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ORIGINAL SCIENTIFIC ARTICLE

Patterns of Evolution in Iranian Tribal Textiles

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Abstract Ever since the publication of *The Origin of Species*, anthropologists and archaeologists have been in turns enchanted and repulsed by the idea that cultural diversity can be explained by a Darwinian model of descent with modification. Over the last decade, this debate has intensified following the publication of a number of studies that have sought to reconstruct cultural histories using modern computational methods of phylogenetic analysis imported from biology. In this paper, I focus on evolution of tribal textile assemblages in Iran and Central Asia. Using cladistic phylogenetic analysis, I show that similarities and differences among the assemblages can be largely explained in terms of descent with modification from ancestral assemblages. Interestingly, the phylogenetic signal in design characters is just as strong (if not stronger) than the signal in technical characters. This may seem surprising given that techniques, like genes, are transmitted "vertically" from mothers to daughters whereas designs are frequently transmitted "horizontally" among peers. However, a closer examination reveals that the transmission of designs between weavers mainly occurs within, rather than between groups, and that, as in many cultures past and present, there are important constraints on the latter. This highlights that differences in the ways in which genes and cultural traits are transmitted among individuals should not be assumed to lead to differences in macro-level patterns of evolution, as many archaeologists and anthropologists have supposed.

Keywords Cultural phylogenies · Material culture · History of Anthropology · Iranian tribal textiles · Cladistics

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Introduction

In 1875, the pioneering anthropologist and collector Henry Augustus Pitt Rivers sketched out the basis for a Darwinian approach to material culture: "Human ideas, as represented by the various products of human industry, are capable of classification into genera, species, and varieties, in the same manner as the products of the vegetable and animal kingdoms, and in their development from the homogeneous to the heterogeneous they obey the same laws" (Pitt Rivers 1875:307). At the time, Pitt Rivers' ideas seemed to be a logical progression of evolutionary theory, which was believed to be applicable in many fields other than biology. For example, Darwin suggested that there were "curious parallels" between the evolution of languages and species, since in both cases new forms arise through gradual processes of descent with modification (Darwin 2005 [1871]:676). This view was endorsed by August Schleicher, the father of modern historical linguistics, who argued that the Indo-European languages were all derived from a single common ancestral language that gradually differentiated into separate branches like "Romance," "Germanic," etc. Pitt Rivers was convinced that similar processes could explain the evolution of material culture diversity, and accumulated a vast collection of objects from all over the world with the aim of reconstructing the "root forms" of human art and technology.

As well as sharing the same goals, Victorian biologists, linguists and anthropologists confronted many of the same problems. Foremost among these is the Problem of Missing Links, i.e. the lack of physical evidence to reconstruct the past. There are enormous gaps in the fossil record and the archaeological record, while the relatively recent origins of literacy mean that little is known about languages that were once spoken but are now extinct. However, while we cannot observe ancestral species and cultures directly, some of the features survive in the form of inherited traits (homologies) shared by their descendents. For example, humans, chimpanzees and gorillas all share a number of characteristics that were probably inherited from an as-of-yet undiscovered common ancestor, including relatively large brains and an extended period of infancy. Since many ideas and skills are, like genes, passed on from generation to generation, early anthropologists believed that many cultural traits could be similarly traced back to ancient societies (e.g. Tylor 1871). They even reconstructed lineages for specific artifact traditions that were directly modelled on the branching phylogenies used by biologists and linguists (Fig. 1).

In the middle of the twentieth century, this approach was attacked by anthropologists who argued that the laws of cultural inheritance are fundamentally different from the laws of biological inheritance: whereas physical traits can only be transmitted "vertically" from parents to their offspring, cultural traits can be borrowed "horizontally" from any number of sources. Moreover, while members of other species are not usually able to interbreed with one another, there are no inherent constraints on communication among humans belonging to different social groups. As the great American cultural anthropologist, Franz Boas, put it "animal forms develop in divergent directions, and an intermingling of species that have once become distinct is negligible in the whole developmental history. It is otherwise in the domain of culture. Human thoughts, institutions, activities may spread from one social unit to another. As soon as two groups come into close contact their cultural traits will be disseminated from one to the other" (Boas 1940:251). This contrast was famously depicted by Boas' student, Alfred Kroeber in his diagram "The Tree of Life and the Tree of the Knowledge of Good and Evil," which showed how the branches on the tree of life grow and then split, whereas those on the tree of culture are tangled together (Fig. 2).

