The Evolution of Material Culture Diversity among Iranian Tribal Populations

SEVEN

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AWIDELY HELD view in anthropology suggests that the processes of cultural and biological evolution differ greatly. An early expression of this view can be found in Kroeber's 1948 volume Anthropology: Race, Language, Culture, Psychology and Prehistory. Kroeber suggested that

the course of organic evolution can be portrayed properly as a tree of life, as Darwin has called it, with trunk, limbs, branches, and twigs. The course of the development of human culture in history cannot be so described, even metaphorically. There is a constant branching-out, but the branches also grow together again, wholly or partially, all the time. . . A branch on the tree of life may approach another branch; it will not normally coalesce with it. The tree of culture, on the contrary, is a ramification of such coalescences, assimilations, or acculturations. (138)

More recent writers have evoked this contrast by likening cultural evolution to a "braided riverbed" (Moore 1994) or "entangled bank" (Terrell 1988) as opposed to the "family tree" model used to depict the relationships among species. In the last few years, this view has been challenged by a number of studies (e.g., Collard and Shennan 2000; Gray and Jordan 2000; Tehrani and Collard 2002; O'Brien, Darwent, and Lyman 2001; Jordan and Shennan 2003; Collard, Shennan, and Tehrani 2006). Using methods of phylogenetic reconstruction developed by evolutionary biologists, these studies have sought to evaluate how well cultural patterns fit a branching, treelike model of evolution in which ancestral traditions split into new ones. The majority of these studies have failed to support the suggestion that cultural evolution is always more complex and intertwined than genetic evolution. Thus, instead of rejecting the family tree model out of hand, anthropologists should evaluate the contributions made by different evolutionary processes to patterns in the ethnographic and archaeological records on a case-by-case basis.

In this chapter, we aim to contribute to empirical research in this area by investigating the relative importance of branching and blending processes in the evolution of material culture diversity among tribal populations in Iran. Our study builds on a previous study in which phylogenetic methods were applied to a data set comprising decorative characters from textiles

99

produced by five Turkmen tribes between the eighteenth and early twentieth centuries, with a view to testing the braided riverbed/entangled bank model of cultural evolution (Tehrani and Collard 2002). We carried out two sets of analyses (Tehrani and Collard 2002). The first focused on artifacts produced prior to the colonization of Turkmen territories by Imperial Russia in the late 1800s, and we found that approximately 70 percent of the similarities among the tribes' woven assemblages in this period can be accounted for by the family tree model. The second set of analyses focused on artifacts produced after 1881. The results of these analyses also suggested that the pattern of design variation is most consistent with the family tree model, although the percentage of resemblances among the tribes' weavings that could be accounted for by this model decreased to around 60 percent. Based on these two sets of results, we concluded that cultural evolution among the Turkmen over the last two hundred years was more compatible with the family tree model than the braided riverbed/entangled bank model.

Here, we seek to go beyond our earlier study (Tehrani and Collard 2002) and provide a more comprehensive understanding of material culture evolution among the tribes of western Central Asia. An important reason for pursuing this goal is that, for most of their history, Turkmen tribes enjoyed a level of autonomy from state governments that was unusual for tribes in the area (see, e.g., Irons 1974; Tapper 1991). This appears to be mainly due to the inaccessibility of the remote, frontier regions that they inhabited. Given that we (Tehrani and Collard 2002) found evidence that branching processes became less important in Turkmen cultural evolution after they were incorporated into the Russian Empire, it is possible that cultural evolution among tribes that have a longer history of interacting with state governments may be more consistent with the braided riverbed/tangled bank model. With this in mind, the data set we analyze includes data taken from textiles produced by several Iranian tribal groups who were less remote and less

autonomous than the Turkmen as well as data from textiles created by two Turkmen tribes.

