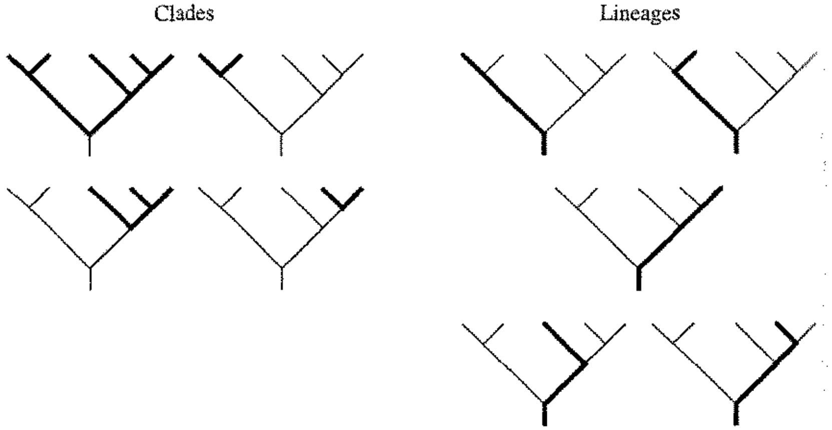

Figure 6.10 Clades versus lineages. All nine diagrams represent the same phylogeny, with clades highlighted on the left and lineages on the right. Additional lineages can be counted from various internal nodes to the branch tips (after de Queiroz 1998).

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

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CHAPTER 7

PHYLOGENESIS VERSUS ETHNOGENESIS IN TURKMEN CULTURAL EVOLUTION

Mark Collard and Jamshid Tehrani

INTRODUCTION

The processes responsible for producing the similarities and differences among cultures have been the focus of much debate in recent years, as has the corollary issue of linking cultural data with the patterns recorded by linguists and by biologists working with human populations (eg, Romney 1957; Vogt 1964; Chakraborty *et al* 1976; Brace and Hinton 1981; Cavalli-Sforza and Feldman 1981; Lumsden and Wilson 1981; Ammerman and Cavalli-Sforza 1984; Boyd and Richerson 1985; Terrell 1986, 1988; Kirch and Green 1987, 2001; Renfrew 1987, 1992, 2000b, 2001; Atkinson 1989; Croes 1989; Bateman *et al* 1990; Durham 1990, 1991, 1992; Moore 1994b; Cavalli-Sforza and Cavalli-Sforza 1995; Guglielmino *et al* 1995; Laland *et al* 1995; Zvelebil 1995; Bellwood 1996a, 2001; Boyd *et al* 1997; Shennan 2000, 2002; Smith 2001; Whaley 2001; Terrell *et al* 2001; Jordan and Shennan 2003). To date, this debate has concentrated on two competing hypotheses, which have been termed the 'genetic', 'demic diffusion', 'branching' or 'phylogenesis' hypothesis, and the 'cultural diffusion', 'blending' or 'ethnogenesis' hypothesis (Romney 1957; Vogt 1964; Kirch and Green 1987; Moore 1994a, 1994b, 2001; Guglielmino *et al* 1995; Bellwood 1996b; Collard and Shennan 2000; Hewlett *et al* 2002).

According to the phylogenesis hypothesis, the similarities and differences among cultures are primarily the result of cultural assemblages dividing as the communities that produce them repeatedly split, grow and then split again. The strong version of the hypothesis suggests that 'Transmission Isolating Mechanisms' or 'TRIMS' (Durham 1992) impede the transmission of cultural elements among contemporaneous communities. TRIMS are akin to the barriers to hybridisation that separate species, and include language differences, ethnocentricism, and intercommunity violence (Durham 1992). The phylogenesis hypothesis predicts that the similarities and differences among cultures can be represented by a cladogram. The hypothesis also predicts that there will be a strong association between cultural variation and linguistic, morphological and genetic patterns (eg, Ammerman and Cavalli-Sforza 1984; Cavalli-Sforza *et al* 1988, 1994; Kirch and Green 1987, 2001; Renfrew 1987; Sokal *et al* 1989, 1991; Bellwood 1995, 1996b, 2001; Cavalli-Sforza and Cavalli-Sforza 1995; Chikhi *et al* 1998, 2002; Diamond and Bellwood 2003).

In contrast, supporters of the ethnogenesis hypothesis (eg, Terrell 1987, 1988, 2001; Moore 1994a, 1994b, 2001; Dewar 1995; Terrell *et al* 1997, 2001) believe that it is unrealistic 'to think that history is patterned like the nodes and branches of a comparative, phylogenetic, or cladistic tree' (Terrell *et al* 1997: 184). Instead, they argue that the biological, linguistic and cultural evolution of our species is best characterised by 'a constant flow of people, and hence their genes, language, and culture, across the fuzzy boundaries of tribes and nations, spreading within a region such as the Plains or the Southeast within a few generations, and across the continent in a few more' (Moore 2001: 51). That is, according to the ethnogenesis hypothesis, the patterns of similarity and difference among cultural assemblages are chiefly a consequence of individuals copying each other's practices, exchanging ideas and objects, and marrying one another. The ethnogenesis hypothesis predicts that the similarities and differences among cultures can best be represented by a maximally-connected network or reticulated graph (Terrell 2001). It also predicts that there will be a close relationship between cultural patterns and the frequency and intensity of contact among populations, the usual proxy of which is geographic proximity.

Recently it has been asserted that ethnogenesis has been the major cultural evolutionary process in the ethno-historical period and is likely to have always been more significant than phylogenesis in cultural evolution (eg, Terrell 1987, 1988, 2001; Moore 1994a, 1994b, 2001; Dewar 1995; Terrell *et al* 1997, 2001). The pervasiveness of human interaction obviously cannot be denied. In the words of Bellwood (1996b: 882), 'humans flourish in interactive groups, and total isolation of any human group has been very rare in prehistory'. However, in our view there is good reason to question whether ethnogenesis has always been the dominant cultural process. First, the archaeological record shows that extensive movement of materials and artefacts across boundaries does not automatically obliterate cultural traditions (eg, Pétrequin 1993; Shennan 2000, 2002). Secondly, ethnographic work indicates that in non-commercial settings cultural transmission is often both vertical and conservative, with children learning skills from their parents with relatively little error (eg, Childs and Greenfield 1980; Greenfield 1984; Hewlett and Cavalli-Sforza 1986; Shennan and Steele 1999; Greenfield *et al* 2000). Thirdly, recent work in psychology suggests that humans may possess evolved cognitive mechanisms that lead them to interact preferentially with individuals who are similar to themselves (Buston and Emlen 2003) and to be prejudiced against individuals from unfamiliar ethnic groups (Gil-White 2001; Schaller *et al* 2003). Fourthly, empirical and theoretical research suggests that, as counterintuitive as it may seem, interaction between people can actually lead to the emergence of cultural distinctions where none previously existed (eg, Barth 1969; Hodder 1982; McElreath *et al* 2003).

In addition to the foregoing general points, it is not clear that the assertion regarding the dominance of ethnogenesis is supported by the empirical contributions to the phylogenesis versus ethnogenesis debate that have been published to date (Welsch *et al* 1992; Moore and Romney 1994, 1996; Guglielmino *et al* 1995; Roberts *et al* 1995; Welsch 1996; Collard and Shennan 2000; Borgerhoff Mulder 2001; Hewlett *et al* 2002; Jordan and Shennan 2003). Several of these studies have focused on cultural variation among villages on the North Coast of New Guinea, using geographic distance and linguistic affinity as proxies for ethnogenesis and phylogenesis, respectively. Using regression and correspondence analysis of presence/absence data, Welsch *et al* (1992; see also Welsch 1996) found that the material culture similarities and differences among the villages are strongly associated with geographic propinquity, and unrelated to the linguistic relations of the villages. In contrast, correspondence and hierarchical log-linear analyses of frequency data carried out by Moore and colleagues indicated that geography and language have equally strong effects on the variation in material culture among the villages (Moore and Romney 1994; Roberts *et al* 1995). Moore and Romney (1996) obtained the same result in a reanalysis of Welsch *et al*'s presence/absence data using correspondence analysis, thereby accounting for one potential explanation for the difference in findings, namely the use of different datasets. Thus, it is not yet clear from the work carried out on the material culture of the north coast of New Guinea whether the similarities and differences among the villages are the result of ethnogenesis exclusively, or a combination of both phylogenesis and ethnogenesis (see Shennan and Collard, Chapter 8 this book).