While the majority of anthropologists and archeologists accepted Boas and Kroeber's arguments, it is only very recently that they have tested them using empirical data. Here, I describe a study of Iranian tribal textiles that was designed to test the competing models of material culture evolution proposed by Pitt Rivers and Boas. Following previous researchers (e.g. Collard et al. 2006), I shall refer to these models as "phylogenesis" and "ethnogenesis." Under phylogenesis, new cultural assemblages evolve through the bifurcation (splitting) of ancestral assemblages, whereas under ethnogenesis cultural assemblages evolve through borrowing and blending among neighboring traditions. Phylogenesis is analogous to biological speciation, whereas ethnogenesis can be compared to the mixing of pure metals to create alloys, or the separation and recombination of river channels (Moore 1994).

Case Study: Iranian Tribal Weaving[1]

The evolution of rug weaving is a classic example of the Problem of Missing Links. The craft is practiced throughout the Middle East and Central Asia, but the poor preservation of textiles over time means that very little is known about its origins and development. It is likely that rug weaving was developed by nomadic pastoralists, who have easy access to raw materials such as wool from their sheep and goats and the ingredients for dyes extracted from wild plants and insects. Furthermore, a textile-based material culture is well adapted to the tribes' mobile lifestyle since, unlike items made from wood or clay, textiles can be folded and rolled. Today, tribal women continue to manufacture a wide range of items, from the tents they live in to colourful rugs and bags for storing and transporting goods between winter and summer pastures. Each tribe has its own distinctive weaving style, although many designs and techniques are shared by different groups. It has often been claimed that these similarities can be traced back to common ancestral tribes. However, this hypothesis needs to be tested against the alternative possibility that contact and exchange among groups might have led to borrowing and blending among their weaving traditions.

Iranian textiles present an especially interesting context for investigating the phylogenesis/ethnogenesis problem because of the ways in which craft knowledge is transmitted among weavers. Between 2001 and 2003, I spent 6 months living among the tribes and interviewed over 60 weavers (all of whom were women, since weaving is an exclusively female activity) about how they learned to weave. The interviews revealed important differences in the ways that techniques and designs are transmitted. Techniques are almost always passed on from mother to daughter, usually at a young age (between 9 and 14 years old), over a period of several years. During their apprenticeship, young weavers also build up a repertoire of designs by collaborating with and imitating their mothers. However, whereas adult weavers rarely acquire new techniques once they begin to work independently, they frequently copy designs from their peers. We can therefore hypothesize that while the transmission of weaving techniques follow similar pathways to the transmission of genes (i.e. they are transmitted "vertically" between generations), the transmission of designs is likely to be much more complicated (since they can be transmitted "vertically" between generations and "horizontally" within generations).

To test this hypothesis, my colleagues and I used a phylogenetic technique known as cladistics. Cladistic analysis focuses on variation in the constituent parts, or "characters," of a group of taxa. In biological species, characters may

[1] For further information about the research summarized here, please refer to Tehrani and Collard (2009) and Tehrani et al. (2010).

