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Investigating cultural evolution through biological phylogenetic analyses of Turkmen textiles

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Abstract

The debate on the evolution of culture has focused on two processes in particular, phylogenesis and ethnogenesis. Recently, it has been suggested that the latter has probably always been more significant than the former. This proposal was assessed by applying cladistic methods of phylogenetic reconstruction to a data set comprising decorative characters from textiles produced by Turkmen tribes since the 18th century. 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 defeat by Tsarist Russia in 1881, which is associated with the sedentarisation of nomadic Turkmen and their increasing dependence on the market. The results indicate that phylogenesis was the dominant process in the evolution of Turkmen carpet designs prior to the annexation of their territories, accounting for c.70% of the resemblances among the woven assemblages. The analyses also show that phylogenesis was the dominant process after 1881, although ethnogenesis accounted for an additional 10% of the resemblances among the assemblages. These results do not support the proposition that ethnogenesis has always been a more significant process in cultural evolution than phylogenesis.
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Keywords: Cultural evolution; Phylogenesis; Ethnogenesis; Turkmen; Woven textiles; Cladistics

Introduction

The extent to which the evolution of culture is analogous to biological evolution has been the subject of considerable debate in recent years, as has the corollary issue of linking patterns in the ethnographic and archaeological records with genetic and linguistic data (e.g., Ammerman and Cavalli-Sforza, 1984; Bateman et al., 1990; Boyd and Richerson, 1985; Boyd et al., 1997; Cavalli-Sforza and Feldsman, 1981; Chakraborty et al.,

1976; Collard and Shennan, 2000; Durham, 1991; Kirch and Green, 1987; Lumsden and Wilson, 1981; Moore, 1994a; Renfrew, 1987; Shennan, 2000; Terrell, 1986, 1988; Terrell et al., 2001; Whaley, 2001; Zvelebil, 1995). A major focus of the debate is the relative importance of two processes that Moore (1994a,b) has termed “phylogenesis” and “ethnogenesis”. In the former, cultural evolution is a result of the progressive subdivision of cultural assemblages that takes place as populations split and give rise to new ones. In ethnogenesis, in contrast, cultural evolution occurs through the borrowing and blending of ideas and practices, and the trade and exchange of objects, among contemporaneous populations.

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Cultural phylogenesis is analogous to biological phylogenesis, the process by which new species appear, whereas ethnogenesis is akin to gene flow within a species. Cultural phylogenesis is expected to produce a strong association between cultural patterns and genetic and linguistic data. Ethnogenesis, on the other hand, is predicted to yield a close relationship between cultural patterns and the frequency and intensity of contact among populations, the usual proxy of which is geographic proximity. Phylogenesis is normally represented by a “family tree,” “dendrogram” or “cladogram,” and ethnogenesis by a “trellis,” “lattice” or “reticulated graph” (Terrell, 2001).

Recently, it has been asserted that ethnogenesis has been the major cultural evolutionary process in the ethnohistorical period and is likely to have always been more significant than phylogenesis in cultural evolution (e.g., Dewar, 1995; Moore, 1994a,b, 2001; Terrell, 1987, 1988, 2001; Terrell et al., 1997, 2001). These authors 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, p. 184) and 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, p. 51). However, the veracity of this assertion is open to question as the debate on the relative importance of phylogenesis and ethnogenesis has so far been dominated by contributions that are theoretical and/or qualitative in nature (e.g., Atkinson, 1989; Bellwood, 1996; Boyd et al., 1997; Dewar, 1995; Durham, 1990, 1991, 1992; Kirch and Green, 1987; Moore, 1994a,b; Shennan, 2000; Terrell, 1986, 1988, 2001; Terrell et al., 1997, 2001; Whaley, 2001). A number of quantitative studies have been published (e.g., Collard and Shennan, 2000; Guglielmino et al., 1995; Moore and Romney, 1994, 1996; Roberts et al., 1995; Welsch, 1996; Welsch et al., 1992), but there is a pressing need for further empirical assessments of the issue. With this in mind, the present paper describes a case study in which biological phylogenetic methods were applied to cultural data with a view to shedding light on the relative importance of phylogenesis and ethnogenesis in cultural evolution.

The case study dealt with the evolution of culture among the Turkmen. 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 distinguished further by aspects of their diet, social institutions, and material culture (Barthold, 1962; Irons, 1975; Khazanov, 1983; Wood, 1973). The majority of Turkmen live in Turkmenistan, northern Iran, and northern Afghanistan; smaller populations 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 Fig. 1. Each group comprised a territorially defined union of kin-based entities and is by convention referred to as a “tribal confederacy” (Irons, 1975; Tapper, 1979, 1991). These confederacies were structured according to a hierarchical, segmentary pattern of genealogical relationships that were defined through patrilineal descent, and which determined the membership of households (*yurt*), residence groups (*obas*), and lineages (*il*) (Irons, 1975).

Turkmen cultural evolution was examined in relation to woven artefacts produced by them since the 18th century. Light, hardwearing, and capable of being made on portable looms, these artefacts met the requirements of the Turkmen’s highly mobile, nomadic lifestyle. Moreover, the materials used to produce the weavings were easily acquired from local resources. 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 (Mackie, 1980; Thompson, 1980; Whiting, 1980). 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 mundane: 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).