Three empirical studies have examined cultural evolution in African societies: Guglielmino *et al* (1995), Borgerhoff Mulder (2001) and Hewlett *et al* (2002). The first of these explored the roles of phylogenesis, ethnogenesis and local adaptation in the evolution of 47 cultural traits among 277 African societies. Models of the three processes were generated, and then correlation analyses undertaken in which language was used as a proxy for phylogenesis, geographic distance was used as a proxy for ethnogenesis, and vegetation type was used as a proxy for adaptation. These analyses found that most of the traits fit best the phylogenesis model. The distributions of only a few traits were explicable in terms of adaptation and even fewer traits supported the ethnogenesis model. Hewlett *et al*'s (2002) results were less clear-cut than those of Guglielmino *et al* (1995) but they nevertheless supported the phylogenesis hypothesis. Hewlett *et al* (2002) investigated the processes responsible for the distribution of 109 cultural attributes among 36 African ethnic groups. Using phenetic clustering and regression analysis, they tested three explanatory models: demic diffusion, which is equivalent to phylogenesis; cultural diffusion, which is equivalent to ethnogenesis; and local invention. Hewlett *et al* found that 32% of the cultural attributes could not be linked with an explanatory model, and that the distributions of another 27% of the cultural attributes were compatible with two of the models. Of the remaining cultural attributes, 18% were compatible with demic diffusion, 11% were compatible with cultural diffusion, and just 4% were compatible with local invention. The results of Borgerhoff Mulder's (2001) analysis of correlations between cultural traits associated with kinship and marriage patterns in 35 East African societies were more equivocal. In this study, analyses of phylogenetically controlled data supported roughly half the number of statistically significant correlations returned by analyses of phylogenetically uncorrected data. These results failed to support Borgerhoff Mulder's preferred hypothesis, which is that adaptation to local environments plus diffusion between neighbouring populations erases any phylogenetic signature. Were that the case, then the correlations between different traits in the phylogenetically controlled analysis would have returned very similar results to a conventional statistical analysis of the raw data, which was not the case. However, Borgerhoff Mulder's results also do not lend unqualified support to the phylogenesis hypothesis either, since a high proportion of correlations remained unaffected by phylogenetic correction. In these cases, the trace of descent is obscured either by a relatively fast rate of cultural evolution and adaptation, or by the mixing and merging between cultural groups that has been reported in ethnographic and historical sources on East African societies. Thus, two of the three African studies offer strong support for the phylogenesis hypothesis, while the third is equivocal regarding the relative importance of phylogenesis and ethnogenesis.

Three other empirical contributions to the phylogenesis/ethnogenesis have been published. One of these investigated the relative contribution of phylogenesis and ethnogenesis to cultural evolution by applying phylogenetic techniques from biology to assemblages of pottery from Neolithic sites in the Merzbach valley, Germany (Collard and Shennan 2000). The analyses indicated that, while both phylogenesis and ethnogenesis were involved in generating the patterns observed among the Merzbach pottery assemblages, phylogenesis was the dominant process. The second study used regression analysis to examine the interrelationships among genetic variability, geographic distance, degree of Caucasoid admixture, and cultural and linguistic dissimilarity in seven Chilean Indian populations (Chakraborty *et al* 1976). The analyses returned significant correlations between geographic distance and genetic distance, geographic distance and cultural dissimilarity, and genetic distance and cultural dissimilarity. Linguistic dissimilarity and degree of Caucasoid admixture were not significantly correlated with the other variables or with each other. The third study used multivariate and cladistic methods to examine Californian Indian basketry variation in relation to linguistic affinity and geographic proximity (Jordan and Shennan 2003). The analyses suggested that the variation observed among Californian Indian baskets is best explained by ethnogenesis rather than phylogenesis.

Thus, based on the empirical studies that have been published to date, the suggestion that ethnogenesis has always been a more important cultural evolutionary process than phylogenesis (Terrell 1987, 1988, 2001; Moore 1994a, 1994b, 2001; Dewar 1995; Terrell *et al* 1997, 2001) is not supportable. Phylogenesis appears to have been at least as important as ethnogenesis in generating the New Guinea and Neolithic datasets, and it was clearly also a major process in producing the African datasets. In this paper we further test the hypothesis that ethnogenesis is a more important cultural evolutionary process than phylogenesis. We do so by applying a method of phylogenetic reconstruction that is widely used in biology to attribute data derived from decorated textiles produced by Turkmen groups between the 18th and 20th centuries (see also Tehrani and Collard 2002).

MATERIALS AND METHODS

The Turkmen are an ethnic group who speak a language that belongs to the Oghuz-Turkic branch of the Altaic language family, and who are further distinguished by aspects of their diet, social institutions and material culture (Barthold 1962; Wood 1973; Irons 1975; Khazanov 1983). Currently, most Turkmen live in Turkmenistan, northern Iran and northern Afghanistan. Smaller populations of Turkmen are found in Iraq, Syria and Turkey. The migration of Oghuz-Turkic tribes from the Mongolian Steppes to these parts of Central Asia was first recorded between the 10th and 11th centuries (Barthold 1962; Jahn 1980). Although today the Turkmen are mostly settled agriculturalists, traditionally they were tent dwelling nomadic pastoralists who raised sheep, goats and other livestock.

The study focused on five groups of Turkmen: the Ersari, Salor, Saryk, Tekke and Yomut. The geographic distribution of these groups during the 19th century is shown in Figure 7.1. Each group comprised a territorially defined union of kin-

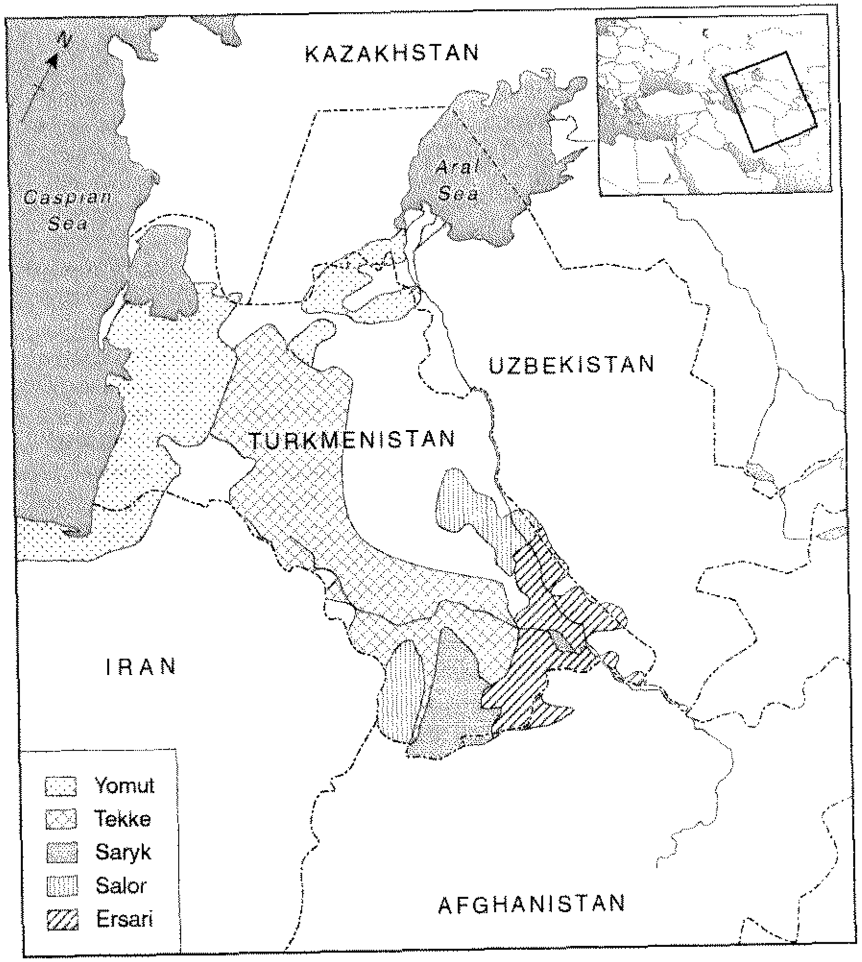

Figure 7.1 Geographic distribution of the Esari, Salor, Tekke and Yomut groups of Turkmen during the 19th century (from Tehrani and Collard 2002; reproduced with permission of the publisher).

based entities, and is by convention referred to as a 'tribal confederacy' (Irons 1975; Tapper 1979, 1991). Tribal confederacies were structured according to a hierarchical, segmentary pattern of genealogical relationships that are defined through patrilineal descent, and which determine membership of households (*yurt*), residence groups (*obas*) and lineages (*il*) (Irons 1975).

