CHAPTER 6

CULTURAL PHYLOGENETIC HYPOTHESES IN ARCHAEOLOGY: SOME FUNDAMENTAL ISSUES

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Phylogeny – the genealogical history of a group, in which ancestor-descendant relationships are hypothesised – has long been a focus of anthropological study. The basis of this focus is the notion that cultural forms of various scales are descended from other forms. The phenomena of interest, however, irrespective of whether they are belief systems, lexical constructs or artefacts, are rarely observed in original chronological sequence. Constructing such a sequence might suggest phylogenetic relationships, but the chronological ordering does not answer questions of heritability and of which form was ancestral to, and thus produced, another. That is a phylogenetic question, and to answer it requires the use of phylogenetic methods, several of which appeared early on in Americanist anthropology. These included seriation, the comparative method, and the direct historical approach. All rested on the implicit assumption of phylogenetic descent. By the 1930s some were beginning to suspect that, as in biology, patterns of descent could be mapped by using homologous characters (Kroeber 1931). Biologists, however, had a theory – genetic transmission – to explain relationships; anthropologists mentioned cultural transmission but built no theory around it. They adopted the view that two things similar in appearance must be related, instead of the theoretically informed view that two things are similar because they are related (Simpson 1961).

Three factors have led to renewed anthropological interest in phylogeny during the past two decades: (1) an exponential increase in linguistic and genetic data (eg, Cavalli-Sforza *et al* 1988, 1994); (2) advances in analytical and computing methods; and (3) the view that human culture is phenotypic (eg, Rindos 1985) and cultural transmission is an inheritance system and a source of variation (eg, Boyd and Richerson 1985). But there is still no consensus regarding what is evolving, what analytical units are needed to track culture change, and what phylogenetic patterns have to say about the evolutionary processes that shaped them. Phylogeny is an important issue for archaeology – not that it isn't for anthropology – because of that discipline's access to portions of past phenotypes. Only archaeologists have access to the entire time span of culture, and their data can be treated as primary phylogenetic information. Archaeologists should ask historical questions because the answers are critical to understanding why cultural manifestations occupy particular positions in time and space.

Here we examine two issues that underlie attempts to unravel cultural phylogeny: (1) differences between two phylogenetic models in use in biology today – evolutionary taxonomy and phylogenetic systematics (cladistics); and (2)

their roles in constructing hypotheses of cultural phylogeny. The heart of both concerns classification and units. Despite acceptance of the validity of Darwin's (1859) theory of descent with modification, there is a lack of consensus in biology over what a species is and what kinds of information are contained in phylogenetic trees. These problems exist in archaeology and anthropology, but here there is an additional problem: the term 'cladistic' often is used to refer to any branching model of cultural phylogeny. Without an appreciation of what cladistics is, the kind of model it produces, and how it differs from evolutionary taxonomy, criticisms of phylogenetic studies of cultural phenomena will never be resolved.

Both phylogenetic models have value for certain analytical purposes. Evolutionary taxonomy is a multipurpose method that reveals similarities and differences among units of various taxonomic rank and gives approximate ancestor-descendant relationships. A taxonomic tree implies an interval-scale measure of time, an interval-scale measure of formal differences, and a particular form of ancestral taxon. Cladistics is strictly a phylogenetic method. It suggests the order of appearance of certain morphological characters, which are used to place taxa in a hypothesised order of appearance with no reference to interval-scale time and no reference to overall difference in form. It places all taxa at branch tips, and no 'real' ancestral taxon is identified. Cladistics creates hierarchical patterns that consist of nested sets of taxa, whereas evolutionary taxonomy searches for a natural order of taxa within a hierarchical framework.

CULTURAL PHYLOGENETIC STUDIES: A BRIEF OVERVIEW

The phylogenetic studies conducted in anthropology and archaeology during the last 20 years fall into two categories: (1) analyses that trace lines of descent back to a common ancestor and then examine the processes that underlie the geographic distribution and development of descendants (eg, Kirch and Green 2001; Renfrew 1987, 2000c); and (2) comparative studies that rely on understanding patterns of descent in order to examine the distribution of adaptive features (eg, Holden and Mace 1999; see the review in Borgerhoff Mulder 2001). The modern comparative method is designed to escape what Francis Galton pointed out in 1889: comparative studies of adaptation are irrelevant if we cannot rule out the possibility of a common origin of the adaptive features under examination. To escape Galton's problem requires a working knowledge of the phylogeny of the taxa included in the analysis.

Both kinds of studies can involve archaeological and genetic information, but one feature shared by both is their heavy reliance on linguistic analysis to create the basic phylogeny. Language phylogenies form the hypothesised patterns of cultural descent, with subsequent analysis dependent on the correctness of the linguistic trees (Figure 6.1). The method used to construct linguistic trees is similar to cladistics (Hoenigswald and Wiener 1987), with some major differences, including the identification of ancestors.

Most studies using linguistic data employ reasoning similar to that of Borgerhoff Mulder (2001: 106): (1) linguistic phylogenies offer better resolution of
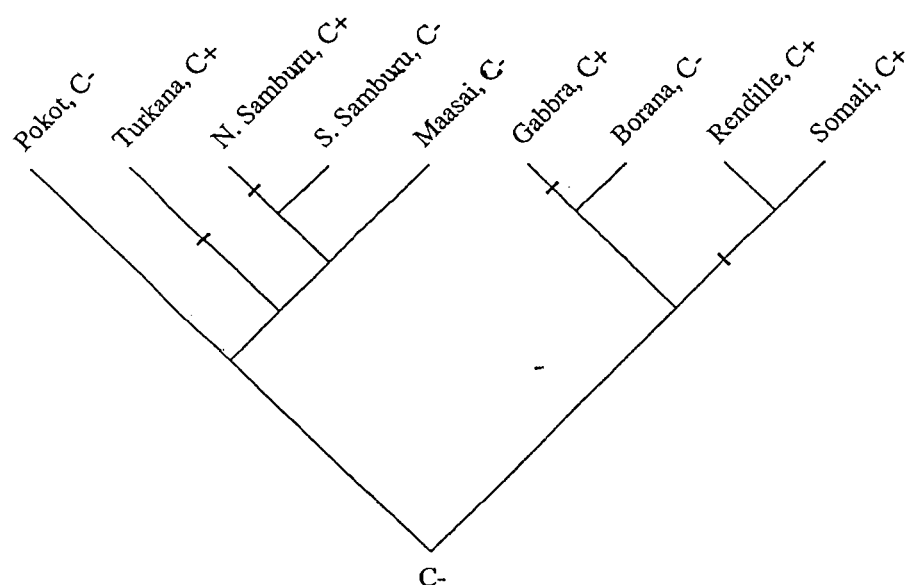
Figure 6.1 A phylogeny of nine Kenyan pastoralist cultures based on linguistic similarity, showing (C+) camel-keeping cultures and (C–) cultures without camels. Bars represent point of introduction of camels (simplified from Mace and Pagel 1994).

sister groups than do genetic phylogenies; (2) linguistic data are available for more groups than are genetic data; and (3) linguistic differences are easy to analyse because they evolve in a phylogenetic manner. Objections to these points, especially number 3, have been voiced. As Mace and Pagel (1994: 552) note, 'unlike biological phylogenies, in which a true pattern of vertical descent exists, cultural phylogenies, even if predominantly vertical, will contain many instances of populations interbreeding and the horizontal transmission ... of cultural elements ... [regardless of] the mechanism of or motivation for the adoption of the element', where horizontal transmission comprises diffusion, copying and borrowing. Those mechanisms have been explanatory mainstays in anthropology and archaeology, although in and of themselves they explain nothing. Only when explicitly made part of theory do they have explanatory power.

Critics of the phylogenetic approach cite three problems. First, they claim that phylogenists view history and its attendant taxonomy as a theory of causal ordering. Secondly, they claim that reconstructing cultural phylogeny is virtually impossible *regardless* of the underlying epistemology because any phylogenetic signal has been overwhelmed by the reticulate and rapid nature of cultural evolution. Thirdly, critics claim that language, culture and biology are unrelated; thus any study that uses language as a basis for examining biological or cultural phylogeny is fatally flawed. We consider each in turn.

TAXONOMY AND CAUSAL ORDERING

We find no evidence that phylogenists view taxonomy as a theory of causal ordering. Terrell (1988: 648) cites Gould (1986) as a source of that view and then says: 'even when we can picture biological speciation as a temporal pattern of descent with modification resulting in reproductive isolation (true "branching" in an evolutionary sense), the pictured fact of speciation alone tells us little, if anything, about causes and processes leading up to speciation.' Gould was referring to the fact that Darwinian evolution provides a theoretical warrant for the Linnaean taxonomic system (see also Padian 1999). A hierarchical taxonomy does not tell us about the 'causes and processes leading up to speciation'. It isn't designed to. Similarly, a cultural taxonomy cannot inform us about process. Terrell has conflated pattern and process.

