Evolutionary Biology: Mechanisms and Trends

Bearbeitet von
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Chapter 2
Cultural Cladistics and the Early Prehistory of North America

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Abstract Anthropology has always had as one of its goals the explanation of human cultural diversity across space and through time. Over the past few years, there has been a growing appreciation among anthropologists that the approaches biologists have developed to reconstruct the evolutionary relationships of species are useful tools for building and explaining patterns of human diversity. One of these methods is cladistics, which is a means of creating testable propositions of heritable continuity—how one thing is related to another in terms of descent. Cladistics has now been applied to a number of cultural data sets. Here we discuss several of these studies, paying particular attention to a series of related papers in which we have applied cladistics to stone tools in an effort to shed light on the early prehistory of North America. Together, these studies demonstrate that cladistics can be fruitfully applied to a range of questions concerning cultural evolutionary processes and events in prehistory.

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2.1 Introduction

Anthropology has always had as one of its chief goals the explanation of human cultural diversity across space and through time. Over the past few years, there has been a growing appreciation among anthropologists that the methods biologists have developed to reconstruct the evolutionary, or phylogenetic, relationships of species can help them achieve this goal. One such method is cladistics, the extension of which into the cultural realm is based on the recognition that cultural traits—tools, religion, kinship systems, and the like—comprise any number of parts that act in concert to produce a functional unit. The kinds of changes that occur over generations of, say, pottery manufacture are constrained in that new structures and functions usually arise through modification of existing structures and functions—descent with modification—as opposed to arising de novo. As with DNA, the history of cultural changes is recorded in the similarities and differences of the traits as they are modified over time by subsequent additions, losses, and transformations (Brown and Lomolino 1998). Our impression is that the increasing use of cladistics to study cultural diversity can be attributed to numerous factors, perhaps the primary one being a growing recognition that genes and culture are both systems of information transmission, and therefore can be analyzed in a similar manner (Boyd and Richerson 1985; Cavalli-Sforza and Feldman 1981; Mesoudi 2011).

In the following sections we (1) discuss the role cultural transmission plays in creating phylogenies; (2) summarize how cladistics works; (3) review some of the ways in which cladistics has been used in anthropology; and (4) describe several related studies in which we have applied cladistics to stone tools in an effort to shed light on the early prehistory of North America.

2.2 Cultural Transmission and Phylogeny

Phylogeny depends on the transmission of information irrespective of mode. This means that cultural transmission is as legitimate a mechanism for creating phylogenetic relationships as genetic transmission is. Using language that Cavalli-Sforza and Feldman (1981) borrowed from epidemiology, cultural transmission can be vertical in the sense of parent to offspring, analogous to genetic transmission, but it can also occur in the opposite direction—from offspring to parent. It can also be horizontal—between people of the same generation—as well as oblique—through unrelated people of different generations.

There are, however, those who object to using phylogenetic methods to study culture history. These objections take several forms. First, it has long been argued by certain anthropologists that phylogenetic methods cannot be applied to cultural objects because cultural objects do not breed (Brew 1946). Obviously, this is true in a strict sense; stone tools, ceramic vessels, musical instruments, and the like do

not have sex, become pregnant, and give birth. However, objects are replicated with greater or lesser fidelity of replication as a result of cultural transmission; therefore, toolmakers and the like are *cultural* descendants of other toolmakers. Cultural transmission creates *traditions*—persistent configurations in single technologies or other systems of related forms (Willey and Phillips 1958). Traditions are collections of related *lineages*, and both phenomena reflect transmission, persistence via replication, and heritable continuity.

It has also been argued that because of the nature of cultural evolution it is difficult to recognize the phylogenetic signal of cultural lineages (e.g., Tëmkin and Eldredge 2007; Terrell et al. 1997). Under this view, cultural evolution is seen as a vastly different kind of process than biological evolution, with a faster tempo and often a different mode—reticulation—both of which act to swamp all traces of phylogenetic history and thus reduce the cultural landscape to little more than a blur of interrelated, hybrid, forms (e.g., Tëmkin and Eldredge 2007; Terrell et al. 1997). Cultural evolution probably is, in most respects, faster than biological evolution, and cultural evolution likely quite often involves reticulation, but these aspects are not particularly problematic theoretically. It is well-documented that biological evolution often involves reticulation (e.g., Russell et al. 2010), especially in the plant kingdom, but this has not precluded phylogenetic analysis. The same applies to the cultural realm.

2.3 Building Cladograms

Cladistics, first developed in the 1940s by the German entomologist Willi Hennig (1950, 1965), is today one of the main methods of phylogenetic reconstruction used in biology (e.g., Cap et al. 2008; Lycett et al. 2007; Mallegni 2007; O'Leary and Gatesy 2008; Smith and Grine 2008). The central tenet of cladistics is that not all phenotypic similarities are equally useful for reconstructing phylogenetic relationships. Cladistics divides phenotypic similarities into three kinds. *Synapomorphies* are similarities between two or more taxa that are inherited from the taxa's most recent common ancestor; *symplesiomorphies* are similarities between two or more taxa that are inherited from a more-distant common ancestor; and *homoplasies* are similarities resulting from processes other than descent from a common ancestor, such as convergence, parallelism, and horizontal transmission among lineages (Collard and Wood 2001; Sanderson and Hufford 1996). Of these three types of similarity, only synapomorphies are informative with regard to phylogenetic relationships.

Based on a model of descent with modification in which new taxa arise from the bifurcation of existing ones, cladistics defines phylogenetic relationships in terms of relative recency of common ancestry. Two taxa are deemed to be more closely related to one another than either is to a third taxon if they share a common ancestor that is not also shared by the third taxon. The evidence for exclusive common ancestry is evolutionarily novel, or *derived*, character states. Two taxa are

inferred to share a common ancestor to the exclusion of a third taxon if they exhibit derived character states that are not also exhibited by the third taxon.