BACKGROUND

Woven textiles are ubiquitous in the material culture assemblages of Iranian tribal groups. Produced exclusively by women, who typically begin learning to make them between the ages of six and ten (Irons 1980; Amir-Moez 2002; Beck 1991; Tehrani 2004), they fulfill a wide range of functions, from the mundane and utilitarian to the ornamental and ceremonial. Among the most commonly made items are colorful hand-knotted rugs, saddlebags, animal trappings, packing bands, salt bags, tent canopies and decorative hangings, articles of clothing, and small pouches for carrying cutlery. One reason for the popularity of woven textiles in these groups is that a textile-based material culture is well suited to the nomadicpastoralist lifestyle that was pursued by most tribal communities in Iran until recently (Irons 1980; Digard 1981, 2002; Mortensen and Nicolaisen 1993; Amir-Moez 2002; Tapper 2002). Objects woven from wool are relatively easy to carry on seasonal migrations, because they can be folded or rolled. Equally importantly, the materials and equipment required for weaving are straightforward for tribeswomen to obtain locally and transport between camps.

Iranian tribal weavings have long fascinated Western collectors (Spooner 1986; Helfgott 1994), and a large body of literature is dedicated to understanding the sources and relationships of Iranian tribal weaving traditions (e.g., Housego 1978; Eiland 1982, 1987; Thompson 1980, 1983; Opie 1981, 1992; Mallett 1998; Parham 1996; Stone 2004). However, research in this field has been hindered by two problems in particular. One is that textiles are fragile and liable to decay rapidly. The consequence is that few ancient textiles have the potential to provide insights into the early history of weaving. Moreover, even when such discoveries do occur (e.g., Rudenko 1970), there is invariably

insufficient evidence to make any direct link between tribal populations in the distant past and those of today. The other problem is that many of the theories that have been put forward by oriental rug specialists are highly speculative because they are based on evidence that has been selected according to predetermined criteria of "authenticity" (Spooner 1986).

Obviously, little can be done about the first of the aforementioned problems. However, we believe that it is possible to overcome the second by adopting a more rigorous approach to the reconstruction of Iranian tribal weaving traditions. More specifically, we advocate employing what is now the most widely used technique for reconstructing phylogenetic relationships among species and other taxa—cladistics (Quicke 1993; Kitching et al. 1998).

Based on a null model in which new taxa arise from the bifurcation of existing ones, cladistics defines phylogenetic relationship in terms of relative recency of common ancestry. Two taxa are deemed to be more closely related to one another than either is to a third taxon if they share a common ancestor that is not also shared by the third taxon. Exclusive common ancestry is indicated by shared evolutionarily novel or "derived" character states. Two taxa are inferred to share a common ancestor to the exclusion of a third taxon if they exhibit shared derived character states that are not also exhibited by the third taxon.

In its simplest form, cladistic analysis proceeds via four steps. First, a character state data matrix is generated. This shows the states of the characters exhibited by each taxon (e.g., presence/ absence of a chin). Next, the direction of change among the states of each character is established. Currently, the favored method of accomplishing this is outgroup analysis (Arnold 1981). This entails examining a close relative of the focal taxa to determine which character states are derived (those found only among the focal taxa) and which are ancestral (those shared by one or more of the focal taxa and the outgroup). Having determined the probable direction of change for the character states, the next step is to construct a branching diagram of relationships for each character. This is done by joining the two most derived taxa by two intersecting lines, and then successively connecting each of the other taxa according to how derived they are (figure 7.1). Each group of taxa defined by a set of intersecting lines corresponds to a clade, and the diagram is referred to as a cladogram. The last step is to compile an ensemble cladogram from the character cladograms. Ideally, the distribution of the character states among the taxa will be such that the character cladograms imply relationships among the taxa that are congruent with one another. Normally, however, some of the character cladograms will suggest relationships that are incompatible. This problem is tackled by generating an ensemble cladogram that is consistent with the largest number of characters and therefore requires the smallest number of ad hoc hypotheses of character appearance to account for the distribution of character states among the taxa.

