

11. CONSERVATION GENETICS OF MALLEEFOWL

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Abstract

Defining appropriate genetic units for the management of Malleefowl is one of the key objectives of the Malleefowl Recovery Plan. We recently obtained funding from the Australian Research Council's *Linkage Grants Scheme* to examine genetic variation in populations of Malleefowl throughout their range, estimate genetic diversity and isolation, define biologically relevant management units, and assess the risk of extinction. The information will enable us to develop management approaches that incorporate genetic considerations when considering strategies for minimised extinction risk. The project is a collaboration between the Universities of Melbourne and Wisconsin (USA), the South Australian Museum, the South Australian Nature Foundation, the Victorian Department of Sustainability and Environment and the Malleefowl Preservation Group, and will run from 2007 to 2011. We are keen to encourage collaboration and participation from additional participants, in order to maximise the quantity and diversity of genetic material that will be available for analysis.

Introduction

Over time we have become more and more interested in using genetic tools to study either animal behaviour or populations of animals. We have worked mainly on mating systems of birds and recently on conservation genetics of bird species. Malleefowl seem to be one of those groups that are crying out for some sort of genetic study and doing genetic work is a priority that has been identified in the Recovery Plan from the very start. What we want to do today is to advertise what the project is about and to appeal to you to get involved where possible in the project.

Malleefowl Populations Today

As we all know, one of the big problems to do with the conservation of Malleefowl is that their range has contracted and particularly that contraction has had a consequence that populations of Malleefowl are small now and also very isolated. We know that small populations, composed of few individuals, are likely to be vulnerable to reduced genetic variation. That is a problem because inbreeding with closely related individuals, the whole population mating together, can lead to weakened offspring and the population can be weakened through random loss of alleles, which happens over time in any small population. The problem is trying to work out whether or not this is an issue for Malleefowl because we know nothing about genetic variation in Malleefowl populations. The aim of this study, we define, as addressing that gap in our knowledge and trying to contribute something that will be useful for the future national conservation of Malleefowl. So although we are new faces at this particular Forum, we hope very much that by the time the next Forum rolls along in three years time, we shall have been able to do a lot of work on this genetic variation, and will be able to discuss some of these conservation issues with a bit more information about genetics.

So why are these genetic data useful, why are they, we would say, essential to understand what the current status of Malleefowl is? Just to give you some examples of how knowledge of genetic structure could be useful, it will indicate how isolated, for example, populations are from each other. Now we know that populations are geographically isolated and how far they are from each other, but that does not show us how genetically different they are. Genetic structure will allow us to tell how genetically isolated those populations are from each other. We also know that we have reasonably good population sizes for some locations, but just because we have population sizes, that does not actually tell us what the effective population size is, nor does it tell us how many individuals could effectively breed in the population. The genetic aspect will provide us with a window to try to find out whether or not small populations are genetically viable. All this should add to management options. We have talked about examples where in particular locations numbers are going down and where one management option, for example, might be to reintroduce birds from other areas, or eggs from other areas. Now if we do that without any understanding of what the genetic profile is of the birds we are going to reintroduce, we are flying blind when it comes to addressing that genetic problem unless we

know whether or not the birds we are going to introduce are genetically very different, and that might be one of our aims, or genetically very similar and that might be an alternative management strategy. In terms of population management genetic information is likely to be useful in captive breeding programs, in pointing out how we should insert habitat corridors, etc.

There are a few things that make Malleefowl interesting in relation to genetic questions in addition to those general sorts of issues. The recent set of population viability analyses conducted on a whole range of threatened species, 19 species in all, estimated that if you get small populations, populations that number less than a thousand individuals, and there are many Malleefowl populations in that boat, on average it takes about 43 years for those threatened populations to go extinct and that is not counting the effects of potential threats, like foxes and other predators, issues of rainfall and climate. Just by virtue of being a small population, 43 years on average is about what it takes for the population to disappear. That is if there is no inbreeding; if there is inbreeding then that reduces by about 15% to 37 years. Malleefowl have strong site fidelity, they tend to stay in one location. Now the young obviously disperse but that site fidelity does suggest restricted dispersal, so the males have restricted gene flow, and maybe you get quite genetically structured populations that are a bit different between one site and another. The other thing that is interesting to me is that we assume that Malleefowl are monogamous. Having studied the mating systems of a number of different bird species that were all presumed to be monogamous, including things like black swans and fairy wrens, we have to say we are monogamy sceptics. But we think it would be great to use some of these genetic tools to actually find out exactly what the mating system of Malleefowl is, and to show that they are genetically monogamous. Or conversely, if they are not entirely monogamous, but certain males are managing to mate with more than one female, the fact that males are not monogamous is also going to have genetic consequences, because its going to increase genetic drift.