Following several recent studies (Collard and Shennan, 2000; Foley, 1987; O’Brien et al., 2001), the evolution of Turkmen weaving traditions was investigated using the method of reconstructing



Fig. 1. Geographic distribution of the Esari, Salor, Saryk, Tekke, and Yomut groups of Turkmen during the 19th century (after Mackie and Thompson, 1980).

phylogenetic relationships that is currently favoured in biology—cladistics (Ax, 1987; Eldredge and Cracraft, 1980; Hennig, 1950, 1965, 1966; Kitching et al., 1998; Minelli, 1993; Page and Holmes, 1998; Quicke, 1993; Schuh, 2000; Wiley, 1981; Wiley et al., 1991). 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) that 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 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 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 (e.g., 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 (Collard and Shennan, 2000; O'Brien et al., 2001). Most significantly, in both cases we require a model that explains the distribution of resemblances among the taxa in the absence of prior knowledge of how those resemblances arose. Given that the bifurcating tree model is simpler than the reticulated graph model, 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 which 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 the bifurcating tree model poorly, then ethnogenesis could be inferred to have been the most significant process. This approach is comparable to those adopted in recent studies of Neolithic pottery, Palaeoindian point technology, manuscript traditions, and languages (Collard and Shennan, 2000; Gjessing and Pierce, 1994; Gray and Jordan, 2000; Hoenigswald and Wiener, 1987; Lee, 1989; O'Brien et al., 2001; Robinson and O'Hara, 1996). We believe it is preferable to the regression-based approaches that have been used previously to investigate cultural evolutionary processes (Guglielmino et al., 1995; Moore and Romney, 1994, 1996; Roberts et al., 1995; Welsch, 1996; Welsch et al., 1992), because the latter may inflate the significance of ethnogenesis. As noted earlier, geographic proximity is usually employed as the proxy for ethnogenesis. However, 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 latter's importance and understate the importance of phylogenesis.

Turkmen woven textiles represent an interesting data set to investigate processes of cultural evolution for three reasons in particular. First, there are grounds to believe that both phylogenesis and ethnogenesis contributed to the evolution of the Turkmen tribes' textiles. On the one hand, historical and ethnographic evidence indicates that the Turkmen frequently interacted not only with each other, but also with urban societies and neighbouring states (Agadzhanov and Karryev, 1978; Barthold, 1962; Irons, 1974; Jahn, 1980; Mackie, 1980; Tapper, 1991; Wood, 1973). This suggests that ethnogenesis may have been important in their cultural development. An obvious example of external influences on the Turkmen is their conversion to Sunni Islam (Azadi, 1975; Barthold, 1962; Irons, 1975; Mackie, 1980). On the other hand, the effect of ethnogenetic processes could have been mitigated by the fact that many of the Turkmen groups' interactions with the societies surrounding them and with each other were hostile in character. For example, Turkmen tribes routinely raided villages in Afghanistan and the Iranian province of Khorassan

for women and livestock, and suffered fierce retaliation from militias and mercenaries sponsored by the Qajar dynasty (Barthold, 1962; Irons, 1974). Significantly, Durham (1990, 1991, 1992) has argued that hostility among populations is one of the factors that can lead to cultural phylogenesis being a significant cultural evolutionary process.

Second, there is reason to suppose that the cultural evolutionary processes operating among the Turkmen may have changed in the second half of the 19th century. During this time, Tsarist Russia annexed large parts of Central Asia. Following successive heavy defeats by Russian troops at Merv in 1857 and Gok Tepe in 1881, the long-term resistance of Turkmen tribes to state authority was gradually eroded. By the early 20th century, most Turkmen had been forced to settle and adopt agriculture. Deprived of monetary income from the sale and ransom of slaves kidnapped from Persian and Afghan villages, and liable for state taxes, the Turkmen became dependent on the market through the sale of cash crops and craft goods, especially carpets (Bacon, 1980; Irons, 1974). Thus, the settlement of the Turkmen can be associated with two major patterns of change: political subjugation to state authorities, in which tribes were forced to abandon their nomadic lifestyle and traditional structures of leadership; and the intrusion of the market, which transformed the Turkmen's pastoral economy. Given the nature of these changes, it seems likely that they would have resulted in a greater role for ethnogenesis in Turkmen cultural evolution.

Third, Turkmen weavings are the subject of a debate among collectors of antique Central Asian carpets and textile specialists that echoes phylogenesis/ethnogenesis controversy. On the one hand, some of those interested in oriental woven artefacts have developed a nomenclature that identifies Turkmen weavings with specific tribes, based on detailed analyses of design, colour, and structural properties (e.g., Azadi, 1975; Moshkova, 1977; Pinner et al., 1980; Thompson, 1980). Qualitative assessments of the tribal origin of Turkmen textiles (e.g., 'Tekke carpet,' 'Salor tent bag,' etc.) reflect an underlying assumption that individual pieces belong to a homogeneous craft tradition preserved by successive generations of weavers in each tribe. This assumption is based on the claim that "the [Turkmen] craftswoman is conservative; she strictly upholds the customs of her craft, preserving age-old forms, repeating the

patterns which she has been taught, and which have become hallowed by tradition” (Ponomaryov, 1980, p. 29). The close correlation between cultural and genetic histories implied by this approach is clearly reminiscent of the phylogenesis model of cultural evolution. On the other hand, critics such as Spooner (1986) argue that the taxonomy employed by oriental textile specialists has little basis in the actual conditions or tribal context of carpet production. Instead, Spooner (1986) suggests that the alleged “conservatism” and “traditionalism” of Turkmen weavers are part of a mythology promoted by the carpet trade to feed the Western fascination with tribal cultures and our preconceptions about them. This idea has influenced historical and anthropological studies of the tribal carpet industry. For example, researchers such as Helfgott (1994) and Baker (1995) have highlighted the role of regional markets in the development of tribal weaving styles, claiming that they have always been influenced by urban and court fashions. If this were correct, then it would suggest that ethnogenesis was more important than phylogenesis in the evolution of Turkmen woven artefact assemblages, particularly in the post-settlement period when market forces exerted a greater hold over the economy of the tribes (Helfgott, 1994; Mackie, 1980).

In light of the foregoing, our study addressed two questions. First, did phylogenesis or ethnogenesis dominate the evolution of Turkmen textile designs prior to the Turkmen’s defeat by Tsarist Russia? Second, 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?

