans, and domestic animals. Global concern has grown over the risk of emerging infectious diseases from zoonotic origins due to this increasing rate of contact. With Madagascar's rampant rate of human population growth and deforestation, its incredible species diversity, the widespread presence of domestic and invasive species, and its evolutionary isolation, it can be viewed as a potential location for future disease risk. Consistent baseline health monitoring of lemur populations provides an effective tool for evaluating wildlife health and preparing for future disease occurrences. Limited, disconnected surveys of lemur health have been conducted, yet there remains a need for more extensive, country-wide evaluations that also assess diseases of invasive species, domestic animals and humans. Our study investigates how spatial, climatic, anthropogenic, and conservation factors affect the occurrence*

of infection on an island-wide scale in Madagascar. We are incorporating lemur health data from 15 reserves throughout the island with habitat characteristics and evaluations of the human pressures affecting each site. By utilizing statistical and geospatial tools, we are assessing the characteristics of sites that exhibit the highest infection rates; these data will assist in predicting potential problem areas in the future. By studying the interactions of spatial patterns, habitat quality, and anthropogenic pressures, we can more accurately assess the health of lemur populations in Madagascar and provide valuable information for reserve design. These data can also inform public health, conservation, economic, and social policy strategies to address disease risk within a multidisciplinary framework.

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howler monkey (BHM; *Alouatta pigra*) has survived in small rainforest remnants in fragmented landscapes characterized by high contact rates with humans and domestic animals, providing an opportunity to study pathogen exchange among different populations. Due to their close phylogenetic relationship with humans, NHP are models and sentinels for zoonotic and anthrozoönotic diseases. Both TB and DEN are important infectious diseases in human populations worldwide and may occur in non-human primates in Mexico. In the southern Mexican state of Campeche we collected sera in three sampling periods of three consecutive years (2006-2008). We obtained sera from 58 individuals belonging to 13 groups of BHM, inhabiting 9 areas with different degrees of habitat fragmentation and 1 troop from the Biosphere Reserve of Calakmul. We used ELISA Platelia NS1 Ag test for dengue virus and we have not found positive BHM; parallel studies have reported positive bat species including *Carollia perspicillata*, *Desmodus rotundus*, and *Uroderma bilobatum* for DEN at the same study sites. In spite of the high prevalence of positive cases of DEN in human and bat populations in the state of Campeche, our results suggest that this pathogen may not affect BHM. The results for the screening of anti-*Mycobacterium* antibodies are still pending. The DEN virus results provide baseline health information on BHM and warrant further research to understand the dynamics of this pathogen.

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**DISEASES SURVEILLANCE IN WILD MEXICAN  
NON-HUMAN PRIMATE POPULATIONS**

**A**ccelerated deforestation is causing loss and fragmentation of primary habitat of the three species of the Mexican nonhuman primates (NHP). The effect of habitat loss and fragmentation on several infectious diseases in New World non-human primates has been scarcely researched. Some diseases that could possibly affect New World NHP, such as tuberculosis (TB) and dengue (DEN), had not been studied in wild primates in Mexico previously. In Mexico, the black

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**PATTERNS OF INFANT MORTALITY AND CANCER DEATH IN ALABAMA, U.S.**

*Public health has close relationships with local social, economic, and environmental conditions. One approach to study these relationships is to correlate large-scale public health data with available concurrent information about the surrounding environment to identify potential public health issues. The objective of this study is to use recent information of infant and cancer mortality in Alabama counties as a case study to test their relationships with social, economic, and environmental conditions at a large scale by the support of GIS, data categorization, and correlation analysis. The results indicate that infant mortality was significantly higher in African-American and other minority populations than in white populations, but cancer mortality was higher in white populations than in African-American and minority populations. There was no significant difference in infant mortality rate between populations in the urban counties and the rural counties, although the mortality rate of cancers was significantly higher in the rural population than in the urban population. Mortality rates for cancers in wealthy counties were lower than in poorer counties. Both the infant and cancer mortalities were lower in counties with higher plant and vertebrate species richness. The emergent spatial pattern suggests that the incidences of infant and cancer mortality were higher in the Sipsey/Warrior River Basin, Coosa/Tallapoosa River Basin, and Conecuh River Basins. This study provides new insight for understanding mortality of infants and cancers at large scales.*

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**GENETIC VARIATION DRIVES SOURCE-SINK EVOLUTION IN PATHOGEN EMERGENCE**

*Laboratory observations show that pathogens can readily mutate to infect new hosts; yet successful pathogen emergence in nature seems comparatively rare. What factors contribute to successful pathogen emergence? One hypothesis is that migration from populations that support growth (i.e. sources, usually native host populations) facilitates adaptation in populations that fail to sustain growth (i.e. sinks, often novel host populations) by delivering beneficial mutations sampled from the sources' standing genetic variation. This hypothesis applies whether the novel host population is a new host type (host shift) or merely a new population of an existing host type in a heterogeneous landscape (range expansion). We expect, however, that migration from sources should have the greatest benefit for emergence of the range expansion type, since selection on source and emergent populations is likely to be congruent. By contrast, since host shifts often involve fitness tradeoffs between native and novel hosts, thus benefits accrued from migration from sources are expected to be limited. We tested this prediction by allowing lineages of RNA bacteriophage Phi6 to evolve on a novel Pseudomonas host under sink conditions while manipulating the emergence scenario: host shift or range expansion. Results were compared with sinks receiving migrants of an unevolved ancestral genotype to control for the effect of genetic variation in source populations. As predicted, adaptation was greatest in the range expansion treatment and did not occur in the ancestral control. However, considerable adaptation also occurred in the host shift treatment, despite demonstrable disruptive selection between phage populations growing on native and novel host types. This surprising result*



*underscores the importance of both migration and standing genetic variation in the process of pathogen emergence.*

