

The Flaws of Phylogeny as History: A Pacific Islands Case Study

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Abstract

Prehistorians have long been interested in tracking the histories and migrations of past populations in a regional context. Phylogenetic reconstructions drawn largely from the methods and assumptions of historical linguistics have been a popular tool for achieving this goal, particularly among the island societies of the Pacific. Some scholars believe such reconstruction faithfully track population histories and reflect coherence in the evolution of human biology, language, and culture. In this paper, we examine the assumptions necessary to the method, revealing the weaknesses of this program to infer the complexities of history. Using the Pacific Islands as a case study, we show that patterns of similarity can result from divergent evolution in relative isolation or under conditions of continuing interaction. While phylogenetic models provide one measure of similarity, they prove too simplistic in unraveling patterns of human relatedness.

Introduction

Scholars working in the Pacific have long assumed that the remote islands of Polynesia would have remained relatively or effectively isolated following their initial colonization. This isolation would allow the comparative use of linguistics in particular to reconstruct prehistoric settlement order better than in most parts of the world (e.g., Churchill 1912; Elbert 1953; Emory 1946, 1963; Green 1966; Kirch and Green 1987). Indeed, the underlying assumption of isolation in the family tree model of linguistic subgrouping has pervaded multiple lines of research for immediate origins and settlement order within Polynesia. Scholars from outside the region (e.g., Moore 1994:14) critical of a cladistic approach to tracing ethnogenesis have even suggested that “the pure cladistic model finds an excellent illustration among the island cultures of Polynesia.” A similar position is expressed in work by Kirch (1984) and Kirch and Green (1987). They argue that the evidence of archaeology and physical anthropology “essentially confirms the linguistic subgrouping model” (Kirch and Green 1987:436 [437]).

In research over the past several decades concepts of origins, settlement order, and isolation of island communities have been shaped by use of the family tree model to reconstruct prehistory. This position is quite explicit in Kirch and Green’s (1987) paper “History, phylogeny, and evolution in Polynesia.” Using a linguistic-based, cladistic method, analysts rigorously construct patterns of uniquely shared linguistic (lexical, morpho-syntactic, phonological) innovations among demonstrably related languages (figure 1). Unique sharing, it could be assumed, marks branches of historical development in isolation from other languages. This method allowed early researchers like Kenneth Emory (1946, 1963; also Elbert 1953; Green 1966; Pawley 1966) to construct a family tree showing the branching of Polynesian languages. Emory and others assumed this family tree mapped the settlement order and subsequent isolation of human populations in the island Pacific (figure 2). The method would show origin, they believed, as unique innovations occurred in the isolated “homelands” that followed colonizing splits before new islands were settled. The model structured research and interpretation of prehistory for decades. Indeed, attempts to

confirm the hypothesized order led to marked circularity in regional research. The model was also adopted by ethnologists such as Mead (1957), Goodenough (1957), and Sahlins (1958)--who pressed the model into service to explain the divergent and convergent evolution of culture in isolation, with the notion of a "control" from common ancestry. The family tree model is derived methodologically and substantively from linguistics, yet the parallels with cladistic methods in biology have been cited in support of its use in anthropology. Thus, use of the family tree to infer history has been called the "phylogenetic approach" (Kirch and Green 1987). The approach remains pervasive in current thinking, despite the contradictions it raises (e.g., Kirch and Green 1987; Irwin 1992; Terrell et al. 1997).

The "Phylogenetic Approach" and Reconstructing History

As Moore (1994:12-13) describes "the most elementary form of the cladistic process of bifurcation is modeled after the biological notion of speciation." Species bifurcate geographically or behaviorally and gradually diverge until an evolutionary point is reached where the two can no longer exchange genetic material. Moore (1994:13) continues and suggests "an anthropological theory based on this simple model would take as a premise that each human society is a unit of evolution, maintaining its homogeneity in language, culture, and physical type through time, occasionally bifurcating into daughter societies." Moore questions the existence of such an idealized "irreducible social species." Yet notions of such a "unit" of evolution is integral to the so-called "phylogenetic approach," particularly as espoused by Kirch and Green (1987:434) or Bellwood (1996). But human populations, and their respective languages, are not species. In biology, cladistic theory is successful largely because a species, once formed, does not borrow genetic material from other species (Moore 1994:13). As Moore (1994:13) points out, humans notoriously borrow language, culture, and mates from other groups making the issue in the cladistic-ethnogenetic debate one of how significant borrowing might be. Furthermore, borrowing, or transmission, among humans is potentially continuous, including modes of vertical, horizontal, and oblique (see Boyd and Richerson 1985;

Cavalli-Sforza and Feldman 1981).