Turkmen cultural evolution was examined via woven artefacts produced by them between the 18th and 20th centuries. These artefacts were ideally suited to the highly mobile and physically demanding lifestyles of Turkmen households in this period. They were light and resilient, and the materials needed to manufacture them were available locally. Wool of appropriate quality for spinning the pile, weft and warp was obtained from the Turkmen's livestock, and dyes were extracted from native plants and vegetation (Mackie 1980; Thompson 1980; Whiting 1980). The weaving itself was carried out on simply constructed portable looms that could be easily carried among other household objects during the migration between summer and winter camps. Accordingly, woven artefacts were ubiquitous among the Turkmen, comprising the bulk of their material culture and fulfilling a wide range of functions from the ceremonial to the mundanely utilitarian: camel hangings for wedding processions, ornamental carpets for tent floors, saddle bags, tent bands, door rugs, salt bags and even small pockets for carrying spoons (Azadi 1975). An equally important reason for focusing on Turkmen textiles is that they are well represented in a number of European and American museums. There is thus an abundance of potential data with which to investigate processes of cultural diversification among the Turkmen.

Cultural evolution among the Ersari, Salor, Saryk, Tekke and Yomut was investigated in relation to two periods of Turkmen history. The first period covers the 200 years prior to 1881, when the tribes were still largely nomadic-pastoralist and organised according to indigenous structures of leadership based on segmentary descent groups. The second period begins with the defeat of the Turkmen by the imperial Russian army at the Battle of Gok Tepe in 1881. Following this defeat the Turkmen tribes were 'pacified', subjected to external political control, and pressurised into adopting a sedentary life. Deprived of monetary income from the sale and ransom of slaves kidnapped from Persian and Afghan villages, and liable for state taxes, the Turkmen eventually became dependent on the market through the sale of cash crops and craft goods, especially carpets (Irons 1974; Bacon 1980).

With the differences between these periods in mind, we addressed two questions in our study. First, did phylogenesis or ethnogenesis dominate the evolution of Turkmen textile designs prior to the Turkmen's defeat by Tsarist Russia? Secondly, did the contributions of phylogenesis and ethnogenesis to the evolution of Turkmen textile designs change following their pacification and settlement by the Russian colonial authorities?

In line with Foley (1987), Collard and Shennan (2000), O'Brien *et al* (2001, 2002) and Jordan and Shennan (2003), the evolution of Turkmen weaving traditions was investigated using cladistics, which is the method of phylogenetic reconstruction that is currently preferred in biology (Hennig 1950, 1965, 1966; Eldredge and Cracraft 1980; Wiley 1981; Ax 1987; Wiley *et al* 1991; Minelli 1993; Quicke 1993; Kitching *et al* 1998; Page and Holmes 1998; Schuh 2000). Based on a null model in which new taxa arise from the bifurcation of existing ones, the cladistic method of phylogenetic reconstruction entails generating a tree diagram (cladogram) which links taxa in such a way that the number of hypothesised changes required to account for the similarities among them is minimised. We employed the cladistic method because we believe that the problem of determining the relative contribution of phylogenesis and ethnogenesis to the ethnographic and archaeological records is akin to the problem of reconstructing phylogenetic relationships among species. In both cases the key challenge is to distinguish the similarities resulting from shared ancestry (homologies) from those due to mechanisms other than shared ancestry (homoplasies). While the processes responsible for generating biological and cultural homologies are not the same (gene transfer versus social learning), and those responsible for generating biological and cultural homoplasies probably also differ (eg, independent evolution versus diffusion), the two problems are sufficiently similar in terms of epistemology and ontology to warrant the application of cladistic methods to cultural data. Most significantly, in both cases a model is sought that explains the distribution of resemblances among a group of taxa in the absence of prior knowledge of how those resemblances arose. Given that the bifurcating tree model represents the simplest way of linking a group of entities, its use as the null model to reconstruct phylogenetic relationships among species and to assess the significance of phylogenesis and ethnogenesis can be defended in relation to the principle of parsimony, the methodological injunction that states that explanations should never be made more complicated than is necessary (Sober 1988). Once a tree model has been generated for a group of taxa, it is possible to classify the similarities among them as homologous or homoplastic. Homologous similarities support relationships that are compatible with the tree model, whereas homoplastic ones suggest relationships that conflict with the tree model.

In our study we assumed that if the data fitted the bifurcating tree model with little systematic conflicting signal, then phylogenesis could reasonably be inferred to have played a more important role than ethnogenesis in the generation of the data. Conversely, if the data fitted poorly on the bifurcating tree model, then ethnogenesis could be inferred to have been the most significant process. This approach is comparable to those adopted in recent studies of manuscript traditions, languages, Neolithic pottery and prehistoric projectile points from eastern North America (Lee 1989; Hoenigswald and Wiener 1987; Gjessing and Pierce 1994; Robinson and O'Hara 1996; Collard and Shennan 2000; Gray and Jordan 2000a; O'Brien *et al* 2001, 2002; Gray and Atkinson 2003). We believe that the cladistic approach is preferable to the regression-based methods that are often used to investigate to cultural evolutionary processes (eg, Welsch *et al* 1992; Moore and Romney 1994, 1996; Roberts *et al* 1995; Guglielmino *et al* 1995; Welsch 1996; Hewlett *et al* 2002), because the latter may overestimate the significance of ethnogenesis. Geographic proximity is usually employed as the proxy for ethnogenesis in studies that use regression-based methods, but phylogenesis can also be expected to correlate with geographic proximity, since sister groups are likely to be nearest neighbours. Thus, the use of geographic proximity solely as a proxy for ethnogenesis will overstate the latter's importance and understate the importance of phylogenesis. A second problem with regression-based studies of cultural evolution in very localised contexts is their reliance on linguistic relationships as a proxy for phylogenesis, since it is generally much harder to classify dialects than languages or language families. This is certainly the case for the Turkmen populations included in this study. Attempts to reconstruct the relationships among the dialects of Turkmeni spoken by the populations have proven inconclusive to date (Dulling 1960; Grimes 1992).

Sixty textiles were selected from Ersari, Salor, Saryk, Tekke and Yomut woven assemblages. These are described in Table 7.1. Twenty-two of the artefacts are curated at the Victoria and Albert Museum, London, and were studied directly.

Table 7.1 Details of textiles employed in analyses.

1. Pre-Synthetic Dye Period textiles, produced prior to the Russian conquest in 1881

Textile	**Collection**	**Specimen number or source**
Ersari Carpet 1	JD Phillips Jr	Thompson 1980, plate 85
Ersari Carpet 2	Victoria and Albert Museum	T88-1926
Ersari Carpet 3	Museum of Ethnography, Leningrad	Bogolyubov 1973, plate 26
Ersari Carpet 4	Victoria and Albert Museum	272-1906
Ersari Carpet 5	Private collection	Loges 1978, plate 80
Ersari Carpet 6	Hoffmeister Collection	Hoffmeister 1980, plate 13
Ersari Torba 1	Museum of Ethnography, Leningrad.	Tzavera 1985, plate 20
Ersari Torba 2	Museum of Ethnography, Leningrad.	Tzavera 1985, plate 6
Ersari Chuval 2	Macculloch Hall Museum	Thompson 1980, plate 87
Ersari Chuval 3	RE Kossow	Thompson 1980, plate 88
PSDP Tekke Carpet 1	Victoria and Albert Museum	T69-1923
PSDP Tekke Carpet 2	Victoria and Albert Museum	T352-1920
PSDP Tekke Carpet 3	Wher Collection	Dall'Oglio 1983, plate 2
PSDP Tekke Carpet 4	Hoffmeister Collection	Hoffmeister 1980, plate 3
PSDP Tekke Carpet 5	G Dumas and H Black	Thompson 1980, plate 28
PSDP Tekke Chuval 1	Victoria and Albert Museum	T200-1922
PSDP Tekke Chuval 2	Victoria and Albert Museum	321-1922
PSDP Tekke Chuval 3	Victoria and Albert Museum	411QQ-1880
PSDP Tekke Chuval 4	Museum of Ethnography, Leningrad	Tzavera 1984, plate 51
PSDP Tekke Chuval 5	Hoffmeister Collection	Hoffmeister 1980, plate 23
Salor Carpet 1	Museum of Ethnography, Leningrad	Tzavera 1984, plate 4
Salor Carpet 2	L Leifer and E Leifer	Thompson 1980, plate 4
Salor Carpet 3	L Sammlung	Loges 1978, plate 17
Salor Carpet 4	J Phillips	Thompson 1980, plate 5
Salor Chuval 1	Victoria and Albert Museum	394-1880
Salor Chuval 2	Victoria and Albert Museum	2324-1876
Salor Chuval 3	Museum of Ethnography, Leningrad.	Tzavera 1984, plate 7
Salor Chuval 4	Museum of Ethnography, Leningrad.	Tzavera 1984 plate 5
Salor Chuval 5	L Liefer and E Liefer	Thompson 1980, plate 10
Salor Chuval 6	Hoffmeister Collection	Hoffmeister 1980, plate 57
Saryk Carpet 1	Textile Museum, Washington, DC	Thompson 1980, plate 17
Saryk Carpet 2	The Wher Collection	Thompson 1980, plate 18