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TEMPORAL AND SPATIAL ANALYSIS OF  
MICROBIAL CONTAMINATION IN SHALLOW  
DRINKING WATER WELLS IN BANGLADESH

*D*iarrrheal disease is the cause of an estimated 4-6 million deaths in the developing world each year. Improvement and changes in water supply, quality, hygiene, and sanitation all reduce diarrheal mortality and morbidity. However, throughout rural Bangladesh, access to potable water is still a significant problem despite efforts to switch from surface to groundwater extraction. Fecal contamination of groundwater from shallow tube wells is common, but the scope of the problem remains poorly constrained. In order to better understand this problem

113 tube wells less than 100 feet deep, throughout the rural Matlab Upazilla, Bangladesh, were monitored monthly for one year. Over the past year, routine monthly sampling for microbial fecal indicators, sulfate, and other geochemical parameters has indicated a strong relationship between the monsoonal rains and subsequent increase in fecal groundwater contamination. During the dry season in May 2008, 30% of the tube wells were positive for E.coli, whereas during the wet season in August 2008, 80% of the tube wells were for positive for E.coli. However, spatial analysis of E.coli concentrations following each sampling event showed little correlation over distance, indicating that the E.coli concentration in one well is a poor indicator of E.coli concentration in a nearby well. In addition, E.coli concentrations were not correlated with the density of ponds or latrines, both hypothesized as contaminant source areas. As a direct result of these findings, re-analysis of the time series data was undertaken. Each tube well was classified into one of four E.coli concentration trends: i) always low, ii) seasonal, iii) always high, and iv) other. Interestingly, even though E. coli concentrations do not correlate over distance, the attributed classifications do appear to cluster in space. This novel analysis may help us better understand what controls fecal contamination in the subsurface and enable future recommendations for remediation.

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**LOGGING CREATES UNANTICIPATED THREAT  
TO APE HEALTH AND CONSERVATION IN  
EQUATORIAL AFRICA**

*Selective logging is a dominant land use activity in forested areas of the tropics with the potential to provide a sustainable and profitable supply of timber, while simultaneously ensuring biodiversity conservation. However, selective logging results in a suite of alterations in host ecology and forest structure that may alter infection prevalence and infection risk in resident populations. As part of a large-scale investigation of patterns of parasitism and infection risk for apes in logged and undisturbed forest, we collected 48 1-m<sup>3</sup> vegetation plots from trees of species frequented by gorillas and chimpanzees in Republic of Congo. Half of these plots were within the Kabo Logging Concession and half were within the adjacent Goulougo Triangle, an undisturbed forest. We used a modified sedimentation technique to recover infective-stage parasites from vegetative plots for examination by compound scope for infective-stage individuals of nematodes with the capacity to infect apes and/or humans. Infective stage larvae of *Strongyloides stercoralis* were found in 25% of ground vegetation plots in the Kabo Concession, but were found in none of the vegetation plots from Goulougo Triangle. This represents an unanticipated threat to ape health and conservation since *S. stercoralis* was not thought to occur in humans in Equatorial Africa and is associated with hyperinfections with the capacity for high mortality rates in apes and humans.*

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**CO-BENEFITS TO HEALTH AND THE  
ENVIRONMENT OF BICYCLING IN CITIES**

*The adverse health effects resulting from climate change, road crashes, physical inactivity, urban air pollution, energy insecurity, and environmental degradation can all be linked to fossil-fuel energy use in transportation. Though the average car has increased in fuel efficiency due to enhancements in vehicle design, the average number of miles driven has increased dramatically—directly effecting emissions causing pollution such as ozone and particulate matter as well as those potentially leading to climate change. Transportation choices are impacted by the way we design our cities and transportation policies, but if we shift toward more sustainable, multi-modal transportation systems which encourage use of bus, train, bicycling, and walking, we could reduce some of our reliance on passenger vehicles and ameliorate many of the aforementioned consequences. Forty percent of automobile trips in the United States are shorter than two miles and over twenty-five percent are less than one mile, and replacement of these shorter car trips with bicycling or walking could enable most motorists to achieve recommended levels of physical activity. We examined the eleven largest cities in the Midwest to determine the health and environmental co-benefits of replacing short car trips with bicycle trips at personal, local, and global scales, specifically (1) improvement to personal fitness and human health, (2) improvement in local air quality and human health, and (3) global climate change mitigation from reduced greenhouse gas emissions. We conclude that the health and environmental co-benefits of promoting bicycling are substantial, and implementing public policies that encourage low-carbon, less-energy intensive, and active transportation systems could play an important role in meeting targets for air quality and greenhouse gas emissions.*

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**AN EVOLUTIONARY APPROACH TO THE DESIGN  
 OF A ROBUST IMMUNE SYSTEM**

*We propose an evolutionary approach to understanding the design and function of immune systems that will be a useful guide to medical research. Wildlife biologists can facilitate innovative research on disease resistance by identifying model organisms with particularly robust immune systems. We identified such a useful animal species, the brown-headed cowbird (*Molothrus ater*, Icteridae), and have been demonstrating the extent and nature of its unusually effective immune defenses. This cowbird is exposed to an exceptional diversity of parasites due to its life history strategy of brood parasitism, in which it lays its eggs and raises its young in the nests of more than 200 different songbird species across North America. We have shown that this cowbird is exposed to a higher diversity of ectoparasites and blood parasites than are closely-related, non-parasitic species in the same avian family. We demonstrated that the cowbird is significantly more resistant to both native and non-native viruses, including West Nile virus. Recently we began to profile the functional innate responses of leukocytes of cowbirds and compared them to leukocytes of related, non-parasitic avian species. Innate immune defenses are a species' response to pathogens in the earliest stages of infection, and they are a critical determinant of its disease resistance and susceptibility. The innate host defenses*