In using cladistics to investigate Iranian tribal material culture diversity, we are following a precedent set by a number of previous studies (e.g., Foley 1987; Robson-Brown 1996; Foley and Lahr 1997, 2003; Collard and Shennan 2000; Gray and Jordan 2000; O'Brien et al. 2001, 2002; Holden 2002; Tehrani and Collard 2002; O'Brien and Lyman 2003; Rexová, Frynta, and Zrzavý 2003; Cochrane 2004; Collard et al. 2006). This approach is rooted in the observation that the problem of reconstructing human population history from cultural data shares features with the problem of reconstructing the evolutionary history of a group of species (Kirch and Green 1987, 2001). In both cases, the key challenge is to distinguish similarities resulting from shared ancestry (homologies) from similarities due to mechanisms other than shared ancestry (homoplasies). While the processes responsible for generating biological and cultural homologies are not the same (gene transfer vs. cultural transmission), and those responsible for generating the majority of biological and cultural homoplasies probably also differ, the problems



FIGURE 7.1 Example data set and cladogram derived from it.

of establishing relationships of descent among cultural groups and among biological taxa are sufficiently similar in terms of epistemology and ontology to warrant the application of phylogenetic 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. The bifurcating tree model is used because it is the simplest and therefore the most defensible way of linking taxa together. 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 it.

Application of cladistics to the problem of elucidating the sources and relationships of Iranian tribal weaving traditions is facilitated by the nature of the woven artifacts. Like biological phenotypes, Iranian tribal textiles are morphologically complex and can be most accurately

described by identifying the specific traits they exhibit. For example, the face of the saddlebag shown in figure 7.2 incorporates several distinct weaving techniques (pile weaving, weft-faced plain weave, and extra-weft wrapping) and a series of integrated but isolable motifs. It is evident from the literature (e.g., Housego 1978; Thompson 1980; Opie 1992; Mortensen and Nicolaisen 1993) that traits such as these vary considerably among different tribal groups. For example, analyses of textile structures have revealed that there are numerous variations in the technique of pile knotting, in which patterns are generated by the cut ends or "tufts" of dyed yarns woven across the warp (e.g., Thompson 1980; Mallett 1998). The pile weavings of different tribes can be differentiated by a number of criteria such as knot density, whether knots are symmetrical (looped fully around two warp threads) or asymmetrical (looped fully around one warp thread and passed underneath another on either the left or right side), and the relative displacement of alternate warp threads. Flat-woven structures are similarly diverse,



FIGURE 7.2 Saddlebag made by a weaver from the Bakhtiari tribe. Three techniques (bold print) were used to weave the bag face: the foundation consists of weft-faced plain weave in alternating stripes of red and black; the central panel comprises designs (e.g., rooster, infinite knot) woven onto the foundation by extra-weft wrapping; and the end panels are woven in a rough pile weave, with designs rendered by the tufts of the pile (e.g., palmette).

while almost every motif used on tribal textiles can be linked to a large family of related designs (e.g., Stone 2004; Opie 1992). The detailed typologies of design, structure, and technique that have been developed by oriental textile specialists (e.g., Thompson 1980; Mallett 1998; Stone 2004) therefore provide a basis for identifying the characters and character states that are the basic units of cladistic analysis.

MATERIALS AND METHODS

The study focused on woven artifacts produced by four Turkic-speaking tribes and four Persianspeaking tribes. The former included two Turkmen groups, the Yomut and Tekke, and two Azeri-speaking groups, the Qashqa'i and the Shahsevan, while the latter included the Baluch and three groups that employ dialects of Lori, a Persian language related to Kurdish (Grimes 2002): the Bakhtiari, the Boyer Ahmadi Lor, and the Papi Lor. The geographic locations of tribes included in the study are shown in figure 7.3.

The tribes produce a wide range of woven artifacts, as well as some items that are made of felt (e.g., tent walls, caps, and cloaks) and basketry (e.g., containers, mats, and small cages for transporting poultry). The tribes' woven products were studied through material culture monographs (Allgrove 1976; Tanavoli 1985; Mortensen and Nicolaisen 1993; Konieczny 1979; Willborg 2002), museum collections (e.g., Mackie and Thompson 1980; Tzavera



FIGURE 7.3 Map of Iran showing the locations of the territories of the study groups.

