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.

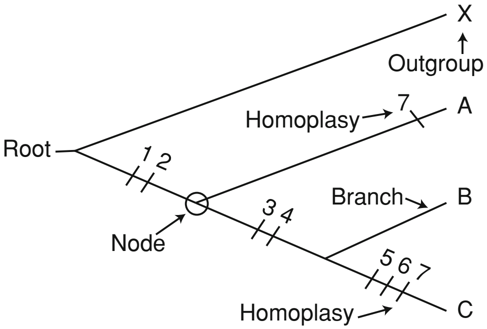
Based on a model of descent with modification in which new taxa arise from the bifurcation of existing ones, cladistics defines phylogenetic relationships in terms of relative recency of common ancestry. Two taxa are deemed to be more closely related to one another than either is to a third taxon if 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 test specific hypotheses. For example, Gray and Jordan (2000) employed cladistic methods to assess the two main competing models regarding prehistory in the Pacific, the express-train model, and the entangled-bank model. The former suggests a rapid dispersal of Austronesian speakers from a homeland in Taiwan around 6,000 years ago through Island Melanesia and into the Polynesian islands of the remote Pacific, whereas the latter contends that the Polynesian colonizers derived from a population in Island Melanesia that had been there for tens of thousands of years. In the entangled-bank model, the cultural and linguistic patterns among Polynesians are the complex result not just of colonization but also of founder effects and continued cultural contact among different islands during the subsequent millennia, with genetic, linguistic, and cultural traits transmitted at varying intensities between populations.

In the entangled-bank model, linguistic patterns largely reflect human interaction and continued cultural transmission rather than the phylogenetic history of the language speakers described by the express-train model. To test these conflicting models, Gray and Jordan (2000) used cladistics to produce a phylogeny of Pacific languages onto which they then mapped the prehistoric events suggested by the express-train model. They found a close fit between the chronological stages of the express-train model and the branching pattern of their language phylogeny. Gray and Jordan concluded that these linguistic patterns result predominantly from colonizing migrations of the language speakers rather than cultural contact since the time of initial colonization.

Holden (2002) conducted a comparable analysis in which she used maximum-parsimony analysis to reconstruct the relationships among 75 Bantu and Bantoid African languages from 92 items of basic vocabulary. As in the Polynesian case, some researchers contend that the Bantu languages evolved rapidly during the Neolithic and Iron Age with the movement of farmers into sub-Saharan Africa, whereas others hold that the evolution is mainly the result of diffusion of Bantu words among neighboring speech communities. Holden's analysis returned a relatively small set of possible phylogenetic trees in support of the tree model of Bantu language history and found these trees to be consistent with the model for the spread of farming in sub-Saharan Africa constructed by archaeologists through chronological analysis of pottery. Holden concluded that the dispersal and diversification of the Bantu languages was linked to the expansion of farming during the Neolithic and Iron Age and that since that time Bantu-speaking communities have not moved to any great extent.

Language trees have also been combined with archeological and molecular data to examine the spread of human populations (e.g., Cann 2001; Renfrew and Boyle 2000), but what about cases where the archaeological record is too old for language phylogeny to be of any help? As we explore below, cultural phylogenies do not have to depend on linguistic data to give them their basic structure; phylogenetic methods can be applied directly to material items, including pottery (Collard and Shennan 2000; Harmon et al. 2006), basketry (Jordan and Shennan 2003), stone tools (Beck and Jones 2007; Buchanan 2005; Buchanan and Collard 2007, 2008a, b; Darwent and O'Brien 2006; Foley 1987; Foley and Lahr 1997; Lycett 2007, 2009a, b; O'Brien et al. 2001, 2002), textiles (Tehrani and Collard 2002), and stone tablets (García Rivero 2010). In the following section, we discuss a series of studies that have applied cladistics to material creature to explore the early prehistory of North America.

