

18. Conservation genetics of Malleefowl

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Extensive land clearance in Australia over the past 100 years has led to wide scale fragmentation of Malleefowl habitat. Consequently, the Malleefowl has suffered a large reduction in range and many populations now exist in small, isolated fragments. Small populations typically have reduced genetic variation because of mating between close relatives (inbreeding) or accelerated random loss of alleles over time (genetic drift). Reduced genetic variation and inbreeding can lead to reduced reproductive output causing further declines in population size and viability (Frankham, 2002). Understanding the vulnerability of Malleefowl in this regard is an essential step in planning their management strategies. This project has three main themes: 1) phylogeography and population structure, 2) mating systems and reproductive behaviour, and 3) landscape genetics. This is the first large scale investigation of Malleefowl genetic variation to be conducted.

Phylogeography and Population Structure

There has been no previous investigation into the genetic structure or phylogeography of Malleefowl and currently the questions surrounding population subdivision remain unanswered. We plan to investigate the level of population structure across the range of Malleefowl to determine:

1. Whether any subpopulations of Malleefowl exist.
2. Whether past or current gene flow is responsible for the current genetic patterns observed.

We will be addressing these questions through analysis of mitochondrial and nuclear genes. The amount of sequence divergence between populations will determine whether populations can be separated as different subspecies. We plan to analyse samples collected across the contemporary range from Western Australia, South Australia, Victoria and New South Wales.

Mating systems and reproductive behaviour

The understanding of genetic variation within a population, as well as the variation in genetic contribution of individuals to future generations, is essential for conservation and management of that species (Quader, 2005). Biased reproductive success can limit populations by reducing genetic variation (Lacy, 1987). Malleefowl have been noted as generally monogamous, although polygamy has been recorded (Weathers, 1988). In most bird species the social mating system is often a poor reflection of genetic parentage (Birkhead & Moller, 1996).

We aim to investigate:

1. Parentage of Malleefowl chicks to determine the mating system of this species.
2. Site fidelity and use of Malleefowl mounds in sequential years
3. Sex ratios of young produced in each mound

This will involve collecting samples from offspring and mound-tending adults. DNA will be extracted and nuclear microsatellite markers will be genotyped to identify the putative parents for each "clutch".

We also aim to document the primary sex ratio of Malleefowl clutches to determine the average proportion of males and females laid in each mound. Biases in the number of a certain sex produced could have large consequences on the survival of a population (for example, if only males are produced for several years).

Landscape genetics

One of the main objectives of the Malleefowl Recovery Plan is to undertake genetic investigation of populations (Benshemesh, 2000) so that management decisions can be made.

Populations of Malleefowl have been subjected to extensive land clearance leading to fragmentation and isolation of a once continuous population. The severity of the impact of this fragmentation and isolation is not yet understood, but Malleefowl are reluctant fliers and apparently do not disperse readily across open country (Frith 1962; Benshemesh 2000). Understanding if and how Malleefowl are moving between remnant patches of mallee will be invaluable in aiding management decisions on the need for habitat corridors between remnants. This part of the study will concentrate on the factors that influence gene flow between isolated fragments in South East South Australia/ North West Victoria. We will use microsatellite markers to determine population of origin and any evidence of immigration between patches.

***Note:** *It is anticipated that this study will be completed in 2012 and the results published in due course.*

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