



Innovation and cultural transmission in the American Paleolithic: Phylogenetic analysis of eastern Paleoindian projectile-point classes



Michael J. O'Brien^{a,*}, Matthew T. Boulanger^a, Briggs Buchanan^b, Mark Collard^{c,d}, R. Lee Lyman^a, John Darwent^e

^a Department of Anthropology, University of Missouri, Columbia, MO 65211, USA

^b Department of Anthropology, University of Tulsa, Tulsa, OK 74104, USA

^c Human Evolutionary Studies Program and Department of Archaeology, Simon Fraser University, Burnaby V5A 1S6, Canada

^d Department of Archaeology, University of Aberdeen, Aberdeen AB24 3UF, UK

^e Department of Anthropology, University of California, Davis, CA 95616, USA

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ABSTRACT

North American fluted projectile points are the quintessential temporally diagnostic artifacts, occurring over a relatively short time span, from ca. 13,300 calBP to ca. 11,900 calBP, commonly referred to as the Early Paleoindian period. Painting with a broad brush, points from the Plains and Southwest exhibit less diversity in shape than what is found in the East, especially for the later half of the Early Paleoindian period. It remains unclear how various fluted-point forms relate to each other and whether the continent-wide occurrence of the earliest fluted-point forms represents a single cultural expression, albeit with regional differences. We used phylogenetic analysis to evaluate fluted-point classes from the eastern United States. Preliminary results suggest that there is both temporal and spatial patterning of some classes and that much of the variation in form has to do with modifications to hafting elements. Although our analyses are presently at a coarse scale, it appears that different kinds of learning could contribute in part to regional differences in point shape.

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Introduction

The earliest well-documented human occupation of North America is marked by the occurrence of bifacially chipped and fluted projectile points. The antiquity of these points—ca. 13,300–11,900 calendar years before present [calBP], a time span referred to as the Early Paleoindian period—was first documented in the American Southwest at Folsom and Blackwater Draw, New Mexico (Cotter, 1937, 1938; Figgins, 1927), where they were found with the remains of extinct animals such as mammoth and large bison. Since those early discoveries in the late 1920s and early 1930s, archaeologists have recovered fluted points throughout the contiguous United States, Alaska, southern Canada, and northern Mesoamerica (Anderson and Faught, 1998, 2000; Anderson et al., 2010; Buchanan and Collard, 2007, 2010; Buchanan et al., 2012; Goebel et al., 2008; Haynes, 1964; Holliday, 2000; Prasciunas, 2011; Sanchez, 2001; Sholts et al., 2012; Smallwood, 2012; Waters and Stafford, 2007).

Point shape was not consistent throughout the Early Paleoindian period. Between ca. 13,300 calBP and 12,800 calBP in the West

and between ca. 12,800 calBP and 12,500 in the East (Gingerich, 2011; Haynes et al., 1984; Haynes, 2002; Holliday, 2000; Levine, 1990) there was a single type of point, termed “Clovis,” which has parallel to slightly convex sides and a concave base, and exhibits a series of flake-removal scars on one or both faces that extend from the base to about a third of the way to the tip (Fig. 1) (Bradley, 1993; Buchanan and Collard, 2010; Morrow, 1995; Sholts et al., 2012; Wormington, 1957).

This description may perhaps give the impression that Clovis points do not vary, but this is not the case. They are, in fact, quite variable—considerably more than is evident in Fig. 1. This brings into focus an issue that we treat in detail later but should mention here: When we said in the preceding paragraph that “there was a single type of point, termed ‘Clovis,’” we should have made clear that what we really mean is something like this: “Despite obvious variation in point shape, archaeologists typically refer to early fluted points by one name—Clovis.” Sometimes other names are used for regional variants—Western Clovis and Redstone, for example—but “Clovis” is the time-honored default label for a morphologically variable category.

The key analytical question is, what accounts for the variation in Clovis point shape? Is it the result of drift—that is, is it random—or is

* Corresponding author. Fax: +1 573 882 3404.

E-mail address: obrienm@missouri.edu (M.J. O'Brien).



Fig. 1. Clovis points from various North American sites. Photo by Charlotte D. Pevny; courtesy Michael R. Waters.

there perhaps an adaptive reason that results in regional patterning? The latter position—what has been called the *regional environmental adaptation hypothesis* (Buchanan et al., 2014)—holds that Clovis groups adapted their hunting equipment to the characteristics of their prey and local habitat, which resulted in regional differences in projectile-point form (Anderson, 1990; Meltzer, 1988, 1993; Smallwood, 2012; Storck and Spiess, 1994; Witthoft, 1952, 1954). The alternate position—the *continent-wide adaptation hypothesis* (Buchanan et al., 2014)—holds that Clovis groups did not adjust the shape of their points in relation to local environmental conditions (Buchanan and Hamilton, 2009; Byers, 1954; Haynes, 1964; Kelly and Todd, 1988; Krieger, 1954; Morrow and Morrow, 1999; Robinson et al., 2009; Sholts et al., 2012; Willey and Phillips, 1958). Recent geometric morphometric analysis of a sample of 241 Clovis points from 30 dated assemblages across North America (excluding the Far West and Southeast) showed that significant morphological differences do occur, both at the gross level of East versus West (using the Mississippi River as a dividing line) and between some subregions, leading Buchanan et al. (2014) to conclude that Clovis people modified their points to suit the characteristics of local prey and/or the habitats in which they hunted. We return to this proposition in the Discussion section.

In the West, especially the Plains and Southwest, Clovis points were followed by “Folsom” points, which tend to be smaller in size than Clovis points and to have more-invasive channel flakes (Ahler and Geib, 2000; Buchanan and Collard, 2010; Collard et al., 2010; Crabtree, 1966; Wormington, 1957) (Fig. 2). Our impression is that Folsom points are more standardized in terms of shape than Clovis points, perhaps reflecting strict requirements imposed by the hafting technique (Amick, 1995; Buchanan, 2006; Judge, 1970; Tunnell and Johnson, 1991). There was no such large-scale standardization in the East, where Clovis points were followed by a host of fluted forms such as Gainey/Bull Brook and Crowfield in the Northeast and Great Lakes region; Dalton, Quad, and Cumberland over much of the South and Midsouth; and Simpson and Suwannee in the extreme Southeast (Anderson, 1990; Anderson et al., 1996, 2010; Bradley, 1997; Bradley et al., 2008; Brennan, 1982; Bullen, 1968; Goodyear, 1982; Lewis, 1954; MacDonald, 1968; Mason, 1962; O'Brien et al., 2001; Robinson et al., 2009; Thulman, 2007, 2012) (Fig. 2). Because of a paucity of radiometric dates from many areas of the East, especially the Southeast (O'Brien et al., 2001), it is in some cases difficult to tell how much of the variation is synchronic and how much is diachronic (see below).

How do we explain what appears to be even greater regional point diversity in the later portion of the Early Paleoindian period



Fig. 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).

in the East than what occurred with Clovis points? Was it a continuation of the regional adaptation proposed by Buchanan et al. (2014) for Clovis variation, or could the diversity at least in part reflect differences in how people learned to make weaponry and how they transmitted that information intra- and intergenerationally? Differences in learning strategies have been suggested as the explanations for geographic patterning in arrowhead form in the Great Basin (Bettinger and Eerkens, 1999), and this hypothesis has been supported by laboratory experiments (Mesoudi and O'Brien, 2008a, 2008b). It is possible that a similar phenomenon structured the patterning evident across much of North America during the post-Clovis portion of the Paleoindian period.

Importantly, the two hypotheses are not mutually exclusive. Anderson and Faught (2000) point out that disruptions in climate and food resources associated with the Younger Dryas (12,890–11,680 calBP), coupled with the disappearance of megafauna (Boulianger and Lyman, 2014; Grayson, 2007; Meltzer and Mead, 1983), can be expected to have led to changes in logistic patterns (but see Polyak et al., 2012). Large-distance movements may have given way to more-localized movements geared toward a wider range of small animals and plants. Anderson and Faught (2000) propose that the distribution of several projectile-point types—Suwannee and Simpson (Fig. 2), for example—within circumscribed ranges in the southeastern United States might reflect the beginning of that trend.

Over a decade ago, we began a series of projects aimed at clarifying the relationships among Paleoindian point forms (Buchanan and Collard, 2007, 2010; Collard et al., 2010, 2011; O'Brien et al., 2012), several of which focused on points from the Southeast (O'Brien and Lyman, 2000, 2003; O'Brien et al., 2001, 2002, 2013). Independent temporal control was largely unavailable for the region—a condition largely unchanged today—but even if it had been available, we were interested in more than simply constructing a chronological record of what came before or after something else. Rather, we were interested in patterns of cultural descent: which point forms were ancestral to which other point forms. To find and evaluate these patterns, we used a method known as *cladistics*, which creates hypotheses of evolutionary descent with explicit rules surrounding changes in the form of things, be they organisms, languages, or artifacts, through time. Cladistics generates *phylogenetic trees*, which are testable hypotheses of relatedness. Trees show change within lineages and can be used

to construct an ordinal-scale sequence of point evolution. Essentially, this means that in certain cases we can potentially determine not only which point form preceded another form but which form was ancestral to another.

In this paper we extend our previous analysis of Paleoindian points from the Southeast. We add specimens from the Middle Atlantic and the Northeast as well as additional specimens from the Southeast. This much broader coverage allows us to detect phylogenetic relationships not seen previously and provides a basis for making preliminary inferences about the transmission of information relative to point manufacture. Although in the following section we refer to well-known point types, in our analysis we used paradigmatic classes because of the ambiguity inherent in existing point typologies. We discuss this in more detail later.