The *pattern* revealed by the Linnean taxonomy was, after 1859, explained by the *processes* comprising Darwin's (1859) theory. The pattern comprises nested taxa of various ranks; groups are constructed on the basis of the formal similarity of each taxon's members, and that is all. Formal similarity results from various evolutionary processes including shared ancestry, parallelism, convergence, and varying degrees of divergence, all of which are in turn driven by natural selection and drift. It took biologists a century to work out the details and we now understand that a set of historical processes provides a *theoretical* explanation for an observed taxonomic pattern.

Critics of cultural phylogenetic studies castigate phylogenists for arguing for the primacy of history as a 'source of law and similarity' (Terrell 1988: 649) – a charge we find unfounded – while at the same time arguing that they *should* be using the ethnographic record as inspiration. But since the 1960s Americanist archaeologists have distinguished between nomothetic and idiographic archaeology, the latter typically being derogated as particularistic history with no explanatory content. This view conflates *history* with *chronology*. The latter comprises a mere temporal ordering of events; the former comprises the ordering and the cause-effect explanations for those events. Americanist culture history is properly named because it involved building chronologies of artefact types and writing explanations, albeit in anthropological terms. Ethnological theory, however, lacked historical explanatory power (Lyman *et al* 1997). Darwinian evolutionary theory is a historical explanatory theory that includes nomothetic processes that operate within the historical contingencies of particular spatio-temporal co-ordinates (Beatty 1995).

Moore (1994b: 931) is emphatic about the necessity of referring to the ethnographic record for interpretive inspiration because without it, 'uniformitarianism' is denied and 'theorists are free to construct whatever bizarre theories they might find agreeable, on whatever basis'. We find this position untenable for several reasons, one being that the ethnographic and ethnohistoric literature offers '*small-scale* observations on societies already under the influence, whether beneficial or malignant, of colonial authorities' (Bellwood 1996a: 883). We do not deny that such research has produced a wealth of insights that must be

considered in efforts to write evolutionary theory in archaeological terms and to adapt biological phylogenetic models to archaeological concerns. We *do* deny, however, that the ethnographic record is a source of uniformitarian laws that govern cultural evolution.

RETICULATION

We agree with the second criticism that cultural evolution *is* often faster than biological evolution and that cultural evolution *can* involve reticulation, but we do not view these as epistemologically problematic. Biological evolution often involves reticulation (Arnold 1997; Endler 1998), but this has not precluded phylogenetic analysis (Nelson 1983; Wagner 1983). The term 'hybridisation' has been used by critics of phylogenetic analyses (eg, Dewar 1995; Moore 1994a, 1994b) to denote any instance of horizontal transmission and thus to signify reticulate evolution. *Hybridisation* produces *hybrids* and 'involves successful matings in nature between individuals from two populations ... which are distinguishable on the basis of one or more heritable characters' (Arnold 1997: 4). Typically, interbreeding members are conceived of as members of separate species – witness Mayr's (1969: 405) definition of hybridisation as 'the crossing of individuals belonging to two unlike natural populations, principally species'. This definition follows the biological-species concept and makes it sound as though hybridisation is not only rare but ontologically messy because the analytical purpose of the biological species *unit* is to study speciation and divergence. Arnold's definition of hybridisation is useful because it avoids restricting the process to interspecific mating, thereby underscoring the issue of the scale of units.

The equation of hybridisation and horizontal-cultural transmission has a deep legacy in anthropology, where 'cultures' have been equated with biological species. Ignoring the issue of the exact scale of a 'culture', hybridisation and horizontal transmission are not necessarily equivalent. Consider the differing scales of the parental units, the offspring units, and the units of transmission. The mating of two parental organisms will produce an offspring with 50% of its genes originating with each parent, a 50/50–F1. The offspring – a hybrid – is an even mixture of its parents' *replicators* (Hull 1988a). Presuming that there are cultural replicators, horizontal cultural transmission may produce an offspring comprised of equal parts of those replicators. But the odds are great that it will not. Whether or not horizontal transmission always produces a 50/50–F1 is not an issue in biology because we know the scale of the replicators that are transmitted. The precise scale of cultural replicators is unknown, but we suspect that their horizontal transmission will rarely result in a 50/50–F1. If one accepts that ceramic technology comprises a lineage, horizontal transmission from another lineage of a replicator concerning how to shape a vessel does not result in a 50/50–F1 because the replicators for paste preparation, preparation and addition of temper, firing, surface treatment, surface manipulation, and other phenotypic traits in the recipient lineage may be unaffected.

Replicators may be transmitted from one lineage to another but not swamp the phylogenetic signal because of the strength of 'vertical transmission in the acquisition of the techniques of artefact production' (Shennan 2000: 821). Horizontal transmission is problematic for phylogenetic studies, but not to the degree suggested by critics. Goodenough (1997: 178) makes an excellent point with respect to language: 'Contact between Japan and the United States has resulted in considerable borrowing in language and culture by Japan and some reverse borrowing by the United States, but their languages and cultures retain their respectively distinct phylogenetic identities.' Innumerable studies have provided the basis for deciding which linguistic characters might be derived characters – bound morphemes and vocabulary, for example – and which might be something else – syntax, for example (Nichols 1996). Borrowing, or introgression (Wiener 1987), leads to a degree of reticulation, but this is in no sense 'hybridisation'.

Paleobiologists who examine the phylogenetic history of extinct organisms must *assume* that the units of analysis – sets of morphometrically similar fossils – comprise distinct taxa (Eldredge and Novacek 1985) and thus do not interbreed. Genetic transmission is assumed to occur *only* within a *lineage* – a line of heritable continuity. Phylogenetic analysis of cultural lineages requires the same assumption. In neither paleobiology nor archaeology can it be *demonstrated* that such is the case. Thus we reject the argument that reticulation precludes cultural phylogenetic analysis. Horizontal transmission is a methodological problem, not a theoretical one.

LANGUAGE, CULTURE AND BIOLOGY

Critics (eg, Moore 2001; Terrell 2001) claim that the comparative method of phylogenists assumes a close correspondence of language, culture and biology. This is false. Early on, Romney (1957: 36) made it clear that one could not assume such a close correspondence, but that language, culture and biology comprised three *independent* lines of evidence for 'a common historical tradition'. His point was to *not* 'presuppose the nature of the relationship, but to establish the pattern in order to consider what factors might affect whether there is a positive, neutral or negative relationship' (Foley and Lahr 1997: 10) among the three. Kirch and Green (2001) refer to Romney's method as 'triangulation'.

The units used in phylogenetic analysis commonly comprise bundles of characters that 'can be transmitted as independent units (ie, even when other aspects of the culture are not passed on)' (Mace and Pagel 1994: 549). Sometimes whole cultures are examined. Terrell (2001: 5) points out that the comparativists' claims are grounded in several problematical assumptions, including '(1) human populations, ethnic groups, cultures, and languages are real things – actual empirical phenomena – and not just convenient analytical fictions; (2) despite births and deaths – and people coming and going – these corporate entities are also historically enduring phenomena [; and] (3) like individuals, such corporate things have ancestors, descendants, relatives, and "patterns of hierarchical descent"'. We agree that these are problematic assumptions for some scales of

analysis. The comparativists understand the problem of units and scale (eg, Mace and Pagel 1994). They would view a cultural phylogeny using 'cultures' as taxonomic units as providing only a broad picture of ancestry. Terrell makes an excellent point about the nonempirical nature of units such as human populations, ethnic groups, and cultures, but he errs in calling them 'analytical fictions'. Explicitly defined units such as 'cultures' can have considerable import *for particular kinds of analysis,* and 'cultures' can be defined differently for different analyses. The real issue is the difference between empirical units and ideational units.

CLASSIFICATION AND UNITS

Today there are deep epistemological disputes regarding biological taxonomy and phylogeny. Many of them concern classification systems and their units. These issues find parallels in anthropology and archaeology, where they rarely receive extended discussion. In evolutionary studies there is no more basic scientific enterprise than classification because it underlies both taxonomy and phylogeny, regardless of whether it is a phylogeny of organisms or of cultural phenomena.

Classification is the creation of units by stipulating the necessary and sufficient conditions for membership within a unit. A *unit* is a conceptual entity that serves as a standard of measurement. *Groups* contain empirical members and have locations in time and space. They are formed extensionally by sorting through a pile of specimens, placing similar specimens together, and using visible properties of the specimens as the basis for the sorting. A problem arises when more specimens are introduced because group boundaries must be reconfigured to accommodate new variation. Units formed in such a manner are often fuzzy amalgams of character states because they conflate the taxon and the specimens in it (Jardine 1969). *Classes* are ideational units that have distributions in time and space. They are defined by *significata* – the necessary and sufficient conditions for membership in a class. A class might have *denotata* – empirical specimens – but it might not. There is no *essential property* that forces a phenomenon to be classified the way it is. Rather, the analyst, on the basis of theoretical concerns and an analytical problem, specifies the *properties of interest* that cause an object or event to be so classified (Lyman and O'Brien 2002; O'Brien and Lyman 2000, 2002b).

