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## BRIEF REPORTS

### *A phylogenetic approach of mythology and its archaeological consequences*

By JULIEN D'HUY

Mythology has provided apparently solid and reliable clues to the meaning of Saharan rock art (see e.g. Le Quellec 2004; Le Quellec et al. 2005). Yet to reveal the mythological meaning concealed in pre-Historic images is an exceptionally difficult task. Rock art images may represent the versions of a myth which are either unknown or diverge substantially from the ones recorded in written sources. As such they may be representative of versions belonging to previous, more archaic stages of development (Devlet and Devlet 2005: 233). This is why we suggest a new and alternative method to study ancient mythology.

There are many parallels between the process of biological and mythological evolution (d'Huy 2012a, 2012b, 2012c). For instance, like genes, mythemes are discrete heritable units, pass from one generation to the next and change slowly. Like biological species, myths evolve into a series of related forms. A number of other parallel features exist, e.g. natural selection vs social selection and trends; biological mechanism of replication vs teaching, learning and imitation; genetic mutations vs innovations and structural transformations; and horizontal gene transfer vs borrowing. Based on similar parallelisms between genetic and other cultural areas, tools from evolutionary biology are being imported to analyse linguistic and cultural phenomena (Nunn 2011). Additionally, some of the most fundamental questions in evolutionary science involve reconstructing ancestral states (Nunn 2011). However, despite these parallels and common goals, prehistorians have not used the quantitative phylogenetic methods that have revolutionised evolutionary biology to reconstruct ancient mythology that can explain rock art.

We used recently a phylogenetic algorithm, Bio-Neighbor-Joining (implemented in the program Splits Tree 3.2), to explore global patterns of the Pygmalion mythological family in Africa. In such stories, a man falls in love with an image of a woman — often a wooden doll. The man believes that it is a real woman; it

becomes alive and marries the master. We constructed a database including the typological variations of the Pygmalion versions (d'Huy 2012a). The presence or absence of mythemes for each version was coded as 1 or 0, respectively, to produce a binary matrix of 58 mythemes in 13 versions. Our results implied that the diversification of Pygmalion versions was consistent with a human expansion from the Afro-Asiatic region to southern Africa ~2000 years ago (Henn et al. 2008).

According to anthropological studies (d'Huy in prep.), we postulate that the more two myths diverge, the more their 'genetic' relationship is distant, geographically and temporally. The same matrix was re-analysed in the phylogenetic package Mesquite 2.75, using a simple model to calculate the parsimony tree-length of the tree and matrix. Character matrices were supplied from data files and the tree was rearranged by sub-tree pruning and regrafting. Finally, we rooted the tree. Archaeological and mythological evidences (d'Huy 2009, 2011a, 2011b; d'Huy and Le Quellec 2009; Le Quellec 2012) agreed that Sahara (Berbers) was a good homeland for a myth that tells us that an image can become alive. A fear of animation may explain why wild animals that constitute a threat, such as felines, elephants and crocodiles, were often represented incomplete in the Libyan rock art: they also were less dangerous and could no longer come alive. One other procedure that constantly appears is that dangerous animals were represented pierced with arrows or simply not represented (d'Huy 2009; d'Huy and Le Quellec 2009; Le Quellec 2012). Moreover, the Berber myths of Pygmalion seem to be much older than a Muslim iconoclasm (d'Huy 2011a) and the Ovidian version of the story (d'Huy 2009). Additionally, a Kabyle version seems to inverse the Egyptian *Tale of two brothers* that dates from the reign of Seti II, who ruled from 1200 to 1194 BP; according to the structural method (Lévi-Strauss 1983), the Egyptian tale may be the product of an old Egyptian borrowing to their Berber close neighbours (d'Huy 2012a). Yet rooting the tree with the Kabyle (Berber community in northern Algeria) version could be claimed to bias the analysis in favour of our own theory. We thus rooted the tree with two versions of the mythological family: the Greek and the Bara. Both versions were closely related (d'Huy 2012a) but also were the more geographically distant. Additionally, the Bara settled on an island that did not allow for great population

