

ARC Linkage Project LP0776322. Sunnucks, Radford, (CIs), Melville, Joseph, Newell (PIs) How much habitat and what configuration maintains natural levels of connectivity in southeast Australian native birds?

We have made considerable progress in organization, fieldwork and laboratory work in the few months since this project began, in Oct 2007.

Team recruitment and development:

We appointed a postdoctoral associate with strong track record in avian molecular population genetics Dr Sasha Pavlova. A biologist with decades of experience in avian population biology, Assoc. Prof Alan Lill, is leading the field teams and field training program. With the assistance of Birds Australia to promote and advertise the project, Dr Pavlova and Assoc. Prof Lill have generated a network of skilled field volunteers. An additional fieldwork assistant, Naoko Takeuchi, is set to be appointed shortly, and we have identified prospective Hons and PhD students: one of each at Monash (Linda Grootendorst and Yessica Rico), and one of each at the Museum of Victoria (Rebekka Bray and Shandiya Balasubramaniam, cosupervised at U Melb).

Planning and administration:

Significant administration has been completed, including permitting, ethics permission, training, obtaining registered bird leg bands, ordering of field and laboratory equipment, consultation with landholders etc. A stakeholders' meeting was conducted at the Museum of Victoria on Oct 26, 2007, where the project received significant endorsement from senior Birds Australia representatives. We have held three major science planning meetings with different interest groups, which have yielded detailed confirmation of sampling locations, set in train activities including the generation of a prior model of expectations for the dispersal abilities of different species of birds through the landscape.

Connectivity model:

With Matt White and Graeme Newell at ARI, we are developing an *a priori* model of landscape connectivity for selected species based on expert opinion of the ability of individuals to move across different land-uses, and probability distributions of movement distances derived from banding recoveries. These models will produce 'resistance surfaces' for our study landscapes that reflect our current state of knowledge about functional connectivity. We will then compare the modelled connectivity with genetic distances derived from our field sampling, which is an empirical measure of functional connectivity.

Fieldwork:

In an on-going program, so far, seven weeks of intensive fieldwork in a cross section of the experimental landscapes have been conducted. Despite difficult weather conditions, the outcomes have been encouraging – using adaptative approaches to mist-netting, there have been over 500 bird captures (Table 1), though some species are proving difficult to catch and the abundance of others is lower than expected. Genetic sampling and other processing of the birds has been going well. The considerable logistics of the major field effort are running smoothly.



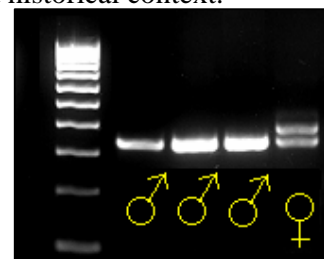
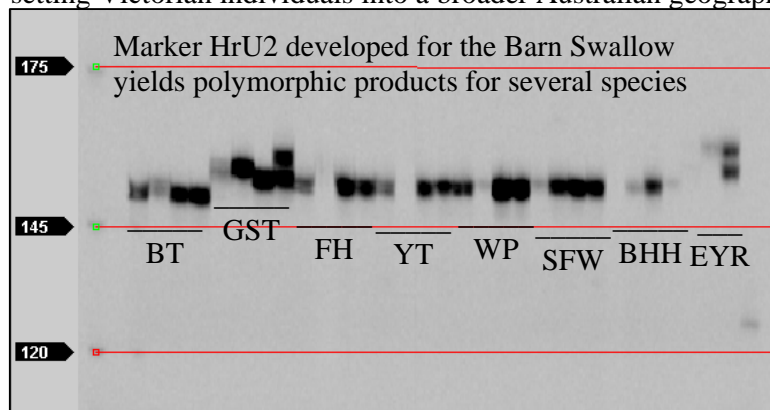
Table 1. Catching success of target species across sampled landscapes: BT- Brown Treecreeper, WPH- White-plumed Honeyeater, EYR- Eastern Yellow Robin, FH-Fuscus Honeyeater, GST- Grey Shrike-thrush, SFW- Superb Fairy-wren, YTH- Yellow-tufted honeyeater, BHH- Brown-headed Honeyeater, SP- Striated pardalote, WB- Weebill.

Dates	Landscape/ Sites	BT	WPH	EYR	FH	GST	SFW	YTH	BHH	SP	WB	Total
7.11.07- 11.11.07	Axe Creek LS51LR3	8		3	12	2	3	7				35
19.11.07- 23.11.07	Crosbie LS25LR3/4	17			33	1		5	1			57
10.12.07- 14.12.07	Havelock LS56 LR1/LR4	16	1	1	2	2		5	1			28
14.01.08- 18.01.08	Tunstalls LS15Rp3	10	27									37
21.01.08- 25.01.08	Tunstalls LS15Rp1/ Continuous	20	60		5	2	10			1		98
28.01.08- 1.02.08	Dunolly DCF3/DCF2	5			65			57	16	3	1	147
4.02.08- 8.02.08	Stuart Mill LS6LR3	17	71		1			21		1		111
	Total	93	159	4	118	7	13	95	18	5	1	513

Laboratory work

After a significant bioinformatics effort, we have obtained ~180 primer pairs for single locus nuclear markers in birds and are beginning to test and optimize them in the target species. Some of the markers are species-specific, and others are expected to be of broader utility. Nine of 12 markers tested so far yielded appropriate products at least for some species. Sexing PCRs are working well, and have been used to test the effectiveness of different sources of DNA, including plucked breast feathers and blood samples treated in different ways. For example, we can extract usable DNA from material remaining after blood cell counts and other blood work.

Approximately 30 samples each of the 6 target and 6 backup species have been supplied by PI Leo Joseph from the Australian National Wildlife Collection (ANWC) and will be used for setting Victorian individuals into a broader Australian geographic and historical context.



DNA sexing of GST:
females yield two bands,
males just one

As well as standard approaches, we are investigating the feasibility of some novel approaches based on a subset of >250 nuclear markers that emerged in 2007 from international avian genomics efforts, and are cooperating with other researchers working on Australian bush birds.

Outputs:

2007: Herrod, Pavlova, Sunnucks & Radford. Using genetic tools to quantify the movement of six passerine species within and among landscapes. Ornithological Congress. Perth, Dec. Poster.

Plans for next 6 months:

Continue the field work, test and optimize genetic markers, begin wide-scale genetic screening.