The Project

We are not sure if you are familiar with Australian Research Council Linkage Projects, so we will tell you a little bit about what they are and how they operate. The idea is that these are a set of grants that are set up to try and support collaboration between university and industry partners, and the industry partner can be defined as anything from a Non-Government Organisation, a state organisation, or a community organisation, where there is some kind of mutual benefit because both parties are trying to work towards a particular goal. The idea is that the industry partners, as they are called, make a contribution to the project, and that contribution can be in terms of funding, cash for the project, or an in-kind contribution, supporting the project by helping in various ways, and that the Australian Research Council also provides funding, so that it becomes a value-added set up. This project involves collaboration between three of us, Steve Donnellan at the South Australian Museum, Raoul Mulder, at the University of Melbourne, and Peter Dunn at the University of Wisconsin. You might ask why is the University of Wisconsin, involved in Malleefowl research. Well, the reason is that Peter Dunn has a lot of experience working on prairie chickens in the United States, and prairie chickens are an interesting conservation story. It has a few parallels with the Malleefowl situation, although it is a bit more dire in the case of the prairie chicken, the Illinois population was down to about 50 individuals, Peter led a study that was conducted as an exact parallel to this genetic study, on the prairie chicken, and established priorities for relocations to the point where the prairie chicken in Illinois is now doing really well. That is a good sign and his work is a model for what we might be able to do with Malleefowl. Steve Donnellan at the South Australian Museum has been interested all along in this project, and has started to accumulate a range of genetic material for reference. The industry partners involved so far, and we'd love to have more partners involved in the project, the South Australian Museum, the SA Nature Foundation, the state Department of Environment in Victoria and the Malleefowl Preservation Group.

Let us give you an overview of the four broad goals that the project has. Obviously the first thing we want to do is try and estimate genetic variation across Malleefowl populations in Australia, and our hope is that this will be a national project. It will be a shame if we have to try to focus it in one or other state. That would ignore the fact that Malleefowl do not respect state boundaries, and we want to be able to say something about genetic variation across the range of the species. We shall be using a couple of different genetic markers for estimating mitochondrial or nuclear DNA to find out more about genetic variation. Those markers are useful as a way of being able to work out mating system of Malleefowl. As we mentioned before we should like to find out more about the genetic mating system of Malleefowl. With that information we should then set up a whole series of models that are asked to

look at what are effective populations of Malleefowl, how big the populations should be and how big the gene flow might be between different populations; and how isolated are they from each other genetically. And from there, what we can do is to find biologically relevant management protocols based on that kind of structure. And we shall also try to model at what rate populations might be going extinct, how likely they are to disappear. One of the nice things is that there are Malleefowl samples in a whole range of different museums around the world and we are slowly and systematically going through those collections to get as many samples as we can. That will give us some idea of what genetic variation might have existed in historic populations of Malleefowl. When we look at contemporary populations it is sometimes hard to say whether or not the level of genetic variation we find is relatively low or relatively high. If we can compare what we find in contemporary populations with birds that have been found more than fifty or a hundred years or even longer ago, then that too will give us a window on whether or not there has been a loss of genetic variation in particular parts for a very long time. In terms of our sampling what we have at the moment is what has been collected at the South Australian Museum, about 210 tissue samples, that come from 34 sites, a couple in New South Wales, mostly sites in South Australia, a few in Victoria and Western Australia. Obviously we are hoping that this is a tiny sub-set of the range that we are going to find. One of the useful things about the monitoring network that has been set up, is that it is an important resource in terms of trying to get genetic samples from many different sites across the range of Malleefowl. If we had done the project five years ago we do not think we should have been in nearly the same position in terms of trying to find out the genetic variation that we are in now with the monitoring set up. If you think that you might be able to be involved in helping to gather samples then we would like to hear from you.

The great thing about doing DNA analyses is that there are a lot of very useful samples that we can get from material that is easy to collect and not invasive. For example feathers that are found on mounds are a great source of DNA. We have talked to a number of people at the meeting already who have revealed to me that they have treasure troves of bags of feathers, individually marked and categorised by mounds; that is a gold-mine of information. Feathers are easy to collect and great for DNA analysis if just wrapped in an envelope. Obviously where people are involved in captive breeding programs, for example zoos, it might be possible to get a blood sample from a captive bird or chick that can be stored in alcohol. And even road-kills or decayed left over fox kills that you might find, still can provide us with useful DNA if you get a bit of muscle from them. So it is early days; we literally only just found out that we have got funding for this project and we shall be working on getting a systematic approach to the collection of samples. That involves sending out information sheets that tell people exactly what we want, to try to get information, to integrate into the monitoring system, and to set up kits for people to use for the collection of samples. The first step for you is to get in touch with us and we shall try and get as many people as possible too. We are very open to any ideas, suggestions or advice that people have, and to receive sample collections for the study.