



NEWINGTON ARMORY – SYDNEY OLYMPIC PARK
SATURDAY 13 MARCH 2010

The Australian Bird Study Association held its Scientific Day and Annual General Meeting on Saturday 13 March 2010 at Newington Armory in Sydney Olympic Park. The Scientific Day consisted of a series of talks around the theme: “DNA – What secrets does it hold for the study of Australian birds?”. The first speaker was Graham Cam who gave an introduction to genome analysis and outlined the rapid progress that this research field has made and is continuing to make. The talks then progressed into DNA and its impact on the study of birds including systematics, reproduction, relationships and song.

Convener:
Graham Fry
Australian Bird Study Association

ABSTRACTS

Compiled by GRAHAM FRY

The impact of DNA studies on the higher systematics of Australian birds

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The use of DNA-based approaches to the relationships among birds has resulted in major changes to the classifications used only a few decades ago. Starting with the pioneering DNAxDNA hybridisation studies of Charles Sibley and his colleagues and moving on to the ubiquitous use of DNA sequencing, avian systematics was demonstrated to be disproportionately influenced by external morphology. Thorough rearrangements of relationships within several higher avian orders, particularly the Passeriformes, have resulted. Nonetheless, there are still many questions that have not been addressed or that are proving difficult to resolve.

DNA sequences, species, subspecies, what is it all about, and why can it be so hard to get a straight answer from DNA in species-level taxonomy these days?

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The new edition of the Slater Field Guide listed some 25 possible new species of Australian birds, pending taxonomic research. It encouraged birdwatchers to seek these out and see them because taxonomic decisions might eventually be made about whether they are species or subspecies. But who will make those decisions and on what sort of data will they be based? Will the same kind of data sets and taxonomic decision-making processes be used that have for so long dominated species-level bird taxonomy? This talk builds on two premises

related to this question. First is that at some level we all hope(d) even if we didn't say it that there would be some kind of 1:1 correlation between the external phenotype of different bird populations and their DNA-based "tags"; the answer to our taxonomic problems would magically follow from that. Second is that what DNA data have done is taken the way we think about species-level taxonomy, cut it into pieces, thrown the pieces in the air and challenged us to be innovative in how we reassemble them. Third, I explore the premise that the question of whether two or more populations are different species or subspecies of one species is either no longer very interesting or not where the primary biological interest lies. This arises from the observation that DNA data have opened a lens on a whole other way of thinking about these issues as well as what they mean for management and conservation and how science should advise and inform management. Examples in the talk will illustrate these ideas.

From the aviary to the Kimberley: assortative mating for head-colour morph and genetic constraints on reproduction in wild Gouldian Finches

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Historically, investigations into the decline of the endangered Gouldian Finch *Erythrura gouldiae* have predominantly focused on environmental factors such as food availability and habitat disturbances. Recent studies on captive populations have demonstrated that genetic incompatibilities between the different head-colour morphs (black and red) have the potential to constrain reproduction by reducing offspring survival in mixed-morph pairs. The prevalence and strength of such effects in remaining wild populations, however, are not known. By provisioning a free-living Gouldian Finch breeding population with custom-designed nest-boxes, this study has been the first to gain access to offspring and their DNA, and subsequently begin to evaluate these phenomena in the wild. Over a three-year project, we have monitored reproduction and sampled genetic material from over 100 breeding pairs and their offspring from a population in the east Kimberly region of Western Australia. The observational data to date suggest that individuals are pairing and breeding at random with respect to head-colour morph, and that mixed-morph pairs do not suffer the fitness costs that were predicted. However, experience with other avian systems suggests that behaviours such as extra-pair copulation and facultative egg-dumping are likely to be occurring, and could be altering the genetic quality of offspring. The only way we can determine the frequency and effects of these behaviours is to analyse the genetic data for levels of relatedness within identified family groups. Costly genetic effects tend to be compounded in small, isolated populations, such as those experienced by Gouldian Finches today. Understanding how these effects interact with other environmental and demographic effects will allow for a holistic approach to the conservation and management of this species.

What can molecular data tell us about Meliphagoidea: the largest radiation of Australian songbirds?

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DNA analysis can tell us a lot about the evolutionary relationships among Australian songbirds. In turn, to know the relationships opens up interesting questions of trait evolution and species distributions. In this presentation some surprising relationships are uncovered, a past taxonomic error is corrected, and the limits of presently available data and methods are explored.

Song and genetics: crucial connections

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Birdsong is an unique form of communication that is learned rather than inherited. However, there are still many ways in which an individual's genes might affect its capacity to sing. Physiology, growth and development are all factors that are partly determined by genetics but are directly related to singing ability. Population genetics also influence the formation of dialects or local 'accents' in populations. Here I discuss the importance of including genetic data on analyses of song adaptations by introducing a current project investigating the effects of urban noise on song development in the Silvereye *Zosterops lateralis*.