Background

As noted above, usual practice is to place the Clovis period between ca. 13,300 calBP and 12,800 calBP in the West and between ca. 12,800 calBP and 12,500 in the East (Gingerich, 2011; Haynes et al., 1984; Haynes, 2002; Holliday, 2000; Levine, 1990), although more-restrictive date ranges have been proposed (e.g., Waters and Stafford, 2007). Our assessment of the data from the Debra L. Friedkin site in central Texas (Waters et al., 2011), however, suggests that Clovis may be considerably older than usual practice suggests (Buchanan et al., 2014). There, the Buttermilk Creek Complex (BCC), which is posited to be pre-Clovis in age and underlies a Clovis assemblage, may actually be a Clovis assemblage, albeit one that is missing a few kinds of tools (including Clovis points) and manufacturing by-products often found at Clovis sites in the West. If so, and the dating of the BCC is accurate—and, despite questions that have been raised (Morrow et al., 2012), we see no reason to suspect that the dating is not accurate (Driese et al., 2013; Jennings, 2012)—the appearance date of Clovis is pushed back to as early as 15,000 calBP.¹ This is perhaps not surprising, as the general expectation in archaeology and palaeontology is that most first-appearance dates are underestimates. Taphonomic processes are such that the probability of a given first-appearance date being too young is high. Thus, the discovery of a Clovis assemblage older than the known Clovis first-appearance date was to be expected (Waguespack, 2007)—an expectation made all the more realistic when one considers that less than two dozen or so North American Clovis sites have been directly radiocarbon dated (Waters and Stafford, 2007). In other words, we have an exceptionally small sample to begin with.

Jennings and Waters (2014) recently presented the results of three comparisons made between the BCC and Clovis components from several western Clovis sites—including the identified 2.5-cm-thick Clovis component that overlies the BCC at Debra L. Friedkin—that in their opinion demonstrates that BCC is “distinct from but similar to Clovis [and] could represent an ancestral assemblage from which Clovis is derived” (pp. 25–26). The comparisons were in terms of (1) site-level behaviors in stone reduction and site-use activities; (2) technological and typological trait lists; and (3) phylogenetic relatedness. Not surprising, there were differences between the BCC and other assemblages. Similarly, it was unsurprising that from a phylogenetic standpoint the BCC was most related to the overlying Clovis component at Debra L. Friedkin and less related to Clovis sites in Arizona (Blackwater Draw [Boldurian and Cotter, 1999; Cotter, 1937, 1938] and Murray Springs [Haynes

and Hemmings, 1968; Haynes and Huckell, 2007; Hemmings, 1970]). Abundant evidence from both eastern and western Clovis assemblages indicates substantial variation in lithic toolkits. For example, Meltzer (1988) showed that different toolkits were used by Paleoindians in two different subregions of the East and, in an earlier study focused on a single tool type, Wilmsen (1970) argued that Clovis and later Paleoindian end scrapers were used differently between the East and West. In the East they were used for wood and bone working, whereas in the West they were used primarily for butchering and hide working.

Given that cladistics is the approach that underlies the analysis we present here, we applaud Jennings and Waters's use of the approach—similar to what Buchanan and Collard (2008a) did in their reassessment of relationships among Denali, Nenana, and Clovis assemblages—in an attempt to sort out phylogenetic relatedness with respect to the BCC and Clovis. We would, however, like to see more, and larger, samples used in the cladistic analysis and an attempt made to control for spatial variation. Still, whether one quibbles over whether the BCC is early Clovis or something slightly earlier, and perhaps ancestral to Clovis, the significance of the BCC for what it tells us about a critical period in North American prehistory is not in doubt.

Where did Clovis point manufacture originate? It has long been suspected that Clovis points originated in the West—the earliest radiocarbon dates (not all of them are universally accepted [e.g., Waters and Stafford, 2007]) are from the Aubrey site in northern Texas (ca. 13,450 calBP) and the Sheaman site in Wyoming (13,210 calBP)—but one credible date from the Southeast—Sloth Hole in Florida (Waters and Stafford, 2007), at 12,900 calBP—falls inside the 13,300–12,800 calBP date range. With the exception of six radiocarbon dates on hawthorn (*Crataegus* sp.) seeds from Shawnee-Minisink in Pennsylvania (Dent, 2007; Gingerich, 2007), at ca. 12,865 calBP, the earliest dates from sites in the Northeast with large numbers of fluted points—Bull Brook in Massachusetts (Byers, 1954; Robinson et al., 2009), Vail in Maine (Gramly, 1982), and Debert in Nova Scotia (MacDonald, 1968)—consistently fall later than the earliest fluted-point dates in the West (Bradley et al., 2008; Curran, 1996; Haynes et al., 1984; Levine, 1990; Miller and Gingerich, 2013; Robinson et al., 2009).

Based more on the fact that the earliest dates in the Northeast are later than those in the West, together with an almost complete lack of dates from the Southeast, archaeologists have long assumed that Clovis points originated in the West and spread eastward. There was, however, an exception. Observing that a greater number of points and a greater richness of point forms occurred in the Southeast than elsewhere in North America, Mason (1962) concluded that fluted points were not a western invention that had been diffused to eastern parts of the country, perhaps as Plains groups escaped the drying effects of the terminal Pleistocene. Rather, it was the other way around:

the distributional and some of the typological evidence, as currently understood, would not seem to favor the proposed western origin for the development of Clovis points and the Llano complex. On the contrary, fluted points of every description except Folsom are far more numerous in the East, particularly in the southeastern United States, than they are in the Southwest or on the High Plains; and this area also has produced the greatest diversification in fluted point styles. On these grounds, then, it is defensible to suggest the southeastern United States, and not the West, as a possible “homeland” of the Clovis complex. (Mason, 1962: 234–235)

Mason's proposal was endorsed in some quarters, either tentatively or wholeheartedly (e.g., Bryan, 1991; Griffin, 1977; Meltzer, 1988; Painter, 1983; Stanford, 1991), although he had few quantita-

¹ Dating at Debra L. Friedkin was done through optically stimulated luminescence of terrace sediments. Two OSL ages immediately below the Clovis horizon date to 14,350 ± 910 BP and 14,070 ± 910 BP, and two ages at the top of the Clovis horizon date to 13,780 ± 885 BP and 13,090 ± 830 BP. The latter age agrees with Waters and Stafford's (2007) accepted age of Clovis.

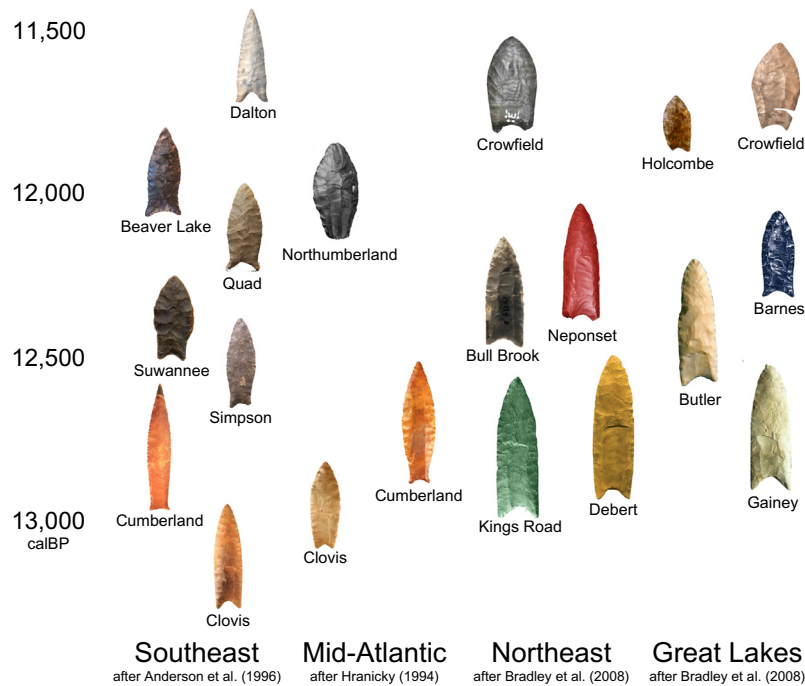


Fig. 3. Proposed chronological sequences of Early Paleoindian-period projectile points from the eastern United States. The time scale reflects our proposed alignment.

tive data to support his proposition. Two decades later, Louis Brennan, editor of *Archaeology of Eastern North America*, attempted to address this deficiency by initiating a survey of fluted point finds in the eastern United States. Brennan (1982) reported 5280 fluted points from east of the Mississippi River, with almost all respondents to the survey noting that their counts likely underestimated the “real” count by a considerable amount. Although laudable, Brennan’s survey was sharply criticized for a variety of reasons (e.g., Griffin, 1983; Haynes, 1983; Moeller, 1983), most having to do with sampling bias, yet the basic concept of statewide and continental surveys of fluted points remains relevant to modern research questions (e.g., Anderson, 1990, 1991; Anderson and Faught, 1998, 2000; Anderson and Gillam, 2000; Anderson et al., 2010; Faught et al., 1994; Stanford and Bradley, 2012; Steele et al., 1998).

Mason’s hypothesis of a southeastern origin for fluted points remains controversial, but there is general agreement with his statement that eastern North America contains a greater number of fluted points (Anderson and Faught, 1998, 2000; Stanford and Bradley, 2012; Steele et al., 1998) as well as a greater diversity of fluted-point forms than western North America (Anderson and Faught, 1998, 2000). Archaeologists, however, have yet to reach consensus on how, if at all, these various point forms relate to one another (O’Brien et al., 2001, 2002). In creating sequences of point forms for the Paleoindian period, such as those in Fig. 3, researchers have relied on chronological data from other regions and on intuitive models of stylistic evolution of points (Anderson et al., 1996; Bradley et al., 2008; Curran, 1996; Faught, 2006).