*are dedicated to containment of pathogens, holding infections to a level that can be resolved by the ensuing development of acquired immune mechanisms. Our preliminary findings indicate that the leukocytes isolated from brown-headed cowbirds have significantly greater functional activities than the leukocytes from red-winged blackbirds (*Agelaius phoeniceus*, Icteridae). Profiling the cowbird's array of immune defenses promises to reveal the design and function of a highly effective vertebrate immune system, valuable to biomedical researchers responsible for defending human populations against emerging zoonoses and global transmission of non-native pathogens.*

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**HEALTHSCAPES.ORG: A TOOL FOR MAPPING  
 ENVIRONMENT-BASED VULNERABILITY TO  
 INFECTIOUS DISEASE EMERGENCE**

*The last three decades have seen a global rise of emerging infectious diseases derived mostly from animals and linked to changes in underlying environmental and socio-economic conditions. The growing understanding of these multiple drivers of disease emergence has spurred calls for proactive, holistic approaches to disease that simultaneously consider human, animal, and environmental sectors. We propose the development of HealthScapes.org (combining issues of health and landscapes), a web-based system that will assemble, interpret, and report data/information that indicates state, change, and vulnerability*

(risk) to infectious diseases. HealthScapes will strategically link data from a number of near-real-time environmental monitoring satellite platforms, as well as historical data on local and regional land use, climate, and sociodemographic data. This mapping project will monitor, organize, and integrate these ecosystem-based data to identify, map, and display vulnerable regions for emerging infectious diseases (EIDs) and their causative components (e.g. insect vectors, their breeding sites and temporal variation in site suitability), build stakeholder understanding and dialogue about the interrelationships between public health and ecosystem health with respect to these EIDs, explore the affects of global and regional environmental changes on disease emergence, and support policy-relevant assessments of conservation, development, and/or disease management programs. HealthScapes seeks to illuminate where hotspots of “vulnerability” exist with respect not only to emergent and resurgent disease, but also to novel disease agents. While causal mechanisms may be elusive, HealthScapes will provide a framework to leverage disease-relevant knowledge from existing online metadata sources, satellite and other environmental data, site-specific health, environment, and socio-demographic data, and from the bi-direction flow of information from end-users. Our efforts will enhance “One-Health” risk-based surveillance already underway by moving upstream to identify prerequisite ecological conditions predictive of ensuing disease outbreaks.

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**ENVIRONMENTAL BIOMARKERS AS METHODS TO DETERMINE THERMAL AND PATHOGENIC STRESS IN CORALS**

*Environmental stress biomarkers can be used as molecular tools for the early detection of pathogenic and thermal stress in the symbiotic algae living in the tissue of corals; this can be an effective approach in preservation of coral reef health and biodiversity. We have found that an extra-cellular, unidentified molecule produced from a cluster of novel Vibrio bacterial pathogens found in coral Yellow Band disease (YBD) inhibits cell cycle mitosis between 60-99% in symbiotic coral cells called zooxanthellae; while simultaneously affecting expression and regulation of HSP60 and 70 in vivo. Heat shock proteins (HSP's) are highly conserved proteins found in induced apoptotic cells due to stress. Symbiodinium clade sub-types; A, B, C, and D are affected by the toxins produced when corals are suffering from YBD. We have found an HSP-70 related protein in thermally stressed Vibrio infected Symbiodinium using HSP-70 specific antibodies. This putative HSP70-related protein is expressed highly in clade C, at low levels in clade A, but not in clades B and D; consistent with observed patterns of sub-type thermal tolerance. Dysfunction of cell protective mechanisms such as NADH dehydrogenase is also implicated during Vibrio exposure at higher temperatures. A WST-Cell viability assay was used to determine peak NADH enzyme activity of all Symbiodinium clade sub-types exposed to the toxin molecule. Enzyme activity was at peak levels during 24hr treatments following no enzyme activity between 48-72hrs. The enzyme deficiency following 24hr indicates impairment in the electron transport chain, affecting ATP energy production that is needed during mitotic cell division and cellular respiration in symbiotic zooxanthellae living in the tissues of corals. Using Symbiodinium subtypes*



as in vitro models can allow researchers to detect early molecular signals as bio-markers associated with environmental stress during coral thermal stress and disease infection.

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**STREAM ECOLOGICAL INTEGRITY IS INVERSELY  
RELATED TO HUMAN CANCER MORTALITY IN  
WEST VIRGINIA, U.S.**

*Assessments of ecological integrity are commonplace for biological conservation, but their role for public health remains largely unexplored. We tested the prediction that human cancer mortality rates would be negatively related to the ecological integrity of streams in West Virginia. We characterized ecological integrity using an index of benthic macroinvertebrate community structure (West Virginia Department of Environmental Quality data) and we used data from the Centers for Disease Control and Prevention to quantify age-adjusted human cancer mortality rates. Ecological integrity was negatively related to total cancer mortality ( $p < 0.01$ ). We detected significant variation among cancer types: respiratory, digestive, urinary, and breast cancer mortality rates were related to ecological integrity but genital and oral cancers were not. Smoking rates were also related to cancer, but did not account for the observed effects of ecological integrity. However,*

*an index of coal mining intensity was positively related to cancer mortality ( $p < 0.01$ ) and negatively related to ecological integrity ( $p < 0.001$ ). Spatial analyses also revealed cancer clusters that corresponded to areas of low ecological integrity and high coal mining intensity. Our results demonstrate significant linkages between ecological integrity and cancer in West Virginia, and suggest important effects of coal mining on ecological and human communities. We conclude that assessments of ecological integrity can be highly relevant for public health and that stream biota may serve as sentinels in this regard.*

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**SUPRAMAP – LINKING PATHOGEN GENOMES  
WITH VIRTUAL GLOBES TO FIGHT EMERGING  
INFECTIOUS DISEASES**

*Emerging infectious diseases present critical issues to public health and economic welfare. As demonstrated by the response to Severe Acute Respiratory Syndrome (SARS) and avian influenza, novel diseases are being addressed via rapid genomic sequencing. However, our ability to make sense of these data lags behind acquisition. First, phylogenetic analyses of large*