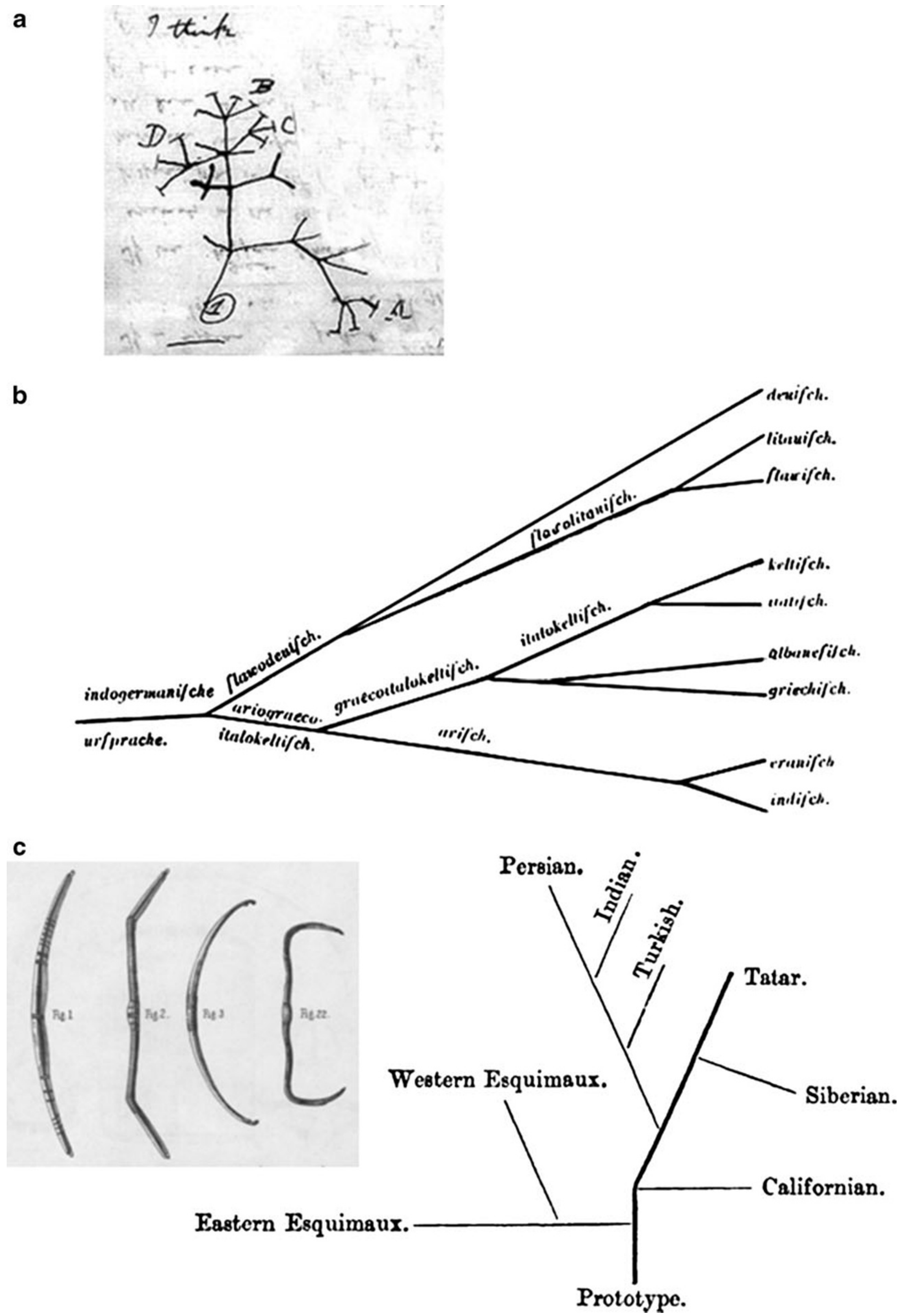

Fig. 1 Branching lineages drawn by Darwin (1837) for species (**a**), Schleicher (1869) for Indo-European languages (**b**) and Balfour (1889) for cross-bows (**c**)

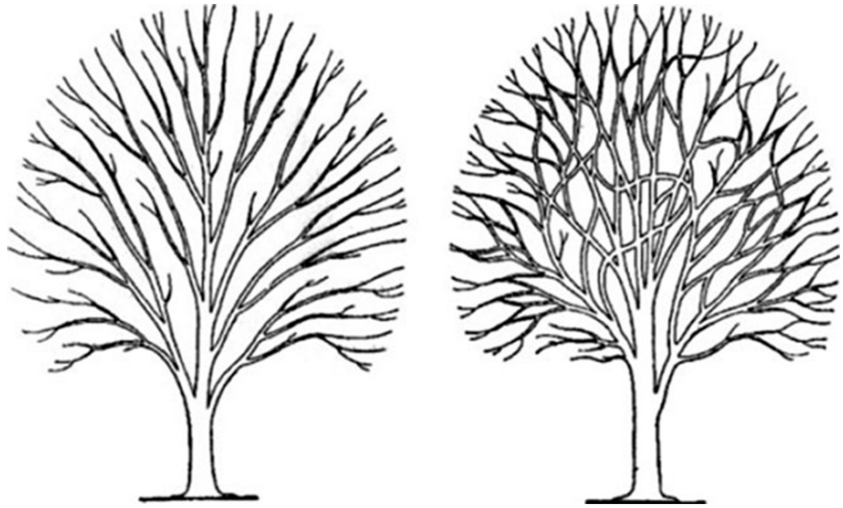

Fig. 2 Kroeber's "Tree of Life and Tree of the Knowledge of Good and Evil—That is, of Human Culture" (Kroeber 1948)

