NEWS AND COMMENTARY

Molecular genetics

Bloodthirsty amazons?

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Malarial mosquitoes might appear to be poor model organisms for population genetics, not least because the majority of workers who study them are driven by a desire to do them irreparable harm. Nonetheless, advances in molecular genetics are fast making *Anopheles* mosquitoes into valuable systems for studies of speciation and of both man- and climate-mediated evolution (Stump *et al.*, 2005). Lisa Mirabello and Jan Conn discuss how mitochondrial sequence data suggest patterns of climate-induced change in the abundance of the Latin American malaria vector *Anopheles darlingi* (Mirabello and Conn, 2006).

South America and the Amazon basin in particular have long been the areas of choice for studies of biodiversity. These studies have revealed that the Amazon basin is not a homogeneous environment with all species widely distributed. Rather, there are a series of discrete areas with their own endemic flora and fauna. These 'islands of endemism' are thought to date from the Pleistocene. Efforts to explain these patterns have generated a number of incompletely congruent hypotheses (Moritz *et al.*, 2000; Hall and Harvey, 2002), which variously invoke sea-level changes, environmental gradients and forest fragmentation resulting from reduced rainfall.

The problem in resolving these hypotheses is that there are few definitive tests that can discriminate between them, and that for many species the necessary molecular data are lacking. These molecular tools are readily available for *Anopheles* mosquitoes. However, for many *Anopheles* species their dependence on man would make them unreliable witnesses for more ancient events. This paradigm was developed from the pioneering work of Mario Coluzzi and colleagues, who suggested that the distribution of *Anopheles gambiae* in Africa is likely to result from man-mediated environmental change.

In particular, the agricultural revolution in sub-Saharan Africa (somewhere after 10 000 years before present) could have facilitated the spread of this mosquito and resulted in its continent-wide distribution. The logic behind this idea is that pre-Neolithic human populations were unlikely to have been large enough to drive the evolution of a mosquito with a predilection for human blood. *Anopheles gambiae* populations do indeed show molecular signatures of recent population expansion, and it has been proposed that similar historically recent (~10 000 years before present) population expansions are likely to be found in the majority of primary vectors and indeed pest species (Donnelly *et al.*, 2002).

Mirabello and Conn show that *A. darlingi* does not show traces of such a recent population expansion and that its present day distribution may result from more ancient processes. This would fit with *a priori* predictions, as *A. darlingi* is less dependent upon man for both bloodmeals and larval habitats and therefore is less likely to be affected by man-mediated environmental change. Given the wealth of molecular markers available for *A. darlingi* and the relative ease with which they, and closely related species, can be collected, they may well be ideal organisms for dating periods of endemism within the Amazonian basin, and factors (eg reduced rainfall/sea level changes, etc) that may be concomitant. Using sequence data from the mitochondrial cytochrome oxidase subunit I from 19 sites throughout Latin America, they observed a pronounced differentiation between samples from south and central America. Similar patterns have been observed in the *Rhodnius* (Triatominae) vectors of Chagas disease, where the pattern was thought to be a result of vicariance events within the Pliocene (~2.4–3.7 My) (Monteiro *et al.*, 2003). Within the South American group of *A. darlingi* there were two further

clusters termed northern Amazon and south America, which may well be important for the dating of Pleistocene events. The latter two clusters are particularly interesting, as they appear to be coincident with proposed sites of endemism within the Amazonian basin (Hall and Harvey, 2002). The northern Amazonian cluster neatly corresponds to the endemic area termed Guiana, and the south American cluster, in the main, comprises specimens from Para and Belem endemic areas. Furthermore, the pattern of haplotype diversity (eg see Figure 1 in Mirabello and Conn) suggests that an increased sample size may well permit the resolution of this catch-all cluster into constituent parts.

While to date there has been concordance in the patterns of demographic change revealed by diverse markers systems in *Anopheles* species, there is a need to extend these studies to additional genomic markers and more samples to look at the boundaries of the distribution of these putative endemic Anophelines. Furthermore, the dating of the changes observed is reliant upon mutation estimates derived from other insect orders and it would be preferable if bounded estimates of mutation rate could be obtained from within the Diptera.

It would be imprudent to argue that these neotropical mosquitoes should be a conservation priority, but they may well be important tools for explaining the faunal history of the Amazon basin. MJ Donnelly is at the Vector Research Group, Liverpool School of Tropical Medicine, Liverpool L3 5QA, UK.

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Further Reading

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