There is a distinct lack of consensus in biology over the epistemological status of the most basic unit, the species (Ereshefsky 2001; Hull 1997; Wheeler and Meier 2000), in part because of a failure to appreciate the dichotomy between empirical ('real', or 'natural') units and ideational ('created') units. Given that organisms are visible things, it is not surprising that the units used to categorise them are viewed as natural. Neither should it be surprising that species units have come to be viewed by some as individuals (Hull 1988b). Many of the things that intraspecific organisms do – interact, communicate, interbreed – can be observed. If we conceive of these interactions as definitive of the species, it becomes a simple matter of elevating the entire collection of individual organisms to the level of *an* individual.

As Holsinger (1984: 297) put it, a species is defined by the 'interactions that its members have with one another and by their cohesiveness in certain processes'. This defines a biological species – 'groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups' (Mayr 1942: 120). This definition is reasonable if we can observe the interactions. What happens when we cannot? Does this put paleontologists out of business? No. The solution is to rewrite traditional evolutionary theory in paleontological, not biological, terms. Part of this rewriting comprises punctuated equilibrium (Eldredge and Gould 1972; Gould and Eldredge 1993), which views (1) fossil-species units as equivalent to extant biological species because of the formal stasis of each; and (2) formal variation in fossils as a result of genetic variation (Eldredge 1999).

Mayden (1997) recently counted nearly two dozen distinct species concepts, enough for Hull (1999: 44) to note that 'we are drowning in a sea of species concepts'. We side with those who recognise that a species is a unit constructed for a specific analytical or applied biological purpose (Cracraft 2000; Dupré 1999; Hull 1999). Those purposes might be for managing biodiversity or for studying phylogenetic history. One's analytical goal dictates which one of the several available species concepts, and thus which kind of unit, is the most appropriate. This perspective has significant implications for anthropology and archaeology. Recall Terrell's (2001) point that one of the problems with the comparativists' position is their claim that ethnic groups, cultures and languages are real. It is not difficult to conceive of cultures as empirical entities, nor is it difficult to view cultural groups as natural units. Individual humans within a group coexist, communicate and interbreed. If we view these interactions as group-maintaining activities, it is a simple matter to elevate the natural group to the level of Individual – capitalised to denote an aggregate of discrete phenomena as opposed to a single discrete phenomenon (lower cased).

An individual, whether an organism or a cultural phenomenon such as a ceramic vessel or a ritual, has a developmental history, or *ontogeny*. Similarly, an Individual has a developmental history. It can add and shed pieces continually – individuals come and go – but for some period of time the Individual appears very much like it did the last time we looked. Boyd *et al* (1997) refer to the conservative part of the Individual (our word, not theirs) as the *core tradition*. After a time, the Individual changes enough in terms of phenotypic characters – language, customs, technology, and so on – that we label it as a different Individual. This is anagenetic evolution – the result of a slow buildup of change that gradually turns Individual A into Individual A'. Alternatively, for whatever reason, part of group A fissions and the daughter part moves some distance away from the parental part. After a time, the two Individuals develop different tool traditions, customs and the like, and after more time they have difficulty communicating with each other. This is cladogenetic, or branching, evolution.

We agree with Terrell that units such as cultures are not real. Rather, they are ideational units created for specific analytical purposes and should be defined on the basis of explicit criteria. The specimens, whether individuals or Individuals, placed in a class are empirical, and together constitute the denota of the class.

Groups extracted from classes are not 'convenient analytical fictions' (Terrell 2001: 5). If theoretically informed definitions are employed, such groups can be used in cultural phylogeny, just as species are used in biological phylogeny. Or, as we discuss later, specific *parts* of cultures can be examined from a phylogenetic standpoint.

ANALYTICAL FRAMEWORKS

Units are useful only if they are placed in a framework that allows us to measure differences among them. Two analytical frameworks are important here: evolutionary taxonomy and cladistics. Both are hierarchical systems, and both are often referred to as systems of classification. Our interest is in the basic structure of each system and in the kind of information that can be derived from each. The varying information content of each is a product of structural differences – a point that is underappreciated in discussions of cultural phenomena and that has significant implications for phylogenetic studies.

EVOLUTIONARY TAXONOMY

Taxonomic classification produces a hierarchical arrangement of classes of varying rank in which characters are weighted and considered in order of their suspected importance such that classes at one rank include parts that are classes at lower ranks (Valentine and May 1996). In Figure 6.2 there is a class E, but if lower levels of exclusivity are used, the classes become E1 and E2. At an even lower level of exclusivity, the classes are E1a, E1b, E2c, and E2d, and at the lowest level the classes – called *terminal taxa* – are E1aI, E1aII ... E2dVIII. Note the vertical asymmetry of a hierarchical system: units at one level can be related to only a single unit at the next higher level but can be related to any number of units at the next lower level (Knox 1998). In taxonomic classification the significata of a class reflect an order constructed by the analyst. In Figure 6.2 characters a and b are relevant only for defining subordinate classes E1aI, E1aII, E1bIII, and E1bIV. This
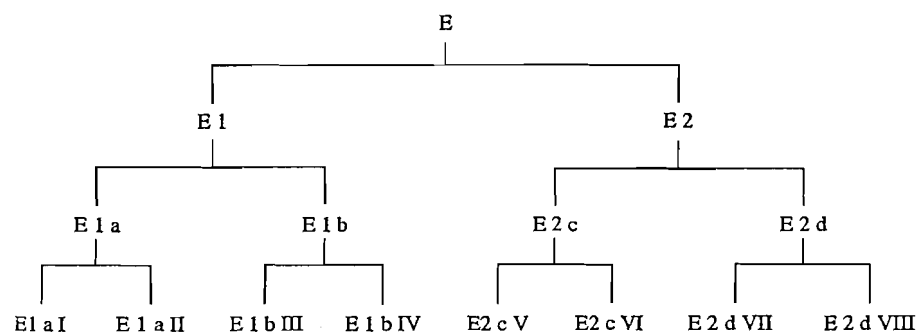

Figure 6.2 A taxonomy of classes at increasing levels of exclusivity (from O'Brien and Lyman 2000).

does not mean that phenomena assigned to, say, class E2cV do not display characters a or b; it means *only* that classes subordinate to E2 are not defined by characters a and b. The particular character that makes the phenomena assignable to class E2 is more important in the judgment of the analyst than is the character that results in phenomena being assigned to E1. Characters a and b are irrelevant to further sorting of phenomena in E2, and characters c and d are irrelevant to further sorting of phenomena in E1. Thus the features that comprise significata are said to be 'weighted'.

Taxonomies can be created from the top down or from the bottom up. The most familiar upward classification is the Linnaean taxonomic system. Each unit ideally comprises organisms that are more similar to each other than any is to an organism in another unit of parallel, superior or subordinate rank, producing 'gaps' between parallel taxa (Mayr 1969; Simpson 1961). Each particular taxon of a rank comprises a group of specimens, whether discrete organisms at the species rank or taxa of rank T_j within a taxon of rank T_{j+1}. Although the various levels of the Linnaean taxonomy can be said to house empirical referents – organisms – it is usually the case that only the lowest levels – species – are treated that way (Ereshefsky 2001). It is only because species are members of genera, genera are members of families, and so on, that we can identify a particular organism as representing a particular genus or family. This method of ordering is used to reflect the degree of formal similarity among the taxa being categorised.

The development of the Linnaean system as the predominant means of representing patterns of taxonomic grouping was independent of any evolutionary perspective. Darwin used the taxonomic pattern as independent evidence supporting the centerpiece of his theory – descent with modification – and was adamant about the rationale for biological classification: 'I believe that the *arrangement* of the groups within each class, in due subordination and relation to the other groups, must be strictly genealogical in order to be natural' (Darwin 1859: 420). Darwin knew that despite his emphasis on descent with modification as the basis of natural classification, he could err in his assignments of organisms to particular taxonomic units and hence be wrong in his assessment of ancestor-descendant relationships. Thus he emphasised that not all morphological characters were equally useful in making assignments: Characters that result from common ancestry – homologs – are useful; those that result from functional convergence – analogs – are not. The key is in being able to distinguish between the two.

That the Linnaean system simultaneously evaluates *both* similarity and descent has implications for cultural phylogenetic studies insofar as the model on which some of them are based does much the same thing. In the biological model, phenotypic similarity is used as a proxy for genetic similarity: The greater the phenotypic similarity between two organisms or groups of organisms, the closer the inferred genetical relationship between them (Simpson 1961). Phenotypic similarity/dissimilarity can also be used as a gauge of evolutionary distance: the greater the similarity, the less evolutionary modification of a descendant and hence the closer the relationship to its immediate ancestor. Cultural taxonomies share these features.