*datasets comprised of many viral genomes are computationally difficult. Such analyses require novel algorithmic approaches, large amounts of memory, and parallel architectures. Next, even once satisfactory phylogenetic trees are produced, we have hardly begun to understand how disease-causing organisms evolve and travel over various hosts and geography to become epidemics. To these ends we have created an interactive genomic and geographic map using phylogenetic trees and geographic information systems to reconstruct the evolution and spread of avian influenza lineages (H5N1) and other diseases. By examining a phylogenetic tree of H5N1 projected onto a virtual globe we can study visually where key genotypes in viral proteins are correlated with host shifts and resistance to therapeutic drugs and their statistical significance. We develop a user-friendly web based application called SUPRAMAP. The application supports a workflow connecting analysis of raw sequence data to parallel computing in POY4 and visualization of the biogeography of the lineages. At [supramap.osu.edu](http://supramap.osu.edu) we have created an interface where users can register, upload raw data files, name projects, and organize sets of data files into jobs to be executed on a computing cluster. Once the user starts a job, the system performs an alignment and phylogenetic tree search in parallel using POY4, generates a tree and statistics on the POY run, and finally, generates a Keyhole Markup Language (KML) file with the tree and mutations it implies suitable for viewing with Google Earth and other software such as NASA Worldwind or ArcGIS. Although emerging infectious diseases provide exciting use cases, SUPRAMAP is applicable to many biogeographic problems across the sciences.*

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**AGENT-BASED SIMULATION OF MALARIA  
TRANSFER IN THE AMAZON**

*Malaria is a major health problem in both urban and rural Amazonia. We offer an approach to understanding the spatial dynamics of malaria transmission by modeling the recent re-emergence of the disease, through an epidemic phase and a more recent transition to endemism, in Iquitos, Peru. In this Amazonian region, climatic change, demographic instability, and landscape fragmentation are among a unique set of local spatial variables underlying transmission dynamics. Traditional non-spatial and population-based epidemiological models lack the ability to resolve the interactions among these variables. We have used an agent-based model to explore the interactions among social, ecological, and biological factors controlling malaria transmission in the Peruvian Amazon. Agent-based models present a new opportunity for spatially explicit definition and exploration of causal factors and influences of transmission between mosquito vectors and human hosts. Three interacting sub-models representing human decisions, vector dynamics, and environmental factors interact to simulate the dynamics of transmission. The resulting emergent behaviors offer insight into the epidemiological events of the past two decades in Iquitos. Preliminary model results indicate that mosquito populations in the area are sensitive to climate change. These findings are related to the climatic effects of El Niño during the epidemic period. Additionally, consideration is given to potential model validation and agent handling strategies. Finally, we recommend the model as an information tool for policy-makers and health agents in formulating strategies to prevent epidemic events as well as focus their interventions on geographic locations where malaria is endemic in Iquitos and other regions of Peruvian Amazonia.*

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**THE FEVER PITCHES NORTH: THE RISE OF  
DENGUE FEVER IN THE AMERICAS**

*D*engue fever infects up to 100 million people, causes a half million hospitalizations and 22,000 deaths annually in more than 100 countries, yet many North Americans know little about it. However, in a situation analogous to West Nile Virus a decade ago, global warming in conjunction with international travel and transport may set the stage for a public health crisis. A new NRDC analysis mapped dengue cases reported in the Western Hemisphere since the mid-1990s and more closely examined the distribution of mosquito vectors and environmental conditions in the U.S. that contribute to increased vulnerability to dengue fever. Results show that a dramatic increase in dengue has occurred in recent years in the U.S. and its neighbors to the south. The overall number of dengue cases nearly tripled between 1995 and 2007, growing from nearly 336,000 cases in 1995 to over 900,000 cases in 2007. Dengue hemorrhagic fever cases in that same time period more than tripled, rising to over 26,000 cases by 2007. In the United States, there have been a total of 4,062 cases of imported and locally-transmitted dengue in the U.S. between 1995 and 2005. When cases in the Texas-Mexico border region cases are included, the numbers soar to over 10,000.

*The mosquitoes that can potentially transmit this disease have become established in a swath of 28 states across the south and mid-Atlantic regions. Many of these areas also face threats, such as flooding and sub-standard housing, that make them increasingly vulnerable to dengue transmission. To combat dengue and other vector-borne diseases, new multi-scale partnerships will be needed among local communities, regional health agencies, and national governments to strengthen systems that monitor and map climate-sensitive environmental conditions, improve health surveillance, and work toward international data sharing.*

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**CONTROLLING SCHISTOSOMIASIS IN IRRIGATED  
AGRICULTURAL REGIONS OF CHINA:  
AN INTEGRATED ECOSYSTEM APPROACH**

*S*chistosomiasis remains a major public health problem in the tropics and subtropics and represents a class of infectious diseases with strong environmental links. In a previous study based on a mathematical model coupled with field epidemiological observations, we showed that chemotherapy or chemotherapy plus sporadic mollusciciding, as commonly practiced in many endemic areas, would not achieve broadly sustainable control of transmission in the irrigated agricultural environment in China. The findings highlighted that the goal of eliminating transmission will require environmental modifications and/or improved sanitation facilities to reduce transmission potential. Here we report on a 10-year longitudinal study in 16 villages in Sichuan, China for controlling schistosomiasis through an

*integrated ecosystem approach complemented with medical interventions. In addition to chemotherapy, in these villages a set of environment-oriented measures including alteration of crop structure, waste management through anaerobic digestion systems, lining of irrigation ditches, and forestation were initiated in the early 1990s. The trends of schistosomiasis prevalence of infection in villagers, snail density and habitat areas, and environmental measures were compared over the 10-year period. Human prevalence of infections ranging from 10-30% at the beginning of the project was reduced to less than 1% in 2005, in which the reduction was significantly related to environmental measures. The modeling analyses indicated that in these villages, effective reproduction ratios of the parasite,  $R_e$ , a measure of transmission potential of the parasite, were less than 1, implying that the transmission would not persist. The simulation analysis suggested that transmission would die out in about 5-8 years. Key characteristics of sustainable control in this type of environment are summarized in the study.*