Materials and methods

The data set comprised details of decorative characters found on 60 woven artefacts produced by five Turkmen tribal groups: the Ersari, Salor, Saryk, Tekke, and Yomut. Twenty-two of the artefacts are curated at the Victoria and Albert Museum, London, and were studied directly. The other 38 artefacts belong to well-documented private museum collections from Russia, Germany, and the USA. These were studied using published photographs and technical descriptions (Bogolyubov, 1973; Dall’Oglio, 1983; Hoffmeister, 1980; Loges, 1978; Thompson, 1980; Tzavera, 1984, 1985).

The textiles selected from Ersari, Salor, Saryk, Tekke, and Yomut woven assemblages are listed in Table 1. These tribes’ weavings can be discriminated using three structural characteristics (Thompson, 1980). The first is whether the knot used to tie the pile around the warp is symmetrical or asymmetrical. In the former case, the pile is tied around a pair of warps, while in the latter it loops over one warp and passes under the other, remaining open on one side. The second is the side on which an asymmetrical knot opens. The third is whether or not the weft shots, which pass between each row of knots and through the warps, are depressed, raising the pile knot. To discern these characteristics, one folds the artefact lengthways along a column of knots and traces the passage of the loop between two warp yarns. The weavings produced by the Salor have asymmetrical knots open on the left, those produced by the Tekke have asymmetrical knots open on the right, and those produced by the Ersari have asymmetrical knots open on the right and depressed wefts. Saryk weavings employ symmetrical knots with raised warps, while Yomut weavings employ symmetrical knots with depressed warps.

Six taxa were included in the study. The taxa comprised the “design vocabularies” for the weavings produced by the tribal confederacies. That is, each taxon consisted of the totality of design types expressed in a set of weavings. The Tekke weavings were divided into two categories: those coloured with natural dyes and those coloured with synthetic dyes. These were referred to as the pre-synthetic dye period or PSDP Tekke and the synthetic dye period or SDP Tekke, respectively. The synthetically dyed Tekke weavings, which are available in abundance, were included for the purpose of identifying possible changes in the Turkmen material cultural evolution associated with the Russian colonisation of Central Asia in the 19th century. This watershed in Turkmen history coincides with the use of chemical dyes and has been used as a dating method by specialists to differentiate antique pieces from modern examples of Turkmen weaving (Whiting, 1980). For the other four tribes, only naturally dyed products were included, since in some cases, such as the Salor, there are no examples of synthetically dyed products in the collections from which the sample was drawn, while in other cases synthetically dyed artefacts are poorly represented.

Table 1
 Details of textiles employed in analyses

Textile	Collection	Specimen number or source
1. Pre-synthetic dye period textiles, produced prior to the Russian conquest in 1881		
Ersari Carpet 1	J.D. 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	R.E. 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		
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 study employed 90 characters. These were decorative in nature and were derived from major field ornaments, minor ornaments, and border motifs featured on the textiles (Fig. 2). The ornaments and motifs were classified according to whether they occurred on a carpet or a bag, their shape, and specific variations in their design. Characters were then defined in such a way that they could be scored as either present or absent. 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. The characters are listed in

Appendix A and the character state data matrix is shown in Appendix B.

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, PSDP 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 data set contains a statistically significant phylogenetic signal (Archie, 1989; Faith, 1990; Faith and Cranston, 1991). However, following criticism (e.g., 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 taxonomic data set is randomly permuted (reshuffled) multiple times without replacement and the length of the most parsimonious cladogram is 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 data set 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 (e.g., Collard and Wood, 2000; Gibbs et al., 2000), the data set derived from the 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, PSDP 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 (Kitching et al., 1998; Minelli, 1993; Quicke, 1993; Schuh, 2000; Wiley et al., 1991). 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

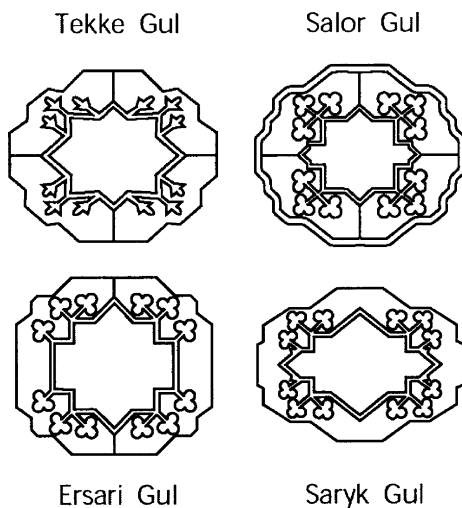


Fig. 2. Examples of characters used in analyses. Known as ‘guls,’ these carpet ornaments are distinguished by their distinctive, lobed shapes. Relationships between the designs of each are also evident. Thus, in the field between the border and central ornament there are projectiles that take the form 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.

cladogram and data set, i.e., it is a measure of the number of homoplasies in a data set (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 (i.e., 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, 1985). However, following several recent critiques (e.g., Carpenter, 1992; Kluge and Wolf, 1993), it is now considered by many researchers to be a 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 1000–10,000) are randomly sampled with replacement from the character state data set, with the character state assignments being retained in each sample. Minimum length cladograms are then computed from these subsets of data and a list of clades that comprise the cladograms is compiled. Thereafter, the percentage of clades yielded by the resampled data that support the most parsimonious cladogram returned for the original data set is calculated. Data sets that fit the bifurcating model with little conflicting signal will return higher percentages of support in the bootstrap analyses. Although there is no consensus on exactly how high this percentage should be, a number of researchers (e.g., 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 program'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 uninformative characters. To interpret the results of parsimony and bootstrapping analyses, it is necessary to determine the direction of evolutionary change for each character. This is usually ac-

complished with the aid of an outgroup (Kitching et al., 1998). In both analyses, the Yomut were used 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; Grimes, 1992; Wood, 1973). Furthermore, students of Turkmen textile traditions (e.g., 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 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 the 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 was evaluated with the CI and with a 10,000 replication bootstrap analysis. Thereafter, the cladogram topology, the 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 data set. 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 a 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 data set 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, PSDP Tekke, Salor, Saryk, and the Yomut fit the bifurcating tree model associated with cultural phylogenesis. The parsimony analysis returned a single most parsimonious cladogram, which is depicted in Fig. 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 clado-