Epistemological and ontological alignment of the Linnaean taxonomic pattern with Darwin's evolutionary processes was fully realised in the mid-20th century as part of the neo-Darwinian synthesis and the simultaneous emergence of the 'new systematics' (Huxley 1940). The latter comprised an effort to align new understandings of evolutionary – particularly genetic – processes with taxonomic pattern. The new systematics did three things. First, it explicitly acknowledged the critical role of homologous characters (Simpson 1945) and focused on *primitive characters* because they evolved slowly and could be traced through the successive species of a lineage. *Derived characters* changed over time rapidly because they were adaptively plastic. Together, primitive and derived characters provided a guide to grouping taxa into various ranks. Primitive characters reflected ancient relationships and taxa of high rank, whereas derived characters reflected more recent relationships and taxa of low rank. Secondly, the new systematics took Linnaeus's dictum that the taxon produces the definitive characters as evidence that the biological taxonomy was 'natural' and thus reflected genealogy. And thirdly, it adopted a new definition of species as reproductively isolated populations and added physiology, behaviour, ecology and biogeography to the morphological data that had previously been used to classify organisms. These newly considered data were thought to allow one to test the phylogenetic implications of the biological taxonomy, and thus emerged what came to be called *evolutionary taxonomy.* Insofar as the results of applying the procedures of the new systematics reflect descent *with* modification – process *and* pattern – the various taxonomic groups are thought to be 'natural'.

The conciliation of the Linnaean taxonomic pattern with the phylogenetic processes of descent and speciation demanded that the former be conceived of in a particular way. Figure 6.3a shows a phylogenetic tree with branches and a stem incorrectly conceptualised as Linnaean taxa of different rank. Time is implied to pass from bottom to top. Figure 6.3b shows the same phylogenetic tree but with the various branches grouped correctly into Linnaean taxa; again time passes from bottom to top. Figure 6.3c is a dendrogram showing the Linnaean taxonomic relationships among terminal species (signified by dots) of Figures 6.3a and 6.3b. The dendrogram is not a phylogeny, and thus time is not included or implied, but note that the horizontal lines connecting vertical lines denote relationships and are topologically like those in Figure 6.3b. Keep in mind Figure 6.3b when reading the following.

CLADISTICS

Cladistics, or phylogenetic systematics, employs a subset of homologous characters to hypothesise phylogenetic relationships. This subset comprises shared derived character states termed *synapomorphies*, defined as homologous character states held in common by two or more taxa and their immediate ancestor but no other taxon. *Symplesiomorphies*, or shared ancestral (primitive) character states, are homologous character states held in common by an entire set of related lineages (Figure 6.4).
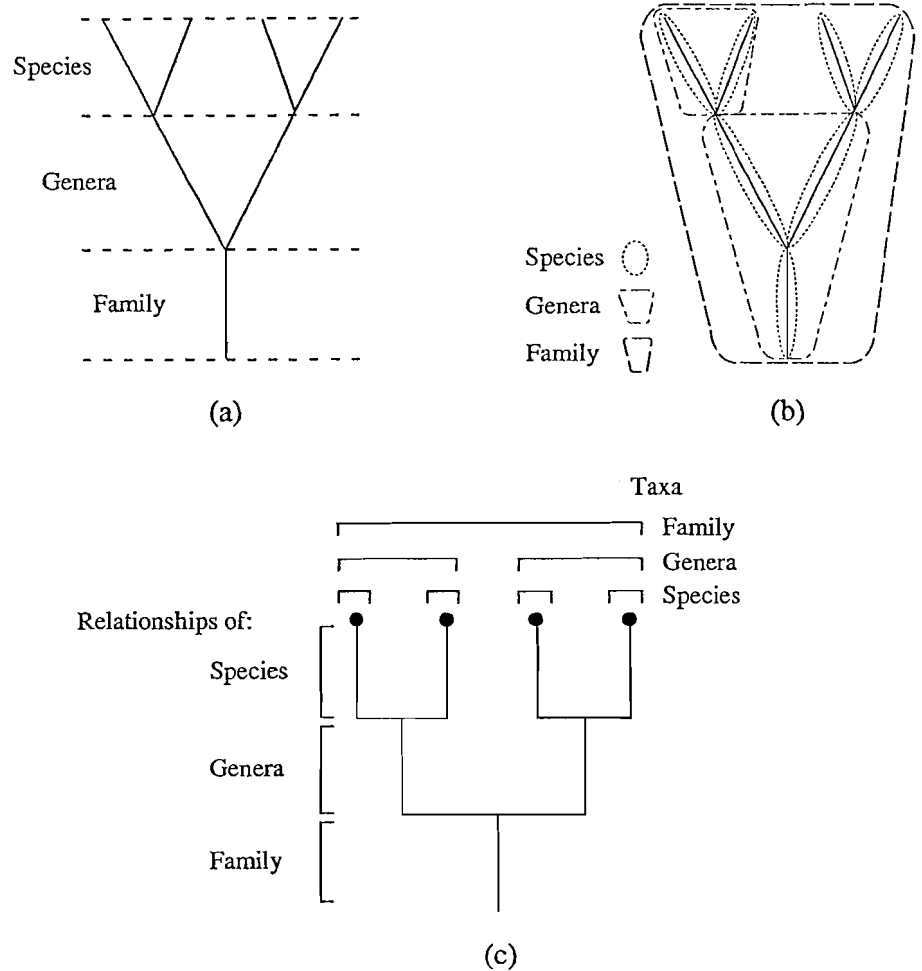
　　　　　　　　The Evolution of Cultural Diversity

(a)

(b)

(c)

Figure 6.3 Hierarchical structures showing phylogeny and the relationships of higher and lower taxa (after Simpson 1961).

Cladistic analysis produces an unrooted tree such as the one at the top of Figure 6.5 (synapomorphies used to generate the tree are not shown). The diagram tells us only that *on the basis of certain characters*, Taxon A and Taxon D are more similar to each other than either is to Taxon C or Taxon E. Whether Taxon B is more similar to either Taxon A or Taxon D than it is to either Taxon C or Taxon E is ambiguous. A measure of similarity is generally not the ultimate goal of cladistics. That goal is to arrange the taxa in phylogenetic order. The theoretical basis for the ordering can be Darwinian evolutionary theory (descent with modification), which is not to say that the theory provides independent *support* for cladistics. If we *could* say this, then we would be assured that descent 'explains pattern similarity, modification explains pattern differences, and their combination can explain any pattern that
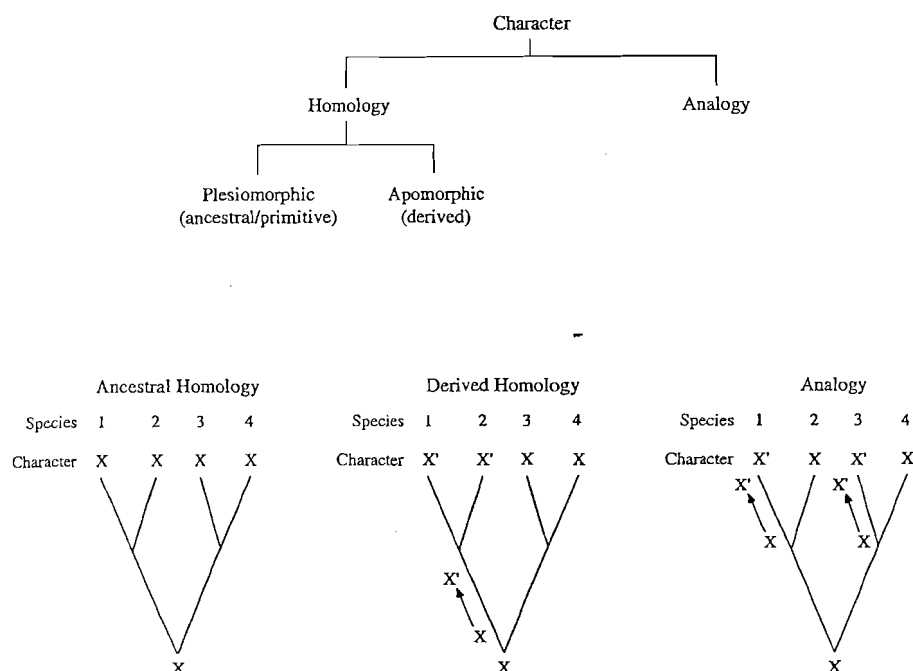
Figure 6.4 Kinds of characters and their relationship to determining phylogenetic history: top, a taxonomic classification of kinds of characters; bottom, three phylogenies showing ancestral homology, derived homology, and analogy (convergence). In all three depictions x is the ancestral character state, x' is the derived character state, and arrows denote the points at which the character state changes (after Ridley 1996).

might be observed' (Brower 2000: 151). Such a notion is both metaphysical and unverifiable (Popper 1974). A strength of cladistics is its nonreliance on evolutionary theory as a *necessary* ontological basis (Brower 2000). This leaves unanswered the question of *why* the ordering appears the way it does, which some find unacceptable (Kluge 2001). The most accommodative theory for why an ordering appears a certain way is descent with modification.

