

## TRICHOMONAS SPECIES IN WILDLIFE AND THE ROLE OF PARASITES AND OTHER PATHOGENS IN UNDERSTANDING AVIAN MIGRATION

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Very little is known of the key principles that govern pathogen emergence and maintenance and the legitimate role pathogens may play as natural accelerants of diversity and change in ecosystems. The aim of this PhD project is to assess pathogen and host diversity in migratory and sedentary populations of the pied imperial pigeon (*Ducula bicolor*) as a model to explain key principles that govern pathogen emergence, survival and diversity in spatially isolated versus open, interconnected, ecosystems. The project will take a theoretical and practical approach to show how knowledge of the pathogenic microbial organisms and endoparasites of a host species can provide and explain life history information about that host.

Most of the research into the ecological effects of host:parasite relationships has been done on metazoan or protozoan parasites with little consideration to viral, bacterial or fungal infectious agents. Here it is proposed to capitalise on the unusually extensive knowledge base of *Columbiforme* pathogens to explain how the diversity and prevalence of pathogens impacts on the ecology of migratory pied imperial pigeons. The project aims to detect and genetically analyse key, well characterised pigeon pathogens, namely *Trichomonas gallinae*,<sup>7,11-13,21,22,29,30,33-35</sup> *Haemoproteus columbae*,<sup>2,6,16,17,19,23,25,31,32</sup> *Enterococcus columbae*,<sup>5,15,24,27</sup> *Columbid circovirus*<sup>1,20,26,36</sup> and *Chlamydophila psittaci*<sup>3,4,37</sup> in oropharyngeal and cloacal swabs as well as blood samples collected from pied imperial pigeons. This range of infectious agents provides a spectrum of relatively well host-adapted organisms that should behave as independent genetic markers of pathogen dispersal. Particular emphasis will be placed on better understanding the phylogeography of Trichomonads, because the prevalence of infection is likely to be high and this will enable sensitive analysis of genetic information.

### TRICHOMONAS SPP. AS A SIGNATURE TOOL

*T. gallinae* is host adapted to *Columbiformes* whereby it resides in the oropharynx and crop of infected but otherwise clinically normal adults. It is capable of causing severe disease in other bird species including predatory raptors which are very susceptible to the infection. Transmission of trichomonads between pigeons is by direct contact with oral secretions.

Trichomoniasis is one of the earliest diseases recognised in birds, having been described in literature initially as a disease of birds of prey. While the metamonad protozoan responsible for this disease, *Trichomonas gallinae*, is still observed to cause disease in a range of wild birds of prey, it has come to be associated more with the pigeons and doves (Order Columbiformes) which appear to be its natural host. *T. gallinae* is found worldwide where pigeons and doves occur. It has been described from many species of Columbiformes of various genera. Most significantly it has been reported from species such as the Mauritius Pink Pigeon (*Columba mayeri*) which are threatened or endangered.

This organism inhabits the upper gastrointestinal tract, especially the oral cavity, oesophagus and the crop and in the Rock Dove or domestic pigeon (*Columba livia*), typically does not cause lesions. This is likely to be the case in other columbid species. When it does cause clinical disease, this is characterised by the development of caseous stomatitis, ingluvitis or oesophagitis, with lesions occasionally penetrating the epithelium into the deeper soft tissues of these regions, especially the head. In severe cases, most commonly seen in young birds, these lesions can result in loss of condition and death. Experimental trials in *C. livia* and *Patagioenas fasciata*, the Band-tailed Pigeon, the development of clinical signs has been associated with infection with particular strains of *T. gallinae*. These trials also experimentally demonstrated the potential for *T. gallinae* to cause acute mortalities in columbiform birds.

The potential for trichomoniasis to cause declines in wild dove or pigeon populations or to confound captive breeding programs has been documented in several species, most notably the endangered Mauritius Pink Pigeon,<sup>8-10,21</sup> however the mechanisms for emergence of this apparently widely distributed organism as a pathogen of significance in particular species is poorly understood.

