



Australian Government
Department of Agriculture,
Fisheries and Forestry



Charles Sturt
University



Industry &
Investment

AVIAN MIGRATION AND MOVEMENT OF PATHOGENS IN THE AUSTRALO-PAPUAN CONTEXT

PROJECT SUMMARY

Background

Highly Pathogenic Avian Influenza (HPAI) has been considered, and remains a threat to domestic animal and human health globally; and its introduction to Australia is a key biosecurity concern. There is increasing evidence and acceptance within the scientific community that the movement of migratory birds likely has played a role in the dissemination of H5N1 HPAI which arose in Asia, arguably the most important strain of HPAI in over half a century. Lack of knowledge on the ecology and connectivity of populations of migrating birds has been identified as a key deficiency hindering refined modelling and thus meaningful recommendations for efficient risk mitigation by most authors examining the epidemiology of the recent epidemic.

Despite recent advances in both field ecology and spatial analysis there remains a significant challenge in the assessment of connectivity between populations of migratory birds. Satellite telemetry, radio telemetry, light stable isotope ratio analysis and phylogenetic analysis are the cornerstones of modern migratory ecology. These techniques, while of increasing value in the analysis of movements of populations and their reproductive connectivity (relatedness within and between populations), only indirectly inform us about connectivity as it relates to the **transmission of infectious organisms**, which clearly is the most important ecological characteristic when considering the distribution of novel pathogens.

The high resolution phylogenetic analysis of commensal organisms in a host species is a theoretically and practically promising method for the determination of relevant population connectivity. Studies probing deep evolutionary questions of population movements have been highly informative in humans (Moodley et al, 2009, Science), while the use of phylogenetics in epidemiological investigations have provided evidence for unexpected inter- and intraspecific connectivity (eg *Trypanosoma cruzi* in Latin America, Hendra and Nipah viruses in Australia and Malaysia, SARS in south-east Asia). However the use of this technique to provide **pre-emptive** knowledge of pathogen transmission risk between populations has not been validated. This is unfortunate as, pre-emptive risk analysis will promote a more efficient and effective application of biosecurity-related surveillance and management particularly where resources must be spread over a large area.

This project directly addresses this technological deficiency, by employing the strengths of team members in epidemiology, molecular genetics and spatial analysis to test an avian migratory model, with the objective of validating the technique to

allow it's more general application by ecologists and other researchers involved in the biosecurity of Australia.

Objectives of this project:

- determine population connectivity in an Australian migrant bird species through the analysis of commensal infectious organism population structure using phylogenetics
- determine the key life history characteristics of infectious organisms which promote their use in the determination of population connectivity in migratory bird populations
- provide a model for further investigations into population connectivity in migrating birds in Australasia

The activities of the project include the trapping of birds of a particular migratory species at sites across northern Australia and in Papua New Guinea, East Timor and Indonesia and the sampling, marking and release of these birds. Captured DNA from samples will be subjected to molecular techniques designed to produce data of sufficient detail to allow sophisticated phylogenetic analysis of six very different infectious organisms. Comparison of these population structures with the distribution and population structure of the host will be performed to identify key connections between populations which permit the movement of infectious organisms.

In summary the project will develop and refine technologies for the survey, containment and control of wildlife diseases, consistent with the control of emergency animal diseases. It will also develop and refine wildlife disease control and surveillance techniques that can be used in an emergency animal disease incident. Through the postgraduate training of a veterinarian in field disease ecology skills it will also significantly add to the national team of trained personnel who are competent to perform roles in wildlife disease control.