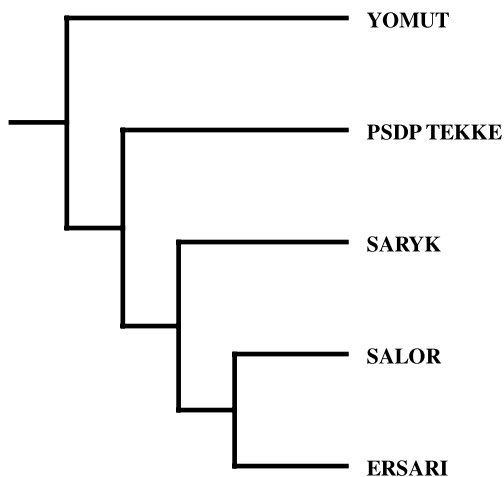


Fig. 3. Most parsimonious cladogram obtained in the analysis designed to determine the relative contributions of phylogenesis and ethnogenesis to the evolution of Turkmen textile designs, prior to the Russian invasion of Central Asia.

gram 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 outnumber homoplastic ones. Thus, the results of the second analysis indicate that the data fit the bifurcating tree model well.

Two sets of analyses were 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 the Yomut fit the bifurcating tree model compared to the data for the Ersari, PSDP Tekke, Salor, Saryk, and the Yomut. Parsimony analysis of the data for the Ersari, Salor, Saryk, SDP Tekke, and Yomut returned a single most parsimonious cladogram (Fig. 3). 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, PSDP 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. A 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 the 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, bootstrapping was used to identify which non-Tekke group contributed most to the ethnogenesis of the SDP Tekke assemblage. The results of these analyses are presented in Table 2. The analysis in which the Salor weavings were excluded returned

Table 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	Clade	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

Taxa, groups included in analysis; Clade, clades supported by 50% or more of the bootstrap replicates; BC, percentage of bootstrap cladograms in which the clade appeared.

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 PSDP 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 the 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.

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 colonisation of Central Asia. The analyses indicated that in this period the evolution of Turkmen textile designs was dominated by phylogenesis. The PTP test suggested that the data contain a phylogenetic signal and the parsimony analysis indicated that the data fit well the bifurcating tree model associated with cultural phylogenesis. The fit between the model and data is not perfect, indicating that ethnogenesis played a role in the evolution of Turkmen culture. But the CI and the results of the bootstrap analysis suggest that ethnogenesis was considerably less important than cultural phylo-

genesis. 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 (cf. 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 the Russian conquest of Central Asia.

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 c.60% of the interassemblage resemblances are homologous and c.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 intertribal borrowing of designs and motifs, but again independent invention cannot be entirely discounted as a source of 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. It is worthy of note in connection with this that Salor textiles were the most valued Turkmen products in the West, the main market

for antique Turkmen woven products (Opie, 1992; Spooner, 1986; Thompson, 1980).

How do these results compare to previous quantitative assessments of cultural evolution? Several contributions to the phylogenesis/ethnogenesis debate have focused on the material culture variation among villages on the North Coast of New Guinea, using geographic distance and linguistic affinity as proxies for ethnogenesis and phylogenesis, respectively (Collard and Shennan, 2001; Moore and Romney, 1994; Moore and Romney, 1996; Roberts et al., 1995; Welsch, 1996; Welsch et al., 1992). The authors of these studies have reached conflicting conclusions. Using regression and correspondence analysis of presence/absence data, Welsch and colleagues found that the similarities and differences among the village assemblages are strongly associated with geographic propinquity and are unrelated to the linguistic relations of the villages (Welsch, 1996; Welsch et al., 1992). 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, 1996; Roberts et al., 1995). Moore and Romney (1996) obtained the same result in a reanalysis of Welsch and colleagues' presence/absence data using correspondence analysis, thereby accounting for one potential explanation for the difference in conclusions, namely the use of different data sets. Most recently, Collard and Shennan (2001) conducted a reanalysis of Welsch and colleagues' presence/absence data set using the mantel test and three methods from biological phylogenetics: parsimony analysis, optimisation analysis, and relative apparent synapomorphy analysis. Collard and Shennan (2001) found a considerably better fit between language and material culture than between geography and material culture, although the fit between the language and material culture data was far from perfect.

Three other quantitative assessments of the significance of phylogenesis and ethnogenesis as cultural evolutionary processes have been published recently (Borgerhoff Mulder, 2001; Collard and Shennan, 2000; Guglielmino et al., 1995). The first of these explored the roles of phylogenesis, ethnogenesis, and adaptation in the evolution of 47 cultural traits among 277 African societies (Guglielmino et al., 1995). Models of the three processes were generated and then correlation analyses were undertaken in which the 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. However, the results of a smaller-scale investigation into correlations between cultural traits associated with kinship and marriage patterns in 35 East African societies were more equivocal (Borgerhoff Mulder, 2001). 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 the author's hypothesis that adaptation to local environments plus diffusion between neighbouring populations would erase any phylogenetic signature from the data. 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. However, these results 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 (Borgerhoff Mulder, 2001, p. 101). The third study tested Moore's (1994a,b) claim that ethnogenesis is more important than phylogenesis in generating the cultural patterns (Collard and Shennan, 2000). This was accomplished by applying phylogenetic techniques from biology to assemblages of pottery from Neolithic sites in the Merzbach valley, Germany. 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. Thus, Moore's claim was not supported.

