

Biogeography Off the Tracks

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Received 10 December 2012; reviews returned 4 February 2013; accepted 14 February 2013
Associate Editor: Susanne Renner

We write to convey our concerns that some methods of panbiogeography and their mainstream evolutionary journals continue to publish articles that, in our view, present misleading accounts of biological evolution. Specifically, panbiogeographic studies of spatial distributions, which connect all distribution points to form a biological history (e.g., Craw 1988; Heads 2011, 2012), our conc rg 0 01(e)11.9(v)39.9 (points of tracks, main massings, which identify more diverse regions of the distribution; and baselines, which represent major landscape features traversed by tracks. First, as a general criticism, the meaning of a track is ill defined. Specifically, Craw et al. (1999) (p. 20) state that tracks "... give shape or expression to the space and time that necessarily intervenes between disjunct localities," a hazy description underpinning a mysterious approach. If tracks are meant to indicate paths of dispersal or vicariant events, there is also no apparent reason why they should take the minimal distance (although indeed they are rarely depicted as great circle distances). Second, it is not always clear how the tracks are arrived at. Although they purport to be minimal spanning acyclic graphs, the specific tracks drawn are sometimes not the shortest available, but are seemingly swayed by locations of main massings within distributions. For example, it is not clear why Australasian ratites are linked by a track through an Indian Ocean baseline, rather than by a track from China to Papua New Guinea to create a shorter network (Fig. 1a). Third, the main massings are said to represent "... the greatest concentration of biological diversity ...," including taxonomic, genetic, phenotypic, or behavioral characteristics (Craw et al. 1999, p. 21), but it is unclear how this diversity is objectively quantified. Fourth, track analysis and ancient vicariant scenarios are often discordant with respect to phylogenetic reconstructions (e.g., track analysis suggests a closer relationship of moa and kiwi [Fig. 1a], yet moa is more closely related to rhea [Fig. 1b]). Fifth, as with many methods, accumulating fossil data (e.g., new Montana record; Fig. 1a) and consideration of extinction events (which will be common over geological timeframes; van

([Campbell 2008](#); [Heenan et al. 2010](#)). Corroborating these geological findings, molecular data from numerous species independently indicate that biotic relationships between the Chathams and mainland New Zealand are far too young for the panbiogeographic conclusions to be considered plausible ([Paterson et al. 2006](#); [Goldberg et al. 2008](#); [Wallis and Trewick 2009](#); [Heenan et al. 2010](#); [Goldberg and Trewick 2011](#)). For example, the oldest estimated divergence of contemporary Chathams and mainland sister taxa known to date is 14 Ma for the Chatham Island forget-me-not (*Myositidium hortensium*), whereas most other Chathams...mainland species divergences appear < 3 Ma ([Heenan et al. 2010](#)). Overall, multiple independent lines of evidence clearly indicate that the modern Chathams biota was established by transoceanic dispersal, and not by ancient vicariance.

Practitioners of the panbiogeographic approach

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