1984), and field surveys conducted in western Iran in the summer of 2001 and spring of 2002 (Tehrani 2004).

Textiles produced by Arab Bedouin of Jordan were also sampled (Weir 1976) in order to provide an outgroup for the analyses. The Bedouin are a useful outgroup for current purposes because, although they are geographically, culturally, and linguistically distinct from both the Turkish- and Persian-speaking Iranian tribes, their crafts are believed to constitute a related tradition based on the materials, techniques, and designs they use (Weir 1976).

A total of 150 characters were identified. They included techniques of preparation and fabrication (e.g., spinning, knotting, etc.), the use of different materials (e.g., wool, goat hair, dyes, etc.), and decorative features (e.g., carpet designs, border patterns, etc.). Characters were defined in such a way that they could be scored as either present or absent.

After coding, the data set was subjected to a two-stage analysis. The aim of the first stage was to generate a cladogram or set of cladograms that best represented patterns of descent for the eight tribal assemblages. This was accomplished with the branch-and-bound search routine of the phylogenetics software program PAUP* 4 (Swofford 1998). PAUP* 4 was employed because it is widely used in evolutionary biology; its branch-and-bound search routine was selected because it is guaranteed to find the most parsimonious cladogram(s) for a given set of data (Swofford 1998).

The second stage of the analysis aimed to establish how well the most parsimonious cladogram accounts for the pattern of similarities and differences among the tribal assemblages. This was achieved with two goodness-of-fit measures-the Consistency Index and the Retention Index-and the phylogenetic bootstrap. The Consistency Index is a measure of how parsimonious evolution has been for a given combination of cladogram and data set; that is, it is a measure of the number of homoplasies in a data set (Kitching et al. 1998). A Consistency Index of 1.0 indicates that the data are perfectly congruent with the cladogram (i.e., the cladogram requires no homoplastic changes to be hypothesized), and homoplasy levels increase as the Consistency Index decreases toward o. The Retention Index is a measure of the number of



homoplastic changes that a cladogram requires independent of its length (Farris 1989a, 1989b). A maximum Retention Index of 1 indicates that the cladogram requires no homoplastic change; and as the level of homoplasy increases, the index approaches o. Whereas the Consistency Index and Retention Index measure the overall fit between the tree and patterns in the data set, the phylogenetic bootstrap is a technique for measuring support for individual clades (Felsenstein 1985; Sanderson 1995). It involves generating cladograms by creating fictional data sets the same size as the original by randomly resampling characters from the original data set with replacement a large number times (in this case, ten thousand) and calculating the percentage of replicates that support a given clade. Data sets that fit the bifurcating model with little conflicting signal will return high bootstrap support percentages and vice versa. As with the parsimony analysis, all three of the techniques described here were carried out in PAUP* 4.

RESULTS

The cladogram favored by the parsimony analysis is shown in figure 7.4. It suggests that the Yomut, Tekke, Shahsevan, Qashqai, Boyer Ahmad, Bakhtiari, and Papi share a common ancestor to the exclusion of the Baluch. The clade composed of Yomut, Tekke, Shahsevan, Qashqai, Boyer Ahmad, Bakhtiari, and Papi is then subdivided into two subclades. The first comprises two groups that speak similar dialects of Turkmen, a Turkic language: the Yomut and the Tekke. The second clade comprises a linguis-

Outgroup Yomut Tekke Shahsevan

Qashqa'i Boyer Ahmad Bakhtiari

FIGURE 7.4 The most parsimonious cladogram obtained from the Iranian tribal craft traits data. The percentages at the nodes represent the level of support given to each clade in the bootstrap analysis.

tically heterogeneous group of tribes. The Shahsevan and Qashqai both speak Turkic languages. However, the latter are included in a clade with three Persian Lor-speaking groups: the Boyer Ahmad, Bakhtiari, and Papi. These three groups comprise a clade that excludes the Qashqai, suggesting their craft traditions are descended from a more recent common ancestor. Within this clade is a further subclade comprising the Bakhtiari and Papi.