It was with these complex issues in mind that we began our cladistic analysis of Paleoindian points from the eastern United States (O’Brien et al., 2001). Cladistics was first developed in the 1940s by the German entomologist Willi Hennig (1950, 1965, 1966) and today is 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*, or *shared derived traits*, are similarities between two or more taxa that are inherited (derived) from the taxa’s most recent com-

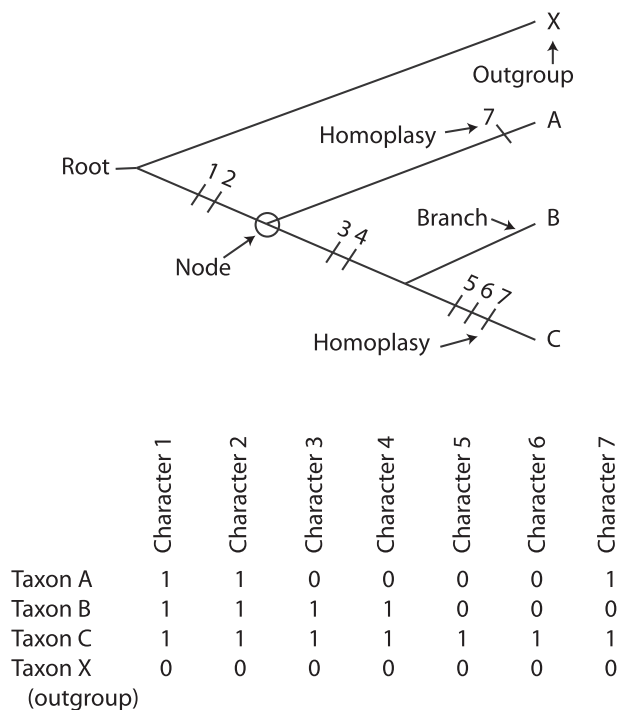


Fig. 4. An example of a tree of evolutionary relationships generated by means of cladistics, together with the character-state data matrix from which it was derived. Trees of evolutionary relationships generated with cladistics are usually referred to as “cladograms,” which are read from the tips to 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 characters 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.

mon ancestor; *symplesiomorphies*, or *shared ancestral traits*, 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 between and among lineages (Collard and Wood, 2001; O'Brien and Lyman, 2003; Sanderson and Hufford, 1996). Of these three types of similarity, only synapomorphies are informative with regard to phylogenetic relationships.²

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 share derived character states (synapomorphies) that are not also shared with the third taxon.

In its simplest form, cladistic analysis proceeds via four steps. First, a character-state matrix is generated. This shows the states

² Here are a couple of examples of different kinds of characters. All mammals have a vertebral column, as do animals placed in other categories. The presence of vertebrae is one criterion that we use to place organisms in the subphylum Vertebrata. The vertebral column is a *homologous* character shared by mammals, birds, and crocodilians, and it suggests that at some remote time in the past, the organisms in these taxa shared an ancestor. But if we want to pick a character to organize the taxa phylogenetically, we would not choose “presence of vertebrae.” Given that all three taxa possess that character, it cannot help us sort out relatedness. As another example, birds and bats both have wings, and those characters share properties in common, yet we classify birds and bats in two widely separate taxonomic groups because birds and bats are only distantly related phylogenetically. This is because these two large groups diverged from a common vertebrate ancestor long before either one of them developed wings. Therefore wings are of no utility in reconstructing lineages because they evolved *independently* in the two lineages after they diverged. Independently evolved characters are referred to as *analogues*. Interestingly, the difference between homologous and analogous characters is at the center of one of the more extreme hypotheses put forward for the origin of Clovis peoples. Based on similarities between Clovis points and Solutrean points from western Europe, which date no later than 17,000–16,500 calBP (Straus, 2000), Stanford and Bradley (2012) speculate that Clovis points arose from an Atlantic pre-Clovis maritime archaeological culture that represented the expansion of Solutrean-age peoples from Europe. Numerous lines of evidence contradict the idea that Clovis is descended from the Solutrean and, by extension, suggest that the similarities between Clovis points and Solutrean points are homoplastic (O'Brien et al., 2014). We focus on just three here. First, there are large chunks of Solutrean culture, including rock art, that are missing from Clovis assemblages (Straus, 2000). As Straus et al. (2005) point out, for the Solutrean origin of Clovis to make sense, there would have had to have been a cultural as well as a genetic amnesia on the part of Solutrean colonists once they arrived on the North American continent. Second, Eren et al. (2013, 2014) used a combination of experimental and archaeological analysis to evaluate the key trait—overshot flaking—that Stanford and Bradley argue supports the hypothesis that the Solutrean is ancestral to Clovis. Eren and colleagues found that overshot flaking is most parsimoniously explained as a technological by-product rather than a complex knapping strategy and concluded that it cannot be considered to be good evidence for an ancestor–descendant relationship between the Solutrean and Clovis. Additionally, virtually no evidence for overshot flaking exists among any of the putative North American pre-Clovis assemblages. As such, even if it were a complex knapping strategy, it would be a convergent similarity between the Solutrean and Clovis rather than a similarity indicative of ancestor–descendant relationships. Third, there is a significant chronological problem with Stanford and Bradley's hypothesis, which perhaps is even more serious than all the other problems put together. Needless to say, for the Solutrean to give rise to pre-Clovis, the Solutrean must precede it. However, if the pre-Clovis dates and artifact contexts Stanford and Bradley (2012) cite in defense of their argument are correct—and we do not believe they are (O'Brien et al., 2014)—we would be forced to conclude, based on Stanford and Bradley's own data, that western Europe was colonized by people from North America, not the other way around. How many times have homologous relations been posited on a much less evidence than what has been brought to bear in the Solutrean–Clovis debate? The number is probably countless. In addition, the two proponents of the Solutrean-origin hypothesis, Bruce Bradley and Dennis Stanford, have seen more Clovis-age tools than most of us combined, and Bradley is an expert flintknapper who knows Clovis stone-tool technology inside and out. If they can be wrong in assessing homologous relations, then that should give us some reason to pause (O'Brien, 2010). We might ask ourselves if it wouldn't be better to rely on some of the phylogenetic methods discussed here rather than on experience and intuition.

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 derived they are. 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. We refer to such a cladogram as the “most parsimonious” solution.³ An example of an ensemble cladogram is shown in Fig. 4.

There are numerous techniques for measuring the goodness of fit between a data set and a given cladogram. The most commonly used are the consistency index (CI) (Kluge and Farris, 1969) and the retention index (RI) (Farris, 1989a, 1989b). 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 dataset 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 (see O'Brien and Lyman (2003) for discussion).

Methods other than cladistics have been used to reconstruct phylogenetic relationships. These are termed *phenetic* approaches and include such methods as hierarchical clustering (Sokal and Sneath, 1963). These approaches, however, are of dubious merit from an evolutionary standpoint because the algorithms used do not search for shared derived characters (synapomorphies). In fact, they do not distinguish between homologous and homoplastic traits, let alone between shared derived and shared ancestral traits (symplesiomorphies). Rather, they look for overall similarities among sets of objects and then group the most similar sets together. Work carried out in biology over the last half century has demonstrated that overall similarity can be expected to be a poor

³ There are grounds other than parsimony for creating trees, including two probabilistic methods, maximum likelihood and Bayesian Markov chain Monte Carlo. With maximum parsimony, trees are evaluated on the basis of the minimum number of character-state changes required to generate the data on a given tree, without assuming a specific distribution. With the probabilistic methods, the criterion for evaluating a topology—the probability of the data, given the tree—is calculated with reference to an explicit evolutionary model from which the data are assumed to be distributed identically (Kolaczowski and Thornton, 2004).

guide to phylogenetic relationships. The same applies to cultural phenomena (O'Brien and Lyman, 2003).

Until roughly two decades ago, cladistics' sole use had been in the biological realm, but the method is becoming increasingly important in the social sciences as well (e.g., Beck and Jones, 2007; Bouckaert et al., 2012; Bower, 2012; Buchanan and Collard, 2007, 2008a, 2008b; Buckley, 2012; Currie and Mace, 2011; Currie et al., 2010; Darwent and O'Brien, 2006; Fortunato and Jordan, 2010; García Rivero and O'Brien, 2014; Gray and Atkinson, 2003; Gray and Jordan, 2000; Gray et al., 2009; Holden and Mace, 2003; Jennings and Waters, 2014; Jordan and Shennan, 2003; Jordan et al., 2009; Matthews et al., 2011; O'Brien et al., 2008, 2012; Platnick and Cameron, 1977; Rexová et al., 2003; Tehrani, 2013; Tehrani and Collard, 2002; Tehrani et al., 2010). The logical basis for applying cladistics to artifacts is the same as it for applying it to fossil hominin cranial remains and other biological datasets: Artifacts are complex systems, comprising any number of parts that act in concert to produce a functional unit. The kinds of changes that occur over generations of, say, point manufacture are highly constrained in that new structures and functions usually arise through modification of existing structures and functions as opposed to arising *de novo*. Thus, "the history of these changes is recorded in the similarities and differences in the complex characteristics of related [objects]—in the extent to which the characteristics of their common ancestors have been modified by subsequent additions, losses, and transformations" (Brown and Lomolino, 1998: 328).

Materials and methods

For the study reported here, we expanded the original database (O'Brien et al., 2001, 2002) to include fluted points from the Middle Atlantic and Northeast and additional points from the Southeast. This resulted in a sample of 1813 points from 20 US states and 3 Canadian provinces. As with our earlier studies, measurements were recorded from actual specimens as well as from high-quality drawings and photographs. Measurements were coded following the paradigmatic classification used by O'Brien et al. (2001). This form of classification has been proposed by paleontologists (Shaw, 1969) and biologists (Colless, 1985), but it has seen little use in the biological sciences. Its use in archaeology is likewise not widespread, despite its ability to produce objective, replicable analytical units. In contrast to taxonomic classification, paradigmatic classification uses an unordered and unweighted structure of character states to construct classes (Dunnell, 1971). Before starting the classification, the investigator specifies the characters and the states of each character that might be of analytical interest. There is no limit to the number of characters and states that can be included. Each specimen is then classified by noting the states of each character. Any state belonging to a single character can combine with any state belonging to any other character. Whether they actually *do* or not in a particular collection of specimens is a separate, empirical question (O'Brien and Lyman, 2000, 2002).

This classification method contrasts sharply with one based on nominal units such as "types." Although types are commonly used to classify points from eastern North America, there are two major

problems with this approach. One is a lack of redundancy in the characters used to create types. In the case of points, one point type may be defined primarily by blade length and curvature, whereas another point type may be defined by basal shape and curvature. The other problem is that types are *extensionally* defined (Dunnell, 1986; Lyman and O'Brien, 2000), meaning that definitions are derived from the sorting of specimens into groups based on overall similarity and then describing the average properties of each group of specimens. Extensionally defined types are often fuzzy amalgams of character states because such units (types) conflate the taxa and the specimens in them (O'Brien and Lyman, 2002).

These problems led Haynes (1983: 24) to comment that classification of fluted points in the East was "highly subjective" (see also Ellis, 2004). With respect to Clovis points, Table 1 lists six descriptions of "Clovis" points, including the first general description of which we are aware (Wormington, 1957), as well as a specific description of specimens from the Clovis type site, Blackwater Draw (Hester, 1972). The only commonality among the descriptions is that "Clovis" points have concave bases and are fluted. Here is what Faught (2006: 171) had to say about the classification of Paleoindian points from Florida: "Fluted points are universally classified as Clovis, regardless of whether the base is straight or waisted, or what the basal shape is." As far as we can tell, Paleoindian sequences from the East are based in large part on fluting: If a point is fluted, then by definition it is earlier than an unfluted point, even if two specimens are identical in every other aspect.