When the results of the present study are taken together with those of previous quantitative assessments of cultural evolution it appears that, contrary to what has been claimed by some researchers (e.g., Dewar, 1995; Moore, 1994a,b, 2001; Terrell, 1987, 1988, 2001; Terrell et al., 1997, 2001), phylogenesis cannot be discounted as a process in cultural evolution. Phylogenesis was at

least as important as ethnogenesis in generating the New Guinea and Neolithic data sets and it was clearly the major process in producing the African one. Similarly, the present study shows that phylogenesis was considerably more significant than ethnogenesis in the evolution of Turkmen weaving traditions. Thus, the results of the quantitative studies of cultural evolution that have been reported in recent years argue strongly in favour of case-by-case empirical assessments of the relative contributions of phylogenesis and ethnogenesis to cultural evolution (Collard and Shennan, 2000; see also Whaley, 2001). Simply assuming that ethnogenesis is the dominant process, as Terrell (1987, 1988, 2001), Terrell et al. (1997, 2001), Moore (1994a,b, 2001) and others (e.g., Dewar, 1995) have advocated, is not supportable.

One aspect of the present study that is particularly noteworthy is the continued dominance of phylogenesis over ethnogenesis following the subjugation of the Turkmen by Tsarist Russia. As noted earlier, the defeat of the Turkmen by Russian forces was associated with a number of traumatic political and economic transformations. These included the forced settlement of nomadic Turkmen; their incorporation into the administrative machinery of a colonial state; an increasing dependence on the market; and in the Soviet period an active state policy of de-tribalization to create a unified “socialist Turkmen nation” (Bacon, 1980; Bennigsen and Wimbush, 1986). These changes, especially the Turkmen’s involvement in the market for Oriental textiles, have been argued to have greatly affected the transmission of weaving knowledge among the Turkmen. According to Spooner (1986, p. 230), for example, “The Western interest in Turkmen carpets has had the effect of alienating the Turkmen from their own forms of artistic expression. Before, they worked with designs embodying symbols that were for them extensions of their social identity. Now these symbols have become the property of others. To repossess them, they must now find out from others what they mean.” Accordingly, it was anticipated that the assemblages from the Russian era would show a greatly increased role for ethnogenesis in Turkmen cultural evolution. However, although the assemblages in question conformed to this expectation, the increase was a relatively minor one of 10%. Phylogenesis remained the dominant process, accounting for 60% of the resemblances among the tribes. This result indicates that phylogenesis can persist in the face

of major social and political changes, and strongly reinforces the suggestion that ethnogenesis should not be assumed to be the dominant cultural evolutionary process.

It has been pointed out recently that, even when cultural evolution has been dominated by phylogenesis, there is no reason to assume a priori that cultural histories should be correlated with population histories (Shennan, 2000). Nonetheless, in view of the important role of phylogenesis in the evolution of Turkmen culture, it is reasonable to ask whether the hypotheses of relationships obtained in the parsimony analyses of the textile data reflect the tribes’ genealogy. To date, no phylogenetic analyses of Turkmen linguistic or genetic data have been published, so a formal assessment is not possible. However, there are three other lines of evidence that pertain to the genealogical relationships of the Turkmen and which can therefore be used to evaluate the textile data-derived hypotheses of relationships. The first of these is ethnohistory. The primary source of information on the origins and history of the Turkmen tribes studied here is Abu’l Ghazi, who as the Khan of Khiva between 1643 and 1663 waged a series of military campaigns against the Turkmen. Toward the end of his reign, Abu’l Ghazi wrote a formal genealogy describing the descent of the Turkmen, based on their oral traditions and the history of the Turkic peoples of Central Asia produced by Rashid al-Din in the 11th century (Barthold, 1962; Jahn, 1980; Wood, 1973). Abu’l Ghazi reported that southeast of the Caspian Sea in the region of Khorassan there existed a powerful confederation comprising five tribes. Dominant among these were the Salor, who are listed by Rashid al-Din as one of the original descendants of Oghuz, the mythical ancestor of all Turkic and Mongolian peoples (Jahn, 1980). Four other tribes—the Ersari, Saryk, Tekke, and Yomut—were designated as the ‘Outer Salor’. Abu’l Ghazi claimed that, according to Turkmen oral traditions, only the Saryk and Tekke shared actual genealogical connections with the Salor (Azadi, 1975; 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 or the Yomut.

In contrast to the ethnohistorical evidence, the other two lines of evidence support the hypotheses of relationships suggested by the textile data. One of these lines of evidence is the clan names used by

the tribes. According to Wood (1973), the Ersari, Saryk, and Salor clan names are derived from an exclusively Oghuz lexicon, whereas the Tekke and the Yomut clan names include Persian influences. Moreover, the Ersari, Salor, and Saryk have a number of Oghuz clan names in common that they do not share with the Tekke or Yomut. Thus, the clan names support the hypotheses of relationships derived from the textile data, since they also suggest the Ersari, Salor, and Saryk are more closely related to one another than any of them is to the Tekke or the Yomut. The other line of evidence that supports the textile data-derived hypotheses of relationships is the geographic distribution of the tribes. As shown in Fig. 1, the Ersari, Salor, and Saryk lived close to the oases at Sarakhs and Bokhara, while the Tekke and Yomut lived in Khorassan. Given the fact 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.