Saryk Carpet 3	Von Luxburg Collection	Hoffmeister 1980, plate 60
Saryk Carpet 4	L Sammlung	Loges 1978, plate 24
Saryk Carpet 5	Hamburg Museum of Ethnographic Art	Loges 1978, plate 25
Saryk Chuval 1	Victoria and Albert Museum	T96-1923
Saryk Chuval 2	Victoria and Albert Museum	T73-1925
Saryk Chuval 3	Private Collection	Loges 1978, plate 30
Saryk Chuval 4	J Straka and M Straka	Thompson 1980, plate 20
Saryk Chuval 5	Hoffmeister Collection	Hoffmeister 1980, plate 50
Yomut Carpet 1	Victoria and Albert Museum	854-1876
Yomut Carpet 2	Victoria and Albert Museum	272-1906
Yomut Chuval 1	Victoria and Albert Museum	T357-1987
Yomut Chuval 2	Victoria and Albert Museum	311-1884
Yomut Torba	Museum of Ethnography, Leningrad	Tzavera 1985, plate 19

2. Synthetic Dye Period textiles, produced after the Russian conquest in 1881

Textile	**Collection**	**Specimen number or source**
Tekke Carpet 1	Victoria and Albert Museum	T71-1948
Tekke Carpet 2	Victoria and Albert Museum	T69-1923
Tekke Carpet 3	Victoria and Albert Museum	T17-1980
Tekke Carpet 4	Museum of Ethnography, Leningrad	Tzavera 1984, plate 29
Tekke Carpet 5	Museum of Ethnography, Leningrad	Tzavera 1984, plate 30
Tekke Chuval 1	Victoria and Albert Museum	T72A-1948
Tekke Chuval 2	Victoria and Albert Museum	T167-1965
Tekke Chuval 3	Victoria and Albert Museum	T97-1923
Tekke Mafrash	Victoria and Albert Museum	T200-1922

The other 38 artefacts belong to private and museum collections from Russia, Germany and the USA, and were studied using published photographs and technical descriptions (Bogolyubov 1973; Loges 1978; Hoffmeister 1980; Thompson 1980; Tzavera 1984, 1985; Dall'Oglio 1983). Each group's weavings can be identified by the techniques used in their manufacture. Most important among these are the type of knot used to tie pile yarns around the warp, and the relative depression of the warp caused by the tension of the weft shots that pass between each row of knots (Thompson 1980). The knots used in Saryk and Yomut weavings are looped around two warp threads (symmetrical knot), while Salor, Tekke and Ersari knots are looped around one warp thread and pass under another thread (asymmetrical knot), remaining 'open' on one side. Salor knots are open on the left side, whereas Tekke and Ersari knots are open on the right. The depression of the warp in Ersari and Yomut weavings distinguishes them from the Tekke and Saryk textiles with which they share the same knot types respectively. Each taxon comprised the 'design vocabulary' (ie, the motifs, patterns and ornaments) expressed in each group's weavings, as determined by the structural typology described above. One further taxon was included for analysis: Tekke weavings produced following the Russian conquest. These can be distinguished from earlier Tekke textiles by the use of synthetic chemical dyes, which replaced natural dyes (produced from plants, minerals and insects) shortly after the Battle of Gok Tepe in 1881 (Whiting 1980). This taxon, which henceforth will be referred to as the SDP (Synthetic Dye Period) Tekke, was included for the purpose of investigating possible changes in Turkmen cultural evolution in the period following the tribes' defeat by Russia. Only synthetically dyed textiles produced by the Tekke were chosen because they are considerably better represented in the collections from which the sample was drawn.

The study employed 90 characters, which were derived from the ornaments, motifs and patterns used to decorate the textiles (Figure 7.2). These were classified according to whether they occurred on a carpet or a bag, their shape, and specific variations in their design. The occurrence of each character in the taxa was scored on a presence/absence basis. Care was taken not to double count similarities among taxa. For example, if ornament Y was found on the carpets of taxa 1, 2 and 3, but only on the bags of taxa 1 and 2, then two characters were generated: 'presence/absence of ornament Y on carpets' and 'presence/absence of ornament Y on bags'. However, if another ornament, X, was found only on the bags of taxa 1 and 2, only one character was used – 'presence/absence of ornament X' – since there was no need to register the fact that the ornament was found on bags in both taxa. Once the data were coded, a matrix was constructed in which the taxa were listed in the row headings, and the characters listed in the column headings. Details of the characters and a copy of the matrix are presented in Appendix 1.

Two analyses were carried out to assess whether phylogenesis or ethnogenesis dominated the evolution of Turkmen material culture prior to their subjugation by Tsarist Russia. The first sought to determine whether or not the data for the Ersari, Tekke, Salor, Saryk and Yomut contain a phylogenetic signal. The data were analysed with the permutation tail probability (PTP) test. The PTP test was originally proposed as a method of determining whether or not a given dataset contains a statistically significant phylogenetic signal (Archie 1989; Faith 1990;

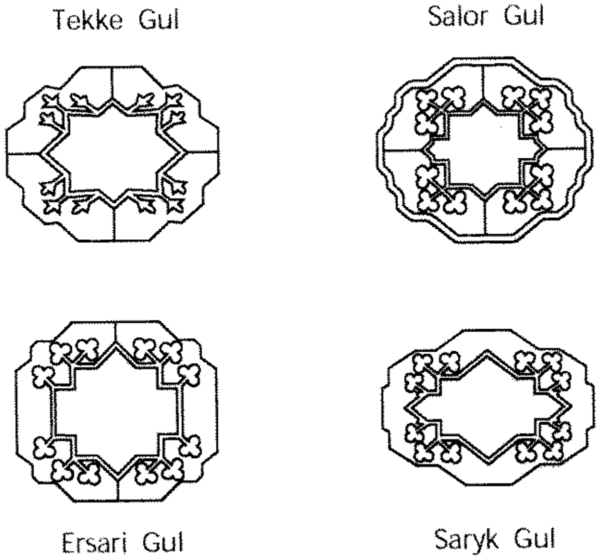

Figure 7.2 Examples of characters used in analyses (from Tehrani and Collard 2002; reproduced with permission of the publisher). Known as 'guls', these carpet ornaments are distinguished by their distinctive, lobed shapes. Relationships between the designs of each are also evident. Thus, in field between the border and central ornament there are projectiles that take the form of 'darts' in the Tekke gul, or 'clovers' in the Salor, Ersari and Saryk guls. Further distinctions within the latter category can be made according to whether the clovers have one stem, as in the Salor case, or two, as in the Ersari gul.

Faith and Cranston 1991). However, following criticism (eg, Carpenter 1992; Steel *et al* 1993), it is now considered to be a heuristic device rather than a statistical test (Kitching *et al* 1998). In the PTP test, a dataset is randomly permuted (reshuffled) multiple times without replacement, and the length of the most parsimonious cladogram computed after each permutation. Thereafter, the length of the most parsimonious cladogram obtained from the unpermuted data is compared to the distribution of lengths of the most parsimonious cladograms yielded by the permutations. If the original cladogram is shorter than 95% or more of the cladograms derived from the permutations, then the dataset is considered to contain a phylogenetic signal. The PTP test was carried out in PAUP* 4 (Swofford 1998). Following recent applications of permutation-based analyses in biology (eg, Collard and Wood 2000; Gibbs *et al* 2000), the dataset derived from Turkmen textile assemblages was permuted 10,000 times.