Placing taxa in historical sequence is done by creating a rooted tree, or *cladogram.* Placing taxa in putatively *correct* historical sequence rests on the ability to distinguish between symplesiomorphic and synapomorphic character states. Without that ability, we would have no way of choosing among the myriad rooted trees possible. Figure 6.5 shows seven possible rooted trees for the five taxa shown in the unrooted tree, any of the seven of which is as likely as any other. Whether a character state is ancestral or derived is termed *character polarity.* Figure 6.6 shows three rooted trees that track the evolution of projectile-point lineages that stem from a common ancestor. For simplicity we track a single character, fluting, for which two character states are possible, fluted and unfluted. Over time, Ancestor A, which is unfluted, gives rise to two lines, one of which, like its ancestor, is unfluted and the other of which *is* fluted (Figure 6.6a). The character state 'fluted'
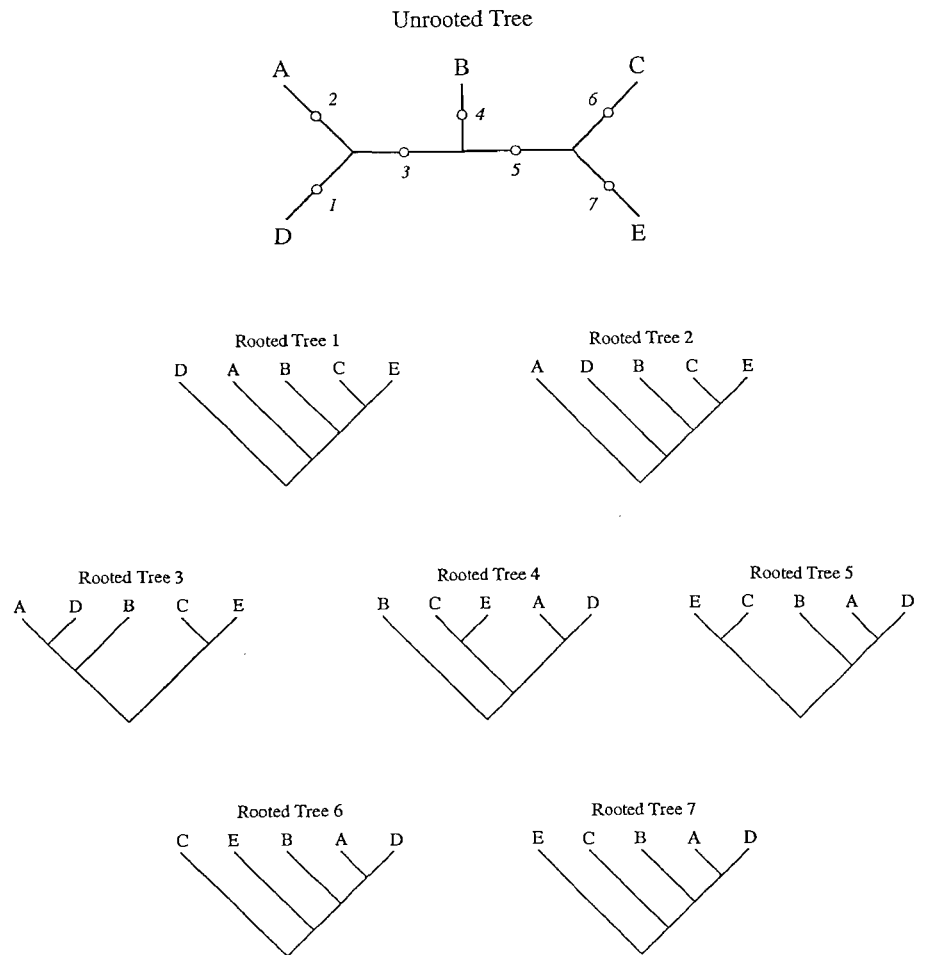
Unrooted Tree

Figure 6.5 The difference between an unrooted tree (top) and rooted trees (bottom). Note that an unrooted tree says nothing about phylogeny; all it shows are intertaxon relationships based on shared synapomorphies (not shown). The tree can be rooted at any of seven points, usually through selection of an outgroup. Once rooted, a tree is phylogenetically informative.

in Taxon 2 is apomorphic; it is derived from the ancestral character state, 'unfluted'. In Figure 6.6b, Ancestor B (old Taxon 2) gives rise to two new taxa, 3 and 4, each of which carries the derived character state, 'fluted'. Here 'fluted' becomes a synapomorphy. In Figure 6.6c, in which two descendant taxa have been added, fluting is now an ancestral character *relative* to taxa 5 and 6 because it is shared by three taxa and two ancestors. But relative to taxa 3, 5, and 6, fluting is synapomorphic because it is shared by three taxa and their immediate common ancestor, B. Thus, depending on where in a lineage one begins, a trait can be apomorphic or plesiomorphic. Convention is to place *nodes* at the points where
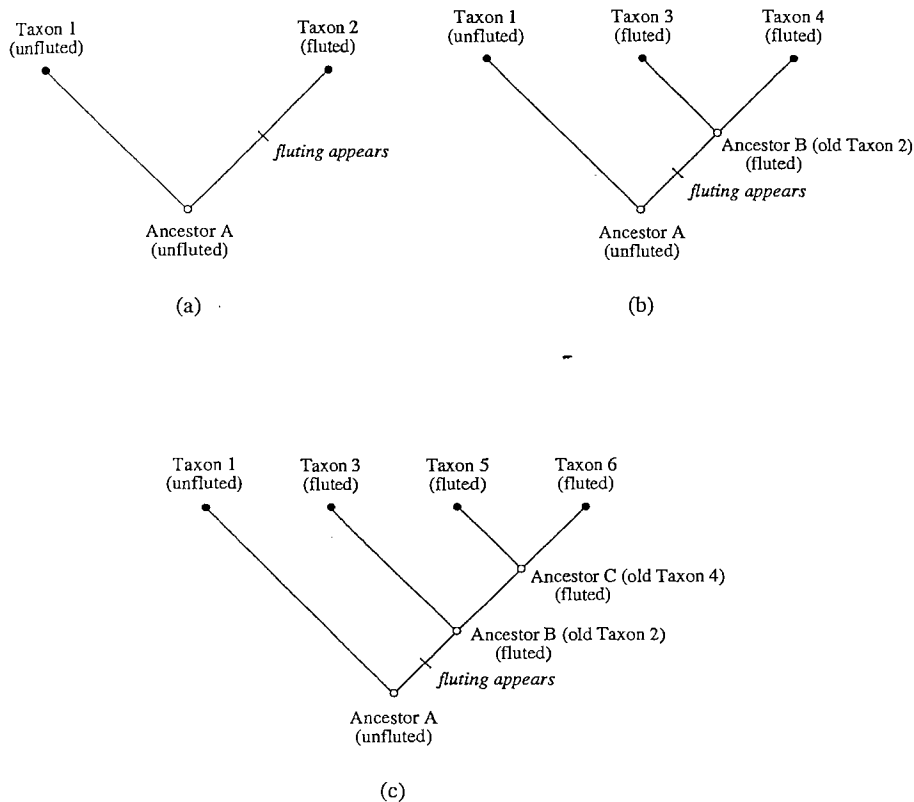
(a)

(b)

(c)

Figure 6.6   Phylogenetic trees showing the evolution of projectile-point taxa. In (a), fluting appears during the evolution of Taxon 2 out of its ancestral taxon. Its appearance in Taxon 2 is as an apomorphy. In (b), Taxon 2 has produced two taxa, 3 and 4, both of which contain fluted specimens. The presence of fluting in those sister taxa and in their common ancestor makes it a synapomorphy. In (c), one of the taxa that appeared in the previous generation gives rise to two new taxa, 5 and 6, both of which contain fluted specimens. If we focus attention only on those two new taxa, fluting is now a plesiomorphy because it is shared by more taxa than just sister taxa 5 and 6 and their immediate common ancestor. But if we include Taxon 3 in our focus, fluting is a synapomorphy because, following the definition, it occurs only in sister taxa and in their immediate common ancestor (from O'Brien *et al* 2001).

branches meet and to refer to the nodes as ancestors that produced the *terminal taxa* (those at the branch tips).