To be clear, we are not claiming that there is no role in archaeology for extensionally derived units such as point types. As shorthand mnemonic devices they serve a useful purpose in conveying coarse-grained information that aids communication. They are not, however, robust enough to use in the kinds of analysis reported here—a point underscored by Thulman (2012: 1599):

Types based on limited samples of isolated specimens usually fail to capture the variation in point form due to manufacturing variability and resharpening. Appending suffixes such as "oid" (ex., Folsomoid) or "like" emphasize the variability but do not hone the definitions. Even though these problems are apparent and occasionally discussed (e.g., Kimball, 1996), archaeology as a discipline has an inertia that keeps it dependent on "type specimens" and traditional point descriptions.

Characters and character states

Each class in our classification comprises eight characters, each of which has a variable number of character states (Fig. 5). The characters are defined as follows:

- I. Height of maximum blade width—the quarter section of a specimen in which the widest point of the blade occurs.
- II. Overall base shape—qualitative assessment of the shape of the basal indentation.
- III. Basal indentation ratio—the ratio between the medial length of a specimen and its maximum length; the smaller the ratio, the deeper the indentation.

Table 1

Six published descriptions of the Clovis point type. Note that the only commonality among all six is that Clovis points are fluted and have concave bases.

	Length	Width	Parallel sides	Convex sides	Concave base	Sides fluted	Basal constriction	Retouch	Basal grinding	Flute length
Wormington (1957)	1.5–5"		x	x	x	2			x	1/3–2/3
Ritchie (1961)	1–5"		x	x	x	1–2			x	
Prufert and Baby (1963)			x	x	x	1–2	Never			
Roosa (1965)		Max. at midline			x	1–2		Never		
Hester (1972)	2–6"	1–2"		x	x	2	Slight	x	x	1/3–2/3
Cox (1986)			x	x	x	2		Never	x	<1/2

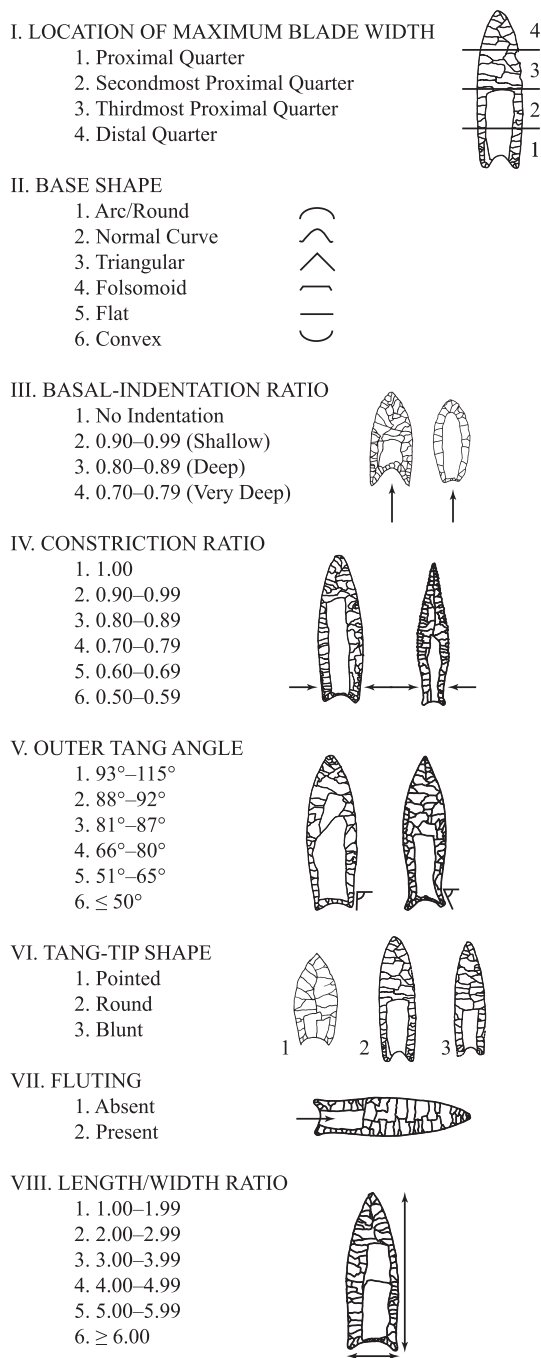


Fig. 5. Characters (roman numerals) and character states (Arabic numerals) used in the analysis.

The choice of which characters to use was based on expectations as to which parts of a point would change most over time as a result of cultural transmission and thus create a strong phylogenetic signal (O'Brien et al., 2001). Considerable variation exists in the size and shape of fluted points, so we selected characters I, IV, and VIII in order to explore changes in size and shape. All three avoid potential bias that could be introduced by using direct measurements of length and width—bias created by some points having been resharpened (Flenniken and Raymond, 1986). Our experience with Paleoindian points, in conjunction with published studies (e.g., Beck, 1995; Hughes, 1998; Musil, 1988), suggested that the hafting element is a likely region in which to find other characters that would be useful in phylogenetic analyses. The haft area, as Thulman (2012) notes, is also the least likely to have been altered from its original form since manufacture (Ahler, 1971; Goodyear, 1974; Hoffman, 1985; Musil, 1988; Thulman, 2006). Four characters—II, III, V, and VI—were selected to monitor changes in such features as base shape, the shape of tang tips, and the angle formed by a tang relative to the long axis of a specimen.

Character VII has only two states: fluted and unfluted. This bears discussion because we have stated up to this point that our interest is in fluted points. If so, why would we include unfluted points in our sample? The answer is found in the unsystematic nature of traditional point typology discussed above. For example, the literature is rife with discussions of such types as fluted Daltons, unfluted Clovis, and the like. What, for example, does one do with a point that has all the characteristics that one normally associates with Dalton (Fig. 2b) except it is fluted? Ignoring, for the moment, that such a specimen is an obvious potential phylogenetic link between Clovis and Dalton (O'Brien, 2005; O'Brien and Lyman, 2000; O'Brien and Wood, 1998), it seems appropriate to not be too worried about the issue. For one thing, how does one define fluting in the first place? Here is what Bruce Bradley, a knapping expert familiar with Paleoindian points, had to say on the subject:

Technological fluting is where basal thinning is done by the removal of one or more flakes that proportionally reduce the longitudinal thickness of the biface. This involves the removal of flakes that travel past the point of maximum longitudinal thickness. It makes no difference whatsoever if the resulting flake scars are retained in subsequent flaking. Morphological flutes, on the other hand, are simply basal flake scars that extend past the point of the hafting element and are visible on the finished object.

With these definitions, it is possible to have points that were technologically fluted but are not morphologically fluted, if the channel scars are removed by subsequent flaking. It is also possible to have points that are morphologically fluted but whose basal flakes did not extend past the point of maximum longitudinal thickness. These did not technically thin the preform. (Bradley, 1997: 54–55)

In two short paragraphs Bradley reduced the mystique surrounding fluting, showing that it is nothing more than the removal of longitudinal flakes from the base of a point to thin it. Both Clovis points and Dalton points were fluted, although the visual effect on each often differs. In scoring our character VII, we followed Bradley's distinction. If a specimen clearly showed evidence of morphological fluting, it was coded as "fluted." If it showed only technological fluting, it was coded as "unfluted."

Taxa and trees

Our classification of the 1813 points in the sample resulted in a total of 763 classes. From these, we selected a subset of those classes that contained four or more specimens ($n = 41$), accounting for

- IV. Constriction ratio—the ratio between the minimum blade width (proximal to the point of maximum blade width) and the maximum blade width; the smaller the ratio, the higher the amount of constriction.
- V. Outer tang angle—the degree of tang expansion from the long axis of a specimen; the lower the angle, the greater the expansion.
- VI. Tang-tip shape—the shape of the tip ends of tangs.
- VII. Fluting—the removal of one or more large flakes (≥ 1 cm long) from the base of a specimen and parallel to its long axis; subsequent flake removal may obliterate earlier flake scars.
- VIII. Length/width ratio—the maximum length of a specimen divided by its maximum width.

Table 2

Number of projectile points, by state or province, used in the phylogenetic analysis.

State	Count
Alabama	40
Arkansas	8
Florida	2
Georgia	4
Indiana	2
Kentucky	16
Maine	12
Massachusetts	8
Mississippi	8
Missouri	20
New Brunswick	1
New Hampshire	1
New Jersey	1
New York	13
North Carolina	3
Nova Scotia	1
Ohio	1
Ontario	1
Pennsylvania	23
South Carolina	1
Tennessee	40
Vermont	2
Virginia	10

218 specimens (Table 2). There was nothing particularly significant about having a minimum of four specimens per taxa; we used it as a crude means of controlling for idiosyncrasies arising from such things as different flaking qualities of raw materials. Following O'Brien et al. (2001), we labeled our taxa using abbreviations of the type names assigned to points within each class (Fig. 6 and Table 3). One outcome of our classification, certainly not unanticipated, was the lack of congruence between previously named projectile-point types and the classes we created. Our sample was derived in large part from specimens illustrated in the literature, and hence we knew which type name had been assigned to any particular specimen. After the classification was completed, it was not uncommon to have four or more type names used to refer to specimens in the same class. Class 21234312, for example, contained specimens distributed across four named types—Beaver Lake, Dalton, Quad, and Suwannee (Figs. 2 and 3). All of those point types have been described in the literature and are typically thought of as discrete units. In reality, they are anything but discrete units and are plagued with the same problems as Clovis (Table 1).

Subsequently, the computer program PAUP* (v. 4) (Swofford, 1998) was used to generate phylogenetic trees. The first step in the procedure is to provide the program with a starting point for tree construction—that is, where the trees should be rooted. This requires that an “outgroup” taxon be designated as the starting point. Any taxon can serve as an outgroup, but the closer the phylogenetic relationship is between outgroup and ingroup taxa, the better the chances of determining character polarity (the direction of change from one character state to another) (O'Brien and Lyman, 2003; O'Brien et al., 2002). Given the age of the taxa—projectile-point classes—with which we were dealing, it was difficult to select an appropriate ancestral taxon from outside those classes. The earliest accepted point type in North America is Clovis. If Clovis points are ancestral to the remainder of the sequence, and we assume they are, then it would make sense to select them as the outgroup, but specimens of what most archaeologists would term Clovis points occur in 25 of the 41 classes.