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*demonstrated that greater tolerance of mutational change is associated with virus adaptability in a new niche, a finding generally relevant to evolutionary biology, and informative for elucidating how pathogens might evolve to emerge in new habitats and/or overcome novel therapies. Here we investigate the unknown question of how genetic robustness evolutionarily arises, by testing the hypothesis that genetic robustness evolves as a corollary to evolved environmental robustness. We do this by evolving viruses to differing levels of environmentally robustness, and then assaying their genetic robustness by exposing them all to the same set of specific mutations and measuring how their fitness changes. The relationship between environmental and genetic robustness is important because it could explain how evolvability itself may evolve, and because it can inform our ability to better predict disease emergence. Habitat disturbance is known to be associated with the emergence of new diseases, but this relationship is assumed to be driven by increased probability of human encounter with new pathogens. However, an intimate relationship between the evolution of environmental and genetic robustness offers an alternate mechanistic explanation for this observation, by suggesting pathogen adaptation to environmental disturbances may predispose the pathogen to successfully undergo emergence on new hosts.*

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**ENVIRONMENTAL ROBUSTNESS AND  
 PATHOGEN EMERGENCE**

*The ability for an evolving population to adapt to a novel environment is achieved through a balance of robustness and evolvability. Robustness is the invariance of phenotype in the face of perturbation and evolvability is the capacity to adapt in response to selection. We have previously*



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**THE U.S. NATIONAL ECOLOGICAL OBSERVATORY NETWORK (NEON): A NEW LARGE FACILITY INITIATIVE**

*The National Ecological Observatory Network (NEON) is a national-scale research platform for analyzing and understanding the impacts of climate change, land-use change, and invasive species on ecology. NEON partitions the United States into 20 ecoclimatic domains using a statistical analysis of ecoclimatic variables and vegetation patterns. Each domain hosts one fully instrumented NEON Core Site located in a wildland area as well as two relocatable sites (which move every 5 years) to capture land use change gradients (60 sites total). Collectively, the domains represent ecological and climate variability across the continental United States, Alaska, Hawaii, and Puerto Rico. NEON features sensor networks and experiments, linked by advanced cyberinfrastructure to record and archive ecological data for at least 30 years. Using standardized protocols and an open data policy, NEON will gather essential data for developing the scientific understanding and theory required to manage ecological challenges. NEON data will be gathered from the level of the gene and the organism to the continental scale. The scaling strategy requires a mixture of human and instrumental measurements. At individual sites, NEON will support fixed towers with sensor arrays to provide comprehensive data on climate, air quality, productivity, soil characteristics, and water quality. The observatory will also track patterns in organismal communities including: soil microbes, plants, algae, insects, birds, and small mammals. Infectious disease is one of the key areas of importance to NEON. Trained observers will monitor pathogens in small mammals (*Peromyscus* species) and mosquitoes. Surveillance of hantavirus, Lyme disease, West Nile Virus, and dengue will*

*be provided by NEON and additional host samples will be archived to enable monitoring of newly emerging pathogens. The success of NEON will be measured by the widespread use of the open database and infrastructure to analyze broad scale patterns and stimulate new areas of environmental research.*

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**A MULTIDISCIPLINARY APPROACH FOR UNDERSTANDING THE HEALTH OF GLOBALLY ENDANGERED MARINE TURTLES AT THE PALMYRA ATOLL NATIONAL WILDLIFE REFUGE**

*Marine turtles face significant health threats, and may be sentinels of ecosystem health. Understanding the health status of globally endangered marine turtles at the remote Palmyra Atoll, where they are removed from pervasive human influence, will provide a baseline for understanding health and human impacts on these animals. We are therefore researching marine turtle health in the context of their distribution and abundance, ecological interactions, and feeding ecology along the atoll, as well as migratory relationships to other regional groups. Our data reveal green turtle juveniles and adults forage at Palmyra throughout the year, and were most commonly sighted along the southern flats, where algal food resources were also observed. Most of the turtles examined (n = 41) had good body weights (range: 7.2 - 94.2 kg) and sizes (range: 39.2 - 91.5 cm straight carapace length). Although most were active, four turtles were in relatively poor body condition. We did not*

detect tumors, including those suggestive of fibropapillomatosis, a serious disease reaching epidemic proportions elsewhere. In contrast to populations under significant human pressure, dead turtles rarely strand at Palmyra, and all observed serious injuries appeared to be associated with shark interactions. Our next steps will be to continue investigating the health of these turtles, focusing on hematology, parasitism, and other infections. Contaminants are of interest due to possible plans to restore the lagoon system, with the potential to release pollutants left by previous inhabitants including the U.S. Military. Because highly migratory turtles protected at Palmyra may face health threats and mortality when moving to other localities, we also report genetic results ( $n = 41$ ) indicating this is a mixed-stock drawn from various regional nesting areas. The data will be key in devising a management plan for sea turtles at Palmyra, and advances understanding of population dynamics and health.

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harbor a greater diversity of viruses due to evolutionary co-divergence of hosts and pathogens; 2) species with larger colony sizes will harbor more viruses due to an increased probability of viral establishment and enzootic persistence in larger populations. Our dataset was limited to 30 bat species with data available for population genetic structure and viral diversity. Most of these bat species had only 1-4 associated viruses, but a few bats had multiple viral associations. We ran Pearson product moment correlations and general linear models to evaluate univariate and multivariate effect, respectively. As hypothesized, we found a trend of increased viral diversity in species with stronger population structure (higher  $F_{ST}$ ), and increased viral diversity with larger colony sizes. The general linear model with colony size and  $F_{ST}$  was significant and explained a quarter of the variation in the viral diversity data. This study is the first, to our knowledge, to link population genetics and demographics with emerging infectious disease across an entire order of animals. Our results highlight the importance of host ecology and evolution in understanding viral diversity. It will be interesting to see if these trends hold true as population genetic and viral surveillance data accumulate for other bat species—this may lead to a predictive framework to target the discovery of novel, zoonotic pathogens in wildlife.

