

## RESEARCH STATEMENT

Ravinder N. M. Sehgal

### INTRODUCTION

My research examines the effects of infectious diseases on the ecology and evolution of birds. Birds are susceptible to similar diseases as humans, but are not subject to the complexities of human socio-economic and cultural patterns. Thus they provide a superior system to directly determine how ecological changes such as deforestation and habitat fragmentation affect the prevalence, and spread of disease. To study these ecological parameters which underlie the recent outbreaks of infectious diseases threatening both birds and humans, I am employing a broad multidisciplinary approach that takes advantage of my expertise in molecular and cellular biology, instrumentation, and fieldwork, as well as scientific collaborations which I have established as an Assistant Professor at San Francisco State University.

As a graduate student at the University of California, San Francisco, I learned the fundamentals of genetics, biochemistry, molecular biology and cell biology. I have also worked in the private sector developing instrumentation for the analysis of blood diseases. As a postdoctoral fellow, I embarked on the challenging path of study that I will pursue for the remainder of my scientific career; the study of infectious diseases in birds. I took advantage of my skills in molecular biology to develop methodologies for the detection and analysis of avian blood parasites. Using these methods, I showed that avian trypanosomes appear to exhibit no host or geographic specificity. On the other hand, infectious nematode microfilariae appear to be relatively host-specific. For these studies, I did extensive fieldwork in Africa, mist-netting and taking blood and morphological measurements of rainforest birds. The intention of this work was to develop as an evolutionary ecologist, studying the interrelationships of disease, natural hosts and their environments. My laboratory skills and knowledge of molecular mechanisms give me a rare perspective in the fields of ecology and evolutionary biology. In addition, the contacts that I developed over the years have yielded fruitful collaborations with well-known scientists. For example, I work closely with Dr. Gediminas Valkiūnas, of Vilnius University; the author of *Avian Malaria Parasites and other Haemosporidia*. With other scientists, notably Dr. Tom Smith at the Center for Tropical Research at UCLA, I work to form a multidisciplinary team that will answer fundamental questions regarding the effects of infectious diseases on the ecology and evolution of birds.

My *long-term goal* is to understand how ecological changes affect the prevalence and evolution of avian diseases, and use this information to make informed decisions pertinent to the conservation of biodiversity. The *objectives* of my current work are to determine the prevalence, and evolutionary relationships of blood-borne diseases in populations of avian hosts that range from small to large, disturbed to pristine and across a variety of environmental gradients. *My central hypothesis is that higher variance exists in the prevalence of infectious diseases among bird populations in forest fragments than populations in larger contiguous forests, and that ground cover changes result in an increase in the spread of disease.* The rationale for this research is that once we ascertain basic ecological factors that contribute to the spread of disease, we shall be able to predict how future land use changes may affect disease outbreaks; and thus gain a better understanding of how anthropogenic changes affect disease.

## RESEARCH

### Africa

For at least the next two years, with funds I have received from the NSF-NIH program in Ecology of Infectious Diseases, I will continue to collaborate with scientists at the Center for Tropical Research at UCLA<sup>1</sup>. Over the past 20 years, a unique set of more than 15000 individual blood and feather samples have been collected from over 200 rainforest bird species in a variety of habitats across Cameroon, Equatorial Guinea, the Ivory Coast and Uganda. Sampling sites have included locations in the ecotone (the transitional region between the contiguous rainforest and savanna), in primary and secondary rainforests, and in sites experiencing intensive logging. Significantly, the samples include sites both before and after degradation, permitting a unique examination into the direct effects of human induced habitat alterations. I use the complementary techniques of blood smear analysis, established PCR-based detection methods, and molecular phylogenetics, to study the pathogens that cause avian malaria, trypanosomiasis, and filariasis. In conjunction with my collaborators, we employ satellite imagery data to assess the ecological correlates of disease prevalence. These data will provide information about changes in temperature, rainfall, forest fragmentation and greenness over a longitudinal time frame, as well as data for cross-sectional comparisons between habitat types.