The second stage of analysis examined how well this cladogram fit patterns in the data. The Consistency Index of the cladogram was 0.60, as was the Retention Index. Thus, both the Consistency Index and Retention Index suggested that a clear majority of the resemblances among the assemblages could be accounted for by the branching pattern of descent represented by the cladogram. The bootstrap analysis returned strong support for each of the clades represented in the cladogram. The support values are shown beside each node in the cladogram (figure 7.4). The most inclusive clade, which comprised all the taxa except the Baluch, was also the most strongly supported one. A Yomut-Tekke clade was also supported by almost all the bootstrap samples (99 percent). A clade composed of Shahsevan, Qashqai, Boyer Ahmad, Bakhtiari, and Papi was also found in a large majority of bootstrap cladograms (78 percent). Subclades within the Shahsevan-Qashqai-Boyer Ahmad-Bakhtiari-Papi clade vary in the strength of support returned by the bootstrap analysis. The best-supported subclade (89 percent) hypothesized a common ancestor for the Qashqai, Boyer Ahmad, Bakhtiari, and Papi

assemblages. The least well-supported subclade consisted of the Boyer Ahmad, Bakhtiari, and Papi (62 percent). There was slightly more support for a subclade comprising the Bakhtiari and Papi (64 percent).

DISCUSSION

The Consistency Index, Retention Index, and the results of the bootstrap analysis indicate that there is a reasonably close fit between the data set and the cladogram, which suggests that branching processes have played an important role in generating the textile assemblages. According to the Consistency Index (0.60), roughly 60 percent of the resemblances among the assemblages can be accounted for by a family tree model. This result is very close to the one returned by the same measure of how treelike patterns of design variation are among contemporary Turkmen populations (CI = 0.61)

(Tehrani and Collard 2002). Thus, based on the results of these two case studies, it would appear that the regional patterns of material culture diversity among tribal groups in western Central Asia are largely, although not exclusively, the product of branching processes.

To put this apparent regional pattern in an even broader perspective, the Retention Index for the eight Iranian tribal textile assemblages can be compared with the Retention Indices obtained by Collard et al. (2006) from a large number of cultural (table 7.1) and biological data sets (table 7.2). The Retention Index is particularly useful for this type of comparative analysis because it is not affected by the number of characters or the number of taxa employed in a study. At 0.60, the Retention Index of the Iranian tribal textile assemblage cladogram falls well within the range of Retention Indices returned by the other cultural data sets, which is 0.42–0.78, and almost exactly matches

TABLE 7.1. Comparison of the Retention Index Yielded by the Iranian Tribal Textile Assemblage Data Set with Retention Indices for 20 Cultural Data Sets

DATA SET	RETENTION INDEX
Gulf of Georgia Salish food taboos and prescriptions	0.57
Neolithic pottery	0.71
Californian Indian basketry	0.71
Eastern North American projectile points	0.70
Coast and inland Salish cultural practices	0.63
New Guinea material culture	0.51
Turkmen weaving designs	0.44
Northwest Coast tribal religion and ritual	0.65
Early Christian doctrinal beliefs	0.61
Iranian tribal weavings	0.60
Northwest Coast archaeology	0.50
Pomo structures	0.52
Oregon Coast tribal puberty rites	0.55
Southern Sierra Nevada tribal death and mourning practices	0.48
Nevada Shoshoni tribal mutilations	0.78
Southern California tribal body- and dress-related practices	0.52
Yuman-Piman warfare-related practices	0.69
Apache-Pueblo houses	0.63
African cultural practices	0.42
Northern Paiute birth rituals	0.43
Northeastern Missouri projectile points	0.66

NOTE: Reported by Collard et al. (2006). The indices are ranked from highest to lowest, and the Iranian tribal textile assemblage Retention Index data set is highlighted in bold.