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**CORRELATES OF VIRAL DIVERSITY IN BATS**

**H**istoric and contemporary host evolutionary dynamics have profound impacts on viral diversity, virulence, and associated disease emergence. Bats have been recognized as natural reservoirs for a diversity of emerging viral pathogens, and are unique among mammals in their vagility and potential for long distance dispersal. We compiled data from the literature on host population genetic structure ( $F$ -statistics), population size, and viral diversity for the order Chiroptera to test two hypotheses: 1) species with more structured populations will

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**SURPRISES IN THE CLIMATE-MALARIA LINK IN THE BRAZILIAN AMAZON**

**G**lobal climatic changes are altering patterns of temperature and precipitation, potentially affecting regions of malaria transmission. The links between changing precipitation and malaria, however, are not well understood, although previous studies have made general predictions of increasing malaria with increasing precipitation. To understand how land use practices may alter malaria patterns in Brazil's Legal Amazon Basin (5.1 million km<sup>2</sup>) we present an analysis of monthly county (n=755) malaria case data and monthly precipitation patterns between 1996 and 1999. Climate data originated from the CRU TS 2.1 half-degree grid resolution climate data set, which globally interpolates station data into monthly grids. We present a hierarchical (random coefficients) log-linear Poisson model relating malaria incidence to precipitation. We also determine the extent of open water and wetlands by using 100 m x 100 m maps from the JERS-1 Synthetic Aperture Radar satellite and calculate the percentage of maximum inundatable open water and wetland coverage in each county. 1.9 million malaria cases are reported by Brazil's Ministry of Health for this period and we find that the seasonal relationship between precipitation and malaria can change depending on the underlying landscape. Regions with few wetlands show a positive seasonal relationship between precipitation and malaria, while areas of high wetlands show a negative seasonal relationship. This result shows that the links between climate

and malaria are more complex than previously believed, and must take into account regional ecological characteristics.

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**URBAN EXPLOITATION AND EPIZOOTIOLOGY OF BLOOD AND GASTROINTESTINAL PARASITES IN THREE VULNERABLE FRESHWATER TURTLE SPECIES IN THE PERUVIAN AMAZONIA**

**W**e studied natural populations of three vulnerable species of freshwater turtles (*Podocnemis expansa*, *Podocnemis sextuberculata*, and *Podocnemis unifilis*) in order to identify epizootiological patterns related to their proximity to urban areas. We examined the physical conditions, collected biometric information and obtained blood, skin and/or muscle biopsies from animals traded in Iquitos; the largest city in the Peruvian Amazon, and captured near rural communities settled along one of the main rivers connecting the city with the Pacaya-Samiria National Reserve (PSNR). This project provides the first baseline hematological parameters (a complete characterization of blood cells of each turtle species,

and total and differential quantification of erythrocyte and leukocyte cells) for evaluating the health status of these species in the wild. We have identified at least two different types of blood parasites: hemogregarines and a second lineage of apicomplexans, previously classified as *Haemoproteus*, but which genetic data revealed to be a new lineage of malaria parasites, sister to those in the genus *Plasmodium*. We have also quantified and partially identified helminth parasites found in the whole gastrointestinal system of 15 *P. unifilis* and 10 *P. expansa* specimens, including nematodes and trematodes. In both species, we found that each section of their gastrointestinal systems (stomach, large and small intestine) have different parasite communities. We are currently correlating hematological parameters with blood and gastrointestinal parasites to detect diseases and analyze if the variables studied show a geographic distribution. The results of this study will be relevant for detecting local and regional epizootiological patterns around urban areas and dispersion of wildlife diseases due to rural-urban trade. This information will provide criteria for implementing appropriate conservation measures for these and other Amazonian species.

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**ANIMALS AS SENTINELS FOR HUMAN LEAD  
 EXPOSURE: TWO CASE REPORTS**

*Because humans and nonhuman animals often share the same environment, there can be concurrent exposure to toxic and infectious agents. As a result, the use of domestic animals as sentinels for these agents is a promising tool. Here we present two cases illustrating exposure of both humans and animals to lead contamination in their environments. Nine dogs in the first case study were removed from a site near a battery plant known to have high soil lead concentrations. Dogs had elevated blood lead concentrations ranging from 12.38 µg/dL to 41.52 µg/dL, though none had clinical signs of toxicosis. The dog owner also had teenage children with access to the contaminated yard. A second case occurred at a farm where cattle deaths were determined to have been caused by lead poisoning based on elevated tissue lead concentrations. Elevated blood lead concentrations were detected in the remaining cattle, a dog, a cat, and a pregnant woman living on the farm. The range of blood lead concentrations in the domestic animals was 8.42 µg/dL (cat) to 85.41 (calf), though clinical signs of lead poisoning were not apparent in these animals. Further testing revealed the source of lead to be paint in the barn and home. Household dogs and cats have been used as sentinels for lead poisoning in humans and may be particularly useful in determining risk of exposure for children. Cattle may also act as a sentinel species for environmental lead contamination.*

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**CORAL YELLOW BAND DISEASE: RECENT INFECTIONS IN THE INDO-PACIFIC LIKELY TO FOLLOW DEVASTATING TREND IN THE CARIBBEAN**

**C**oral Yellow Band disease (YBD) is ubiquitous on Caribbean coral reefs and has had devastating impacts on major reef-building *Montastraea* spp. colonies. Recent data from Bonaire, Netherlands Antilles reveals high frequency of yellow band lesions (86%), similar to rates of infection in the late 1990s (91%). Over the past 10 years, the disease has spread across entire colonies and to adjacent colonies leaving behind increased areas of denuded skeleton. Similar lesions were recently found in the Indo-Pacific on *Diploastrea heliopora*, *Herpolitha* spp. and *Fungia* spp. though occurrence was less frequent. Bacterial isolates were taken from diseased Indo-Pacific corals and inoculated on live Caribbean *Montastraea faveolata* fragments in aquaria. The inoculation experiments resulted in the formation of yellow band lesions at 26°C, which became more virulent as water temperatures were increased. These experiments confirm that the disease is spreading to Pacific coral genera and that corals do not need to be under thermal stress to become infected with YBD. Given projected global temperatures to be on the rise, corals in the Indo-Pacific are likely to follow the same trend as corals in the Caribbean towards higher rates of YBD infection with great loss of biomass.

