

## Thesis summary

**Comparative phylogeography of two rotting-log-dependent springtails from the Great Dividing Range of Southeastern Australia.** Ryan C Garrick, PhD thesis, La Trobe University, Melbourne, 2007.

Phylogeography is a discipline-bridging field that seeks to reconstruct long-term population history, and to identify the processes that have shaped spatial patterns of intraspecific diversity, via integrating population genetics and phylogenetics. An understanding of the relative influence of past climatic changes throughout the Pleistocene versus processes that operate over ecological timescales, and the way these different forces interact with the landscape setting in which species have evolved, can provide critical information for devising conservation strategies. Low-mobility, flightless, habitat-specific invertebrates may be exceptional model organisms for recovering very fine-scale signals of ancient vicariance and range expansion events owing to their ability to maintain viable populations in tiny refuges – refuges too small to support most vertebrates or other taxa with moderate dispersal (Moritz *et al.* 2001). The research reported here focused on two as-yet undescribed species of rotting-log-dependent Collembola (*Pseudachorutinae* Gen. nov. sp. nov. and *Acanthanura* sp. nov.) from cool temperate eucalypt forests at Tallaganda on the Gourock Range, an isolated section of the Great Dividing Range in southeastern New South Wales. The principal aims of this study, which is part of a larger multi-taxon programme, were: (1) to distinguish the predominant underlying processes driving observed spatial-genetic patterns; (2) to determine the extent to which topography, particularly drainage networks, predict the present-day distribution of biodiversity; and (3) to evaluate the degree of phylogeographical congruence between the two springtail species.

Five catchment-based microgeographical regions at Tallaganda were identified *a priori* on the basis of topography, as well as an assessment of the likely palaeoclimatic impacts (i.e. repeated cycles of Pleistocene periglaciation) on the distribution of moist forest habitats (Garrick *et al.* 2004). Based on this landscape model together with a basic understanding of species ecology and life history, testable phylogeographical predictions were formulated. Individuals of each springtail species were intensively sampled at fine spatial scales from rotting *Eucalyptus* logs on the forest floor, and a panel of informative genetic markers capable of detecting population subdivisions and estimating phylogenetic relationships were developed (Garrick & Sunnucks 2006). This approach permitted comparative analyses at hierarchically nested levels – spatially (within and among geographical populations), temporally (ancient, recent and contemporary genetic differentiation of populations) and taxonomically (within and between species). To gain an appreciation of how whole

ecological communities can respond to past changes in the biogeographical landscape, inferences about long-term population history of the two springtails were compared with patterns of biodiversity seen in other co-distributed rotting-log-adapted invertebrates (terrestrial flatworms, velvet-worms, funnelweb spiders), and a vertebrate (the highland water skink), as revealed by related studies centred at Tallaganda.

Both springtail species exhibited considerable genetic differences among geographically localised populations, consistent with expectations for low-dispersal organisms with specific habitat requirements. However, subdivisions were incredibly fine-grained, with marked genetic discontinuities among contemporary populations occurring over distances ranging from several hundred metres to a few kilometres. Migrants and individuals of mixed ancestry are apparently exceedingly rare indicating that current levels of gene flow are very low, and the locations of contact zones largely coincided with catchment boundaries (Garrick *et al.* 2004, 2007). Levels of DNA sequence divergence among individuals from distinct populations were indicative of separations that predate the last several periglacial cycles, perhaps considerably. These genetic differences seem to have been driven by successive periods of isolation in refugia owing to contraction of moist forests into sheltered east-facing montane gullies during Pleistocene periglacial cycles. Indeed, several lines of evidence indicate that the interaction between past climatic changes and topography had a major impact on the evolutionary trajectories of *Pseudachorutinae* Gen. nov. sp. nov. and *Acanthanura* sp. nov. at Tallaganda (Garrick *et al.* 2004, 2007). It is notable that while divergence in allopatry promoted the genetic subdivisions seen today, partial post-mating isolating mechanisms (i.e. endogenous selection against hybrids) probably contributes to their maintenance given that the locations of population contact zones are not clearly correlated with abrupt changes in environmental variables or with ecotones.

Comparative analyses of the two springtail species datasets showed that the general pattern of phylogeographical congruence was accompanied by evidence for marked differences in rates and directionality of gene flow over short to intermediate timescales, indicating that landscape history can exert an overarching influence on genetic structuring, even at very fine spatial scales (R Garrick unpubl. data 2007). Indeed, distantly or unrelated taxa from the same model landscape system show qualitatively similar catchment-based geographical patterns of biodiversity (Sunnucks *et al.* 2006; Hodges *et al.* 2007). Thus, the interaction between topography and palaeoclimatic history seems to have some predictable influences on the locations of areas of endemism in low-mobility, wet-adapted arthropods (and perhaps some vertebrates) in montane temperate forests on the Great Dividing Range (see also Graham *et al.* 2006).

Rotting-log-dependent invertebrates comprise a large proportion of forest biodiversity, yet are a poorly known, understudied ecological community of which members are over-represented on threatened or endangered species lists in areas that have a long history of intensive timber harvesting, such as Europe (Grove 2002). Similar effects of habitat fragmentation are already being seen in Australia (Schmuki *et al.* 2006). The finding that catchment divisions may serve as an excellent surrogate for biodiversity indication in low-mobility invertebrates supports the idea that production forestry can be tailored to conserve such diversity.

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