TABLE 7.2. Retention Indices for Twenty-One Biological Data Sets

DATA SET	RETENTION INDEX
Australasian teal mtDNA	0.94
Corbiculate bee behavior	0.94
Pelecaniforme bird behavior	0.84
Anoles lizards morphology	0.79
Primate behavior	0.73
Strepsirhine primate morphology	0.72
Fossil hominid morphology	0.71
New World monkey morphology	0.70
Ungulate morphology	0.70
Phalacrocoracid bird mtDNA	0.65
Phocid seal morphology	0.60
Hawaiian fruit fly mtDNA	0.50
Hominoid primate cranial morphology	0.49
Carnivore mtDNA	0.47
Mammal mtDNA with emphasis on Malagasy primates	0.47
Carnivore mtDNA with emphasis on Malagasy taxa	0.47
Mammal mtDNA	0.44
Insectivore mtDNA	0.44
Lagomorph mtDNA	0.39
Hominoid primate soft-tissue morphology	0.38
Anolis lizard mtDNA	0.35

NOTE: Reported by Collard et al. (2006). The indices are ranked from highest to lowest.

the mean Retention Index of 0.59. Thus, the fit between the Iranian textile assemblage data set and the cladogram is not atypical for a cultural data set. In view of the long-standing assumption that cultural evolution is much more reticulate than biological evolution, it is perhaps more surprising that the Retention Index yielded by the Iranian textile assemblage data set is also close to the mean of the Retention Indices returned by the biological data sets, which is 0.61. Thus, the proportion of resemblances among the Iranian tribal craft assemblages that can be accounted for by inheritance from ancestral taxa is almost exactly the same as the average for related biological species.

Our results could be interpreted as supporting a model of cultural evolution that is based on speciation theory in biology (e.g., Mayr 1963). This model proposes that culture, along with genes and language, is acquired almost entirely by inheritance from ancestral populations and is only minimally influenced by contact among neighboring groups (e.g., Durham 1990, 1992). However, like many other researchers interested in cultural evolution (e.g., Boyd et al. 1997; Shennan 2002; Jordan and Mace 2006), we consider this model to be too extreme because on the whole it seems that the ideas, skills, beliefs, and behaviors that are present in any given population are not as tight contained as genetic traits are in species. In the Iranian case, for example, many tribespeople speak languages originating thousands of years ago in Central Asia (e.g., Oghuz Turkic languages like Azeri or Turkmen), hold religious beliefs that arose in the Arabian peninsula several centuries ago (Islam), hunt with European-manufactured weapons (rifles), and consume vast quantities of a drink introduced into Iran by the British in the nineteenth century that derives from a plant first cultivated in China (tea) (Digard 2002). Therefore, we do not believe that these cultures should be considered equivalent to biological species in a

FIGURE 7.5 Diagram representing the linguistic relationships among the study populations. The Turkicspeaking groups divide into two branches, Turkmen and Azeri. The Persian-speaking groups comprise the Baluch, who speak a northwestern Iranian language, Balochi, and three groups who speak dialects of another northwestern Iranian language, Lori. (After Grimes 2002.)



literal sense. However, the strength of the phylogenetic signal that we recovered from the material cultural data set also rules out the entangled bank (Moore 1994) or braided riverbed (Terrell 1988) model, which proposes that culture comprises temporary collections of traits that are so ephemeral that it is impossible to retrieve any trace of branching descent (e.g., Terrell 2004).