We selected KDR as our outgroup class. This class contains specimens classified as Clovis (including a point from Kimmswick, Missouri, found associated with mastodon remains [Graham et al., 1981]), Dalton, and Redstone. In earlier studies (O'Brien et al.,

2001, 2002), occurrence seriation had shown KDR to be the earliest class in the sequence. Occurrence seriation is a technique that orders phenomena on the basis of the presence/absence of characters or character states (Dempsey and Baumhoff, 1963; Rowe, 1959). The phenomena to be seriated can be sets of things or individual things. Here, those sets are classes of points. The characters are the traits being used to order the phenomena—those listed in Fig. 5—each of which contains multiple character states.

Within PAUP* we used the *heuristic search* method in three separate runs of 100, 10,000, and 100,000 replicates. Although this method is not guaranteed to identify a single globally optimal tree, it is the most computationally efficient method when dealing with large numbers of taxa.

Results

Each run returned multiple equally parsimonious trees. Consequently, we calculated a 50% majority-rule consensus tree, which places classes in their most common positions across the sample of trees (Swofford, 1991), using the trees returned in the 100-replicate sample. The tree (Fig. 7) has a consistency index of 0.34 and a retention index of 0.72—values that are as high or higher than some accepted trees for biological taxa (Collard et al., 2006). Although several clades are clearly defined, we note the presence of polytomies, or unresolved relationships among taxa—KGain, KD, and Ki, for example. There might be bifurcation points within this group, but the phylogenetic signal is too weak to resolve them. Alternatively, cultural transmission may frequently result in the creation of polytomies, just as genetic transmission does (O'Brien et al., 2001).

Character-state changes

One aspect of using cladistics for examining technological change is that we can move down from the level of class to examine historical change in individual characters (Darwent and O'Brien, 2006). In theory, almost every character change could represent a functional change in the performance of a point, any of which could benefit or hinder its success as a weapon (Beck, 1998). Characters such as weight, blade shape, width, and haft all affect how deeply a point penetrates its target, how much bleeding it causes, how accurately it can be propelled to the target, how far it can be effectively shot, how well the point will withstand impact, and even ease of manufacture (Cheshier and Kelly, 2006; Christenson, 1986; Hughes, 1998; Musil, 1988; Shott, 1997). The design of every point represents a series of compromises among these factors and reflects the needs that its manufacturer perceived as necessary for successful use.

Given that our interest here is phylogeny, we by-pass discussion of presumed functional changes in character states of Early Paleoindian points and focus solely on how some of the changes led to the creation of various classes. The tree shown in Fig. 8 contains 48 character-state changes, represented by boxes. Each box is labeled with a Roman numeral indicating the character that has changed; the subscript Arabic numeral indicates the evolved character state (Fig. 5). White boxes indicate phylogenetically informative changes—those changes that result from descent with modification and not from adaptive convergence or reversal. Black boxes indicate convergent changes in character states, and half-shaded boxes indicate reversals to ancestral states. Recall that for purposes of phylogenetic analysis, only shared-derived character-state changes (synapomorphies) are informative.

The first characters to change were location of maximum blade width (character I) and constriction ratio (character IV). The former changed from the first proximal quarter in the outgroup (KDR) to

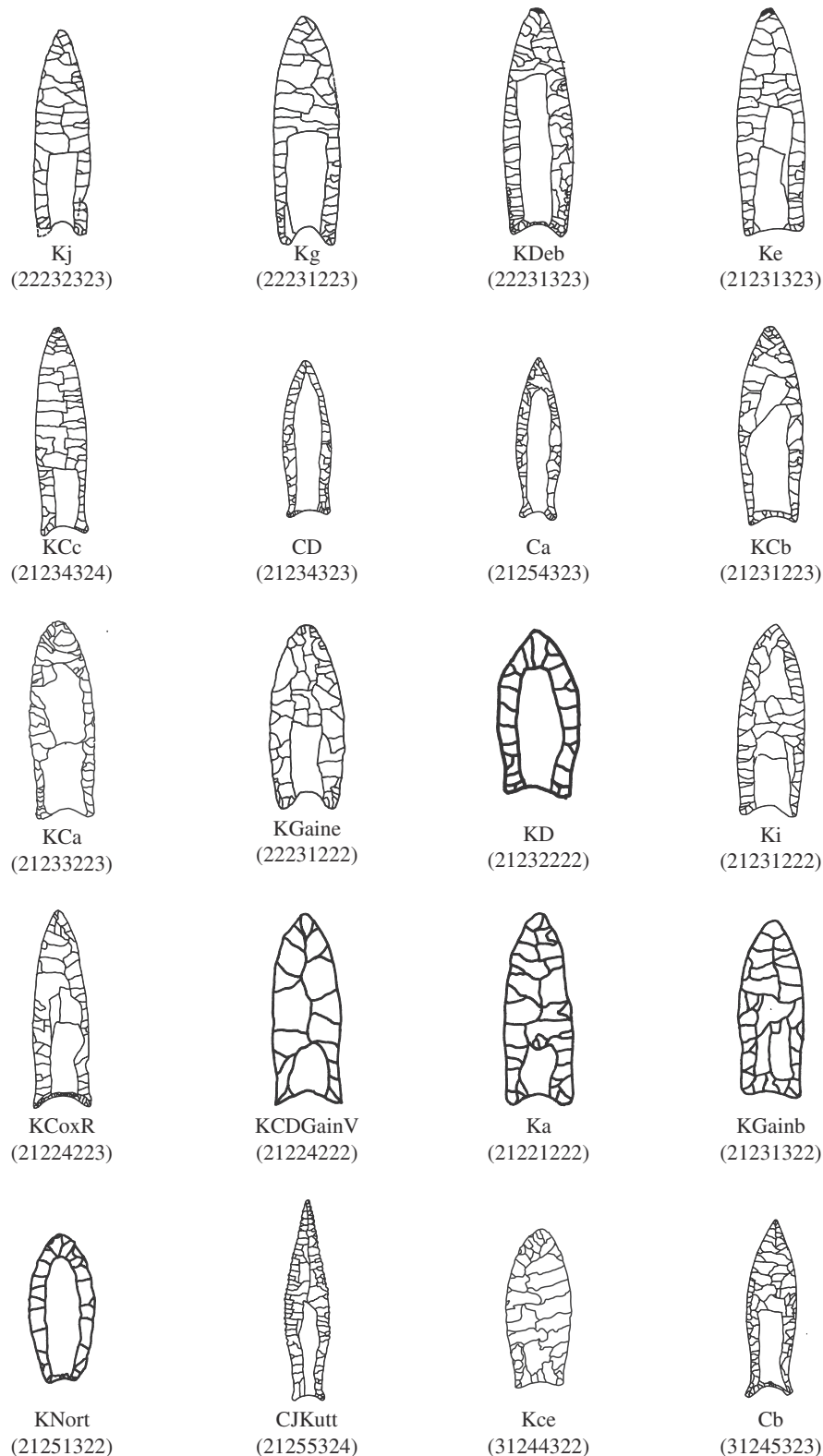


Fig. 6. The 41 projectile-point classes used in the phylogenetic analysis (the asterisk marks KDR as the outgroup).

the secondmost proximal quarter. Constriction ratio changed from state 1 (1.00 [no constriction]) to state 3 (0.80–0.89). These changes resulted in a ghost class—one not represented in our database. An increase in outer tang angle (character V) from this ghost class led to the creation of kg (22231223). A change in tang-tip shape (character VI) from round (state 2) to blunt (state 3) led to the creation of an ancestral form isomorphic with Kj (22232323).

The next character to change was character V (outer tang angle). As with the character-state changes leading to the creation of Kg, tang angle changed from state 2 to state 3. This change led to the creation of an ancestral class isomorphic with KDeb (22231323).

A change in base shape (character II) in the ancestral form isomorphic with KDeb from state 2 (normal curve) to state 1 (round) led to the creation of a form ancestral to a clade (clade VI, shown in



Fig. 6 (continued)

maroon in Figs. 7 and 8) of three classes: KCc, CD, and Ca. All these classes contain points identified in the original reports as Cumberland (Figs. 2 and 3).

A reversal of tang-tip shape (character VI) from blunted (state 3) back to round (state 2) and a decrease in the length/width ratio (character VIII) led to the creation of a class isomorphic with Ki, and this form is ancestral to all other clades in our phylogeny (excluding polytomies): Clade I, which contains high-shouldered, narrow-based, pointed-tang forms; Clade II, which contains relatively parallel-sided and mostly straight-tanged forms; Clade III, which contains point forms with acute-angled tangs, including all of the unfluted forms in the database; Clade IV, which contains

high-shouldered points with relatively shallow bases and narrow basal constrictions; and Clade V, which contains forms with round bases and shallow or slight basal constrictions.

Fig. 9 summarizes the frequencies of changes by character state and type of change—phylogenetically informative or homoplasious (convergence or reversal). Most changes are related to constriction ratio (character IV), tang angle (character V), and tang-tip shape (character VI). Note in particular all the instances of reversal and convergence with respect to outer tang angle, with a trend toward more acute angles, creating “fishtail” points (Fig. 5). All of these characters—constriction ratio, outer tang angle, and tang-tip shape—are related to the hafting elements of a point, reinforcing

Table 3
Projectile-point type names and abbreviations used to create class designations.

Type name	Abbreviation
Arkabutla	A
Barnes	Bar
Beaver Lake	B
Bull Brook	Bull
Clovis	K
Coldwater	Cold
Coxey	Cox
Crowfield	Crow
Cumberland	C
Dalton	D
Debert	Deb
Doo	Doo
Gainey	Gain
Jackson	J
Kuttawa	Kutt
Neponset	Nep
Northumberland	Nort
Quad	Q
Redstone	R
Russelville	Russ
Simpson	S
Suwannee	Suw
Vandale	V
Yazoo	Y

our assumption that this aspect of point technology carries a strong phylogenetic signal, even with the presence of considerable “noise” caused by homoplasy.

