Biogeography Off the Tracks

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We write to convey our concerns that some mainstream evolutionary journals continue to publish articles that, in our view, present misleading accounts of biological evolution. Specifically, we argue that “panbiogeographic” studies of spatiotemporal biological history (e.g., Craw 1988; Heads 2010a, 2010b, 2011, 2012a, 2012b) are detrimental to the progress of biogeography as a discipline. The panbiogeographic approach usually ignores long-distance dispersal and considers alternative hypotheses only within the narrow confines of assumed ancient vicariance. Although previous commentators have already penned epitaphs for the panbiogeographic paradigm (e.g., Cox 1998; McDowall 2004; McGlone 2005; Briggs 2007), some editorial and review processes continue to allow this misleading approach to be promulgated as a useful scientific method. Despite the approach being termed “moribund” (Briggs 2007), recent years have seen an apparent upswing in the number of panbiogeographic studies published (e.g., Kutschker and Morrone 2012; Mercado-Salas et al. 2012; Silva et al. 2012).

Panbiogeography represents a worldview of biology seemingly fixated on ancient earth history and evaluates alternative biological hypotheses only within the limited confines of assumed ancient vicariance. The lack of scope for considering alternative hypotheses makes panbiogeography of dubious utility, especially relative to the far more developed biogeographic methods, accumulating fossil data (e.g., new Montana 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]). 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...
FIGURE 1. Panbiogeographic studies routinely assume that ancient tectonic processes explain modern biological distributions. a) Blue lines show a panbiogeographic analysis of ratite birds (flightless members of superorder Palaeognathae; redrawn from Craw et al. 1999), with “tracks” (straight lines connecting distributional records) supposedly representing ancient tectonically mediated fragmentations of an ancestral taxon, blue squares representing “baselines,” and blue circles representing fossil localities included by Craw et al. (1999). In contrast, recent palaeognath fossil discoveries (red circles) indicate a broader biogeographic history, indicating the past presence of this group from many additional regions of the globe (Houde and Olson 1981; Houde 1986; Houde and Haubold 1987; Leonard et al. 2005; Bibi et al. 2006). b) A well-resolved total evidence molecular phylogeny of Palaeognathae (Smith et al. 2012) reveals evolutionary relationships incompatible with Craw et al.’s (1999) panbiogeographic tracks (e.g., the nonsister relationship of kiwi and moa).

Valen (1973) have the potential to change the network substantially.

Earth and life, so the story goes, evolve together (Croizat 1964), so the possibility of long-distance biological dispersal and establishment is typically discounted or discarded at the outset of the panbiogeographic exercise. Croizat et al. (1974), for instance, explicitly reject “dispersal of species, as a conceptual model of general applicability in historical biogeography.” Although the assumptions of panbiogeography often allow for some “normal” local dispersal (Craw et al. 1999; Crisci 2001; Grehan and Schwartz 2009), we have yet to see an empirical panbiogeographic study that argues for anything other than the primacy of some ancient vicariant process to explain distributional data. Unfortunately, this a priori rejection of long-distance dispersal as an explanation for multitaxon biogeographic pattern ignores abundant evidence supporting this important process (e.g., Muñoz et al. 2004; Renner 2004; de Queiroz 2005; Lomolino et al. 2005; Warren et al. 2009; Ali and Huber 2010; Gillespie et al. 2012; Samonds et al. 2012). Indeed, recent analyses suggest that such dispersal may well be a common and repeated process, mediated by predictable phenomena such as ocean currents, storms, and prevailing winds (Gillespie et al. 2012).