How do we account for the disagreement between the textile, clan name, and geographic distribution data, on the one hand, and the ethnohistorical evidence on the other? One possibility is that, whereas the ethnohistorical 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 knowledge is passed primarily from mother to daughter (Irons, 1980). However, descriptions of Turkmen kinship and marriage patterns (Irons, 1974, 1975) mitigate this explanation, since they suggest that matrilineal descent should be delimited by patrilineally defined endogamous units, namely the clan and tribe. We contend therefore that a more likely explanation for the discrepancies between the ethnohistorical and textile data is that Abu'l Ghazi's genealogy is flawed. There is good ethnographic evidence for the systematic contrivance of genealogies in nomadic societies of the Near East and Central Asia. Anthropologists have long taken an interest in the political functions of oral histories in defining contemporaneous relationships in reference to the past (e.g., Goody, 1977, 1986; Vansina, 1985). It is well known that in societies where kinship, and more specifically descent, provides the major idiom of co-operation, social groups often express their solidarity in terms of common ancestry (Durk-

heim, 1947). In the case of the Turkmen, this tendency is reflected in the polysemantic term *il*, which can refer to both the patrilineal descent group and/or a "relationship of peace" (Irons, 1974, p. 642). Slippage between these two meanings is compounded by the practice of inventing what can be termed "genealogical fictions" to consolidate, and lend moral value to, politically expedient relationships. Irons (1975) explains that fictional genealogies were invoked in the Yomut in cases where fugitive or "client" groups (i.e., groups economically dependent on larger or wealthier residence groups) remained on a long-term basis with their hosts, who would incorporate them into the lineage. A similar phenomenon has been reported to occur among several other nomadic groups throughout the history of Central Asia and the Near East (e.g., Bacon, 1980; Barth, 1964; Linder, 1982; Tapper, 1991). In such cases, it is common for fictional genealogies to reflect the dominance of the more powerful partner in a territorial coalition. This may account for the genealogical connection between the Tekke, Saryk, and Salor reported by Abu'l Ghazi, the Ersari being excluded on account of their strength and independence. Records of the tribes' tribute payments to the Khiva during the reign of Abu'l Ghazi support this hypothesis. These payments were proportional to the number of livestock owned by each tribe and therefore provide an indication of the tribes' wealth. The Tekke and Saryk paid only 8000 sheep each, compared to the 16,000 sheep surrendered by the Salor. The Ersari, on the other hand, paid an equal number to Salor's contribution (Azadi, 1975). Thus, we suggest that Abu'l Ghazi's history of the Turkmen can be discounted as a source of information on the tribes' genealogy in favour of the textile, clan name, and also geographic distribution data.

Turning to more theoretical issues, a useful way of conceptualising the findings of the present study is provided by Boyd et al. (1997). These authors outline a range of models of cultural evolution that form a continuum with regard to the relative contribution of phylogenesis and ethnogenesis. At one end of the continuum is the "cultures as species" model. This sees cultures as coherent units that are insulated from outside influences in some way (e.g., by xenophobic ideologies) and which are therefore derived entirely by descent with modification. The "culture as species" model, which has been supported by Durham (1990, 1991, 1992), can be thought of as the strong phylogenesis model. Next on the

continuum is the model that Boyd et al. label “cultures with hierarchically integrated systems”. According to this model, cultures have “core traditions” and “peripheral elements”. The former arise through descent with modification and can exist over long periods of time, despite high rates of interaction between members of adjacent populations. In contrast, the peripheral elements result from diffusion and change rapidly. A further step away from the “cultures as species” model is the position that Boyd et al. characterise as “cultures as assemblages of many coherent units”. This model denies the existence of a single cultural core, positing instead that cultures are ever-changing constellations of distinct traditions that are inherited from different sources and in diverse ways. The individual traditions may be relatively long lived and originate through lineage splitting, but the cultures themselves are ephemeral and the relationships among them are reticulate. This model corresponds to the “ethnogenesis” hypothesis promoted by Moore (1994a,b, 2001). The fourth model identified by Boyd et al. represents an extreme version of the ethnogenesis hypothesis. Under this model, which Boyd et al. call “collections of ephemeral entities,” there are no cultural traditions, since individuals always make unbiased decisions about how to act on the basis of trial and error and the alternatives to which they are exposed.

The applicability of the models outlined by Boyd et al. (1997) to the evolution of Turkmen culture can be assessed in relation to the CIs of the most parsimonious cladograms and the results of the bootstrap analyses. To reiterate, the CI of the most parsimonious cladogram for the data for the Ersari, PSDP Tekke, Salor, Saryk, and Yomut was 0.68 and the CI for the most parsimonious cladogram for the data for the Ersari, Salor, Saryk, SDP Tekke, and Yomut was 0.61. In the bootstrap analysis of the data for the Ersari, PSDP Tekke, Salor, Saryk, and Yomut, two clades were supported: an (Ersari, Salor, Saryk) clade at 86% and an (Ersari, Salor) clade at 63%. Two clades were also supported in the bootstrap analysis of the data for the Ersari, Salor, Saryk, SDP Tekke, and Yomut. The Ersari and Saryk were grouped together to the exclusion of the other assemblages in 67% of the bootstrap cladograms and the Ersari, Salor, and Saryk were grouped together to the exclusion of the SDP Tekke in 59%. Whilst care must be taken when comparing CIs among different studies (Kitching et al., 1998), it is nonetheless noteworthy that the

CIs associated with the textile-derived cladograms are comparable to those obtained in cladistic analyses of fossil hominid species. For instance, the cladograms presented by Chamberlain and Wood (1987) had CI values between 0.69 and 0.71; Lieberman et al.’s (1996) most parsimonious cladogram had a CI of 0.68; and the two cladograms favoured by Strait et al. (1997) in the most recent cladistic analysis of the early hominids had CIs of 0.59 and 0.58. Likewise, the bootstrap support figures are within, or close to, the 70% confidence interval that has been used recently to determine phylogenetic relationships among biological taxa (e.g., Collard and Wood, 2000; Gibbs et al., 2000; Hillis and Bull, 1993). Thus, there are grounds for discounting the third and fourth of Boyd et al.’s (1997) models—“cultures as assemblages of many coherent units” and “cultures as collections of ephemeral entities”. If either of these models were correct, then the fit between the data and the bifurcating tree model would be poor, which it is not according to the standards used in biology. It is also worth noting that if the evolution of Turkmen textile designs conformed to either the “cultures as assemblages of many coherent units” model or the “cultures as collections of ephemeral entities” model, it would not have been possible to determine the source of homoplasy by sequentially removing taxa from the analysis.

