Modelling real-time migration rates during a population decline

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INTRODUCTION

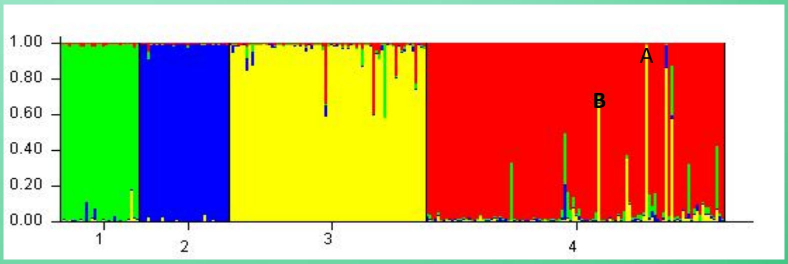
Dispersal is a key life history trait that has important consequences for understanding the ecology and epidemiology. Both are important contributing fundamental information about how diseases can threaten a particular population. Molecular techniques offer an elegant approach to improve our knowledge of the dynamics of pathogen dissemination by making information available that is difficult to observe with conventional methods, such as field data.

All Western Australian woylie (*Bettongia penicillata*) populations, between 2002 and 2004 declined steeply. In the hypothesis that a disease is involved in the Woylie decline, a key piece of information is the extent of woylie movements in the wild.

METHODS

We used a direct estimate of migration rates - or dispersal - (*Nm*) using a Bayesian approach with the program STRUCTURE (Pritchard *et al.* 2000) as well as indirect estimates based on: partitioning of allele frequencies (Hedrick 2000), private alleles (Barton & Slatkin 1986) and complex coalescence-based approaches using the program LAMARC (Kuhner 2006).

RESULTS



Assignment test using STRUCTURE (Pritchard et al. 2000). Admixture model with allele frequencies correlated. Analysis with different models had similar results. Each column represent the genome of an individual. A: first generation immigrants. B: second generation immigrants . 1. Dryandra 2. Tutanning 3. Upper Warren west 4. Upper Warren east


Photo: Sabrina Trocini

The number of migrants per generation
(allele frequency approach)

	Dryandra	Tutanning	UW_W
Tutanning	1.39		
UW_W	2.53	1.28	
UW_E	3.91	1.59	4.31


Photo: Sabrina Trocini

The number of migrants per generation
(coalescent approach). Results for mtDNA.

		Emigrants from			
		Dryandra	TUT	UW_W	UW_E
Immigrants into	Dryandra	--------	0.03	0.18	0.28
	Tutanning	0.00	--------	0.00	0.00
	UW_W	0.06	0.01	--------	0.22
	UW_E	0.31	0.04	0.39	--------

The number of migrants per generation
(private allele approach)

	Dryandra	TUT	UW_W
Tutanning	0.54		
UW_W	0.98	0.75	
UW_E	1.11	0.85	1.40

CONCLUSIONS

There are a range of different methods available to calculate migration rates among populations. Care needs to be taken when considering point estimates, because some of the models have restrictive assumptions that are rarely met in free-range populations. Relative comparison and characterisation of general trends are often indicative of real migration events.

With this study, we have been able to demonstrate that **woylies are capable of moving long distances**, not only within the Upper Warren, but also between populations as far apart as 150 km (Dryandra forest to Upper Warren). The **consistent results** using **different methods and genetic markers** give us confidence that it is not just an occasional event. Therefore, **diseases that involve direct transmission cannot be discounted** as potential contributing factors in the woylie decline.

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