One common, but contentious (Nixon and Carpenter 1993), method for determining polarity is *outgroup comparison*, with outgroup defined as a taxon that is outside the taxa being analysed (the *ingroup*). A character state in the outgroup is likely to have been ancestral relative to the taxa under investigation. Technically, any taxon can serve as an outgroup, but the more closely it is related to the ingroup taxa, the greater the number of character states whose polarity

might be clarified. Selecting an outgroup roots the tree below the intersection of the outgroup and ingroup; ingroup taxa are then arranged in terms of their best fit relative to the character states examined. Although in the simple examples presented thus far all character states evolved only once, such is rarely encountered in real-world situations. More likely a tree will contain multiple character states that show up in lines not related directly through one common ancestor. These are *homoplasies*. One kind of homoplasy results from character state reversals – meaning that character state A changed to state A' and then at some later point in the set of related lineages reverted to state A. This kind of homoplasy is a classification problem (O'Brien *et al* 2001, 2002) because rarely will precisely the same character state re-emerge after it disappears (Dollo's Law). More likely, classification makes it *appear* as if the character state has reappeared. Another kind of homoplasy results from parallelism or convergence – organisms, perhaps because of anatomical and/or environmental constraints (the first the result of common history, the second because of similar environments), independently evolve the same character state (Figure 6.4). All but the simplest cladograms contain homoplasy, and the analytical task is to reduce its influence on phylogenetic hypotheses – probably *the* most difficult problems in cladistic analysis. Homoplasy leads to multiple solutions to arranging taxa, and it is up to the analyst to sort through the solutions and defend why one of them was chosen. Various computer programmes (eg, Swofford 1998) simplify this task and produce indices by which to judge the overall strength of the ordering.

As Ridley (1996: 476) notes, 'outgroup comparison works on the assumption that *evolution* is parsimonious'. This means that when faced with the problem of character polarity, we choose the option that requires the fewest evolutionary events. In Figure 6.6 it is more parsimonious to assume that fluting arose once and only once as opposed to having arisen twice in separate lineages. When faced with specimens in taxa 3 and 4, which exhibit fluting (Figure 6.6b), it is more parsimonious to assume that fluting appeared in Ancestor B than it is to see it as having arisen separately in taxa 3 and 4. That would require two evolutionary steps instead of one. Based on that reasoning, fluting is a synapomorphy as opposed to a case of homoplasy. Our particular view of parsimony, however, has nothing to do with whether evolution is parsimonious; rather, it has to do with logical argumentation: it is more parsimonious to make as few ad hoc phylogenetic hypotheses as possible (Sober 1983).

At the heart of cladistics is the notion of *monophyly*, which is the specification of a historical group (Farris 1974). A *monophyletic group*, or *clade*, is defined as two or more terminal taxa and their common ancestor. In the rooted tree shown in Figure 6.6c, taxa 5 and 6, together with Ancestor C, are in one clade; taxa 3, 5, 6 and their common ancestor, B, are in a second and more inclusive clade; and taxa 1, 3, 5 and 6, together with their common ancestor, A, are in a third and most inclusive clade. Cladistics creates a nested hierarchy of synapomorphies: 'From the point when a feature first appears in phylogenetic history, it will be passed along in some guise (ie in the same or transformed version) to descendent taxa. [By] mapping the distribution of such attributes[,] monophyletic taxa – branches of the tree of life – are delineated, defined, and recognized' (Eldredge and Novacek 1985: 67). Such taxa comprise 'actual historical units' (Eldredge and Novacek 1985: 66).

The taxa are created before an unrooted tree is generated; rooting it on the basis of an outgroup and using synapomorphies to order the taxa (classes) turns them into units that have historical significance.

The hypothetical ordering is testable. Independent temporal information could be used to test the order of character state change, or testing might involve adding new characters and/or character states and omitting those that produce ambiguous phylogenetic signals. A different outgroup might be used to help resolve homoplasy and increase parsimony. Some lament that these procedures might result in an unstable set of taxa because that set is revised with every new analysis (Niklas 2001). This ignores the fact that the correct phylogenetic ordering is being sought and because that ordering is unknown, testing *must* be a part of the analytical procedure. Theory dictates how a result should appear, not what a particular result should be.

PARAPHYLY AND ANCESTORS

Two ontological differences between evolutionary taxonomy and cladistics are important. One concerns paraphyly and the other ancestral taxa. *Paraphyletic groups* are what remain after one or more parts of monophyletic groups are removed. Molecular data suggest that humans, chimpanzees and their common ancestor represent a clade, as do humans, chimpanzees, gorillas and their common ancestors (Figure 6.7). Adding orangutans and a common ancestor creates yet another monophyletic group. Standard practice is to group chimpanzees, gorillas and orangutans together and to refer to them as great apes and to place humans (including fossil hominids) in a separate group, or *grade*. Cladistically the grade 'great apes' is a paraphyletic group when humans are excluded (Figure 6.7).

There are four reasons why paraphyly is acceptable in evolutionary taxonomy. First, paraphyletic groups are easily recognised (Brummitt 1996). Secondly, a consensus as to the general arrangement of groups contributes to the acceptance of paraphyletic groups (van Welzen 1997). Thirdly, there is a general belief that grouping taxa based on commonly held nonsynapomorphic characters provides information about the degree of evolutionary divergence. By keeping humans separate from the great apes, taxonomists emphasise *autapomorphies*, or characters that humans developed that the great apes did not – language, culture, and the like. As the traditional argument goes, the hominid split was so rapid and so pronounced (Figure 6.8) that hominids deserve to be kept in a separate grade. Fourthly, paraphyletic groups are considered to be ancestral groupings. Paraphyletic groups, being based on symplesiomorphies, can be recognised only by the characters they do *not* have. This is why on a rooted phylogenetic tree ancestors are placed at the ends of branches instead of at nodes. Ancestors must, by definition, be totally primitive with respect to their descendants and thus cannot be distinguished as individual taxa. In cladistics a *hypothetical* ancestor comprises the collection of characters and character states (not a taxon) at a node.
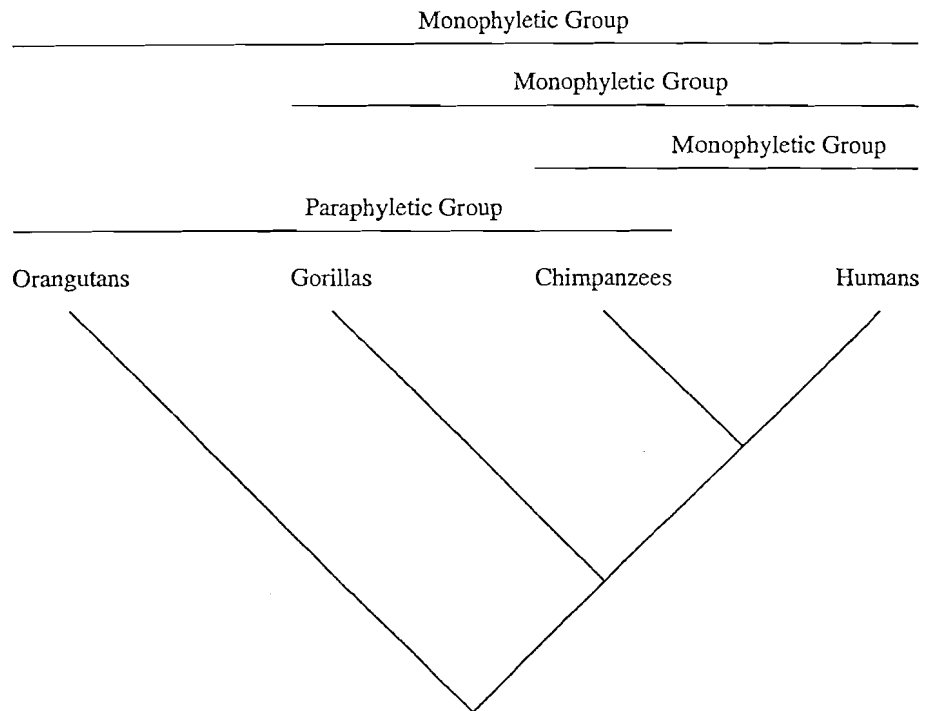
Monophyletic Group
_____

                   Monophyletic Group
        _____

                              Monophyletic Group
                    _____

        Paraphyletic Group
_____

Orangutans   Gorillas   Chimpanzees   Humans

Figure 6.7 Three monophyletic groups (clades) of primates and a paraphyletic group comprising orangutans, gorillas and chimpanzees, but not humans.

