

Reconciling Australia's Linguistic and Genetic Past(s)

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Bouckaert, Bowern, and Atkinson (2018) date the beginning of the expansion of the Pama-Nyungan family throughout Australia to a period between 4 and 7kya. In contrast, two recent gene trees (Malaspinas et al 2016, Tobler et al 2017) provide evidence that Australian population dispersions are ancient, dating to more than 30kya. Malaspinas et al's tree is convergent in many respects with the linguistic tree of Bouckaert, Bowern, and Atkinson (2018), despite the difference in dates, while Tobler et al's tree is not. Tobler et al is based on mitochondrial DNA (inherited through the female line) while Malaspinas et al's is based on full genome coverage.

This leads to a contradiction: if the regional genetic variation depicted in the gene trees is old and the spread of Pama-Nyungan is recent, then Pama-Nyungan must have been spread by cultural diffusion rather than by migration into uninhabited territory. Such a scenario would explain the lack of congruence between Tobler et al's gene tree and the language tree, as well as the 7-fold differences in dating of dispersal. However, in that case, why is the Malaspinas et al tree such a close fit to the observed language tree? Moreover, how do we reconcile the claims of regional stability in the gene trees with the evidence from climatic variation and gaps in the archaeological record, both of which suggest regional dynamics and settlement fluctuations?

In this talk, I suggest several ways in which we might reconcile the gene and language trees, involving the diagnosis of migration versus contact-induced diffusion. First, the gene trees are rather low resolution geographically, with small numbers of individuals contributing and large gaps across the country. Several phylogeographic genetic analyses provide information only at the level of the 'state', a grouping that is not only highly anachronistic but also useless considering that Wati groups (a single subgroup within Pama-Nyungan) span three states. The language tree, in contrast, has high-density coverage from across the family of language locations at the time of European settlement. Secondly, the timing of the breakup of several major Pama-Nyungan subgroups tracks breaks in the archaeological record, as noted by Bouckaert, Bowern, and Atkinson (2018). This provides evidence for migration rather than diffusion. However, in areas where there is no such tracking (especially where the archaeological evidence suggests continued occupation), diffusion is more likely. Thirdly, examining the linguistic and geographical neighbors allows us to distinguish likely migrations (where strong tree-like signal follows topographic features) from other events. Finally, I suggest an approach that would let us detect substrate signal through vocabulary replacement. These methods allow us further insight into the dynamic history of Aboriginal Australia.

Bouckaert, Remco R., Claire Bowern, and Quentin D. Atkinson. "The origin and expansion of Pama-Nyungan languages across Australia." *Nature Ecology & Evolution* (2018): 741-749

Malaspina, Anna-Sapfo, et al. "A genomic history of Aboriginal Australia." *Nature* 538.7624 (2016): 207-214.

Tobler, Ray, et al. "Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia." *Nature* 544.7649 (2017): 180-184.