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**PREVALENCE OF RABIES ANTIBODIES IN TROPICAL BAT COMMUNITIES IN FRAGMENTED LANDSCAPES IN PUEBLA, MEXICO**

**H**abitat loss and fragmentation have caused biodiversity loss, changes in species assemblages, and changes in the prevalence of infectious diseases such as rabies. Rabies virus has been isolated from different species of bats. However, little is known about its transmission dynamics and maintenance mechanisms in bat communities. The aim of this study was to investigate the effects of habitat loss and fragmentation on species assemblages and rabies prevalence in bat communities in different habitat types in fragmented landscapes in Puebla, Mexico. We compared bat diversity and rabies antibody prevalence in three habitat types (forest, edges, and pastures) in large, medium, and small forest fragments. We have obtained blood samples from 74 bats belonging to 4 genera and 17 species and were analyzed by the immunoenzymatic test ELI-Rab at the National Center of Veterinary Microbiology. Species diversity was higher in grasslands (0.89 Simpson index), followed by forested areas (0.87) and edges (0.82). *Sturnira lilium* was the most common captured species in forested areas (28%) and edges (38%) while *Sturnira ludovici* dominated in grasslands (19%). Overall rabies seroprevalence was 82% (60/74). Antibody prevalence at edge sites was 81% followed by grasslands (80%) and forested areas (68%). The high

seroprevalence indicates that rabies virus is endemic in these bat communities and that these species are refractory or able to recover from rabies virus infection. Further studies are needed to understand the role of each species in viral maintenance. At this local spatial scale, our study concludes that the ecosystem is highly homogeneous. Further studies are needed to know the effects of the habitat loss and fragmentation on the bat community assemblages and on the infection dynamics in tropical areas where agricultural activities are established.

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**REPRODUCTIVE STATUS AND HEALTH EVALUATION OF ENDANGERED FORAGING LOGGERHEAD SEA TURTLES AT BAJA CALIFORNIA SUR, MEXICO**

*The critically endangered North Pacific loggerhead turtle (Caretta caretta) nests exclusively in Japan, and juveniles undertake developmental migrations that can last several decades and span the entire Pacific. Juvenile loggerheads*

*aggregate in the rich waters of Baja California Sur, Mexico (BCS), apparently to forage their way to maturity and to fuel their return migration to Japan, where they are thought to remain through adulthood. Because hundreds of loggerheads are accidentally killed in small-scale fisheries along the BCS coast annually, it is essential to verify key life history traits of the BCS foraging population to evaluate the demographic effects of this bycatch mortality. Particularly, the health status of this population has never been addressed. This project encompasses three main goals, which are: i) developing a health assessment of the North Pacific loggerhead population and ii) assessing the reproductive status and sex ratio of individuals caught and stranded and iii) engaging local fishers and families in our conservation research. We conducted fieldwork during the summer of 2008, and conducted 20 necropsies of stranded and bycatch turtles, and collected 15 gonad samples for a complete reproductive assessment. Also, we conducted physical examinations and collected blood samples from juvenile turtles offshore from Playa San Lázaro, BCS. All the turtles examined were active, had normal body weight, were in good overall condition, and showed no fibropapillomas, lesions, or injuries. Preliminary hematological characteristics, including packed cell volume, total protein, and leukocyte counts are presented and compared to available data for loggerhead sea turtles. Results on the gonad assessment showed that more than 90% of the individuals were females, and were juveniles and subadults (reproductively immature). Our preliminary results suggest that this represents a healthy juvenile population, that the observed high mortality is unlikely to be the result of disease and may therefore be due to the high fishing pressure in the area.*

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### IMPACT OF HEMIPARASITE ON TREES OF GOOSEBERRY AND LIVELIHOODS IN BILIGIRI RANGASWAMY TEMPLE WILDLIFE SANCTUARY, SOUTH INDIA

**N**on-timber forest products provide livelihoods for millions of forest dwellers. Soliga indigenous community in Biligiri Rangaswamy Temple Wildlife Sanctuary earn 30-50% cash income from non-timber forest products (NTFPs). More than 40% of this income is derived from fruits of Gooseberry (*Phyllanthus* spp.) alone. An average of 486 tons of fruits is harvested by the Soligas every year. Gooseberry trees are commonly infected by a hemiparasite (*Taxillus tomentosus*) that causes considerable damage leading to mortality of the host tree. My studies have shown that 54% of the trees infected with hemiparasite die. The objectives of the study were to understand the impact of hemiparasite on fruit production and growth of the trees. Of the 350 trees sampled, 100 were infested by hemiparasites, 150 were free of hemiparasites, and hemiparasites were physically removed from 100 trees. All trees were monitored for four years by counting fruit loads and general condition. Results show that hemiparasites had a negative impact on fruit production, tree growth, and fruit and seed weight. Mortality rate was high in trees infected with hemiparasites. Removal of hemiparasites increased growth rate and survival. Soligas believe that hemiparasite densities have increased due to the state prescribed control of fire, which in the past was traditionally used to control hemiparasites. In addition to hemiparasites and fire control, invasive species such as *Lantana camara* are also negatively impacting regeneration of trees and health of forests. Climate change is likely to intensify these effects. However, the health of Gooseberry trees and of forest is directly linked with the economic well being of Soligas. The sanctuary is a part of the Western Ghats biodiversity hotspot. Thus the health of forests and the well being of Soligas are critical to the success of global efforts to conserve biodiversity and cultural diversity.