The second analysis assessed how well the data fit the bifurcating tree model. The data for the Ersari, Tekke, Saryk, Salor and Yomut were subjected to parsimony analysis. This form of analysis identifies the cladogram that requires the smallest number of ad hoc hypotheses of homoplasy to account for the distribution of character states among a group of taxa. That is, it identifies the cladogram that requires the least number of evolutionary changes, the so-called 'minimum length' cladogram (Wiley *et al* 1991; Minelli 1993; Quicke 1993; Kitching *et al* 1998; Schuh 2000). The fit between the data and the cladogram was assessed with the Consistency Index (CI) and with bootstrapping. The CI is a measure of how parsimonious evolution has been for a given combination of cladogram and dataset, in other words, it is a measure of the number of homoplasies in a dataset (Kitching *et al* 1998). The CI for a single character is calculated by dividing the minimum number of character state changes required by any conceivable cladogram (m) by the number of changes required by the focal cladogram (s). The CI for two or more characters is computed as M/S, where M and S are the sums of the m and s values for the individual characters. A CI of 1 indicates that the data are perfectly congruent with the cladogram (ie, the cladogram requires no homoplastic changes to be hypothesised), and homoplasy levels increase as the CI decreases. In phylogenetics, bootstrapping was originally developed as a way of estimating the statistical likelihood of a given clade being real (Felsenstein 1985a). However, following several recent critiques (eg, Carpenter 1992; Kluge and Wolf 1993), it is now considered by many researchers to be an heuristic tool rather than a statistical test (Kitching *et al* 1998; but see Sanderson 1995). In bootstrapping, a large number of subsets of data (normally 1,000 to 10,000) are randomly sampled with replacement from the character state dataset, with the character state assignments being retained in each sample. Minimum length cladograms are then computed from these subsets of the data, and a list of the clades that comprise the cladograms compiled. Thereafter, the percentage of clades yielded by the resampled data that support the most parsimonious cladogram returned for the original dataset is calculated. Datasets that fit the bifurcating model with little conflicting signal will return higher percentages of support in the bootstrap analyses. Although there is no consensus as to exactly how high this percentage should be, a number of researchers (eg, Hillis and Bull 1993) believe that 70% and higher invests sufficient confidence in the accuracy of a phylogenetic hypothesis tested by the bootstrapping procedure. Parsimony analysis and bootstrapping were carried out in PAUP* 4 (Swofford 1998). The programme's branch-and-bound search routine was used to identify minimum length cladograms. The bootstrap assessment was based on 10,000 replications. The CI for the minimum length cladogram was computed in MacClade 4 (Maddison and Maddison 2000), after the exclusion of uniformative characters. In both analyses we designated the Yomut as the outgroup. This is supported by linguistic evidence, since the Yomut dialect and clan names are considered to be distinct from those of the Ersari, Tekke, Saryk and Salor (Dulling 1960; Wood 1973; Grimes 1992). Furthermore, students of Turkmen textile traditions (eg, Thompson 1980) consider Yomut weavings to be stylistically distinct from those of the Ersari, Tekke, Saryk and Salor, which are believed to share a common heritage.

Two sets of analyses were also carried out to investigate whether or not the relative contribution of phylogenesis and ethnogenesis to the evolution of Turkmen textile designs changed following the Turkmen's subjugation by Tsarist Russia. The first examined how well the data for the Ersari, Salor, Saryk, SDP Tekke and the Yomut fit the bifurcating tree model compared to the data for the Ersari, PSDP Tekke, Salor, Saryk and Yomut. To do so, the data for the Ersari, Salor, Saryk, SDP Tekke and Yomut were subjected to parsimony analysis, and the fit between the resulting minimum length cladogram and the data evaluated with the CI and with a 10,000 replication bootstrap analysis. Thereafter, the cladogram topology, CI and bootstrap support figures were compared to those obtained in the analyses of the data for the Ersari, PSDP Tekke, Salor, Saryk and the Yomut. As before, the parsimony and bootstrap analyses were conducted in PAUP* 4, the CI was calculated in MacClade 4, and the Yomut were employed as an outgroup.

The second set of analyses aimed to identify which non-Tekke group contributed most to the ethnogenesis of the SDP Tekke assemblage. This was achieved by sequentially removing the Ersari, Salor and Saryk in successive bootstrap analyses involving the data for the Ersari, PSDP Tekke, Salor, Saryk, SDP Tekke and Yomut. As noted earlier, the higher the bootstrap support for the clades represented in the minimum length cladogram, the lower the number of homoplasies in the dataset. This provides a means of assessing the role of each taxon excluded from the analysis. It was anticipated that the group that contributed most to the ethnogenesis of the SDP Tekke would share the greatest number of homoplasies with the new assemblage. Thus, excluding them from an analysis should yield stronger bootstrap support for the clades included in the minimum length cladogram.

RESULTS

Two analyses were conducted to assess whether phylogenesis or ethnogenesis dominated the evolution of Turkmen textile designs prior to their settlement and pacification by Tsarist Russia. In the first, the PTP test was used to determine whether or not the textile data for the Ersari, PSDP Tekke, Salor, Saryk and the Yomut contain a phylogenetic signal. The PTP test indicated that 177 out of the 10,000 permutations produced cladograms that were as short or shorter than the most parsimonious cladogram obtainable from the unpermuted data. Since this means that more than 98% of the cladograms derived from the permuted data are longer than the minimum length cladogram yielded by the unpermuted data, the results of the PTP test suggest that the dataset contains a phylogenetic signal.

In the second analysis, parsimony analysis, the CI and bootstrapping were used to assess how well the data for the Ersari, Tekke, Salor, Saryk and Yomut fit the bifurcating tree model associated with cultural phylogenesis. The parsimony analysis returned a single most parsimonious cladogram, which is depicted in Figure 7.3. This suggested that the Salor, Saryk and Ersari form a clade to the exclusion of the PSDP Tekke. Within the latter clade, the Salor and Ersari form a clade to the exclusion of the Saryk. The cladogram had a CI of 0.68 after uninformative characters were excluded (n = 43). The 10,000 replication bootstrap analysis returned two clades, one comprising the Ersari and Salor (63%), the other the Salor, Saryk and Ersari (86%), indicating that homologous resemblances greatly outnumber homoplastic ones. Thus, the results of the second analysis indicate that the data fit the bifurcating tree model well.

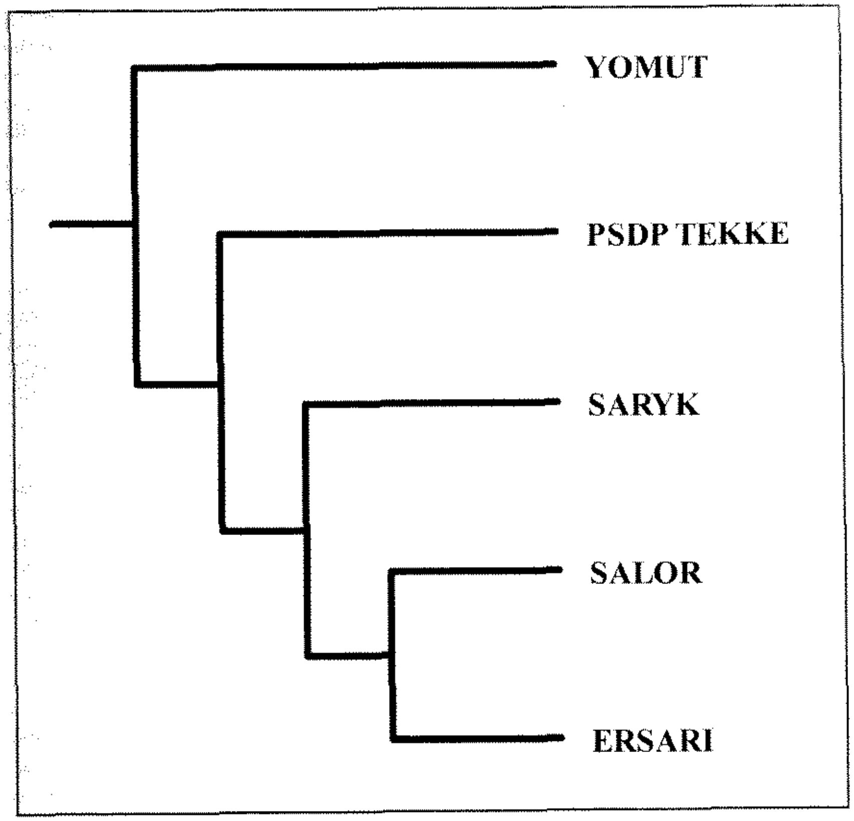

Figure 7.3 Most parsimonious cladogram obtained in analysis designed to determine the relative contributions of phylogenesis and ethnogenesis to the evolution of Turkmen textile designs prior to the Russian invasion of Central Asia (from Tehrani and Collard 2002; reproduced with permission of the publisher).