comprise DNA sequences or morphological traits. In languages, characters are usually based on lists of words, such as core vocabulary items. In the case of material culture, characters consist of stylistic and/or technological elements of assemblages, such as aspects of arrowhead design (O'Brien and Lyman 2003), forms of musical instruments (Temkin and Eldredge 2007), or, in this case, variations in textile ornaments and knotting techniques. It is worth emphasizing that the lack of naturally bounded units in material culture does not undermine the applicability of phylogenetic methods. As O'Brien et al. (2001) have pointed out, "whether a tooth represents one or multiple genes—replicators—is as yet unknown, but this does not hinder the efforts of palaeobiologists to determine and explain the evolutionary histories of the organisms whose phenotypic hard parts they study….Cultural traits conceived as ideas held in the mind of individuals are the replicators that are transmitted…If there is phenotypic change, and if over time enough variation is generated, cladistical analysis might indeed be able to detect the phylogenetic signal" (p.1134).

Cladistic analysis reconstructs relationships among taxa or classes by distinguishing characters that are evolutionarily novel (also termed apomorphic or derived), from those that were present in the last common ancestor of all the taxa under study, which are labelled ancestral or plesiomorphic. The presence of a derived trait in two or more taxa provides evidence that they are descended from a common ancestor of more recent origin than the ancestors they share with the other taxa under analysis. There are several methods to identify which traits are derived and which are ancestral, the most popular of which is outgroup analysis. An outgroup is defined as a taxon that shares a common ancestor with the taxa under analysis (the ingroup), but is of more distant origin than the ancestor the analyzed taxa share with each other. Since the outgroup does not share an exclusive common ancestor with any individual member of the ingroup, it follows that when a character occurs in two states among the study group, but only one of the states is found in the outgroup taxon, the former is considered the derived state and the latter the ancestral state.

Once the direction of change has been established for each character, the next step in a cladistic analysis is to construct a branching diagram that connects taxa according to their relative derived status. This diagram is known as a character cladogram. An example of a character cladogram is shown in Fig. 3 which concerns variations in a type of carpet ornament called a *gul*: the shape of the ornament is similar in all the taxa, but there are several differences in the interior design. In the outgroup taxon and taxon A, we can see what appear to be darts or birds protruding from the heart of the *gul*. In the three remaining taxa, these take a different form—that of clovers. Since the dart/bird form is found in the outgroup and the clover form is found only in the ingroup, we can infer that the clover evolved subsequent to the last common ancestor shared by the ingroup. In other words, the presence of the clover design provides evidence that taxa B, C, and D share a common ancestor that is not shared with taxon A. Studying the *gul* of these three taxa more closely, we can see that it is possible to make further distinctions. Thus, in the case of taxa C and D, the clover is divided into two stems; whereas in taxon B, the clovers have only one stem. Again, this suggests that the clover design has evolved in two forms. If we assume that C/D form is derived with respect to the B form, then this would imply that they share a common ancestor that is not shared with taxon B (although it should be noted that it is equally possible that the B form is derived, in which case we cannot be sure that C and D are more closely related to one another).