2.5 Stone Tools, Cladistics, and the Early Prehistory of North America

The earliest well-documented human occupation of North America is marked by the occurrence of bifacially chipped and fluted projectile points (Haynes 1964) that date roughly 13,300–11,900 calendar years before present [calBP] (Faught 2008; Hamilton and Buchanan 2007). This time period is usually referred to as the *Early Paleoindian period*. Despite the fact that it is marked by the presence of fluted points, the Early Paleoindian period encompassed a range of spatial and temporal variation in such things as settlement pattern, diet, and technology (Haynes 2002; Meltzer 1993). The picture that has emerged for the first several 100 years of the Early Paleoindian period is one of hunters who targeted a wide range of large game animals, including mammoth, mastodon, bison, and, in the eastern woodlands, caribou (Cannon and Meltzer 2004; Spiess et al. 1985; Surovell and Waguespack 2009). In contrast, later hunters, at least those in the West, appear to have specialized in bison hunting (Amick 1994). The temporal shift in game animals may have resulted from the extinction of the majority of large North American species at the end of the Pleistocene.

There are also significant technological differences between earlier and later weapons. The former are dominated by a fairly standardized stone spear tip referred to as a *Clovis* point—an elongated symmetrical form that exhibits a concave base and a series of flake-removal scars one or both faces that extend upward from the base (Fig. 2.2a). In the West, especially the Plains and Southwest, Clovis points were succeeded by *Folsom* points, which are different in shape and tend to be smaller and have more invasive channel flakes (Collard et al. 2011) (Fig. 2.2c). In the East, Clovis points were followed by numerous fluted forms (Fig. 2.2b, d–f), which some investigators (e.g., Meltzer 2004) have suggested reflect different adaptive strategies employed by regional populations in response to local environmental conditions.

2.5.1 Colonization

Where did the early inhabitants of North America come from? The most widely accepted hypothesis is that hunter-gatherer groups migrated by way of Beringia, the landmass between Siberia and North America that was exposed by sea-level reduction during glacial intervals (Haynes 2005). Once in eastern Beringia, the

Fig. 2.2 Examples of Paleoindian fluted projectile points from North America: **a** Clovis (Logan Co., Kentucky); **b** Dalton (Lyon Co., Kentucky); **c** Folsom (Roosevelt Co., New Mexico); **d** Cumberland (Colbert Co., Alabama); **e** Gainey/Bull Brook (Essex Co., Massachusetts); **f** Crowfield (Addison Co., Vermont)

groups gained entry to the interior of the continent, specifically the Great Plains, by way of an ice-free corridor between two ice sheets that is hypothesized to have opened around 14,000 calBP (Catto 1996). Thereafter, according to this model, the Early Paleoindians spread rapidly throughout North and South America, reaching the Patagonian Plateau within just a few centuries (Fiedel 2000). The speed with which the Early Paleoindian populations colonized the Americas is generally believed to be the result of rapid population growth (Martin 1973).

Although the ice-free corridor route model remains popular, a number of alternative migration routes have been proposed. One is along the Pacific Coast. This pathway, usually referred to as the "Northwest Coast model," suggests that maritime-adapted groups using boats moved along the ice-free western coast and sometime later moved east into the interior of the continent (Dixon 1993; Fladmark 1979). Another possibility is that Early Paleoindians could have rapidly skirted the western coast of North America and established their first substantial colonies in South America. Following the colonization of South America, groups could then have moved northward and populated North America by way of the Isthmus of Panama (Anderson and Gillam 2000). We refer to this hypothesis as the "Isthmus of Panama model." Lastly, a trans-Atlantic voyage from Europe has also been proposed as a possible colonization scenario. The main proponents of this model suggest that a number of similarities between Clovis and pre-Clovis technology on the one hand and 18,000-year-old stone-tool technology from France and Spain on the other indicate a historical connection (Stanford and Bradley 2012). They suggest that the makers of the 18,000-year-old stone tools, the Solutrean people, left what is now northern Spain, traveled along an ice bridge between Europe and North America, and entered North America in the Midatlantic region. We refer to this hypothesis as the "Solutrean model."

Buchanan and Collard (2007, 2008a) applied cladistics on a continent-wide sample of Early Paleoindian points from 25 sites to assess the competing models of colonization as well as several alternative explanations for morphological variation among the points, including adaptation to local environmental circumstances. They used cladistics because the general process of colonization is expected to give rise to historical relationships among populations. This is usually a result of continual population fissioning and reduced contact, if not complete isolation, during colonization and exploration, which can be expected to lead to distinct cultural traditions created through selection and drift of cultural traits. Not only is cladistics amenable to finding such branching patterns in cultural data sets but it also provides a testable means of choosing among competing hypothesis with regard to the particular population history that produced the branching patterns.