## MARKERS OF DISEASE EMERGENCE

Disease emergence in wildlife is a significant threat to biodiversity, agriculture and human health. Examples include emerging infectious diseases such as chytridiomycosis,<sup>14</sup> pilchard herpesvirus and the henipaviruses, which amongst many others have attracted international attention. Disease emergence is commonly associated with a change in connectivity between and within populations of organisms. This can include the direct or indirect connection or fragmentation of populations through mechanisms such as introduction and movement of species and changed population ecology.

The recent expansion of highly pathogenic H<sub>5</sub>N<sub>1</sub> Avian Influenza across Eurasia and Africa has illustrated that there is a need to understand the dynamics of infectious disease emergence, transmission and maintenance in migrating wild birds.

Tools for assessing population connectivity in migratory birds have long been in use. Methods for locating individual birds in space and time such as ring banding, radio and satellite telemetry are popular, as is light stable isotope analysis which can provide an historical account of individual bird movement. Genetic analytical tools such as microsatellite analysis of bird populations help to demonstrate reproductive connectivity between populations. However, these tools do not address levels of connectivity relevant to disease transmission (such as the sharing of food or water resources for example), which is of great relevance to understanding the emergence and maintenance of disease in populations. These complex population interactions are very hard to elucidate using traditional ecological methods.

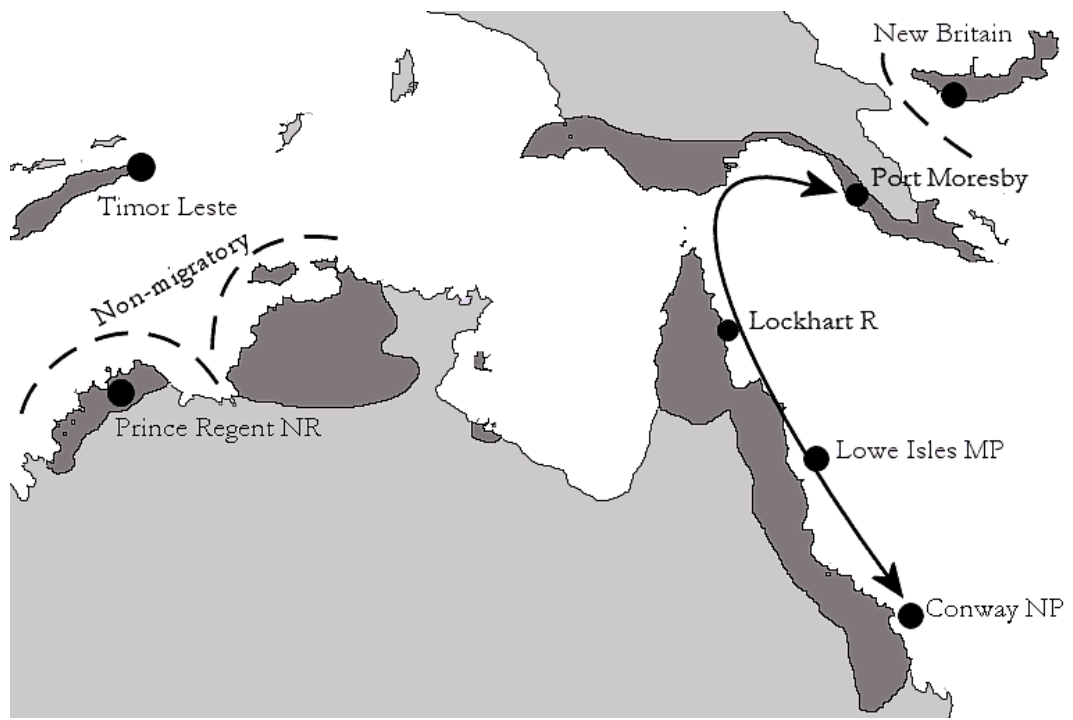
Recent investigation of *Helicobacter* spp in people<sup>18,28</sup> has demonstrated that genetic analysis of infectious organisms can provide an understanding of historical host movement and connectivity. There is a need to investigate whether the phylogenetic analysis of multiple infectious organisms within a host can provide finer scale information on host population connectivity and to validate this tool as a method for investigating such connectivity in migratory birds.

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**Known distribution and presumed migration corridors for the pied imperial pigeon**