Other characters change either moderately or almost not at all. Base shape (character II) has four changes, one a change from normal curve to arc-shaped and three reversals to the ancestral normal-curve state. Blade width exhibits a few reversals and a single

phylogenetically informative change, and length/width ratio exhibits a few instances of reversal and convergence and one phylogenetically informative change.

Geographic distribution of character states and classes

Figs. 10 and 11 show the geographic distributions of character states. At this exploratory stage the point sample contains spatial biases (Table 2), but several distributions are noteworthy. For example, samples from a contiguous area comprising Missouri, Arkansas, Kentucky, Tennessee, Mississippi, and Alabama contain points that have their maximum blade width (character I) in the secondmost proximal quarter. The only other state to have such specimens is Pennsylvania. Virtually all points from the Northeast, the Middle Atlantic, and the Southern Atlantic have their maximum blade width in the secondmost distal quarter. Similarly, almost all points south of Pennsylvania have shallow basal indentation ratios (character III), whereas points with deep indentation ratios are confined to the extreme Northeast. This is not an unexpected occurrence, given that the considerable depth of the basal indentation is a characteristic of Debert points (MacDonald, 1968) and other northeastern types (Bradley et al., 2008; Ellis, 2004) (Fig. 2).

There appears to be little geographic patterning in either outer tang angle (character V) or tang-tip shape (character VI) but strong patterning in fluting (character VII). The only unfluted points are in the Southeast, where in South Carolina and Florida all points are unfluted. We would not make much of the absence of fluting on points from those two states because of the small sample size ($n = 3$ [Table 2]), but the pattern becomes more robust with the addition of samples from the neighboring states of Georgia, Mississippi, and especially Alabama and Tennessee (Fig. 11).

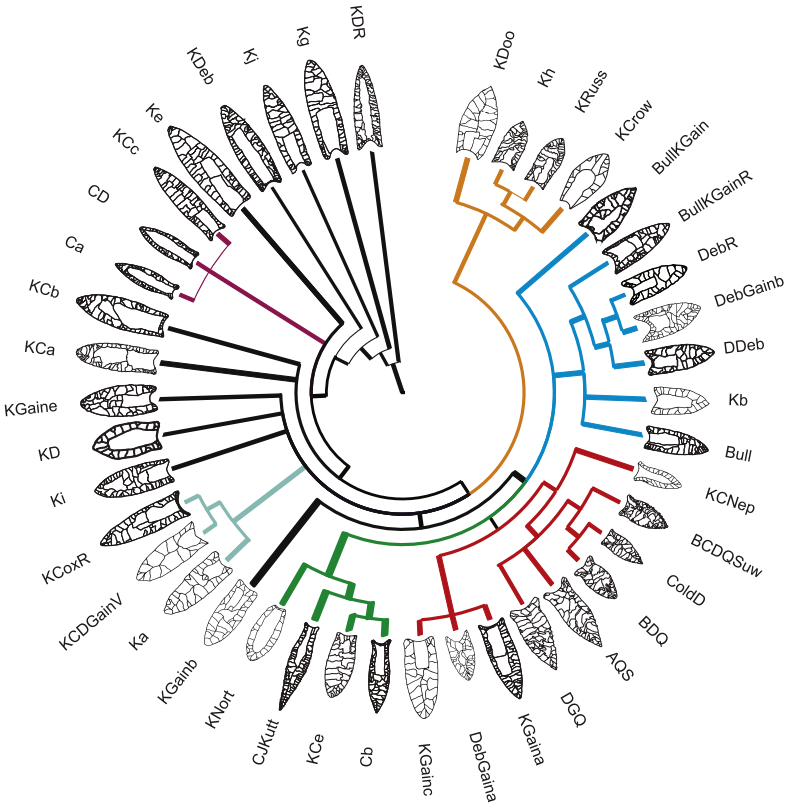


Fig. 7. Fifty-percent majority-rule consensus tree of 41 taxa based on 100 replicates. Various clades are shown in different colors. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

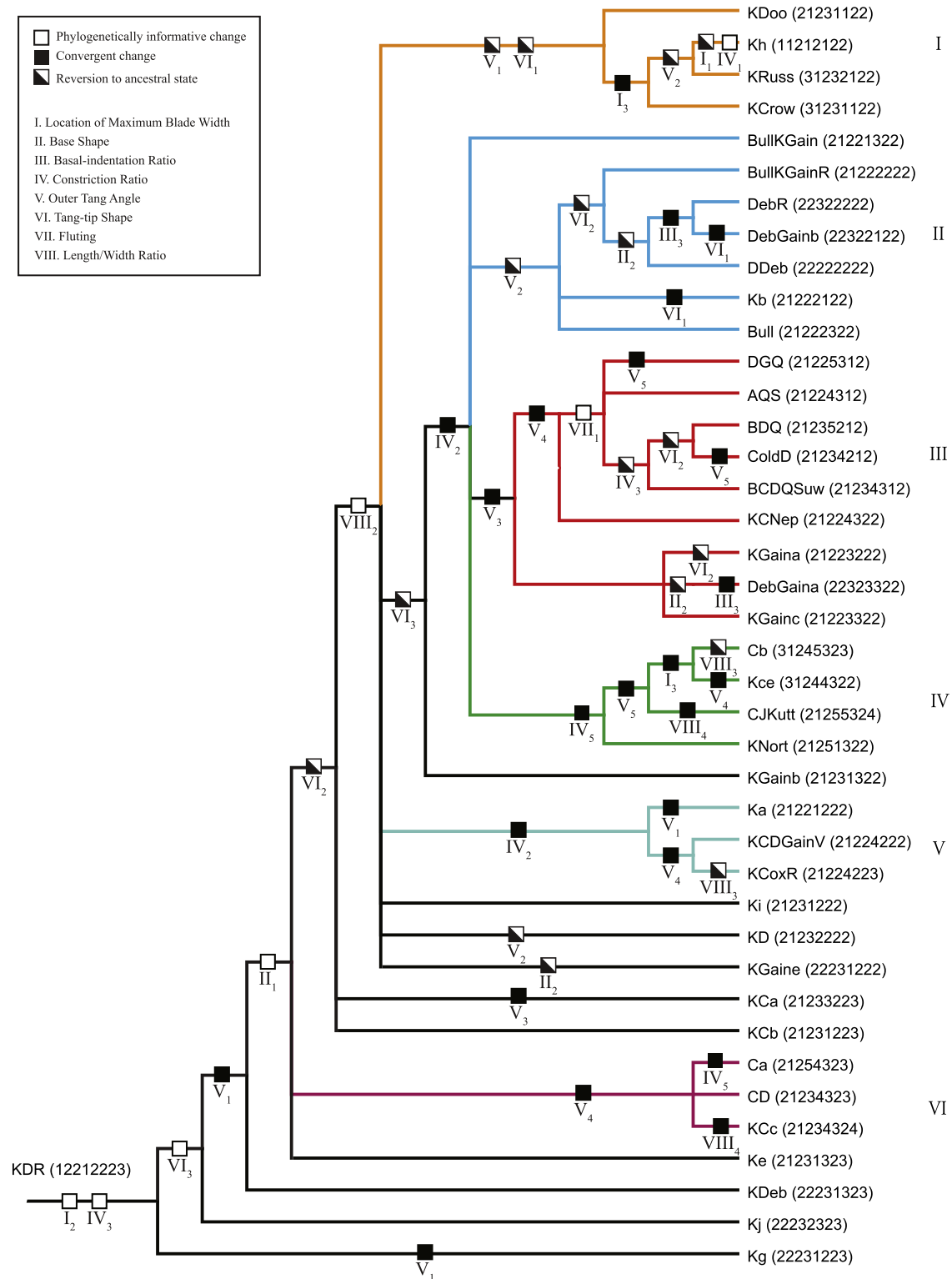


Fig. 8. The same maximum-parsimony tree as shown in Fig. 7 with boxes showing the 48 changes in character states. Roman numerals denote characters, and subscript numbers denote character states. Open boxes indicate phylogenetically informative changes; shaded boxes indicate parallel or convergent changes (homoplasy); and half-shaded boxes indicate characters that reverted to an ancestral state. Clades discussed in the text (I–VI) are shown in color, which match the colors in Fig. 7.

Projecting the consensus tree into geographic space—creating a geophylogeny—allows us to observe the significance of the phylogeny in both time and space (Fig. 12). In particular, a geophylogeny serves as something of an independent test of the validity of a cladistically based phylogenetic hypothesis because it allows us to

determine if an ancestor–descendant pair of taxa are in spatial proximity to one another. If they are not, then it is likely that we have not measured phylogeny but something else. To construct the projection, we first calculated the mean geographic centroid of the county in which each specimen was obtained. These

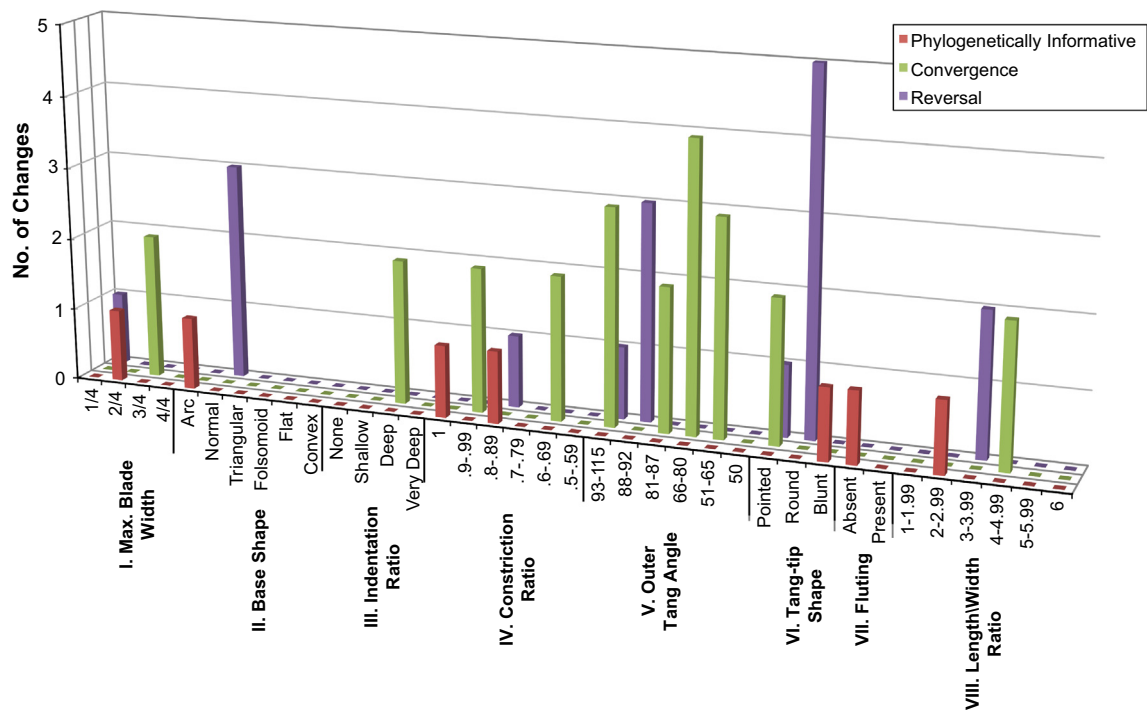


Fig. 9. Frequencies by type of the 48 character-state changes shown in Fig. 8.