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### CLIMATE CHANGE CHALLENGES TO ARCTIC HEALTH: THE CASE OF THE NORTHERN PEOPLES OF YAKUTIA

**R**esearch of communities of indigenous people of Yakutia (*Chukchees, Yukaghirs, Evens, Evenkis*) have shown that climate change creates new threats to the health of these populations. Here I summarize the main impacts of global climate change on the health of these northern peoples:

1. Increased death rate due to increase of natural cataclysms: flooding, strong heat, sharp pressure differences. These include sunstroke, work-related injuries in fishermen and hunters and aggravation of concurrent medical conditions.
2. Deterioration of water quality.
3. Deterioration of traditional food sources due to increases in parasitic loads in fish and game and to deteriorating conditions for storage.
4. Changes in the prevalence of parasites and infectious diseases.
5. Increased probability of disease resulting from the washout of cattle burial grounds.
6. Changes in the distribution on the north of new kinds of trees and grassy plants, which can increase the prevalence of outdoor allergies.
7. Deterioration of conditions for duly rendering appropriate medical care in these remote locations.

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**GENETIC VARIATION IN RAGWEED RESPONSE TO  
 GLOBAL CHANGE: SOMETHING TO SNEEZE AT?**

*Changes in the dynamics of allergy-causing plants could have critical public health impacts in future climate scenarios, yet we know very little about their future genetic structure and performance. We tested whether elevated levels of atmospheric CO<sub>2</sub> would alter the genetic makeup of common ragweed (Ambrosia artemisiifolia L), a plant species that has shown dramatic increases in pollen output under future climate conditions and is the leading cause of allergic airway disease in North America. We demonstrate for the first time that elevated atmospheric CO<sub>2</sub> can reverse the dominance structure of genotypes within ragweed populations. We use functional relationship models to show that ragweed genotypes that are competitively suppressed in size within ambient conditions respond best to elevated CO<sub>2</sub> (and vice versa). These normally suppressed plants also boost their reproductive allocation to that of dominants in high CO<sub>2</sub>. Extending our work to an evolutionary context, we further show that the strength of natural selection on size is dramatically reduced at elevated CO<sub>2</sub>, because an individual's position within the stand size hierarchy becomes less important for reproductive success. Thus, evolution in a changing world could favor genotypes that differ substantially from those that are most abundant today. New arrays of ragweed genotypes may therefore dominate future*

*landscapes, with unknown effects on ragweed's status as a noxious, highly allergenic weed.*

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**ARSENIC IN DRINKING WATER, SOURCES AND  
 HEALTH EFFECTS**

*Over the last three decades, elevated concentrations (> 10µg/L) of arsenic have been detected in drinking water in many countries all over the world. Arsenic is a fairly common in the Earth's crust and is mobilized easily under certain natural conditions, e.g. in geothermal systems or organic rich deltaic environments. Landfills and former herbicide and pesticide factories are also known sources of arsenic. Chronic exposure to elevated arsenic levels causes skin lesions, several types of cancer, cardiovascular disease, and lowers the intellectual abilities of children. Columbia University has been conducting a large research project on the geochemistry, health effects and remediation of arsenic for almost 10 years, funded by the National Institute of Environmental Health's Superfund Basic Research Program. Our efforts have been focused on sites with natural and anthropogenic sources of*



arsenic in Bangladesh, New England, and New Jersey. We have studied the geochemical processes that mobilize arsenic, how arsenic affects human cells on the molecular level, health outcomes due to arsenic exposure and ways how to reduce concentrations, human exposure and improve human health. Our presentation provides an overview of the global arsenic problem and a few examples of major findings based on our research including the following: In Bangladesh, naturally occurring arsenic is mobilized under reducing conditions and increases linearly with groundwater age up to about 40 years. This pattern can be explained by either a variable removal of arsenic from the sediments or a slow mobilization rate. Deeper (>30-100m) groundwater, typically occurring in Pleistocene aquifers tends to have levels of dissolved arsenic concentrations below the drinking water standard. On the health side, studies showed a relationship between the occurrence of skin lesions and arsenic levels. Childhood intelligence was found to correlate negatively with arsenic exposure. In order to reduce arsenic levels in drinking water in Bangladesh, deep, low-arsenic community wells were installed in our research area and a detectable decrease of urinary As was shown, indicating a successful exposure reduction.

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**CAN ECOLOGICAL NICHE MODELING OF HOSTS PREDICT A PARASITE'S DISTRIBUTION?**

*E*cological niche modeling (ENM) is an increasingly used tool in biogeography and ecology that incorporates species' occurrences and environmental variables to estimate species' distributions. We examine the usefulness of incorporating biotic variables into an ENM of the cestode *Echinococcus multilocularis*, which causes human alveolar hydatid disease. This parasite has intermediate (mice and voles) and definitive (canids) hosts and is Holarctic in distribution. In North America it has recently spread from arctic tundra into the prairies of Midwestern North America, although the modern distribution is disjunct with no parasites in boreal forest habitat. We examine *E. multilocularis* ENMs using only climate data, and compare these with ENMs of definitive hosts and ENMs of intermediate and definitive hosts. We found that climate-only ENMs of *E. multilocularis* did not show the expected disjunct distribution. However, ENMs of host distribution appear to be better predictors of *E. multilocularis* distribution. Thus, although ENMs usually incorporate only environmental variables, using biotic variables in some cases may greatly improve predictions of species' distributions. This example also highlights the utility of ENM in better understanding the ecology of parasites and pathogens affecting human health.

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