Two sets of analyses were also carried out to assess whether the relative contributions of phylogenesis and ethnogenesis to the evolution of Turkmen textile designs changed following the Turkmen's subjugation by Tsarist Russia. In the first, parsimony analysis, the CI and bootstrapping were used to examine how well the data for the Ersari, Salor, Saryk, SDP Tekke and Yomut fit the bifurcating tree model compared to the data for the Ersari, PSDP Tekke, Salor, Saryk and Yomut. Parsimony analysis of the data for the Ersari, Salor, Saryk, SDP Tekke and Yomut returned a single most parsimonious cladogram. This suggested that the Ersari and the Saryk are more closely related to one another than either is to the Salor or the SDP Tekke, and that the Ersari, Saryk and Salor are more closely related to one another than any of them is to the Tekke SDP. Following the exclusion of the uninformative characters (n = 43), the cladogram had a CI of 0.61. The bootstrap analysis returned two clades. One comprised the Ersari and Saryk (67%). The other consisted of the Ersari, Salor and Saryk (60%). Comparison of the

CI with that obtained in the analysis of the Ersari, Tekke, Salor, Saryk and Yomut data indicated the presence of a greater number of homoplasies in the data for the Ersari, Salor, Saryk, SDP Tekke and Yomut. Comparison of the results of the two bootstrap analyses also indicated a larger number of homoplasies in the data for the Ersari, Salor, Saryk, SDP Tekke and Yomut. Therefore, the analyses indicate that the relative importance of phylogenesis and ethnogenesis changed following the subjugation of the Turkmen by Tsarist Russia. Specifically, while phylogenesis remained the dominant cultural evolutionary process, ethnogenesis played a more important role.

In the second set of analyses, bootstrap analyses were used to identify which non-Tekke group contributed most to the ethnogenesis of the SDP Tekke assemblage. This was achieved by the sequential removal of the Salor, Saryk and Ersari taxa in consecutive analyses to identify the principal source of homoplasy in the dataset. Since homoplasies are used as a proxy for ethnogenesis, this procedure was devised to reveal which non-Tekke assemblage contributed most to the evolution of the SDP Tekke assemblage. The results of these analyses are presented in Table 7.2. The analysis in which the Salor weavings were excluded returned a well-supported consensus cladogram. In 95% of the bootstrap replicates, a clade comprising the Ersari and Saryk assemblages was identified. In 80% of the bootstrap replicates the Tekke and the SDP Tekke also formed a clade. The analysis in which the Saryk weavings were excluded yielded two clades. One comprised the Ersari and Salor weavings (87%), the other the PSDP and SDP Tekke weavings (73%). The analysis in which the Ersari weavings were excluded returned a single clade, which linked the Salor and the Saryk to the exclusion of the two Tekke assemblages. Together, these results suggest that Salor designs contributed most to the ethnogenesis of the Tekke weavings following the Turkmen's defeat by Tsarist Russia. The analyses also demonstrate that the SDP Tekke design vocabulary borrowed from Saryk weavings, though not as extensively. The contribution of the Ersari to the ethnogenesis of the SDP Tekke assemblage appears to have been negligible.

Table 7.2 Results of bootstrap analyses designed to identify which non-Tekke Turkmen group contributed most to the ethnogenesis of the Tekke weaving following the Russian colonisation of Central Asia.

Taxa = groups included in analysis.

Clades = clades supported by 50% or more of the bootstrap replicates.

BC = percentage of bootstrap cladograms in which clade appeared.

Taxa	Clades	BC
Ersari, PSDP Tekke, Saryk, SDP Tekke, Yomut	(Ersari, Saryk)	95%
	(PSDP Tekke, SDP Tekke)	80%
Ersari, PSDP Tekke, Salor, SDP Tekke, Yomut	(Ersari, Salor)	87%
	(PSDP Tekke, SDP Tekke)	73%
PSDP Tekke, Salor, Saryk, SDP Tekke, Yomut	(Salor, Saryk)	64%

DISCUSSION

Cladistic analyses of Turkmen textiles were carried out to determine whether phylogenesis or ethnogenesis dominated the evolution of Turkmen weaving traditions prior to the Russian annexation of Central Asia. The analyses indicated that in this period the evolution of Turkmen textile designs was dominated by phylogenesis. The PTP test suggests that the data contain a phylogenetic signal, and the parsimony analysis indicate that the data fit the bifurcating tree model associated with cultural phylogenesis reasonably well. The fit between the model and data is not perfect, indicating that ethnogenesis played a role in the evolution of Turkmen culture. However, the CI and the results of the bootstrap analysis suggest that ethnogenesis was markedly less important than phylogenesis. According to the CI for the cladogram (0.68), about 70% of the similarities among the assemblages are homologous, and approximately 30% are homoplastic. This is compatible with the borrowing of designs and motifs being responsible for a third of interassemblage resemblances, although the possibility of independent invention as a source of homoplastic similarities cannot be completely discounted (Mace and Pagel 1994; Mace and Holden 1999). Regardless of the source of the homoplasies, it is clear that phylogenesis was the dominant cultural evolutionary process among the Turkmen prior to their defeat by the Imperial Russian army.

Cladistic analyses were also carried out to ascertain whether the relative contributions of phylogenesis and ethnogenesis to the evolution of Turkmen textile designs altered following their defeat by Tsarist Russia in 1881. The results indicated that the social and economic changes experienced by the Turkmen after 1881 led to a greater role for ethnogenesis in Turkmen cultural evolution. Phylogenesis remained the dominant cultural evolutionary process, but the importance of ethnogenesis increased. The CI associated with the cladogram (0.61) indicated that about 60% of the interassemblage resemblances are homologous, and about 40% are homoplastic. Thus, there is a 10% increase in the number of homoplastic resemblances among the woven assemblages from the period of Russian domination. This is consistent with more inter-tribal borrowing of designs and motifs, but again independent invention cannot be entirely discounted as a source of the homoplasies. If the homoplasies are assumed to result mainly from diffusion, then the analyses indicate that the Salor were a particularly important source of designs and motifs for the Tekke weavers during the Russian era.

Overall, the results of this study do not support the hypothesis that ethnogenesis is the dominant cultural evolutionary process (eg, Terrell 1987, 1988, 2001; Moore 1994a, 1994b, 2001; Dewar 1995; Terrell *et al* 1997, 2001). There is evidence for ethnogenesis in both the pre-1881 and post-1881 Turkmen textile samples, but in both samples it is considerably less significant than phylogenesis. Our study, therefore, concurs with the majority of the other quantitative studies of the relative contribution of phylogenesis and ethnogenesis to cultural evolution.

As noted in the introduction, most of these studies indicate that phylogenesis is at least as important as ethnogenesis in cultural evolution. Thus, it is inappropriate to simply assume that ethnogenesis is the dominant cultural evolutionary process, as some have advocated (eg, Terrell 1987, 1988, 2001; Terrell *et al* 1997, 2001; Moore 1994a, 1994b, 2001; Dewar 1995). Rather, both the phylogenesis hypothesis and the ethnogenesis hypothesis need to be tested in relation to any given cultural dataset (Kirch and Green 1987; Bellwood 1996a; Collard and Shennan 2000; Whaley 2001).