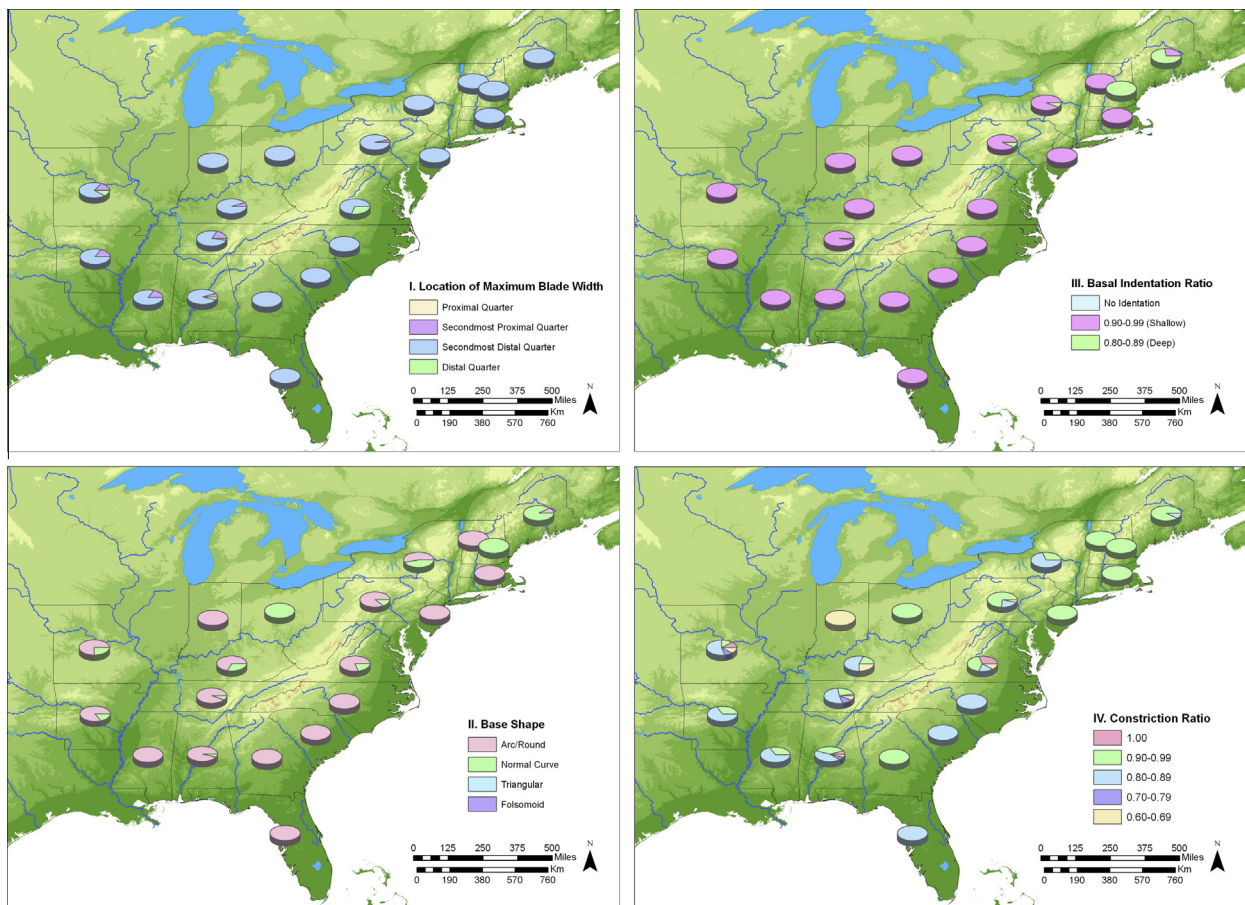


Fig. 10. Geographic distributions of states of characters I–IV: location of maximum blade width, base shape, basal indentation ratio, and constriction ratio.

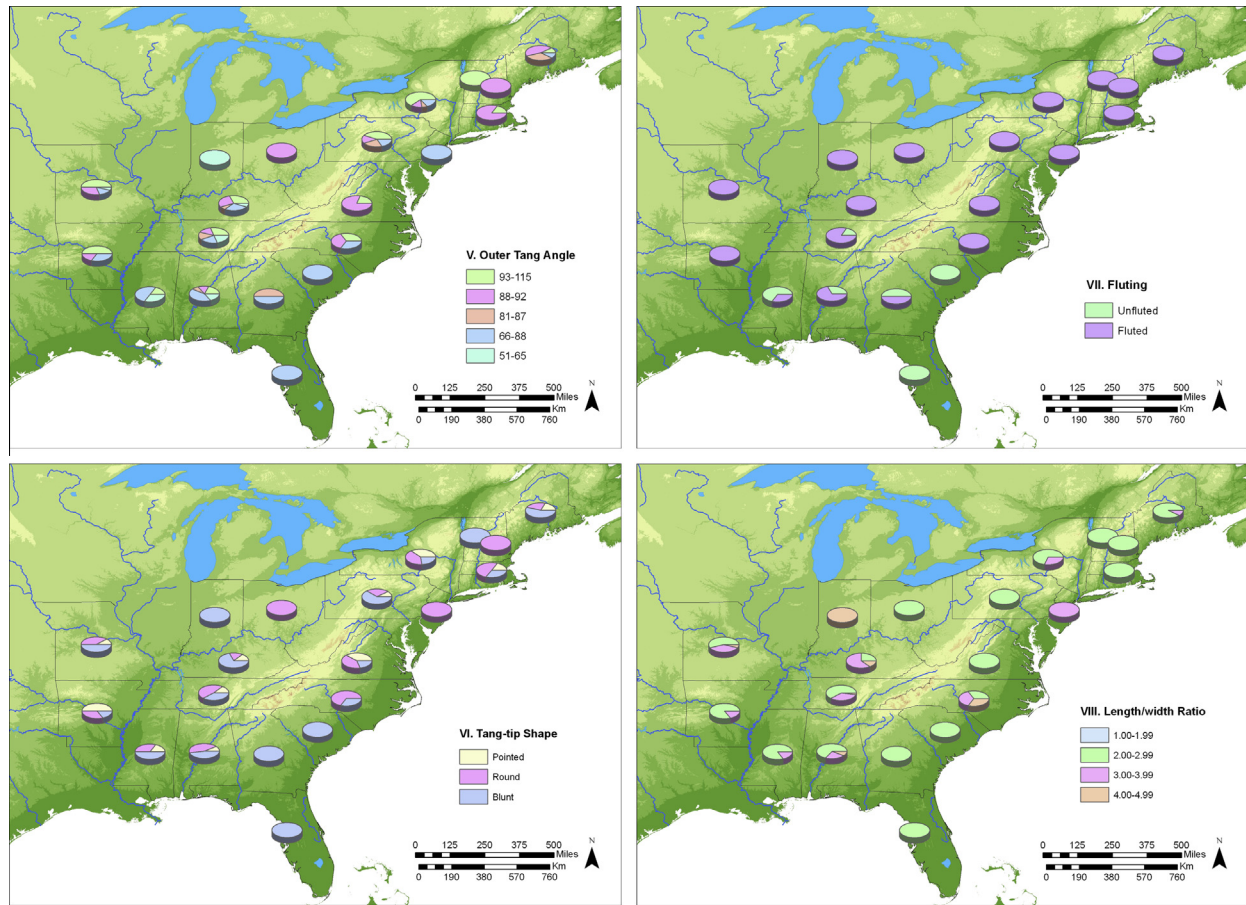


Fig. 11. Geographic distributions of states of characters V–VIII: outer tang angle, tang-tip shape, fluting, and length/width ratio.

coordinates were then used to calculate a spatial envelope representing the geographic distribution of each class. The spatial centroids were then calculated to create a weighted mean representing the center point of each class's distribution. Before discussing the results of this analysis, we again stress that the sample has spatial biases (Table 2).

The classes in Clade I all contain specimens identified as Clovis points, and all are restricted to the Midwest. Classes in Clade II are skewed toward the Northeast and Middle Atlantic regions. Key constituents of the classes are types described as having deep basal indentations—Bull Brook (Byers, 1954), Debert (MacDonald, 1968), and Gainey (Simons et al., 1984) (Figs. 2 and 3). Classes in Clade III show a split distribution: The subclade comprising KGaina, DebGaina, and KGainc is restricted to the northern portion of the study area, whereas all other classes in Clade III have distributions in the southern portion. This is not particularly surprising, given that a key constituent of the subclade is Gainey, a point type that occurs primarily along the southern edge of the Great Lakes eastward, although it is found sporadically throughout eastern North America (Morrow and Morrow, 2002). As noted above, Gainey is also well represented in classes in Clade II.

Classes in Clade IV occur in a northeast/southwest-trending band from the Tennessee River valley northward, generally following the Ohio River valley. This is also not surprising, given the large number of Cumberland points (Fig. 2), a key component of classes in Clade IV, that are found in the Tennessee and central Ohio River valleys (Anderson et al., 2010). Classes in Clade V occur, like those in Clade II, in the Middle Atlantic and Northeast. Classes in Clade VI cluster in the Midwest eastward to the Tennessee River valley. Constituent types include the long, narrow, heavily fluted

Cumberland point. Interestingly, Clade VI shows minimal taxonomic diversity and diverges from the superclade comprising the other clades early in the phylogeny.