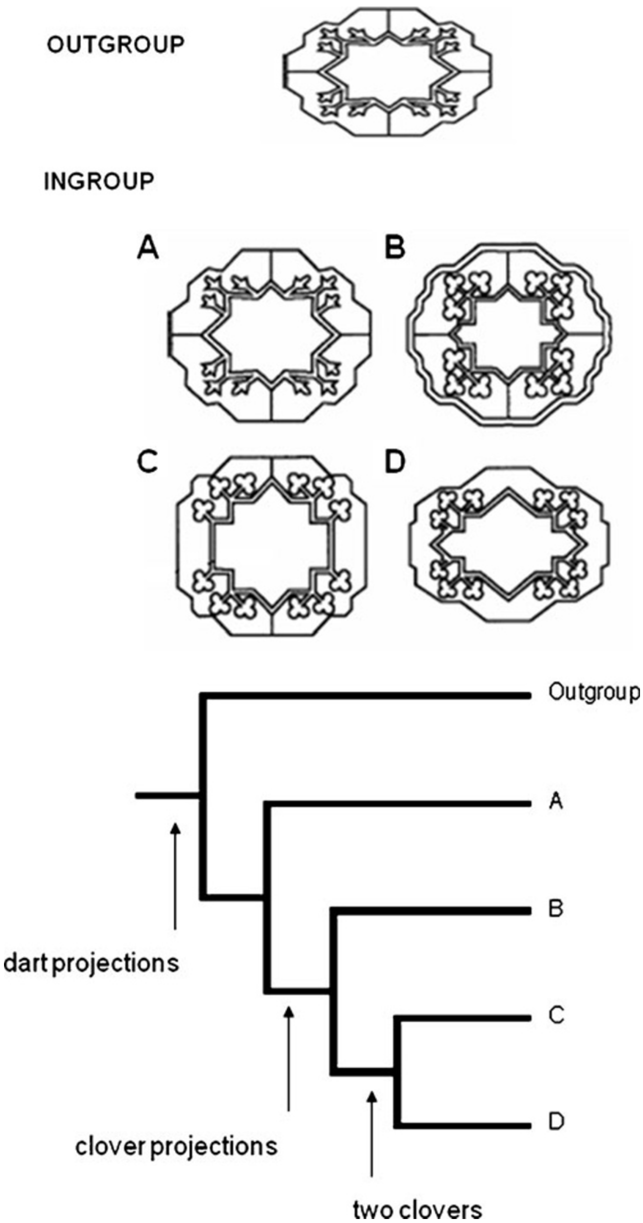

Fig. 3 Character cladogram for a rug ornament known as "gul," which varies from tribe to tribe (**a**–**d**)

If descent and modification were the only cause or source of similarities among taxa, then all the character cladograms would be compatible with one another. Normally, however, a number of the character cladograms will suggest relationships that are incompatible because, as noted earlier, common descent is not the only source of similarity among taxa. How can we sort true family resemblances (known in phylogenetic terms as homologies) from similarities resulting from other processes such as independent evolution and borrowings (homoplasies)? The cladistic approach deals with this problem by generating an ensemble or consensus cladogram that is consistent with the largest number of characters and therefore requires the smallest number of evolutionary changes to account for the distribution of character states among the taxa. This approach is based on the principle of parsimony, the methodological injunction that explanations should never be made more complicated than necessary. Characters that are consistent with the ensemble cladogram can then be classified as homologous (i.e. similarities due to common descent) while those that are inconsistent with it can be classified as homoplastic (i.e. similarities that are due to other processes, such as borrowing and blending among lineages).

If it is true that horizontal transmission leads to complex and tangled patterns of cultural evolution, then, based on the description of craft learning above, we would predict that similarities among the designs used by Iranian tribes would be much more homoplastic than similarities among their techniques. This is because designs are transmitted both vertically and horizontally, whereas techniques are only usually transmitted vertically. We tested this prediction through a cladistic analysis of 122 decorative and technical characters from six tribal groups, the Yomut, Shahsevan, Qashqai, Boyer Ahmad, Papi and Bakhtiari. I employed a prehistoric Western Asian textile assemblage (from the Pazyrk Valley, Siberia, fourth to fifth century BCE) as an outgroup (Fig. 4). The first stage of the analysis inferred the most parsimonious tree for the textile assemblages. The second stage of the analysis examined how well decorative characters (n=80) fitted the tree compared to the technical characters (n=42). The goodness-of-fit for each set of characters was measured using the Retention Index (RI), which calculates the number of homoplastic changes a cladogram requires that are independent of the number of characters in the data (for a more detailed description, see Farris 1989).

Results

The first stage of the analysis yielded a single most parsimonious tree, shown in Fig. 5. It suggests that the material culture assemblages of the Shahsevan, Qashqai, Boyer Ahmad, Bakhtiari and Papi are descended from a common ancestor that is not shared by the Yomut. The weavings of the Qashqai, Boyer Ahmad, Bakhtiari and Papi comprise a clade that excludes the Shahsevan. The branches that are nested within this clade suggest that the Boyer Ahmad, Bakhtiari and Papi assemblages are more closely related to one another than they are to the Qashqai assemblage, and that the weavings of the Bakhtiari and Papi share an exclusive common ancestor.