Pongid Zone   (Zone Now Unoccupied)   Hominid Zone

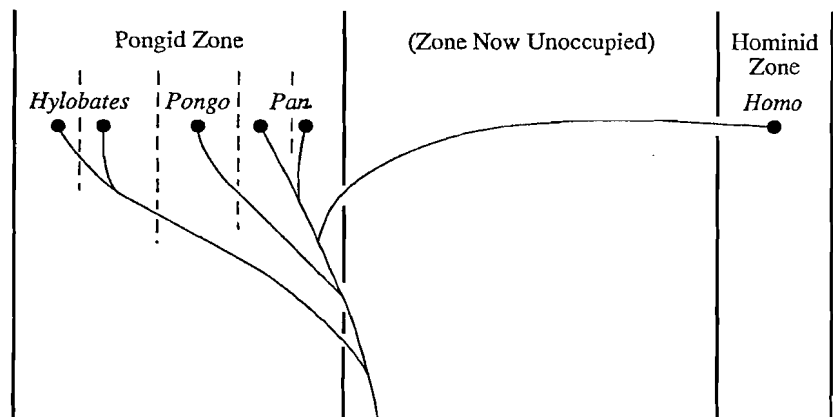*Hylobates*   *Pongo*   *Pan*   *Homo*

Figure 6.8 Adaptive basis for splitting out hominids from pongids and placing each in a separate grade (after Simpson 1963).

Cladistics views speciation as a branching event (anagenesis can occur after a split), with every speciation event producing at least two daughter species. To examine the implications of treating a taxonomic unit as an ancestor, consider Figure 6.9a, in which Taxon A is ancestral to taxa B and C. The three taxa are grouped because they share ABC characters, but B and C are *sister taxa* – they are more closely related to each other than either is to A – because they share BC characters. If A is considered to be the ancestor of B and C, it can be placed at the speciation node *only* if it lacks any distinguishing characters of its own. Otherwise, it would be placed as the sister taxon of the clade comprising B and C. An ancestor cannot exhibit an apomorphy that is not also present in its immediate descendant. We are left with the illogical position that ancestor A can be recognised only because it possesses ABC characters but lacks BC characters. In Figure 6.9b, three avian taxa have been substituted for the letters in Figure 6.9a, with *Archaeopteryx* shown as the ancestor of ostriches and ravens. *Archaeopteryx* has the synapomorphies (eg, feathers) that are found in all birds but lacks the synapomorphies of the ostrich and raven, such as a pygostyle. In terms of unique characters, *Archaeopteryx* simply does not exist – an absurd notion given that its remains have been found; parents do not necessarily cease to exist when their children are born (Sober 1988). To circumvent this illogical position, likely ancestors are placed on a cladistically derived tree as terminal taxa (Figure 6.9c). Cladists accept that in many cases their trees contain *nominal* paraphyletic taxa because of homoplasy, and they work to reduce it.
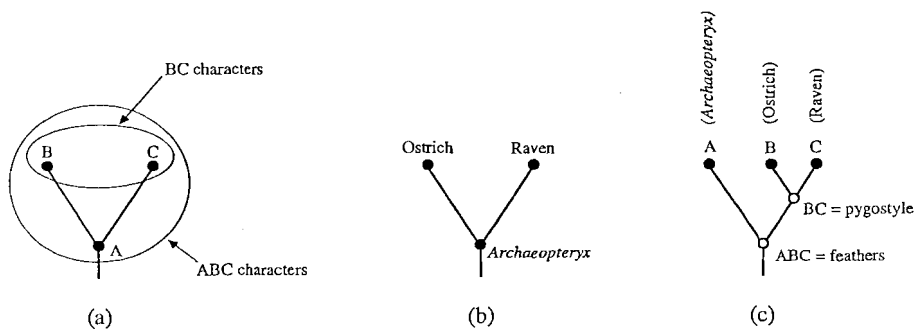

(a) (b) (c)

Figure 6.9 Diagram showing the logical inconsistency involved in treating ancestors as individual taxa and how cladists have solved the problem. In a, three taxa (A–C) form a group because they share three character states (also A–C). Taxa B and C are sister groups because they share BC character states, which A lacks. If A is considered to be an ancestor of B and C, it can be placed at the origin point *only* if it lacks any distinguishing character states of its own; otherwise, it would be placed as a sister group to B + C. As an example (b), *Archaeopteryx*, the traditional ancestor of birds (ignoring more recent findings), has synapomorphies found in all birds, such as the ostrich and raven, but lacks synapomorphies found in the ostrich and raven. Thus in terms of character distribution, the *Archaeopteryx* does not exist. To get around this problem, cladists do what is shown in c: they place ancestors as a sister group to their putative descendants and accept that they must be nominal paraphyletic taxa (after Kitching *et al* 1998).

If real ancestors have no place in cladistics, why do linguists refer to ancestral or 'proto' languages? Historical linguists have long recognised the importance of homologous characters, and they understand that homology statements are similar to synapomorphy statements at different levels. But historical linguists have as one of their goals the identification (reconstruction) of an ancestor – the 'stem group' (Wiener 1987: 221) – and to do this they rely on symplesiomorphies. An ancestor can be identified *only* on the basis of ancestral characters; derived characters cannot occur in *the* true ancestor of a group of related languages. Platnick and Cameron (1977: 383) put it this way: 'Although admitting that in most cases possibly ancestral languages do turn out to have autapomorphies "disproving" such a relationship, linguists consider the failure to find such a character sufficient evidence of actual ancestry.' Most linguists view ancestral languages as real. There is, however, an alternative to labelling specific languages as ancestors: Related languages can be viewed as sister taxa, as shown in Figure 6.1. This is the cladistic method, which shows genealogical relationships without recourse to an ancestor.

RETICULATION IN CLADISTICS

Plotting the genealogy of hybrid taxa creates a reticulate tree, and thus it has been claimed (Sosef 1997) that reticulate evolution arising from hybridisation followed by speciation cannot be accommodated in a system of clades. We disagree. In our discussion of phylogenetic trees we assumed that every split was dichotomous, but this is not always the case. Trees often contain *polytomies*, or points at which a simple dichotomous split cannot be made. Additional data may help to resolve the polytomy, or it might turn out that the polytomy is a result of reticulation. This is an empirical matter. Thus we agree with Platnick (in Harper and Platnick 1978: 360) that 'hybridisation is not a problem for cladistics [, which] merely converts reticulations of two taxa (producing a third hybrid taxon) into trichotomies'. This has enormous implications for cladistic analyses of archaeological and anthropological phenomena, where some reticulation is expected.

WHICH METHOD FOR WHAT GOAL?

On the few occasions when the term 'cladistic' is used in the archaeological and anthropological literature, the author is usually referring to any classificatory architecture that branches. We suspect that the differences between evolutionary taxonomy and cladistics, and the difference between pattern and process, are not well understood. Evolutionary taxonomy and cladistics offer different ways of looking at the world. The former addresses both similarity (pattern) and genealogy (process) whereas the latter addresses genealogy only. Process plays a role in cladistics only when we introduce a theory to explain the pattern. That theory is descent with modification, although other theories (processes) could conceivably explain the pattern as well.

The differences between how evolutionary taxonomy views taxonomic relationships and how cladistics views them are irreconcilable ontologically and methodologically (de Queiroz and Gauthier 1992; Ereshefsky 2001; Mayr 1995). Cladistics creates taxa not on the basis of similarity but on the basis of proximity of descent as defined by synapomorphies. In cladistic analysis there are no known ancestors to any descendent taxa, nor can we identify one. That is why a cladistically derived tree is only an abstraction of reality. This, however, is its strength, not a weakness. Evolutionary taxonomy cannot exist without 'real' ancestors. But it is unlikely, given the vast number of species that must have existed from the beginning of time and the relatively few that have left records, that actual ancestors have been found. Yet evolutionary taxonomists insist that ancestor recognition is integral to the creation of groups – an insistence derived from the perspective that the groups are real. Even in palaeoanthropology, despite the penetration of cladistics (Strait and Grine 1999), 'one cannot avoid the impression that its underlying philosophy has been less thoroughly absorbed' (Tattersall 2000: 7).

If we are interested in producing *phylogenetic* orderings, cladistics is superior to evolutionary taxonomy because genealogy is, theoretically, the *only* thing it tracks. If we are interested in process and pattern *simultaneously*, then evolutionary taxonomy is a viable option. In such cases we must acknowledge that paraphyly will be present and that as a result evolutionary taxonomy cannot *on average* produce as correct a phylogenetic result as cladistics can. Evolutionary taxonomists try to work around this conundrum by moving back and forth between the two methods, first constructing evolutionary taxonomies and then testing derived groupings for monophyly (Mayr and Ashlock 1991). However, only in those cases where exactly the same characters, and *only* those characters, are used to define taxa will there be a correspondence between taxa defined cladistically and those defined by evolutionary taxonomy. All those characters would be putative synapomorphies. The key question is, how would we know that only synapomorphies were used, given that such characters are for the most part indistinguishable from the total set of homologous characters used in evolutionary taxonomy?