In the Pacific, researchers promoting a cladistic model for history argue that borrowing among island populations is detectable. Detection of later sharing by diffusion means that the order presented in the linguistic trees maps an historical sequence of settlement, change in isolation, and then migration (or bifurcation). Thus, we see the common notion of homelands and migrations as chapters in Pacific prehistory. The assumptions of the family tree model have also led some to build essentialist reconstructions called *Ancestral Polynesian Society* (APS, see Kirch 1984; Kirch and Green 1987). The model is explicitly linguistic. But, herein lies the clues to its flaw. As Clark (1979:263) wrote:

borrowing is the direct adoption by one language of lexical items and other features from another language. It is perhaps the major factor that complicates the family-tree model of linguistic relationships.....and frustrates the linguist's attempts to reconstruct history.

In particular, Clark (1979:263) notes the problem of direct and indirect inheritance (i.e., vertical and horizontal transmission) in the closely related languages of Polynesia. The awful truth is that not all forms borrowed among settled island populations are undetectable. There are ample historically-documented cases of this sort in the Pacific. The consequences for historical reconstructions are significant. Instead of family trees mapping origins and settlement order, they reflect degrees of sharing that arise when populations bifurcate, then sharing occurs with interaction largely as a function of geographic proximity. So, in some cases, the traits used to build the models could represent similarities from the last contacts, not sharing directly inherited by "origin." Irwin (1992:195-204) analyzes interisland voyaging accessibility and nicely illustrates the consequences for measures of similarity among Pacific populations. He concludes that "some of the signs that prehistorians have used to track the path of Polynesian expansion may actually belong to a later time" (Irwin 1992:203).

Confronting the Regrettable: Isolation and Interaction Produce the Same Patterns of Similarity

The problems with using family tree models produced by cladistic algorithms to infer historical

processes becomes apparent when we consider even the simplest models of interaction. Developing an illustration of the problem by Relethford (1993), in figure 3, we contrast the consequences of pure interaction versus pure divergence for family trees. Model 1 is based on a simple model of divergence in populations of equal sizes with bifurcation at different times. Populations begin as a single group and over time diverge into a series of sub-groups. This is precisely the sequence imagined in Kirch and Green's (1987) use of the linguistic family tree model. At the bottom of the figure, a dendrogram represents the results of an analysis of similarity between the diverged groups after t generations. Model 2, on the other hand, is based on a model where all populations are of equal size and interact with each other with slightly different probabilities shown by the thickness of the arrows. This model illustrates degrees of interaction or relative isolation among the populations compared. The dendrogram for Model 2 plots similarity assumed to be a simple function of interaction. Irwin (1992) analyzed measures of accessibility and the consequences to make a similar point. Note that the models produce the same patterns of similarity. This parallels Irwin's (1992) observation that geographic measures produced results comparable to those of family tree models or clusters for human biological data. In sum, if we only have a dendrogram or the results of a family tree analysis, we have no way of distinguishing the kinds of underlying processes that model produced the distances. Thus, we have no way to distinguish whether patterns of similarity were produced by historical divergence in isolation, under conditions of differential interaction, or a combination of each. And this problem is not limited to linguistics; Relethford (1993) argues the significance of this problem for genetic data bearing on the Out of Africa versus multiregional debate over modern human origins.

Words of Caution

But these problems have been known for a long time. In 1972, Bruce Biggs, a linguist, warned archaeologists that the settlement of Polynesia could not be viewed as a simple A to B to C sequence. In a section of his paper subtitled "movements of human population not directly derivable from linguistic subgrouping," Biggs (1972:149) argues that

It follows that any simplistic view of Polynesian settlement passing from A to B to C in a sequence which never retraces its steps will be false. It seems likely that as more detailed research is completed in the various fields which contribute to our knowledge of Polynesian prehistory, we will have to substitute for long-discarded theories of successive migrations into Polynesia, a theory of multiple intra-Polynesian migration and settlement.

Biggs (1972:150) goes on to suggest that his

line of argument is intended to suggest that where secondary contact was either sufficiently minor or sufficiently major, individual cases of secondary settlement will be undetectable linguistically. Nevertheless, viewed in its totality, Polynesia provides evidence from several fields that a settlement pattern of the kind postulated here must have prevailed.