When all the characters in the dataset were taken into account, the Retention Index of the cladogram was 0.59. When only technical characters were included, the RI was

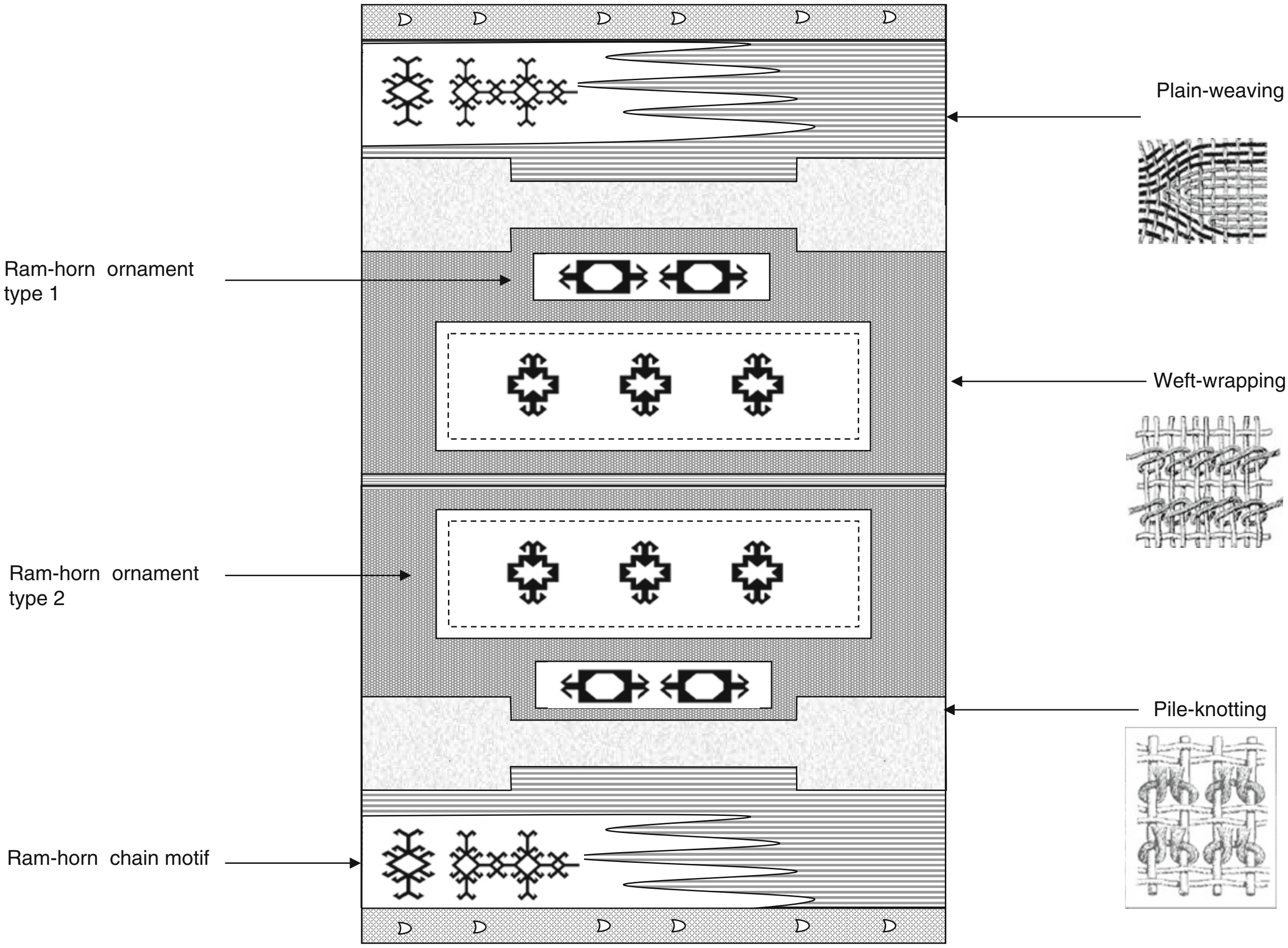

Fig. 4 Examples of decorative and technical characters extracted from a saddle bag

0.588. When only the decorative characters were included, the RI was 0.593. This result contradicted the prediction that designs are more likely to be homoplastic than techniques. Instead, it appears that the phylogenetic signal in designs is at least as strong as the signal in techniques.