We suggest that, for any rigorous scientific approach, the proof of the pudding is in the eating: that is, that results should wherever possible be validated by independent data. In contrast, panbiogeographers have proposed scenarios that seemingly dismiss all other data regarding the history of life on earth. For example, Grehan and Schwartz (2009) reject the wealth of molecular evidence supporting a human–chimpanzee clade, instead proposing a human–orangutan sister relationship that better satisfies assumptions of vicariance. Furthermore, Heads (2010a) invokes an early Jurassic origin for primates, around 100 million years before this clade is generally accepted to have evolved (as based on congruent fossil and molecular data; Goswami and Upchurch 2010). A similarly discordant age is implied by Heads (2011) for the Asteraceae (see Swenson et al. 2012). Additionally, panbiogeographers routinely scorn the role of long-distance dispersal in assembling oceanic island biotas (Heads 2010b, 2011, 2012a), instead invoking continental land bridges and island arcs of little or no geological credibility (see critique by O’Grady et al. 2012). Such extraordinary claims surely demand extraordinary evidence, but these ideas seem to be derived simply by assuming vicariance and ignoring dispersal. When panbiogeographic hypotheses of ancient vicariance conflict with data from geology, palaeontology, and molecular genetics (as they almost inevitably do), panbiogeographers tend to dismiss these other information sources as unreliable. In our view, this attitude is akin to a young-earth creationist insisting that the world was created in 4004 BC, regardless of what geological dating, biogeography, genetics, or palaeontology might independently indicate. We note that a near-exclusive focus on vicariance and dismissal of evidence supporting alternative explanations are not unique to proponents of panbiogeography: such views are also shared by several cladistic biogeographers (Ebach and Tangney 2007).

Application of the panbiogeographic approach to the Chatham Islands biota led to claims that ancient tectonic evolutionary processes stretching back over 100 Ma explained its apparently composite nature with respect to the distribution of relatives on different parts of the New Zealand mainland (Craw 1988). Subsequent geological and palaeontological analyses, however, clearly show that the islands themselves were completely submerged until less than 10 Ma
strive to apply the most appropriate models (Felsenstein 1988; Sarich and Wilson 1967) and their imperfections (Langley and Fitch 1974; Donoghue and Smith 2003) have been known for many years and are mainstream to our understanding of evolution (Nei and Li 2000; Nei and Wilson 1974; Penny et al. 1982). Rather than throwing the baby out with the bathwater, molecular evolutionists test each particular geological time and molecular evolutionary change demonstrated a correlation, albeit imperfect, between molecular clocks (Zuckerkandl and Pauling 1962; Sarich and Wilson 1967) and their imperfections (Langley and Fitch 1974; Donoghue and Smith 2003) have been known for many years and are mainstream to our understanding of evolution (Penny et al. 1982; Graur and Li 2000). Rather than throwing the baby out with the bathwater, molecular evolutionists test each particular geological time and molecular evolutionary change demonstrated a correlation, albeit imperfect, between molecular clocks (Zuckerkandl and Pauling 1962; Sarich and Wilson 1967) and their imperfections (Langley and Fitch 1974; Donoghue and Smith 2003) have been known for many years and are mainstream to our understanding of evolution (Penny et al. 1982; Graur and Li 2000; Nei and Kumar 2000). Rather than throwing the baby out with the bathwater, molecular evolutionists test each particular geological time and molecular evolutionary change demonstrated a correlation, albeit imperfect, between molecular clocks (Zuckerkandl and Pauling 1962; Sarich and Wilson 1967) and their imperfections (Langley and Fitch 1974; Donoghue and Smith 2003) have been known for many years and are mainstream to our understanding of evolution (Penny et al. 1982; Graur and Li 2000; Nei and Kumar 2000). Rather than throwing the baby out with the bathwater, molecular evolutionists test each particular geological time and molecular evolutionary change demonstrated a correlation, albeit imperfect, between molecular clocks (Zuckerkandl and Pauling 1962; Sarich and Wilson 1967) and their imperfections (Langley and Fitch 1974; Donoghue and Smith 2003) have been known for many years and are mainstream to our understanding of evolution (Penny et al. 1982; Graur and Li 2000; Nei and Kumar 2000).