Of particular interest, for reasons discussed in the following section, are the unresolved classes—those that do not fall into one of the six clades. These are represented in black in Figs. 8 and 12. Unresolved classes occur in the Upper Midwest near the junction of the Mississippi and Ohio rivers, northeastward along the Ohio River, and southeastward along the Cumberland River. Class KGaina is the most northeastward of the unresolved classes.

Discussion

The analysis described here, although preliminary, represents another layer of data directed at understanding the social complexities of the Paleoindian cultural landscape. Phylogeny is important in its own right for what it can tell us about character-state changes over time and how those changes are related, but here we are interested in what it might tell us, even in preliminary fashion, about cultural transmission in eastern North America between ca. 13,300 calBP and 11,900 calBP. As a starting point, we are interested in how the data relate to what at first glance appear to be competing proposals for regional differences in Paleoindian point shape.

As background, recall the earlier discussion of studies of Clovis point shape, some of which found that shape was fairly consistent across North America, with variation attributable to drift (Buchanan and Hamilton, 2009; Hamilton, 2008; Hamilton and Buchanan, 2009; Morrow and Morrow, 1999), and another study that found

What specific cultural transmission process(es) within a general framework of social learning could have led to the patterns we see for Clovis points? There appear to be two possibilities. First, knappers could simply copy what they saw. Second, they could be trained in the proper way of making a Clovis point. Given the complexities involved in manufacturing a Clovis point, which can take up to two hours to produce (Whittaker, 2004), we doubt that copying was a profitable strategy. In fact, we are sure it was not. As Sholts et al. (2012) document, even highly skilled modern replicators, although they can mimic Clovis shape precisely—in some cases to the point of fooling professionals and highly knowledgeable collectors—they cannot consistently mimic the flake-removal techniques of Clovis artisans. More likely, they argue, Clovis artisans shared their technical knowledge through one knapper showing another the “proper” way to flake a Clovis point, and so on down the line—or, more precisely, across the landscape.

This conclusion is consistent with the proposal by Hamilton (2008) and Hamilton and Buchanan (2009) that Clovis point shape was a product of strong biased transmission (e.g., Boyd and Richerson, 1985; Henrich, 2001) as opposed to individual learning and guided variation (see below). Within certain subregions, however, point knappers were adjusting shape to fit particular environments while still maintaining basic flaking patterns. Thus the findings of Buchanan et al. (2014) and Hamilton and Buchanan (2009), for example, are not necessarily at odds.

Biased transmission, of whatever form (Laland, 2004; Mesoudi, 2011), is an important process in human learning (Henrich, 2001). Thus it is understandable why biased learning strategies would have played a key role in fluted-point technologies. The manufacture of a Clovis or Folsom point is a complex procedure that would have required a significant amount of investment both in terms of time and energy to learn effectively (Bradley et al., 2010; Crabtree, 1966; Whittaker, 2004). Under these conditions, it is likely that there was significant variation among the level of skill exhibited by toolmakers (Bentley and O'Brien, 2011; Henrich, 2004, 2006)—one does not become a flintknapper, let alone an accomplished one, overnight (Olausson, 2008; Pigeot, 1990)—such that recognized craftsmen could have held considerable prestige (Hamilton, 2008). Prestige bias—learning from (not simply copying) certain individuals to whom others freely show deference or respect in order to increase the amount and accuracy of information available to the learner (Henrich and Gil-White, 2001; Reyes-Garcia et al., 2008)—allows a learner in a novel environment to quickly choose from whom to learn (provided the population is not so large as to “swallow up” highly skilled individuals [Bentley and O'Brien, 2011]), thus maximizing his or her chances of acquiring adaptive behavioral solutions to a specific task or enterprise without having to assess directly the adaptiveness of every potential model's behavior (Atkinson et al., 2012). In a fast-moving and fast-growing population subject to the widespread environmental changes of, say, the North American late Pleistocene landscape, prestige bias would have been a highly effective strategy for social learning (Hamilton, 2008) because under circumstances where ecological conditions change is, say, on a generational scale, the mean trait value is often optimal, leading to frequency-dependent bias, or conformism (Henrich and Boyd, 1998). However, if ecological conditions change faster, social learning may favor individual trial and error or even a combination of the two (Mesoudi, 2008; Toelch et al., 2009).

In their classic model of Clovis colonization of North America, Kelly and Todd (1988) suggest that the speed of colonization was driven by high rates of residential mobility because of the large foraging areas required of a primarily carnivorous diet. Hamilton and Buchanan (2007) note that Clovis colonists would have moved rapidly through large river systems such as the Missouri and Mississippi drainages, leading to an initially rapid rate of colonization

through the midcontinent, which would have then slowed dramatically as diet breadths broadened with the increased biodiversity of the eastern forests (Steele et al., 1998), and as prey size, abundance, and availability changed (Meltzer, 1988).

The phylogenetic tree shown in Fig. 12 lends support to the model of initial rapid colonization. Note the locations of the unresolved classes (shown in black). As we pointed out earlier, they occur in the Upper Midwest near the junction of the Mississippi and Ohio rivers, northeastward along the Ohio River, and southeastward along the Cumberland River. All 11 classes, including the two outgroups, contain specimens identified in the original literature as Clovis points. In some cases, all specimens were identified as Clovis, and in others some were classified as Gainey, Cumberland, Redstone, Debert, and/or Dalton. A working hypothesis based on this distribution would be that the unresolved classes were the products of groups moving rapidly across the landscape—so rapid, in fact, that there was not enough time for a strong phylogenetic signal to develop. There were technological changes, to be sure—they are what define the classes in the first place (Fig. 8)—but there were not enough changes to allow much resolution of phylogeny (Figs. 8 and 12). This conclusion is similar to that reached by Buchanan and Hamilton (2009) as a reason for the lack of regional variation in their study of Clovis point shape. Even though their analysis failed to find the shape variation that sets off the Northeast from other eastern regions (Buchanan et al., 2014), their reasoning is valid.

We suspect, however, that the situation changed in the East sometime after ca. 12,500 calBP—a rough date for the rapid proliferation of fluted-point forms. Reasons for the change perhaps had more to do with shifts in the use of space (territories) by Paleoindian groups than it did with adaptive changes relative to game animals and the physical environment (Anderson and Faught, 2000), or, more likely, it was a combination of the two. Those changes in turn had implications for how information about point technology and performance was transmitted. The difference in transmission, we believe, is analogous to what was documented by Bettinger and Eerkens (1999) in their study of projectile points from the Great Basin. There, points from two adjacent regions differed in the degree to which their attributes, such as weight, width, and length, correlated with each other. Bettinger and Eerkens (1999) attributed the differences to the manner in which prehistoric people of the two regions acquired and transmitted point technology, with one group using primarily guided variation—unbiased transmission plus individual trial-and-error experimentation—and the other using prestige bias (they used the term “indirect bias”), whereby individuals learned the design of a single successful model (Boyd and Richerson, 1985; Mesoudi, 2011; Mesoudi and O'Brien, 2008a, 2008b).

If, as we have hypothesized, the unresolved classes shown in black in Fig. 12 are associated primarily with Clovis groups, then a related hypothesis is that the more-resolved classes, those in clades II–IV, represent later Early Paleoindian points. Fig. 8 shows the numerous character-state changes that produced those classes. Note that all but one change, the loss of fluting ($VII_2 \rightarrow VII_1$) in Clade III, are either instances of convergence or reversal to an ancestral state. The 22 instances of homoplasy argue strongly that Paleoindian knappers were no longer learning the design of a single successful model but rather were experimenting with numerous aspects of points (Lyman et al., 2008, 2009). More evidence in support of this shift in behavior comes from the fact that the 23 character-state changes in clades II–IV represent almost half of all 48 character-state changes represented in Fig. 8.

This apparent pattern of increased experimentation is exactly what one would expect from the guided-variation model, which shows that, in the absence of selection for a particular trait, a population will move toward whichever trait is favored by people's

individual-learning biases. This occurs even when the strength of guided variation is weak (Mesoudi, 2011). Future work will be directed at developing a better understanding of the “fitness” of character states in terms of performance and how and why groups from widely different regions during the late half of the Early Paleoindian period landed on the same fitness peaks in terms of character states—in other words, finding similar solutions to common adaptive problems (O'Brien and Bentley, 2011). Understanding the phylogenetic history of fluted points in the East, especially in terms of the often small changes in characters that occurred through time, provides a solid starting point for delving into some of these highly complex issues.

Conclusions

Phylogenetic analysis represents a break with more traditional approaches to understanding the archaeological record. Still present are issues of chronology and culture change—the mainstays of archaeology—but phylogenetic analysis shifts the emphasis from simple *historical* continuity—A comes before B—to *heritable* continuity—A not only preceded B but gave rise to it (O'Brien and Lyman, 2000). In other words, A and B share a homologous relation. This, of course, is not news to most archaeologists working in the Americas, who have long recognized the difference between homologous similarities and analogous similarities—those that arise through similar, yet unrelated, adaptations to similar environmental conditions. They have also realized the difficulties in distinguishing between the two kinds of traits in the archaeological and ethnological records (e.g., Binford, 1968; Kroeber, 1931). This is where cladistics plays an important role: not only does it allow us to separate homologous and analogous traits but it also allows us to identify the *kinds* of analogs, such as what are shown in Fig. 8. Cladistics is not the only method for determining degree of similarity among sets of objects, but it is the only one that offers a means of assessing ancestor–descendant relationships.

We in no way want to leave readers with the mistaken belief that archaeological applications of cladistics are limited to individual classes of items, such as we highlight with points from eastern North America. Recall our earlier discussion of Jennings and Waters' (2014) cladistic analysis of the Buttermilk Creek Complex tool assemblage from the Debra L. Friedkin site in central Texas and assemblages from several other sites in western North America, using a protocol developed by Buchanan and Collard (2008a) for a similar analysis. These analyses have proved valuable, but we agree with Jennings and Waters' (2014, p. 41) advice: “It is highly probable that assemblage sample-size and site-function differences represent serious problems for assemblage-level cladistics analyses. For future research, looking at the evolution of specific technological lineages may be necessary to overcome the difficulties of examining assemblages in their entirety, the composition of which may vary with site function.” We hope our work reported here will spur other researchers to follow Jennings and Waters' advice.

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