In view of the similarity between the results of the present analyses and those obtained in cladistic analyses of biological taxa, it is tempting to conclude that Turkmen textile design evolution is consistent with Boyd et al.’s (1997) “cultures as species” model. However, we believe this would be a mistake, since it ignores an important difference between the way homoplasies are treated in biological applications of cladistics and the way they were dealt with in the present study. In biological applications of cladistics, homoplasies are treated as “noise” that obscures the phylogenetic “signal”. Providing homoplasies are few in number and/or do not co-vary, they do not interest the biologist in attempting to reconstruct phylogenetic relationships. In the present study, in contrast, homoplasies were treated as “signal”. They were taken to be evidence of ethnogenesis and used to assess the relative contribution of phylogenesis and ethnogenesis to Turkmen cultural evolution. Thus, the finding that the CIs are less than 1 and the bootstrap analyses did not support the clades at 100% is informative. It indicates that ethnogenesis played a role in the evolution of

Turkmen culture, both prior to and during their subjugation by Tsarist Russia. As noted earlier, the CIs suggest that ethnogenesis may be responsible for up to 30% of the resemblances among the assemblages in the pre-subjugation period and up to 40% in the period of Russian domination. Thus, we would contend that “cultures as species” is not an appropriate model of the evolution of Turkmen textile design vocabularies. Rather, Turkmen textile design evolution in both periods can best be conceptualised in terms of Boyd et al.’s (1997) “cultures as hierarchically integrated systems” model, which distinguishes between the descent of core traditions and peripheral elements.

It has been noted that “Reconstructing 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 recognisable history” (Boyd et al., 1997, p. 364). The strength of the phylogenetic signal in the Turkmen textile data clearly indicates that the tribes’ woven assemblages had sufficient coherence to create recognisable history. But what accounts for this coherence? Why was the rate of innovation so low and why was diffusion not more commonplace? Part of the answer to these questions may lie in tribes’ marriage practices. By tradition, the Turkmen were strongly endogamous. Although systematic statistical analyses of Turkmen marriage patterns are lacking, Irons (1975) has estimated that among the Yomut clan 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 the 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, one of the primary mechanisms of diffusion that might be expected to have played a role in Turkmen cultural affairs—the movement of individuals among tribes—does not appear to have operated to any significant degree. It is noteworthy in this context that Durham (1990, 1991, 1992) has suggested that endogamy is one of the mechanisms by which culture evolves phylogenetically, while Moore (2001) has stressed the role of marriage-related movements of individuals

in promoting ethnogenesis. It is also worthy of note that sociologists have found endogamy to be important in the intergenerational transmission of distinctive cultural attributes among contemporary ethnic groups in the USA (Stevens and Swicegood, 1987).

Cultural diffusion among the five Turkmen tribes may also have been inhibited by aspects of the weaving process, especially the way in which weaving was learned and reproduced. Traditionally, weaving was an exclusively female activity. Knowledge of how and what to weave was transmitted from mother to daughter without the aid of writing or patterns. Structural characteristics of, and the designs incorporated into, textiles were learned by imitation and reproduced from memory (Irons, 1980; Moshkova, 1977; Ponomaryov, 1980). Thus, weaving was a skill acquired over many years, one which, according to Irons’ (1980) informants, beginners could not hope to master in a short time. It seems likely that these methods of learning and reproduction may well have helped ensure that diffusion was limited among the tribes. Given the constraints on the transmission and replication of weaving knowledge, it is possible that it was difficult for tribes to adopt the structural characteristics and designs employed by other tribes, particularly when the low level of intertribal marriage is taken into account. This hypothesis could be tested by ethnographic studies of weaving among contemporary Turkmen and other Central Asian weavers.

While endogamy and aspects of the weaving process may have insulated the development of tribes’ woven assemblages from external influences, their residence practices and frequent involvement in conflict seem likely to have encouraged the circulation of designs within the tribes. By tradition, Turkmen residence was patrilocal (Irons, 1974, 1975). It was common for newly married Turkmen women to leave their *oba* if their husband lived in a different one. Marital exchanges between households belonging to separate *obas* were used as a means of consolidating alliances forged during times of conflict, when they would align themselves against a common enemy. Most such conflicts arose through disputes over pasture and water resources, which, when they could not be resolved peacefully, involved military expeditions and persistent feuding (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 *gong-shi*, or “neighbours,” 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). Thus, the prevalence of warfare among the Turkmen, and the strategies they employed to cope with it, may help explain how the homogeneity of each tribe’s woven assemblage was maintained: designs could have moved through the traffic in brides between strategically aligned *obas* and the frequent displacement of families by violent blood feuds.

