PERSPECTIVE

A tale of two worlds: molecular ecology and population structure of the threatened Florida scrub-jay

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Abstract

Elsewhere in this issue of *Molecular Ecology*, Coulon *et al.* provide a detailed analysis of population structure of the threatened Florida scrub-jay (*Aphelocoma coerulescens*) using genetic markers and compare it to that inferred from previous demographic surveys and observed dispersal behaviour in this species. In contrast to previous attempts at such comparisons, estimates from the two methods are reasonably congruent. Although challenges remain, Coulon *et al.*'s analyses demonstrate the potential for closing the gap between these alternative methodologies, and ultimately for future genetic surveys to be used confidently in conservation planning.

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When it comes to applying molecular ecology to conservation, these are good times. Molecular methods are powerful, complex multivariate statistical techniques are numerous and relatively easy to implement, and the theory behind the objective determination of genetically unique units and geographical areas of conservation importance are vibrant areas of activity within the fastest growing field of ecology. Given a reasonably thorough set of genetic samples, obtainable if necessary using noninvasive techniques from hair, dung, or even from museum specimens, it is now possible to infer details about genetic structure of populations using methods that were far outside the realm of possibility a mere decade ago.

Unfortunately, the same cannot be said for more traditional field-based methods of determining population structure by marking and/or using telemetry, techniques necessary to determine variation in dispersal at the individual level. On the one hand, technology has improved such that it is now possible to track organisms as small as dragonflies over long distances (Wikelski *et al*. 2006). Unfortunately, this is not yet easily or cheaply accomplished; tracking those dragonflies required a lot of brute force, including following animals using hand-held antennas, a technique dating back to the 1960s, along with a fair amount of quality time spent trying to follow individuals from a Cessna. Although there is speculation about the potential for a tracking system that could eventually monitor movement of small animals on a global scale (Wikelski *et al*. 2007), most field studies of organisms smaller than several hundred grams currently have little or no access to techniques that will allow detection of animals that move beyond a few kilometres. For these species, which include a majority of the world's fauna, field-based techniques for estimating dispersal and population structure are of limited value, regardless of how intensive they may be, and typically yield results that markedly conflict with those obtained by molecular methods (Koenig *et al*. 1996).

It is therefore a significant achievement that Coulon and colleagues have succeeded in obtaining estimates of population genetic structure by these two disparate methods that are almost identical. The Florida scrub-jay (*Aphelocoma coerulescens*) is found only in low-growing oak scrub of the Florida peninsula, some 1600 km away from the nearest populations of its closest relatives in the western USA and Mexico (Fig. 1). Beginning with a long-term study of its cooperatively breeding behaviour by G. E. Woolfenden and J. W. Fitzpatrick at Archbold Biological Station in 1969, it has since become one of the most intensively studied birds in the world due to its interesting social behaviour, limited range, and threatened status.

This combination of characters has set the stage for a unique integration of Woolfenden & Fitzpatrick's (1984) long-term field study, extensive efforts to survey the species throughout its range (Stith *et al*. 1996), and an intensive effort to genetically sample the population (Coulon *et al*. 2008). The earlier survey efforts, conducted in 1992–1993, were an attempt to exhaustively survey the population, which at the time was estimated to consist of about 10 000 individuals. Based on an observed dispersal distribution indicating that the vast majority of dispersal events are under a few kilometres, combined with the apparent reluctance of birds to travel through unsuitable habitat such that only a small proportion of patches located more than 12 km from a source population are occupied, Stith *et al*. (1996) used a 12-km buffer around extant territories to help define metapopulations demographically. Based on the buffers, they delineated 42 metapopulations, half of which were thought to contain less than 10 pairs and thus deemed to be demographically insignificant.

Although impressive, this attempt to exhaustively survey a species over even its relatively compressed current potential range in the order of 60 000 km^2 is a task that deserves critical scrutiny. Much of the range of Florida scrub-jays, estimated to support about 30% of all individuals (Stith 1999), is privately owned and difficult to access. Scrub-jays are often relatively conspicuous, but if it is possible that ivory-billed woodpeckers (*Campephilus principalis*) have been hiding in parts of Florida almost entirely unnoticed for over 40 years (Hill *et al*. 2006), it is clearly possible that much more than 2% of the population was missed in the 1992–1993 survey, as estimated by Stith *et al*. (1996). Indeed, a later study focusing on three of the metapopulations identified in the 1992 survey indicated that 16% of scrub-jays were missed, largely because they are sometimes found in areas other than well-drained scrub ridges, the criterion by which Stith *et al*. (1996) demarcated suitable habitat (Breininger *et al*. 2006).