In its simplest form, cladistic analysis proceeds via four steps. First, a character-state data matrix is generated. This shows the states of the characters exhibited by each taxon. Second, the direction of evolutionary change among the states of each character is established. Several methods have been developed to facilitate this, including communality (Eldredge and Cracraft 1980), ontogenetic analysis (Nelson 1978), and stratigraphic-sequence analysis (Nelson and Platnick 1981). Currently, the favored method is *outgroup analysis* (Maddison et al. 1984), which entails examining a close relative of the study group. When a character occurs in two states among the study group, but only one of the states is found in the outgroup, the principle of parsimony is invoked (see below), and the state found only in the study group is deemed to be evolutionarily novel with respect to the outgroup state.

After the probable direction of change for the character states has been determined, the third step is to construct a branching diagram of relationships for each character. This is done by joining the two most derived taxa by two intersecting lines and then successively connecting each of the other taxa according to how they are derived. Each group of taxa defined by a set of intersecting lines corresponds to a *clade*, and the diagram is referred to as a *cladogram*. Ideally, the distribution of the character states among the taxa will be such that all the character cladograms imply relationships among the taxa that are congruent with one another. Normally, however, a number of the character cladograms will suggest relationships that are incompatible. This problem is overcome through the fourth step, generating an *ensemble cladogram* that is consistent with the largest number of characters and therefore requires the smallest number of homoplasies to account for the distribution of character states among the taxa. Such a cladogram is referred to a the "most parsimonious" cladogram. An example of an ensemble cladogram is shown in Fig. 2.1.

There are numerous techniques for measuring the goodness of fit between a data set and a given cladogram. The consistency index (CI) and the retention index (RI) are the most commonly used. The CI measures the relative amount of homoplasy in a data set but is dependent on the number of taxa. Thus, the expected CI for a given cladogram must be assessed relative to the number of taxa used in the analysis (Sanderson and Donoghue 1989). The RI measures the number of similarities in a data set that are retained as homologies in relation to a given cladogram. It is insensitive to both the presence of derived character states that are present in only a single taxon (*autapomorphies*) and the number of characters or taxa employed. Thus, it can be compared among studies (Sanderson and Donoghue 1989). Both indices range from zero, which indicates a lack of fit between the cladogram and the data set, to 1.0, which represents a perfect fit.

Methods other than cladistics have been used to create orderings that the analyst assumes are based on evolutionary relatedness. These are termed *phenetic* approaches and include such methods as hierarchical clustering. These approaches, however, are of dubious merit from an evolutionary standpoint because the algorithms used do not search for shared derived characters. In fact, they do not
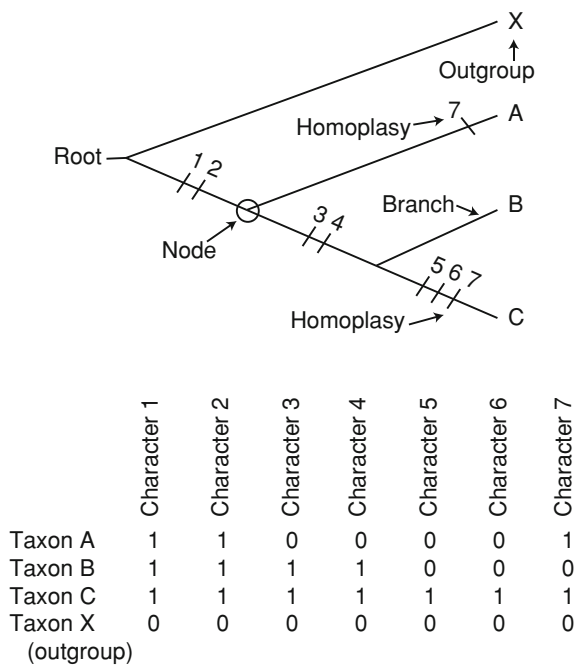
	Character 1	Character 2	Character 3	Character 4	Character 5	Character 6	Character 7
Taxon A	1	1	0	0	0	0	1
Taxon B	1	1	1	1	0	0	0
Taxon C	1	1	1	1	1	1	1
Taxon X (outgroup)	0	0	0	0	0	0	0

Fig. 2.1 An example of a tree of evolutionary relationships generated by means of cladistics, together with the character-state data matrix from which it was derived. Trees of evolutionary relationships generated with cladistics are usually referred to as "cladograms," and are read from the tips to the root. Thus, the cladogram shown here indicates that taxa B and C form a monophyletic group (clade) to the exclusion of taxon A based on the shared possession of derived character states for characters 3 and 4. It also suggests that taxa A, B, and C form a monophyletic group based on the shared possession of derived character states for characters 1 and 2. Taxon C is the most derived taxon, having derived states for character 5, 6, and 7 in addition to the other derived characters. Character 7 is homoplastic, as it is in a derived state in taxa A and C but is not inherited from a common ancestor.

distinguish between homologous and homoplastic traits, let alone between shared derived and shared ancestral traits. Rather, they look for overall similarities among sets of taxa and then group the most similar taxa together. Work carried out in biology over the last half century has demonstrated that overall similarity can be expected to be a poor guide to phylogenetic relationships among species. The same applies to cultural phenomena.

2.4 Phylogenetic Trees in Anthropology

In recent years, cladistics and related methods have been used to examine a range of anthropological problems. Some of these studies have used linguistic data to create phylogenies and then mapped other cultural traits or dispersal patterns to