

## NEWS AND VIEWS

### PERSPECTIVE

## Tracking elusive timber rattlers with molecular genetics

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### Abstract

**Most biologists would agree that understanding the factors that influence gene flow among populations is important, because population connectivity is critical to effective conservation and management as well as to issues such as disease transmission and the degree of local adaptation. Nonetheless, our understanding of the mechanistic determinants of gene flow remains abysmally limited for many types of organisms. Predictably, some of the biggest gaps involve animals that are rare, secretive, and difficult to collect or handle — and thus, remain relatively unstudied for other traits as well. Large venomous snakes have long provided a classic example of such an under-studied group, but the situation has changed dramatically over recent years. The study by Clark *et al.* in this issue builds upon our increasingly sophisticated understanding of snake behaviour, to interpret patterns of gene flow in the light of our emerging knowledge of snake behavioural ecology.**

*Keywords:* connectivity, dispersal, gene flow, snake

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The emergence of snakes as (relatively) popular study organisms has been driven both by technological innovation (the development of miniature radiotransmitters that facilitate relocation of these cryptic animals) and by shifts in public perception (such that snakes are now often seen as wildlife to be treasured rather than enemies to be slaughtered: Shine & Bonnet 2000). The species studied by Clark *et al.* (2007) is the timber rattler (*Crotalus horridus*), an icon of the eastern North American forests and an animal under severe threat from increasing urbanization. These beautifully camouflaged ambush hunters remain inactive and virtually invisible to humans for much of their lives, so that simply obtaining the tissue samples for genetic analysis was a mammoth task. The challenge was simplified, however, by the predictable seasonal aggregation of animals at communal winter retreat sites (hibernacula) in rocky escarpments (Fig. 1). That facet of

rattlesnake biology also identified an obvious focus for any study on gene flow, with hibernacula treated as potentially separate populations.

Perhaps the most exciting aspect from Clark *et al.*'s study is the way they have integrated the availability of thermo-regulatory opportunities into a measure of effective distance between hibernacula. Straight-line distance between a pair of hibernacula did not predict gene flow, whereas a metric that incorporated the ease of travel between the sites — based on the availability of sun-exposed basking sites between the two — was far more successful. It will not surprise any snake biologist that thermo-regulatory opportunities influence usage of alternative routes for a travelling snake — but empirically demonstrating the importance of this behavioural trait for population-level gene flow is an elegant demonstration of the virtues of 'wearing the snake's shoes' (Rivas & Burghardt 2001); that is, looking at a variable such as 'distance between adjacent hibernacula' in the way that a rattlesnake might view it, rather than as perceived by a human with a topographic map on the desk.

How general are the results of Clark *et al.* likely to be? Given the pioneering nature of the current study, there is no way to tell — but speculation may nonetheless be worthwhile. I suspect that the severely cold winters of the rattlesnake site play a large role in producing the patterns detected by Clark *et al.* because those thermal conditions force snakes to aggregate in limited thermally suitable sites during winter, and place a strong premium on basking-site availability for travelling snakes in spring or autumn. Thus, we might expect similar patterns for many populations of relatively low-vagility ectothermic organisms in seasonally cold habitats. Many ectotherm systems fulfil these criteria. Indeed, it is striking that like the rattlesnake population studied by Clark *et al.*, many of the most intensively studied snake populations — such as the red-sided gartersnakes in Manitoba, black rat snakes in Ontario, European adders in Sweden, and Shedao pit-vipers in northern China — occur close to the northern (cold-climate) limit of the species' distribution. The reasons for this strong bias involve both logistics (cold climates force snakes to bask in open areas where they can be captured or observed), the geographical locations of most major research centres (in temperate-zone areas rather than the tropics), and a trend for impending endangerment to be easily recognized in more intensively studied areas. Even within such cold-climate systems, however, details of mating systems may well drive gene flow. For example, we might expect more population structure in a system where mating often occurs before the animals disperse from the overwintering den (like gartersnakes: Manier & Arnold 2005) than in one where mating occurs on the summer range, far from the den (as in rattlesnakes).

Inconveniently for scientists living in temperate regions, however, most snakes actually live in the tropics. Does this matter for the approach suggested by Clark *et al.*? Not really — it is just that the factors affecting rates of gene flow will need to be evaluated afresh, in the light of the spatial distribution of

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**Fig. 1** Timber rattlesnakes (*Crotalus horridus*) emerging from a hibernaculum. Photo credit: Rulon W. Clark.

factors limiting snake mobility and favouring aggregation. Tropical habitats do not eliminate phenomena such as strong natal philopatry in snakes (as in tropical colubrids: Brown & Shine 2007) or dense aggregations in suitable sites (as in sea kraits: Shetty & Shine 2002); but because harsh climatic conditions do not enforce aggregation, rates of gene flow among neighbouring snake populations likely will prove to be higher in the tropics than in the temperate zone. Even where we see strongly subdivided populations, the landscape features that dictate rates of gene flow may be very different from those in the northeastern USA. For example, patches of densely shaded habitat may facilitate rather than discourage snake movement, by protection from critically high heat loads as well as from predators.

More generally, many of the traits that fall into dichotomies in severely cold habitats may prove to be continua in warmer climates, where thermal constraints on snake distributions are relaxed. For example, Clark *et al.* demonstrated that gene flow among den populations was generated mostly by migrating males not females, based on the proportion of mother–offspring vs. father–offspring pairs collected at the same den. In warmer climates, direct molecular measures to detect dispersal are likely to be more appropriate to quantify sex biases in such behaviours (Rivera *et al.* 2006; Keogh *et al.* 2007). The history of snake ecology tells us that much can be learned by focusing on the logistically convenient systems of the cold temperate zone, and the lessons learned there can be used to generate insights that ultimately allow us to widen our knowledge geographically, climatically and phylogenetically. The same may well be true of the application of molecular techniques, and hopefully we will not have to wait too long before we see equally sophisticated analyses of gene flow within tropical systems. Clark *et al.*'s study provides a striking

demonstration of the potential for molecular approaches to clarify topics such as mating systems in highly cryptic animals, virtually unobservable during the mating season, and a salutary lesson in the benefits of embedding such an analysis within a detailed knowledge of the study organism's natural history.

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Richard Shine studies the evolution, ecology and conservation biology of reptiles and amphibians. He has worked extensively on the ecological traits of snakes, and the relevance of those traits to interpreting and ameliorating conservation threats.

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## PERSPECTIVE

### Adapting to winter in wheat: a long-term study follows parallel phenotypic and genetic changes in three experimental wheat populations

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#### Abstract

**Drawing a direct connection between adaptive evolution at the phenotypic level and underlying genetic factors has long been a major goal of evolutionary biologists, but the genetic characterization of adaptive traits in natural populations is**