A further explanation for the conservatism of tribes’ woven assemblages is suggested by Nettle’s (1999) investigation into the evolution of language variation. 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). This danger increases proportionally to the size of a population and the mobility of its members, since the less likely the chances of meeting again, the easier it is for potential co-operators to cheat. Nettle therefore 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. We suspect that Turkmen carpet designs might provide an equally useful identifier since, like language, weaving is learnt at a very early age and over a period of many years (Irons, 1980). It is feasible therefore that the ornaments used to decorate textiles provided a “recognition system” that clearly indicated the identity of their makers. The value of such markers is clear in a situation of endemic feuding, where the accurate identification of co-operators and defectors is literally a matter of life or death. This is especially pertinent given the mobility of the Turkmen, evident in the high numbers of families who temporarily seek refuge among other *obas* to escape “blood responsibility”. In such cases, both the refugee and host need to be able to establish a relationship of trust, which may require a pre-existing familiarity with one another either as individuals or as social groups. In the absence of such familiarity, a recognition system, such as dialect, dress or carpet ornaments, would provide some basis for a reciprocal relationship to be established. Work on

mate recognition systems among animals 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). Thus, it is possible that the conservatism of the Turkmen’s woven assemblages is a consequence of the designs incorporated into them being part of a recognition system. Although a number of writers (e.g., Moshkova, 1977; Ponomaryov, 1980) have argued that carpet ornaments had a “heraldic” value to the tribes, no published description is sufficiently detailed to enable the recognition system view of Turkmen’s design vocabularies to be assessed. Thus, this hypothesis needs to be tested by an ethnographic investigation of the symbolism and function of weaving in contemporary Turkmen society.

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 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 c.70% of the resemblances among tribes’ assemblages and ethnogenesis c.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 A. Characters

These were recorded as present or absent.

- | | |
|---------------------------------------|---|
| 1. Lobed gul | 39. Dyrnak gul: carpet |
| 2. Lobed gul: birds | 40. Dyrnak gul: bag |
| 3. Lobed gul: clovers | 41. Dzhengel |
| 4. Lobed gul: one-stem clover | 42. Dzhengel: carpet |
| 5. Lobed gul: two-stem clover | 43. Dzhengel: bag |
| 6. Archetypal gul | 44. Dzhengel: type 1 |
| 7. Archetypal gul: carpet | 45. Dzhengel: type 2 |
| 8. Archetypal gul: bag | 46. Tauk Noska |
| 9. Archetypal gul: type 1 banner | 47. Tauk Noska: version 1 |
| 10. Archetypal gul: type 2 banner | 48. Tauk Noska: version 2 |
| 11. Archetypal gul: type 1 bracket | 49. Sagdak |
| 12. Archetypal gul: type 2 bracket | 50. Sagdak: star centre |
| 13. Octagonal gul | 51. Sagdak: Gochak centre |
| 14. Octagonal gul: two-headed animals | 52. Memling |
| 15. Octagonal gul: arrows | 53. Memling: carpet |
| 16. Rhomboid minor gul | 54. Memling: bag |
| 17. Rhomboid minor gul: carpet | 55. Constellation |
| 18. Rhomboid minor gul: bag | 56. Carpet Gochak borders |
| 19. Salor Rose | 57. Carpet Gochak borders: simple pattern |
| 20. Salor Rose: carpet | 58. Carpet Gochak borders: cross pattern |
| 21. Salor Rose: bag | 59. Carpet Gochak borders: cross ornament |
| 22. Kurbaghe | 60. Chuval Gochak border |
| 23. Kurbaghe: carpet | 61. Chuval Gochak border: simple |
| 24. Kurbaghe: bag | 62. Chuval Gochak border: complex type 1 |
| 25. Kurbaghe: type 1 | 63. Chuval Gochak border: complex type 2 |
| 26. Kurbaghe: type 2 | 64. Chuval S-border |
| 27. Chemche | 65. Chuval S-border: continuous |
| 28. Chemche: carpet | 66. Chuval S-border: continuous version 1 |
| 29. Chemche: bag | 67. Chuval S-border: continuous version 2 |
| 30. Chemche: type 1 | 68. Chuval S-border: bracketed |
| 31. Chemche: type 2 | 69. Chuval S-border: bracketed version 1 |
| 32. Aina gul | 70. Chuval S-border: bracketed version 2 |
| 33. Aina gul: carpet | 71. Soldat border |
| 34. Aina gul: bag | 72. Soldat border: carpet |
| 35. Aina gul: type 1 | 73. Soldat border: bag |
| 36. Aina gul: type 2 | 74. Soldat border: version 1 |
| 37. Aina gul: type 3 | 75. Soldat border: version 2 |
| 38. Dyrnak gul | 76. Zig-zag border |

- | | |
|------------------------------------|-----------------------------------|
| 77. Triangle border | 84. Star border ornaments: type 1 |
| 78. Triangle border: single | 85. Star border ornaments: type 2 |
| 79. Triangle border: double | 86. Star border ornaments: type 3 |
| 80. Framed cross border | 87. Barmak border |
| 81. Framed cross border: version 1 | 88. Barmak border: carpet |
| 82. Framed cross border: version 2 | 89. Barmak border: bag |
| 83. Star border ornaments | 90. Hooked branch border |

Appendix B. Character state data matrix

Characters are listed consecutively from 1 to 90. See Appendix A for character names. 1 = presence, 0 = absence.

Ersari	1 0 1 0 1 1 1 0 1 0 1 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 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 0 1 1 1 1 1 0 0 0 0 0 0 0 0
Saryk	1 0 1 0 1 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 1 0 0 0 1 1 1 1 0 1 1 0 1 0 1 0 0 0 0 0 1 0 1 1 1 0 0 0 0 0 1 0 1 1 1 1 0 1 1 1 0 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
PSDP Tekke	1 1 0 0 0 1 0 1 1 0 1 0 0 0 0 1 1 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 0 1 0 0 0 1 0 1 0 1 0 0 0 0 0 0 1 0 1 0 1 1 0 1 1 0 1 0 1 1 0 1 0 0 0 0
SDP Tekke	1 1 0 0 0 1 0 1 1 0 0 1 0 0 0 0 0 0 1 1 1 1 1 1 0 0 1 1 1 0 0 1 1 1 1 1 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 1 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 1 0 1 0 1 0 0 0 1 0 1 1 1 1 1 1
Yomut	0 0 0 0 0 1 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 1 1 0 0 0 0 1 0 1 0

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