Prior to testing the competing models, Buchanan and Collard first established if the Early Paleoindian–point data had a significant phylogenetic signal. As mentioned previously, critics of cultural cladistics argue that cultural reticulation is often so severe that it swamps phylogenetic signals. In this scenario, the sharing of cultural traits—for example, the borrowing of manufacturing and hafting techniques of Clovis points—among groups could destroy any branching signal that might have once existed. Alternatively, the *convergence* of cultural traits through similar adaptations can also destroy a phylogenetic signal. This could occur if Early Paleoindians using similar adaptations in similar environments independently developed adaptive solutions to environmental problems.

Buchanan and Collard subjected the Early Paleoindian–point dataset to a series of tests to determine how well the data fit a branching pattern. The dataset consisted of 15 quantitative and qualitative traits recorded for each of the points in the 25 site assemblages, similar to how a biologist or paleobiologist uses morphological data to define species. The quantitative traits were measured using a digitizing technique to extract several distance measures that described individual point size and shape (Fig. 2.3). Buchanan and Collard employed several tests to determine if the data contained a phylogenetic signal. They then used these tests to give an indication of how well the data fit a branching pattern and what percentage of the data could be explained as homoplasy. The tests included a randomization procedure (the permutation tail probability test), goodness-of-fit statistics

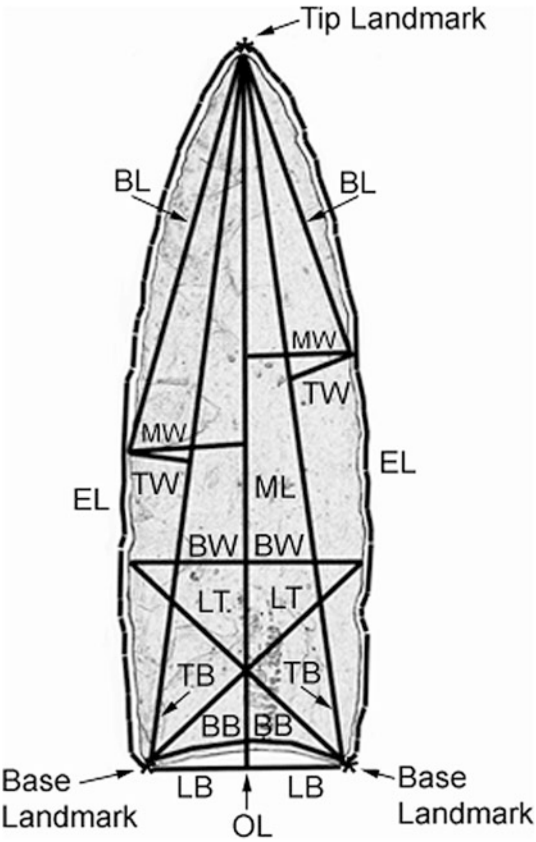


Fig. 2.3 Image of a Clovis point showing approximate locations where 11 interlandmark characters are measured and the locations of the three landmarks: EL, edge boundary length; TB, tip landmark to base landmark; TW, width of tip to base length to maximum inflection position; BL, blade length; MW, maximum width; BB, base boundary length; LB, linear measure of base; ML, midline length; OL, overall length; BW, basal width across proximal third of point; LT, length from base to 1/3 along opposite edge (from Buchanan and Collard 2007)

(the consistency index and the retention index), and the phylogenetic bootstrap, all of which indicated that a significant phylogenetic signal existed in the dataset. This result was consistent with the hypothesis that Early Paleoindian populations colonized the continent by repeated fissioning.

The next step was to assess which colonization model best fit the tree derived from the point data. To accomplish this, Buchanan and Collard converted each colonization model into a hypothetical tree. This was done by arranging the branches in each tree to represent the distinct branching pattern of population fissioning that followed the pattern of each model. For example, the ice-free corridor model contends that Early Paleoindian populations entered the contiguous United States through the southern opening of the corridor located in southern Alberta (represented by the red node in Fig. 2.4) and subsequently moved into the Northern Plains and Northwest regions (represented by the yellow node in Fig. 2.4). Thus, in this model point traditions in the Northwest and Northern Plains are expected to have branched off from their common ancestor in southern Alberta (Fig. 2.4).