Because of these and other issues, there was every reason to fear that Coulon *et al*.'s survey involving 1028 individuals from 21 of the 42 metapopulations screened at 20 microsatellite

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Fig. 1 The threatened Florida scrub-jay (*Aphelocoma coerulescens*). Photo credit: Simon Fellous.

loci would suggest significantly less population structuring among the putative metapopulations than indicated demographically — the typical result of earlier attempts to compare these two approaches. This turned out not to be the case; in general, boundaries of the putative metapopulations and genetic groups were identical or the genetic groups encompassed several neighbouring metapopulations; essentially no putative metapopulation was genetically subdivided and only 30 of the individuals (2.9%, including a genetic group of 22 embedded within a larger, distinct genetic group) were not easily reconciled with the previously inferred metapopulation structure delineated demographically. As the authors point out, these discrepancies are probably due to individuals being missed, but the differences are sufficiently small that they do not point to the serious shortcomings suffered by prior attempts to infer population structure from demographic studies.

The good news is thus that future genetic surveys may provide information regarding population structure of sufficiently high quality that they can be used confidently in conservation planning, at least when conducted in conjunction with thorough sampling. The bad news is that the statistical techniques for analysing the data from the microsatellite sequences are currently bewilderingly complex. Coulon *et al.* for example, performed two different Bayesian analyses to generate spatial patterns of genetic structure from their data, each involving multiple complex steps, at least some of which they developed themselves. Each step involved making various assumptions and required making judgement calls regarding demographic issues key to performing the analyses. Although this does not detract from their accomplishment — indeed, such judgement calls are typical of both molecular and ecological studies, whether acknowledged or not — one has to wonder to what extent the results are dependent on them. Other methods are available (Grivet *et al.* 2008), and it would be quite illuminating to compare Coulon *et al.*'s (2008) results with those produced by other independent groups analysing the same genetic data.

In any case, Coulon *et al.*'s study demonstrates how far molecular ecology has come from the days when studying population structure meant primarily calculating F_{ST} values. Additionally, this work shows how successful a demographic analysis of population structure can be, albeit given an enormous investment of time and effort. Our understanding of metapopulation structure, as well as our confidence in management decisions predicated on genetic structuring, have come a long way.

Unfortunately, despite these advances, conservation measures for *A. coerulescens* lag behind. In the 15 years since the Florida scrub-jay population census in the 1990s, there has been a 37.5–65% decline in all or portions of 10 metapopulations of this species (USFWS 2007). One of the best-studied and most interesting species in North America continues to head in the direction of extinction.

References

Breininger DR, Toland B, Oddy DM, Legare ML (2006) Landcover characterizations and Florida scrub-jay (*Aphelocoma coerulescens*) population dynamics. *Biological Conservation*, **128**, 169–181.

Coulon A, Fitzpatrick JW, Bowman R *et al.* (2008) Congruent population structure inferred from dispersal behaviour and intensive genetic surveys of the threatened Florida scrub-jay (*Aphelocoma coerulescens*). *Molecular Ecology*, **17**, 1685–1701.

Grivet D, Sork VL, Westfall RD, Davis FW (2008) Conserving the evolutionary potential of California valley oak (*Quercus lobata* Née): a multivariate genetic approach to conservation planning. *Molecular Ecology*, **17**, 139–156.

Hill GE, Mennill DJ, Rolek BW, Hicks TL, Swiston KA (2006) Evidence suggesting that ivory-billed woodpeckers (*Campephilus principalis*) exist in Florida. *Avian Conservation and Ecology*, **1**, 2. Available from http://www.ace-eco.org/vol1/iss3/art2/.

Koenig WD, Van Vuren D, Hooge PN (1996) Detectability, philopatry, and the distribution of dispersal distances in vertebrates. *Trends in Ecology & Evolution*, **11**, 514–517.

Stith BM (1999) Metapopulation viability analysis of the Florida scrub-jay (*Aphelocoma coerulescens*): a statewide assessment. Final Report to the Endangered Species Office, US Fish and Wildlife Service, Jacksonville, Florida.

Stith BM, Fitzpatrick JW, Woolfenden GE, Pranty B (1996) Classification and conservation of metapopulations: a case study of the Florida scrub jay. In: *Metapopulations and Wildlife Conservation* (ed. McCullough DR), pp. 187–215. Island Press, Washington, D.C.

USFWS (2007) *Florida Scrub-jay (*Aphelocoma coerulescens*): 5-Year Review: Summary and Evaluation*. US Fish and Wildlife Service, Southeast Region, Jacksonville Ecological Services Field Office, Jacksonville, Florida.

Wikelski M, Moskowitz D, Adelman JS *et al.* (2006) Simple rules guide dragonfly migration. *Biology Letters*, **2**, 325–329.

Wikelski M, Kays RW, Kasdin NJ *et al.* (2007) Going wild: what a global small-animal tracking system could do for experimental biologists. *Journal of Experimental Biology*, **210**, 181–186.

Woolfenden GE, Fitzpatrick JW (1984) *The Florida Scrub Jay: Demography of a Cooperative-Breeding Bird*. Princeton University Press, Princeton, New Jersey.

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