Having demonstrated that the distribution of cultural similarities and differences among the Turkmen groups is more in keeping with the phylogenesis hypothesis than the ethnogenesis hypothesis, it is appropriate to consider the reasons why this is the case. What was it about Turkmen social life between the 18th and 20th centuries that might have fostered the apparent long-term coherence of their weaving traditions? One factor that may have been significant in this regard is their approach to weaving. Judging from ethnographic reports about the Turkmen, learning and reproducing designs was a time-consuming and difficult process (Moshkova 1977; Irons 1980). In contrast to urban workshops, and many modern-day tribal weavers, the Turkmen wove patterns without the aid of written instructions or drawings. Instead, Irons (1980: 35) writes that 'they relied on memory to produce the elaborate designs of their carpets as they wove … One woman told my wife that the ability to weave a Turkmen carpet was like literacy. It is a skill acquired over many years, one that beginners cannot hope to master in a short time'. This type of learning by imitation and memorisation required intense and prolonged contact between teacher and learner. In most cases, weaving skills and decorative patterns were transmitted from mother to daughter (Moshkova 1977; Ponomaryov 1980; Irons 1980). It seems likely that these methods of learning and reproduction may well have helped to ensure that diffusion was limited among the tribes. It is interesting in this regard that fieldwork currently being carried out by one of us (JJT) among the Qashqa'i and other southern Iranian tribes suggests that the introduction of cartoons has provided an important mechanism for the adoption of patterns previously alien or unknown to the weaver or her kinswomen. Once a pattern has been woven from a drawing, the weaver is able to commit it to memory and therefore add it to her repertoire as well as teach it to others.

In addition to the constraints imposed by the Turkmen's approach to weaving, inter-tribal borrowing of designs may have been limited by cultural proscriptions on the movement of women. Among the Turkmen, weaving was carried out exclusively by women. In accordance with the Turkmen's adherence to conservative Sunni Islam, women were generally confined to the domestic sphere and rarely travelled (Irons 1975, 1980). Thus, despite the close geographical proximity of the five Turkmen tribes studied here, gender relations in these societies would have inhibited contacts between weavers from different tribes, particularly for periods sufficient to learn one another's designs.

A third factor that may have helped foster the coherence of the weaving traditions is the Turkmen's strong endogamy. Although systematic statistical analyses of Turkmen marriage patterns are lacking, Irons (1975) has estimated that among the Yomut endogamy accounted for over 90% of marriages. This suggests that marriage outside the tribe was extremely rare. Support for this is found in Turaeva *et al*'s (1985) study of the genotypic frequencies of the ABO and Hp systems in present day Turkmenistan. Their analyses suggested that the geographical subdivision of the Turkmen populations included in their sample – among them Tekke and Ersari groups – coincided with their genetic divergence, and indicated that gene flow among the tribes has been negligible since their formation. Thus, what has been argued by Moore (2001) to be one of the primary mechanisms of ethnogenesis – the movement of females between groups as a result of marriage – does not appear to have operated to any significant degree among the Turkmen.

It is possible that warfare and feuding also contributed to the relative isolation of the Turkmen groups' weaving traditions. Prior to their pacification by Tsarist Russia, warfare and feuding were endemic among the Turkmen (Irons 1974). As Durham (1992) has noted, intercommunity violence is likely to act as a very effective barrier to cultural diffusion. In addition, marital and residential patterns associated with violent conflicts may have been important in maintaining the homogeneity and integrity of each tribe's woven assemblages. Marital exchanges between households belonging to separate residence groups (*obas*) within the tribe were used as a means of consolidating alliances forged during times of conflict with other groups over pasture rights or water resources (Irons 1974). Another strategy employed by Turkmen camps, and even individual families, was to seek refuge among neutral *obas* until the conflict had waned. A feature of Turkmen feuding was the concept of 'blood responsibility', by which close family members of a perpetrator were legitimate targets for revenge (Irons 1974). As a result, most *obas* would have an attached contingent of *gongshi* or refugees who had fled from their original territory in fear of violent reprisals for some act that they or their relatives had carried out (Irons 1974, 1975). These strategies may help to explain how the homogeneity of each tribe's woven assemblage was maintained – designs could have circulated within a tribe through the traffic in brides between strategically aligned *obas* and through the frequent displacement of families by violent blood feuds.

Nettle's (1999) work on the evolution of language variation suggests an additional factor that may have minimised the amount of inter-group transfer of motifs. Nettle proposes that variations in accent, colloquialisms and dialects may have developed in response to the 'freerider problem'. This refers to the perennial danger of co-operating with others who fail to reciprocate altruistic acts (Trivers 1971). Nettle hypothesises that dialects function as 'social markers' that coincide with normal boundaries of reciprocity, making it more difficult for strangers to infiltrate and abuse the system. Since weaving is similar to language, in that it is learnt at an early age and over a long period, Turkmen carpet designs may have provided a useful social marker of the tribe and allegiance of the household in which it was woven. Although craft styles have generally been assumed to be politically neutral, Bowser's (2000) study of pottery styles in the Ecuadorian Amazon shows how decorative ornamentation can be used for signalling and accurately identifying the potter's allegiances. It is not currently known whether

Turkmen carpet designs were used as explicit social markers. However, the potential value of such a recognition system would be seem to be high given the mobility of the Turkmen, evident in the large numbers of families who temporarily seek refuge among other *obas* to escape 'blood responsibility'. In addition, work on animal mate recognition systems indicates that such systems can be expected to be under stabilising selection most of the time, since individuals whose signals and responses diverge from the norm are less likely to be successful in reproductive terms (Paterson 1978; Turner and Paterson 1991). It seems likely that stabilising selection on cultural recognition systems could similarly lead to their long-term coherence. Due to the limitations of the ethnographic record, the hypothesis that textile designs functioned as a sort of cultural recognition system among the Turkmen between the 18th and 20th centuries cannot be tested directly. However, it might be possible to shed light on the veracity of the hypothesis by comparing the diachronic pattern of design stasis and change with the patterns expected to result from stabilising selection and from other evolutionary processes (cf Neiman 1995; Shennan and Wilkinson 2001).

It has been pointed out recently that, even when cultural evolution is dominated by phylogenesis, it should not be assumed that cultural histories correlate with genetic lineages, since the mode of cultural transmission (social learning) and the mode of genetic transmission (sexual reproduction) are different from, and independent of, one another (Shennan 2000). Nonetheless, the available ethnographic descriptions of Turkmen craft learning suggest that it is likely to coincide with genetic transmission, since weaving skills are taught mother-to-daughter. Furthermore, we have specifically highlighted how institutions such as endogamy and marriage alliances might have determined patterns of inter-group and intra-group cultural transmission. So, how does the textile phylogeny compare with what is known about the groups' population history?

Unfortunately we are unable to directly compare the history of the tribes' craft traditions with their population histories since, to date, no phylogenetic analyses of Turkmen linguistic or genetic data have been published. However, there is some ethno-historical data on the origins of the five tribes included in the study, and their genealogical relationships. The most widely accepted source is Abu'l Ghazi, who wrote a history of the Turkmen tribes based on their own oral traditions and the 11th century writings of Rashid al-Din shortly before the end of his reign as Khan of Khiva in 1663 (Barthold 1962; Wood 1973; Jahn 1980). Interestingly, his interpretation of the tribes' relationships does not concur with our cultural phylogeny. The cladogram we derived from the textile data strongly linked the Salor assemblage to the Saryk and Ersari assemblages. Abu'l Ghazi, on the other hand, claims that only the Saryk and the Tekke shared actual genealogical connections to the Salor (Wood 1973). Abu'l Ghazi's genealogy of the Turkmen thus conflicts with the cladograms derived from the textile data, which suggest that the Ersari, Salor and Saryk are more closely related to one another than any of them is to the Tekke.