In addition to the colonization models, Buchanan and Collard constructed hypothetical trees to represent environmental-adaptation hypotheses. They then conducted a statistical test used by phylogeneticists to assess the strength of fit between observed and hypothetical trees (the Kishino-Hasegawa test (Kishino and Hasegawa 1989)). In this test, a *p*-value is calculated for the length difference between a hypothetical tree and an observed tree by comparing the difference to a distribution of length differences obtained from a randomly generated sample of trees. Buchanan and Collard found that the four best-fitting trees were all significantly different from the hypothetical trees. They then compared tree lengths to assess the fit of the hypothetical trees to the observed trees (Jordan and Shennan 2003). Using this approach, the ice-free-corridor colonization model was found to be the one that best accounted for the structure in the dataset and the only model that fit the observed data better than would be expected by random chance.

2.5.2 The Origins of Clovis

What about the origins of Clovis itself? Were the people who made the early fluted points evolved from an earlier culture of people moving eastward from Siberia into Alaska? The Clovis point is almost exclusively an interior United States phenomenon, meaning that tool assemblages identified as Clovis, usually based on the association of the diagnostic Clovis point type with other tools, are found infrequently north of the United States–Canada border, and when they are, they date later in time, probably tools left by people back-migrating into more northern territory.

Two archeological complexes in Alaska that potentially predate Clovis—Nenana and Denali—have figured prominently in discussions about the origins of Clovis over the last decade. Nenana tool assemblages are characterized by large stone flakes and fairly large bifacially flaked tools. In contrast, Denali assemblages contain microblades, which are small, specially prepared cutting tools that are rectangular in shape, and burins, which are small flakes with chisel-like edges used for engraving or carving wood or bone. Neither Denali nor Nenana assemblages contain fluted points, which are the most distinctive feature of Clovis. The question is whether Clovis is related phylogenetically to either, and if so, to which? More specifically, is one the progenitor of Clovis?

Nenana has until recently been considered the oldest cultural horizon in Alaska, with assemblages recovered stratigraphically below Denali assemblages in cases where the two complexes have been recovered from the same site (Bever 2006). However, an assemblage containing microblades recovered from the lowest level of a site in the Tanana Valley is now considered the oldest dated assemblage in Alaska (Bever 2006). Thus, the temporal relationship between Nenana and Denali is uncertain. Accordingly, using age to indicate which of them is most likely ancestral to Clovis is problematic.

Currently, most researchers consider Nenana to be more closely affiliated with Clovis than with Denali—a consensus based primarily on the results of a study reported by Goebel and colleagues (1991) that drew on a dataset comprising 77