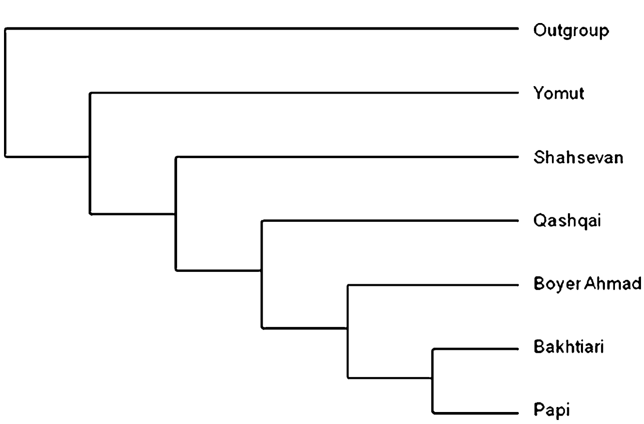

Fig. 5 Most parsimonious tree returned by the cladistic analysis of the tribal assemblages

Discussion

The results of these analyses suggest that the majority of similarities among Iranian tribal material culture assemblages can be explained by a tree-like model of descent with modification. The RI of the complete dataset, the technical characters and the design characters were all around 0.59. Recent computer simulations of cultural evolution suggest that an RI of this value can be interpreted as strong evidence of phylogenesis (Nunn et al. 2010). In the case of weaving techniques, a good fit with the tree model was expected because, like genes, these traits are transmitted vertically between parents and offspring. However, the finding that designs fitted the tree just as well, if not better, was highly surprising given that they are often transmitted horizontally among weavers. Following Boas, Kroeber and most anthropologists and archeologists of the last century, we would have expected the histories of these traits to be much messier and more complicated. Yet, on the contrary, it seems that the evolution of textile designs has been more influenced by phylogenesis than ethnogenesis.

To explain this counter-intuitive result, it is important to remember that even when cultural traits are transmitted horizontally, it is usually far easier to access knowledge from members of the same community than from members of different communities. In this case, there are two specific factors that limit the ability for adult weavers to share designs with women from other tribes. The first is marriage norms. Iranian tribal women usually move from their own village to their husband's village after marriage. This brings them into contact with new potential influences as they socialise with their husband's female relatives and neighbours. However, while the movement of women through marriage contributes to the flow of designs within tribes, it does not lead to exchanges between tribes due to the norm of endogamy, which prohibits intermarriage between tribes. Secondly, broader social norms prevent women in these communities from travelling very far by themselves. Since tribes are territorial, this means that weavers generally stay within the borders of their own group and do not have many opportunities to meet weavers from other groups.

These examples chime with arguments made by the anthropologist William Durham, who has pointed out that, whereas transmission among members of the same group is facilitated by their physical proximity, common language and shared cultural norms, communication among members of different groups is often impeded by the existence of ecological boundaries, language barriers, endogamy and xenophobic prejudices (Durham 1992). Durham suggests that these "Transmission Isolating Mechanisms" may constrain the exchange of cultural information among societies much as reproductive isolating mechanisms prevent gene flow between species. Consequently, despite the clear differences between cultural transmission and genetic transmission at the individual level, cultural evolution at the level of the group may often be very similar to the evolution of species diversity, just as Pitt Rivers asserted. In support of this, a recent study by Collard et al. (2006) compared the "treeiness" of 21 cultural and 21 biological datasets and found that the range and mean RIs were highly similar.

Of course, this is not to deny that many cultural behaviors, beliefs and ideas—from antibiotics and gunpowder to the novel and pop music—have spread across countries and continents in a matter of decades, if not years. The pace and reach of cultural diffusion has increased dramatically with the advent of modern communications media and economic globalization. Perhaps our cultural differences will eventually dissolve altogether in the heat of this melting pot. Yet even then it would be a mistake to draw too strong a distinction between cultural and biological evolution: after all, beyond the vertebrates, hybridization is a common and important evolutionary process. Indeed, it increasingly looks like the differences within genetic and cultural systems are far more important than the differences between them, and that greater cross-fertilization between disciplines would be fruitful for social scientists and natural scientists alike.

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