How are we to account for this conflict? One possibility is that it could reflect the fact that whereas ethno-historical evidence concerns the origins and formation of patrilineal descent groups, the phylogeny we have derived from the textile data represents the history of a matrilineally transmitted tradition, since weaving is primarily learned from mother to daughter (Irons 1980). However, given the strong tendency for Turkmen marriage patterns to coincide with patrilineally defined descent groups (Irons 1975), this explanation seems unlikely. The other possibility is that Abu'l Ghazi's genealogy, based as it is on oral traditions, might be incorrect. Two lines of evidence support this hypothesis. First, the clan names associated with the Ersari, Salor and Saryk are all believed to share a single common etymological root, while those used by the Tekke and Yomut seem to be of mixed origins (Wood 1973). This supports the textile phylogeny, and conflicts with the genealogy of Abu'l Ghazi. Secondly, the geographic distribution of the tribes also supports the textile phylogeny. As shown in Figure 7.1, the Ersari, Salor and Saryk lived close to the oases at Sarakhs and Bokhara, while the Tekke and Yomut lived in Khorassan. Given that there is a strong statistical tendency for territorial groups to coincide with descent groups (Irons 1974), this distribution also supports the suggestion that the Ersari, Salor and Saryk are more closely related to one another than any of them is to the Tekke or the Yomut. Thirdly, evidence from other Near Eastern and Central Asian nomadic societies (eg, Bacon 1980; Barth 1964; Linder 1982; Tapper 1991) suggests that genealogies are frequently contrived by tribes for reasons of political expedience. Therefore, it might be reasonable to conclude that Abu'l Ghazi's genealogy is an unreliable guide to the tribes' population histories and discard it in favour of the textile, clan-name and geographic data, at least provisionally.

CONCLUSIONS

In the study described here, biological phylogenetic methods were applied to designs incorporated into textiles produced by the Turkmen of Central Asia since the 18th century in order to shed light on the relative importance of two cultural evolutionary processes: phylogenesis and ethnogenesis. The analyses focused on two periods in Turkmen history: the era in which most Turkmen practised nomadic pastoralism and were organised according to indigenous structures of affiliation and leadership; and the period following their subjugation by the Russian colonial regime, which is associated with the sedentarisation of nomadic Turkmen and an increasing dependence on the market. The analyses indicated that in the pre-Russian period the evolution of Turkmen woven assemblages was dominated by phylogenesis. Phylogenesis accounted for about 70% of the resemblances among the tribes' assemblages and ethnogenesis about 30%. The analyses also showed that phylogenesis was the dominant process in the Russian period, although ethnogenesis accounted for an additional 10% of the resemblances among the assemblages. These results are comparable to those obtained in other quantitative assessments of cultural evolution, in that they suggest that phylogenesis is an important cultural evolutionary process. The corollary of this is that the recent suggestion that ethnogenesis should be assumed to be the only significant process in cultural evolution is not supportable. Rather, the relative importance of the two processes should be assessed empirically on a case-by-case basis.

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APPENDIX 1

Characters. These were recorded as present or absent.

1. Lobed gul
2. Lobed gul: birds
3. Lobed gul: clovers
4. Lobed gul: one-stem clover
5. Lobed gul: two-stem clover
6. Archetypal gul
7. Archetypal gul: carpet
8. Archetypal gul: bag
9. Archetypal gul: type 1 banner
10. Archetypal gul: type 2 banner
11. Archetypal gul: type 1 bracket
12. Archetypal gul: type 2 bracket
13. Octagonal gul
14. Octagonal gul: two-headed animals
15. Octagonal gul: arrows
16. Rhomboid minor gul
17. Rhomboid minor gul: carpet
18. Rhomboid minor gul: bag
19. Salor Rose
20. Salor Rose: carpet
21. Salor Rose: bag
22. Kurbaghe
23. Kurbaghe: carpet
24. Kurbaghe: bag
25. Kurbaghe: type 1
26. Kurbaghe: type 2
27. Chemche
28. Chemche: carpet
29. Chemche: bag
30. Chemche: type 1
31. Chemche: type 2
32. Aina gul

46. Tauk Noska
47. Tauk Noska: version 1
48. Tauk Noska: version 2
49. Sagdak
50. Sagdak: star centre
51. Sagdak: Gochak centre
52. Memling
53. Memling: carpet
54. Memling: bag
55. Constellation
56. Carpet Gochak borders
57. Carpet Gochak borders: simple pattern
58. Carpet Gochak borders: cross pattern
59. Carpet Gochak borders: cross ornament
60. Chuval Gochak border
61. Chuval Gochak border: simple
62. Chuval Gochak border: complex type 1
63. Chuval Gochak border: complex type 2
64. Chuval S-border
65. Chuval S-border: continuous
66. Chuval S-border: continuous version 1
67. Chuval S-border: continuous version 2
68. Chuval S-border: bracketed
69. Chuval S-border: bracketed version 1
70. Chuval S-border: bracketed version 2
71. Soldat border
72. Soldat border: carpet
73. Soldat border: bag
74. Soldat border: version 1
75. Soldat border: version 2
76. Zig-zag border
77. Triangle border

33. Aina gul: carpet
34. Aina gul: bag
35. Aina gul: type 1
36. Aina gul: type 2
37. Aina Gul: type 3
38. Dyrnak gul
39. Dyrnak gul: carpet
40. Dyrnak gul: bag
41. Dzhengel
42. Dzhengel: carpet
43. Dzhengel: bag
44. Dzhengel: type 1
45. Dzhengel: type 2

78. Triangle border: single
79. Triangle border: double
80. Framed cross border
81. Framed cross border: version 1
82. Framed cross border: version 2
83. Star border ornaments
84. Star border ornaments: type 1
85. Star border ornaments: type 2
86. Star border ornaments: type 3
87. Barmak border
88. Barmak border: carpet
89. Barmak border: bag
90. Hooked branch border

APPENDIX 2

Character state data matrix. Characters are listed consecutively from 1 to 90. See Appendix 1 for character names.

1 = presence

0 = absence

Ersari	1 0 1 0 1 1 0 1 0 1 1 0 1 1 1 0 0 0 0 0 0 1 1 0 1 0 0 0 0 0 0 1 0 1 1 0 0 1 1 1 1 1 0 1 0 1 1 0 0 0 0 1 1 1 1 1 1 0 0 1 1 0 1 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 1 1 0 0 0 0 0 0 0 0
Saryk	1 0 1 0 1 1 1 1 1 1 1 0 1 0 1 0 0 0 0 0 0 1 1 0 1 0 1 1 1 1 0 1 0 1 0 1 0 0 0 0 1 1 1 1 1 0 0 0 0 0 0 1 0 1 0 1 0 1 0 1 1 0 0 1 1 0 1 1 1 0 0 0 0 0 0 0 1 0 1 1 1 0 0 0 0 0 0 0 0 0
Salor	1 0 1 1 0 1 0 1 0 1 0 1 0 0 0 1 1 1 1 0 1 1 0 1 0 1 0 0 0 0 0 1 0 1 1 0 0 0 0 0 1 0 1 1 1 1 0 1 1 1 0 1 0 1 0 1 0 0 0 1 0 0 1 1 1 1 0 1 1 1 1 1 0 1 0 0 1 1 0 1 1 0 0 0 0 0 1 0 1 0
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THE EVOLUTION OF CULTURAL DIVERSITY

A PHYLOGENETIC APPROACH

Edited by

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PREFACE

This book arose proximally out of a session at the Human Behaviour and Evolution Society annual meeting that was held at University College London in 2001. Present at that session were a number of us that were interested in applying phylogenetic methods to understanding cultural diversification, be it in languages, material artefacts or behavioural and bio-cultural traits. For all of us, our interest had arisen some time earlier. In my case, I trained as an evolutionary ecologist working in zoology, then moved into human behavioural ecology; I first wrote about applying phylogenetic comparative methods to cultural evolution soon after I had joined the Department of Anthropology at University College London, when I co-authored a paper with Mark Pagel in 1994 (who at that time was at the Department of Anthropology at Harvard). Clare Holden joined me as a PhD student not long after that and has worked on phylogenetic approaches to linguistic and cultural evolution at UCL ever since. Meanwhile, Stephen Shennan, at the Institute of Archaeology at UCL, had a longstanding interest in evolutionary archaeology, and in 1999 began working on formal phylogenetic approaches to material culture with Mark Collard (in Anthropology at UCL). Archaeology and Anthropology at UCL and Archaeology at Southampton jointly put forward a successful bid to set up the AHRB Centre for the Evolutionary Analysis of Cultural Behaviour, which was up and running by 2000. Most of the contributors to this book have been members of or visitors to the CEACB at some time. We thank all the members of the Centre for their discussions of many of these papers at seminars. And we are grateful to the UK Arts and Humanities Research Board, the Wellcome Trust and the Leverhulme Trust for the funding which has made much of this work possible. This book covers our range of interests in cultural phylogenies and comparative methods to date, and includes much of the pioneering work in this field. But the field is moving forward and growing all the time – hopefully an indication of the value of this approach to understanding the evolution of human cultural diversity.

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London, UK
2005