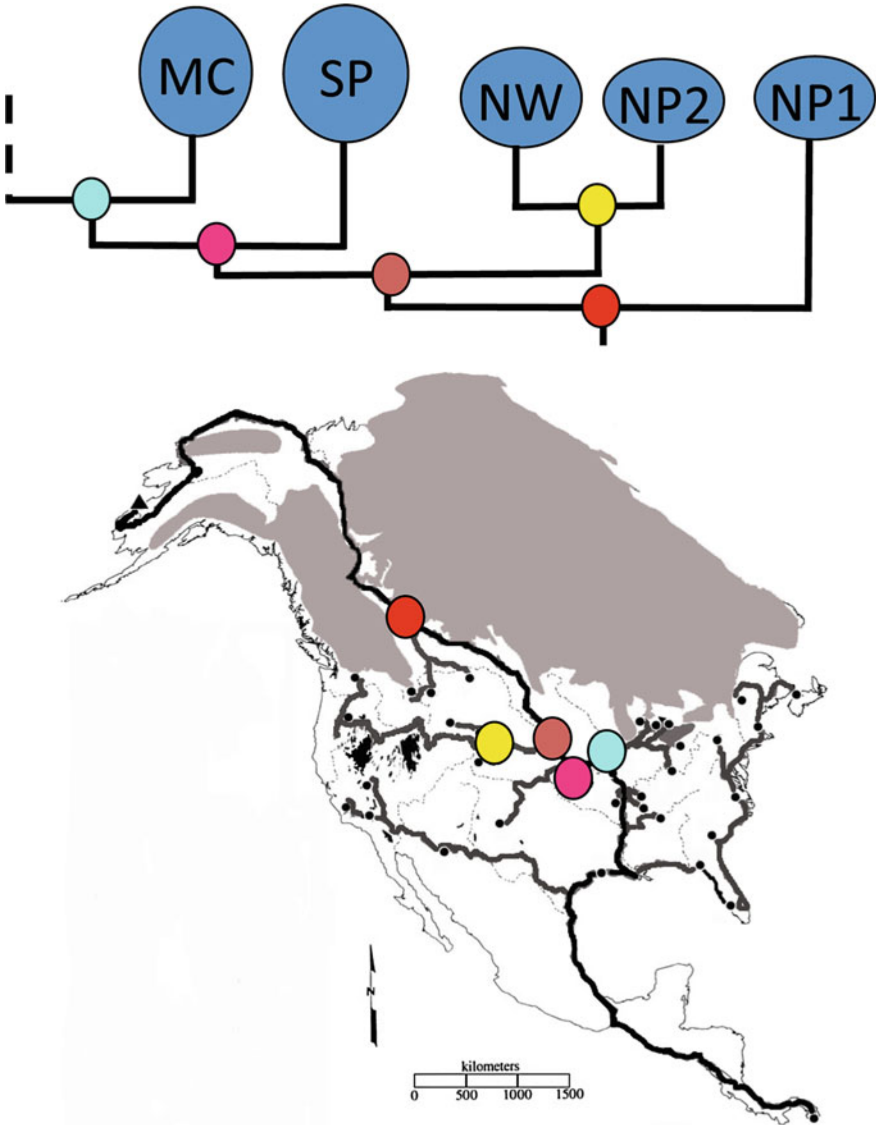


Fig. 2.4 Ice-free-corridor entry model (bottom) showing five hypothesized branching events of a colonizing population using projectile-point data from selected archeological sites. The base map shows a GIS-based least-cost-solution pathway for North American colonization with glacial (stippled) and pluvial lake (black) boundaries reconstructed for 12,000 years calBP (from Anderson and Gillam 2000). The black triangle at the upper left represents the hypothesized starting point of entry. The black dots show the locations of Paleoindian sites identified in Anderson and Gillam's (2000) analysis. The nodes of branching events are shown as colored circles. The tree (top) illustrates the phylogenetic relationship of spatially clustered assemblages of projectile points from each of five colonized regions: *NP1* Northern Plains subregion 1, *NP2* Northern Plains subregion 2, *NW* Northwest, *SP* Southern Plains, *MC* Midcontinent. The colored nodes on the tree, representing branching events, have been plotted on the map. Note the correspondence of the spatial sequence and the phylogenetic sequence

tool types from five archaeological assemblages. Two were assigned to Nenana, two to Clovis, and one to Denali. Goebel and colleagues investigated the relationships among the assemblages using cumulative percentage curves and hierarchical cluster analysis. They found that Nenana clustered more closely with Clovis than with Denali and concluded from this that Nenana was likely ancestral to Clovis (Fig. 2.5 top).

Buchanan and Collard (2008b) subjected Goebel and colleagues' data to a set of phenetic analyses using a suite of different clustering methods and demonstrated that the topology of any of the resulting dendrograms was dependent on the combination of clustering algorithm and distance measure employed. Dendrograms showing Denali as most distant to Clovis were produced but so were dendrograms showing Nenana as being most distant to Clovis. Unlike with cladistics, phenetics provides no objective basis for choosing one dendrogram over another. Next, Buchanan and Collard subjected the dataset to a cladistic analysis and derived results different from the ones presented by Goebel et al. (1991). The cladogram that Buchanan and Collard produced (Fig. 2.5 bottom) strongly suggests that Denali and Clovis are in fact more closely related to each other than either is to Nenana. This suggests that Clovis is either descended from Denali or that Clovis and Denali are descended from an as yet unknown ancestor.