Paraphyly is a consequence of two interrelated factors. First, the classification process, not nature, creates paraphyly as a result of the confusion of empirical and theoretical units. For this reason we reject the notion that paraphyletic groups are 'real'. Secondly, the confusion of pattern and process creates paraphyly. As Lidén (1997: 528) put it, 'The statement "nature creates paraphyletic taxa" is ... based on a much more idealized picture of nature: a concept of atomistic temporally extended species-taxa, psychologically appealing but devoid of empirical and theoretical support'. Cladistically derived trees can contain paraphyly because of homoplasy, but this is nominal paraphyly, not 'real' paraphyly. The addition of more characters or character states, plus the identification of new taxa (classes) could remove the paraphyly (homoplasy) and yield monophyletic groups. Evolutionary taxonomists often make the claim that extinction is the saviour of cladistics because it removes the 'problem' caused by lack of 'real' ancestral taxa, but this is hardly the case. Rather, as van Welzen (1998: 421) put it, 'unknown ancestral taxa are the saviour of paraphyletic groups in Linnaean classification'.

UNITS OF CULTURAL EVOLUTION

The method used to examine cultural phenomena conditions the units used and their scale. Boyd *et al* (1997: 364) observe that tracing 'cultural phylogenies is possible to the extent that there are genealogical entities that have sufficient coherence, relative to the amount of mixing and independent evolution among entities, to create recognizable history'. Tracing phylogenetic history depends on there being a phylogenetic signal strong enough to be detected. They point out that if culture is defined as information transmitted from individual to individual, it is reasonable to posit the existence of a hierarchy of genealogical entities analogous to the genealogical hierarchy of organic evolution. Small elements – such as specific innovations and components of ritual practice, are linked together in larger, potentially transmittable entities – technological systems, religion – which themselves are collected into 'cultures' that characterise human groups of different scales, such as kin groups, villages and ethnic groups. These units can cross-cut one another, and thus the analyst must be explicit in defining the unit being used. The units will create the same paraphyly seen in the Linnaean taxonomic system if we confuse pattern with process and attempt to mix similarity and descent. If we impose a theoretically informed classification on the phenomena being classified as opposed to extracting it *from* the phenomena, then we have a much better chance of avoiding the construction of paraphyletic groups. We have in mind a taxonomy similar to that in Figure 6.2, which in terms of *structure* is no different from the Linnaean system. The difference lies in how the units are created.

UNIT SCALE

Boyd *et al* (1997) offer three models: cultures as species, cultures as collections of ephemeral entities, and cultures as assemblages of many coherent units. Like Boyd *et al*, we find no support for the culture-as-species model, although the literature is replete with references to this culture or that culture, as if they were natural units. Archaeologists (Cullen 1993) and biologists (Gould 1987) routinely equate 'cultures' with species, despite the fact that there is no explicit, generally accepted definition of 'a culture' that incorporates the notion of transmission. Thus any equation of a biological species with a culture is fallacious. Likewise, based on our experience and that of others in detecting phylogenetic signals in the archaeological record (Foley 1987; Foley and Lahr 1997; Kirch and Green 2001; O'Brien *et al* 2001, 2002), we reject the cultures-as-collections-of-ephemeral-entities model. It rests on the premise that 'observable aspects of culture could be the result of units that are beneath the resolution of current methods to observe' (Boyd *et al* 1997: 366). One reason for this lack of resolution might be that change is so rapid that only a weak phylogenetic signal results. The model of cultures as assemblages of many coherent units views the components as 'collections of memes that are transmitted as units with little recombination and slow change, and their phylogenies can be reliably reconstructed to some depth' (Boyd *et al* 1997: 376). How deep we can go hinges on the strength of the 'glue' that holds the

units together and the degree of openness of cultural systems. If we think of the components as memes, how cohesive is a set of memes, and how freely can memes from the outside enter a set and in what frequency?

The two models that hold the most promise – cultures as hierarchical systems and cultures as assemblages of coherent units – are not mutually exclusive, and in fact Boyd *et al* (1997) view them as modes within a continuum. As they point out, it is difficult to put upper and lower bounds on the modes, and perhaps because of that we should view them as nonexclusive, overlapping modes, especially if the models are applied to cultures in general. Central to their model of cultures as hierarchical systems is the existence of a conservative 'core tradition', which is rarely affected by diffusion of units from other groups. New core traditions arise mainly 'by the fissioning of populations and subsequent divergence of daughter cultures. Isolation and integration protect the core from the effects of diffusion, although peripheral elements are much more heavily subject to cross-cultural borrowing' (Boyd *et al* 1997: 365). As for constructing phylogenetic hypotheses, 'reasonably deep core-cultural phylogenies can still be inferred, but this requires disentangling the effects of borrowing by distinguishing core and peripheral elements, and especially by methods to identify elements that "introgressed" into the core' (Boyd *et al* 1997: 365).

We agree that most cultures probably have a conservative 'core tradition' and perhaps it can be identified in modern cultures. It is at the level of tradition that archaeologists can begin to construct testable hypotheses of cultural phylogeny. An archaeological tradition is 'a socially transmitted cultural form which persists in time' (Thompson 1956: 39). Traditions are lineages that can exist at several scales. As in biology, genes, cells and organisms all replicate or reproduce to form lineages; at a higher level, cell lineages make up organisms; and at a yet higher level organismic lineages form populations. Lineages can be represented on a phylogenetic tree as a set of branches that form pathways from the root of the tree (or an internal node) to a terminal (Figure 6.10). Clades comprise multiple, related lineages. Whereas clades are by definition monophyletic, lineages can be paraphyletic or polyphyletic in terms of their lower-level components. In biology, 'organisms making up the later part of a population lineage may share a more recent common ancestor with organisms in a recently diverged but now separate lineage than with the earlier organisms of their own lineage' (de Queiroz 1998: 60). Lineages are patterns of genealogical descent; clades are patterns of phylogenetic relationship.

CONCLUSIONS

Cladistics holds considerable promise for archaeology in terms of generating phylogenetic hypotheses. The phylogenies it produces are starting points from which to begin to answer some of archaeology's evolutionary questions. These could take myriad forms. Do changes in character state relate to artefact function? Do changes in one character or set of characters relate to changes in other characters? Was the change in form the product of selection, the product of drift, or some combination thereof? What was the nature of the selection or drift?
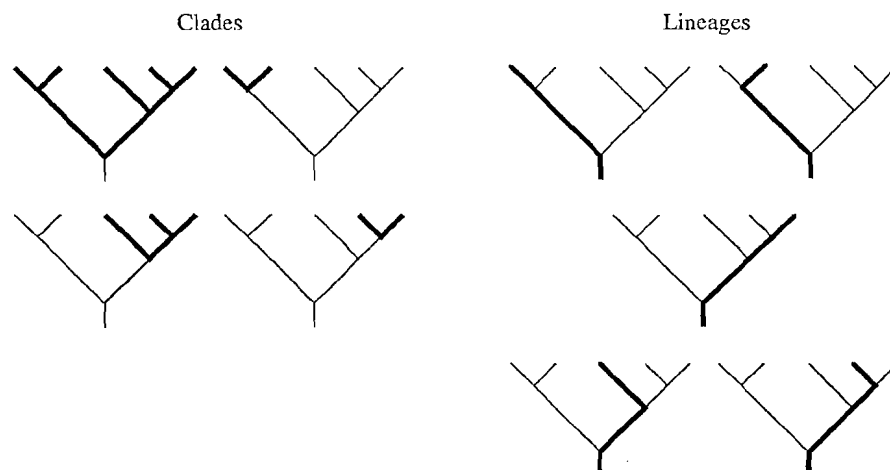
Clades   Lineages

Figure 6.10 Clades versus lineages. All nine diagrams represent the same phylogeny, with clades highlighted on the left and lineages on the right. Additional lineages can be counted from various internal nodes to the branch tips (after de Queiroz 1998).

Archaeologists are uniquely capable of answering these questions, and cladistics offers a means to answer them.

But are we simply borrowing techniques of biological origin without a firm basis for so doing? No. We view cultural phenomena as residing in a series of nested hierarchies that comprise traditions, or lineages, at ever more-inclusive scales and that are held together by cultural as well as genetic transmission. In practice the lines between nested hierarchies and reticulating networks are sometimes blurred, just as without a boundary around the reticulating networks there can be no nested hierarchy and hence no monophyly (Goldstein and De Salle 2000). Such boundaries are often difficult to delimit, but they are by no means beyond our power to determine archaeologically (eg, Bellwood 1996a; Bettinger and Eerkens 1999; Kirch and Green 2001; Lipo *et al* 1997; O'Brien *et al* 2001, 2002).

Cladistics is a method that depends solely on heritable continuity, irrespective of the mode of transmission. Proper use of cladistics in archaeology and anthropology recognises genetic and cultural transmission, both of which play a role in the evolution of such things as tool lineages. If there is phenotypic change, and if over time enough variation is generated, cladistics should be able to detect the phylogenetic signal and we should be able to create phylogenetic orderings that have testable implications.

Acknowledgments