This leaves two other possibilities. The first is that the craft phylogeny might represent what has been called a "core tradition" (e.g., Boyd et al. 1997; Shennan 2002; see also Rosenberg 1994). A core tradition represents a set of cultural traits that is relatively insulated from cultural, linguistic, and genetic exchange with other groups and therefore remains stable for a long period of time. The second possibility is that Iranian tribal craft traditions represent a "package" of cultural traits. The "multiple packages" model of cultural evolution (e.g., Boyd et al.; Shennan 2002) proposes that coherent cultural lineages do not always necessarily coincide with population histories. Some traditions may remain stable even when they are transferred across ethnolinguistic boundaries. A phylogeny for such a tradition may therefore reveal patterns of inheritance from ancestral groups, but it could also include information about how cultural traits spread among more distantly related populations.

To examine which of these models best explains the evolution of Iranian tribal craft traditions, we compared our cladogram with an estimate of the tribe's linguistic affiliations (figure 7.5; cf. Gray and Jordan 2000; Borgerhoff-Mulder 2001; Holden 2002). The comparison revealed that the division of the craft traditions of the Turkic-speaking groups into two separate lineages corresponded to the split between Turkmen speakers (the Yomut and Tekke) and Azeri speakers (the Qashqai and Shahsevan). This fits with the core traditions model of cultural evolution. The hypothesis that the assemblages of the Boyer Ahmad, Papi, and Bakhtiari share an exclusive common ancestor is also compatible with the model because all three speak Lori. However, it appears that these assemblages are more closely related to those of Turkicspeaking groups than they are to the Baluch assemblage, despite the fact that the Baluchi language belongs to the same Indo-Iranian northwestern Iranian family as Lori. This clade, which was found in 100 percent of the bootstrap cladograms, suggests that the craft traditions of the Lor-speaking Bakhtiari, Papi, and Boyer Ahmad are probably Turkic in origin. More specifically, the internal structure of the clade indicates an Azeri source, since the Bakhtiari-Papi-Boyer Ahmad clade is nested within a larger clade that contains the Qashqai and Shahsevan but excludes the Yomut and Tekke. It appears that the ancestral assemblage from which the three Lorspeaking groups' craft traditions derive is the same one that gave rise to present-day Qashqai weavings, since these groups were linked by a clade excluding the Shahsevan that has high bootstrap support (89 percent). Ethnohistorical evidence and the tribes' geographic distributions (figure 7.3) suggest that this common source was

most probably the Azeri-speaking tribes that migrated from the Caspian territories (which the Shahsevan continue to inhabit) to southwestern Iran more than five hundred years ago. The descendants of these tribes later formed the core of the Qashqai tribal confederacy that arose in the nineteenth century (e.g., Beck 1986; Amir-Moez 2002), but some were likely also absorbed by neighboring Lor-speaking tribes (cf. Barth 1961). Although the precise nature of the mechanisms through which the latter acquired their weaving skills requires further exploration, it appears that the structure of the craft traits cladogram reflects both inheritance from ancestral populations and transference across ethnolinguistic boundaries. Therefore, it appears that the multiple packages model of cultural evolution offers the best explanation for the origins and spread of weaving among tribal populations in Iran.

CONCLUSIONS

The case study that we have reported here adds further weight to the recent critique of conventional assumptions in anthropology and archaeology regarding cultural evolution. There is now strong reason to believe that, contrary to what most anthropologists and archaeologists currently assume, the relationships among cultural traditions can often be explained by a branching pattern of descent. The results of our analyses suggested that a majority of resemblances among tribal craft assemblages in Iran can be explained by such a model. However, as we pointed out at the beginning of this chapter, researchers should probably be cautious about generalizing about the processes involved in cultural evolution and consider the evidence for each case independently. Here we have shown that although the patterns in the Iranian tribal craft data set are in many ways typical of those in other cultural and biological data sets, the models required to account for these patterns might vary considerably. In this case, we have argued that a multiple packages model offers a better explanation for the evolution of material culture diversity among Iranian tribal groups than a speciation model, an entangled bank model, or a core traditions model. However, we do not rule out the possibility that these and other models might apply in other cases. We suspect that future research in this field will demonstrate that we are still at a very early stage of understanding how patterns of cultural diversity evolve and how they relate to population histories, genetic patterns, and languages.

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