2.5.3 *The Evolution of Paleoindian Culture in the Eastern United States*

Early Paleoindian colonization of the interior of North America was a rapid process (Buchanan and Hamilton 2009; Hamilton and Buchanan 2007, 2009), taking not more than 500 years or so for occupation to spread to the extreme Southeast and Northeast. During that period, projectile points diversified, especially in the hafting element—the part of a stone point that is affixed to a shaft or foreshaft (Fig. 2.2). This variation is patterned temporally and spatially, although often not in straightforward ways, and archaeologists have created several point types to keep track of the variation.

Tracking ancestry implies that we can not only put things such as point types in their correct historical sequence but that the sequence reflects patterns of descent: which point type evolved out of which other type? To begin to answer this question, O'Brien and colleagues (Darwent and O'Brien 2006; O'Brien and Lyman 2003; O'Brien et al. 2001, 2002) used cladistics to create a phylogenetic ordering of Paleoindian points from the southeastern United States based on morphometric characters similar to those later used by Buchanan and Collard (2007, 2008a).

O'Brien and colleagues began by recording three qualitative and five quantitative characters on a sample of 621 specimens representing a range of projectile point types, including Clovis, Dalton, and Cumberland (Fig. 2.2). They then subjected the specimens to paradigmatic classification in order to cluster them into

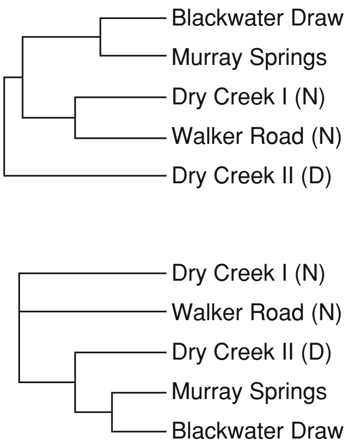


Fig. 2.5 Two possible orderings of five early (pre-13,000 calBP) cultural assemblages from the United States. Two are Clovis assemblages from the American Southwest (Murray Springs and Blackwater Draw), and the other four are from Alaska—two Nenana (N) assemblages and two Denali (D) assemblages. Using overall assemblage similarity, Goebel et al. (1991) see the Nenana complex as being more similar to Clovis than either is to Denali (*top*). They speculate that Nenana may in fact be ancestral to Clovis. Buchanan and Collard's (2008b) cladistic analysis, however, shows that Denali and Clovis are more closely related than either is to Nenana (*bottom*)

taxa with unique combinations of character states. In the next part of the study, O'Brien and colleagues carried out a cladistic analysis of the 17 taxa that contained at least 4 specimens. One of the 17 taxa was selected as the outgroup on the basis of least-step occurrence seriations and chronological considerations; the remainder were treated as the ingroup. The cladistic analysis yielded a single most parsimonious cladogram that had a CI of 0.59, which suggests that it is a reasonable depiction of the relationships among the taxa. In the final part of their study, O'Brien and colleagues used the cladogram to investigate the character-state changes that occurred in the course of the evolution of Paleoindian projectile point form.

Boulanger et al. (2012) subsequently expanded the database to include specimens from the Atlantic Seaboard westward into Tennessee, Kentucky, and Pennsylvania. One of their trees is illustrated in Fig. 2.6. Note the presence of four well-defined clades (labeled 1–4), each containing between four and seven sister taxa. When Boulanger and colleagues plotted the geographic distribution of the taxa, there seemed to be no clear-cut regional differences (larger samples may eventually change that), supporting Buchanan and Hamilton's (2009) conclusions that (1) variation in Early Paleoindian point form across North America was primarily the result of drift (see also Morrow and Morrow 1999) and (2) Clovis-point technology was highly stable and capable of performing well in the diverse environments of the North American Late Pleistocene.