So Biggs (1972) cautioned Pacific researchers against a simple historical reading of linguistic family tree models. His admonition followed what many linguists have long recognized--that family trees do not necessarily track historical patterns of settlement order. For example, in 1933 in a seminal work in linguistics, Bloomfield (1933:311 emphasis added) wrote:

The earlier students of Indo-European did not realize that the family-tree diagram was *merely a statement of their method*; they accepted the uniform parent languages and their sudden and clear-cut splitting, as historical realities.

These words of wisdom from linguists such as Bloomfield and Biggs seem to have been ignored by some in Polynesian research. The long-standing, often implicit, assumption was that islands insured the isolation of communities necessary for the historical interpretation of the linguistic model. Isolation seemed reasonable, not so much in the view of early scholars such as Peter Buck, but later in a kind of reactionary era associated with Andrew Sharp. Sharp countered what he saw as the simplicity of migrationism and by argument downgraded indigenous sailing and navigation capabilities (Finney 1994:257). Recent experimental and simulation research (see Finney 1994; Irwin 1992) has brought a sophisticated understanding of voyaging back to Pacific prehistory.

Rejecting the simplistic family trees as history for the Pacific is not a call to surrender. It is a renewed battle cry to document and analyze multiple lines of evidence for human similarity and difference in the Pacific. Linguistic, genetic, cultural, archaeological, and other lines of investigation will be relevant. Recent work has already shown us promising results.

Conclusions

Some may feel that we have pulled the rug out from under a useful research strategy. Yet a “phylogenetic approach” to prehistory rests on a shaky foundation. The comparative approach of historical linguistics is accorded the certainty of cladistic models in biological reconstructions. However, family trees in linguistics are only *approximately* analogous to clades in biology. Languages are not different species; nor are human populations. Closely related languages, such as those of Polynesia, are hardly immune to change from interaction (Terrell et al. 1997; Hunt and Terrell 1997). The family trees constructed from language may look like *actual histories*; that is precise and accurate overviews of discrete historical events. So their intuitive appeal is understandable. Nevertheless, such trees reflect an unknown and *unknowable* mixture of ancestry and later sharing. Sorting ancestry from contact-induced language change would require identifying *all* borrowed traits (e.g., lexicon), even those forms transformed in horizontal transmission making them appear to follow earlier shifts (e.g., phonological) in the divergence of languages (see Thomason and Kaufman 1988). Complete detection of such forms, likely to be numerous in Polynesia, is an unattainable goal in historical linguistics (e.g., Clark 1979).

Language sharing, like culture, is passed through vertical, horizontal, and oblique transmission between individuals (Boyd and Richerson 1985; Cavalli-Sforza and Feldman 1981). Interaction on varying scales allows this transmission to occur, albeit at variable rates. When the amount of vertical relative to horizontal transmission is high, populations are *relatively* isolated. Critically, the degree of isolation is an empirical question, not an assumption we should accept to fit a particular interpretive algorithm. This observation tells us we have much to learn about unraveling human history.

Now some may argue that where relative isolation is great, a phylogenetic approach has much to offer. However, the critical point is that if interaction occurred *at all* then a ‘phylogenetic’ history derived from linguistic family trees is flawed. Even some interaction over part of the field of interest will confound the interpretation of history from a family tree. As Finney (1993) points out, Easter Island’s position in the

family tree for Polynesia illustrates this point. While Easter no doubt remained well isolated following colonization, continued sharing among other populations in Polynesia made settlement of the island appear to have been remarkably early, and made it impossible to track the source for Easter's earliest colonists.

The far-flung islands of Polynesia have been promoted as the ideal case for a 'phylogenetic approach' using language family trees to infer historical events and relationships (e.g., Kirch and Green 1987; Moore 1994b). However, as we've outlined, there are compelling reasons to question the validity of interpretations drawn from the results of such a research strategy. If we are right, and there are problems in the "ideal" case of the Pacific, then we wonder how well the necessary assumption of isolation will stand elsewhere. For those defending the so-called "phylogenetic approach," we challenge them to address the validity of using synchronic linguistic data to infer history in some minimally certain terms. In its place, we would emphasize the significance of time transgressive data. We see archaeology making its contribution in multidisciplinary research on the origins of human diversity.