We have four specific objectives:

1. *Determine how pathogen prevalence changes over time within differing rainforest habitats, some of which have remained unaltered, and some of which have gone through habitat conversion.*

Based on our previous work, our working hypothesis is that where forest fragment sizes have decreased, we expect to find more variability in pathogen prevalence, and higher variance in infection rates, as compared to larger forest fragments. Because our sampling spans the last 15 years it is possible to compare sites sampled in 1990 with those of today.

2. *Determine the host- and habitat- specificities of blood-borne pathogens to assess the degrees of host-switching that may occur in differing habitats.*

We know that different pathogens have differing degrees of host specificity. We postulate that host switching may occur more readily in small forest fragments or otherwise disturbed habitats.

3. *Determine how the presence of parasitic diseases affects the feather coloration of birds.*

Theories of sexual selection predict that the presence of disease can affect feather brightness. We use reflectance spectrophotometry to measure variation in feather coloration among sites and between infected and uninfected birds.

4. *Determine, using remote sensing data, the environmental variables that best correlate with pathogen prevalence, and develop models that will aid in the prediction of how ecological change will affect disease prevalence and the likelihood of host switching.*

We predict that certain environmental variables derived from remote sensing data will correlate with our disease prevalence data. We employ sophisticated computer programs such as MaxEnt, to build predictive models.

---

<sup>1</sup> <http://www.ioe.ucla.edu/CTR>

This work is novel in that I study wildlife diseases over a broad scale, in a region of the world undergoing rapid deforestation. The data provided by remote sensing allow us to make comparisons over a period of more than a decade, and will establish which ecological factors correlate with disease prevalence. These studies will answer fundamental questions regarding the role of infectious diseases in the ecology and evolution of bird populations.

### California Raptors

I have initiated a project studying the infectious diseases in birds of prey. Through my collaborations with the Golden Gate Raptor Observatory, the Lindsay Wildlife Museum, and the UC Davis Raptor Center I have amassed over 2000 blood samples from individual raptors, mostly hawks of the genera *Buteo* and *Accipiter*. Using PCR, and DNA sequencing, I am studying the interrelationships among the blood parasites of these birds, with the intention to discern how disease can affect the migratory patterns of birds. We have preliminary evidence that infection with parasites delays the onset of migration of the Red-tailed Hawk, *Buteo jamaicensis*. Thus, infection can affect the behavior of the birds. I am also testing hypotheses regarding the spread of parasitic blood parasites from the Old World to the New World. I am presently expanding this project to include raptor samples from Europe, Africa, and Australia. In addition, we are studying parasites of owls, including the threatened Spotted owl (*Strix occidentalis*). We have found that these owls are threatened not only by habitat loss, but also are prone to parasitic infections by strains found in other sympatric owl species.

In collaboration with Dr. Gediminas Valkiūnas, I have developed a project linking traditional parasitology with molecular methodologies. His laboratory houses experts in the identification of avian parasites on thin blood smears. With molecular methods, we can link established species identifications with DNA lineages, and also use phylogenetic approaches to characterize genetic bounds for morphospecies. Identification using morphological criteria is extremely time-consuming and requires a high level of skill. We work with scientists developing a worldwide database that links morphological species with their corresponding DNA sequences to allow for more rapid and precise analyses.

The definition of an emerging infectious disease is one that undergoes an increase in geographical range, an increase in host range, and/or an increase in prevalence. With the research described above, I will explore some of the factors that may contribute to the spread of disease following human induced land use change. However, there are several areas of research that I would like to pursue that would complement these studies. For example, in many cases, there is little information on what insect vectors transmit the avian blood parasites. I would like to understand how host specificity is maintained in certain host-parasite relationships. Are the vectors also host specific, and if not, what are the mechanisms (most likely immunological) that preclude multiple parasite lineages in a single host?

The questions and projects described above will entail years of rigorous research. Several of the projects are suitable for inclusion of undergraduate research. Others will require collaborations between graduate students, and highly specialized scientists. In all, the field of evolutionary ecology with regard to infectious diseases is in its infancy, and I plan to use a synthesis of traditional and modern methodologies to make strides in answering fundamental questions that will impact biomedical research and conservation policy.