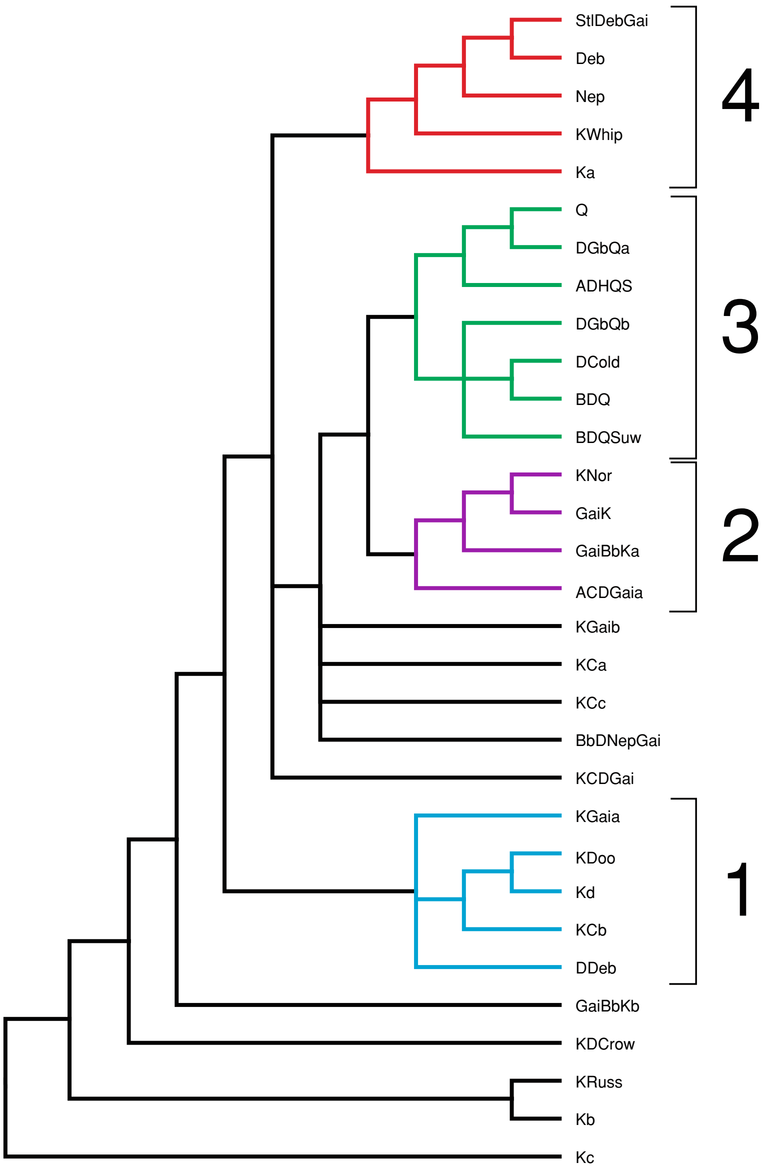


Fig. 2.6 Cladogram showing relationships among 32 projectile-point taxa from the eastern United States (after Boulanger et al. 2012)

2.6 Conclusions

The growing interest in cultural phylogenetics evident over the last few years marks a return to the questions on which the foundation of much of anthropology rests—a return that is important to the growth and continued health of anthropology. Why? Because, as Linder and Rieseberg (2004), point out, a reconstructed phylogeny helps guide interpretation of the evolution of traits by providing hypotheses about the lineages in which those traits arose and under what circumstances. Thus, it plays a vital role in studies of adaptation and evolutionary constraints.

One long-held goal of anthropology has been to explain the historical development of cultural traditions. This is why, as we have pointed out before (O'Brien et al. 2008), issues such as the origins of the use of fire, the rise of urbanism, the appearance of complex sociopolitical organization, the development of agriculture, the effects of the technological development of pottery, and the like have occupied so much anthropological attention. It is impossible to imagine an anthropology that does not have those as central issues. Cladistics, although developed in the biological sciences, offer a means of situating these anthropological problems in a framework that provides a means of creating testable propositions of heritable continuity.

Here we have attempted to lay out in the barest of form how cladistics can offer insights into one important archaeological problem, the initial colonization of North America and the subsequent dispersal of populations. Cladistics offers an objective means of discriminating among competing hypotheses, but more important, the assumption underlying cladistics is that the method provides measures not only of similarity but of similarity resulting from evolutionary relationships. Paleontologist George Gaylord Simpson (1961), using monozygotic twins as an example, made an excellent point: they are twins not because they are similar; rather, they are similar *because* they are twins. That is, they are similar because they share a common history. Cladistics helps us understand that common history, whether it be a history of organisms or of projectile points.

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