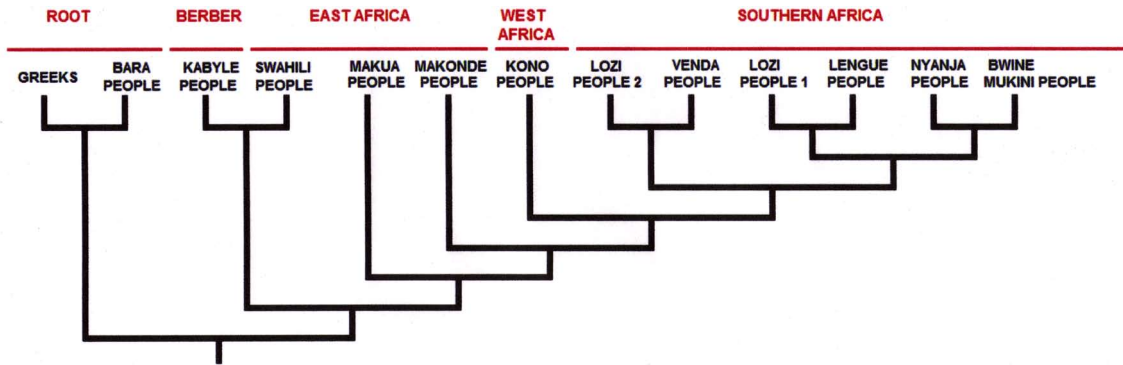


Figure 1. Phylogenetic tree of Pygmalion mythological family inferred with Mesquite 2,75.

expansion and mythological diversification. Similarly, the Greek version has been borrowed by the Greeks from the Berbers (d’Huy 2011b) and remained isolated for most of its history from African versions. So the Greek and Bara versions probably preserve one of the first versions of the Pygmalion family. The tree is shown in Figure 1, and its topology is in agreement with the tree obtained by the Bio-Neighbor-Joining algorithm and a Berber origin of the myth (d’Huy 2012a). The tree also shows a diffusion of the tale from the Afro-Asiatic region to southern Africa.

An analysis of the tree produced a consistency index of 0.60 and retention index of 0.52. The CI is commonly used to measure the extent of homoplasy (resemblance not due to inheritance from a common ancestry, convergence) and the RI is used to measure synapomorphy (derived states shared by two or more taxa and their most recent common ancestor) in the data. High CI and RI values (for example, greater than 0.60) are usually indicative of low horizontal transmission (Nunn et al. 2010), yet a RIs corpus for biological data sets usually ranges from 0.35 to 0.94 (Lycett et al. 2009). Consequently, horizontal transmissions (borrowings between neighbouring tribes) did not seem a problem for the phylogenetic mythological comparative method (d’Huy in prep.), because it appeared that the majority of mythemes were transmitted vertically from parents to daughter populations and are consequently relatively conservative. A lower CI or RI would refute this assertion.

The orderly and geographically consistent phylogenetic signal shows that phylogenetically analysed mythological pattern can preserve a signal that is consistent with old human migrations. The results show a diffusion of the tales from the Nilo-Saharan region to southern Africa and this is consistent with the geographic distribution of the E3b1f haplogroup. The genetic data suggest an expansion through Tanzania to southern-central Africa, independent of the migration of Bantu-speaking peoples along a similar route ~2000 years ago (Henn et al. 2008). Whereas memes can travel without migration, myths seem to be related to the people’s history (d’Huy 2012a, 2012c, in prep.). Consequently, the study of myths can be useful to reconstruct large and ancient movements of populations. To be accepted, our results imply that the past populations did not get very far, but this is in agreement with the E3b1f diffusion and the analysis of microsatellite data.

What was the ancestral state of the Pygmalion myth? We recreated the first state for the Pygmalion family by applying to each mytheme of this family maximum likelihood or parsimony reconstructions (i.e. phylogenetic reconstruction methods). We only selected highly confident reconstructed mythemes (probability of more than 75% with the maximum likelihood method and of 100% with the parsimony method). Figures 2 (maximum likelihood) and 3 (parsimony) provide an example of how we did this; the analysed mytheme was ‘the sculptor is a human

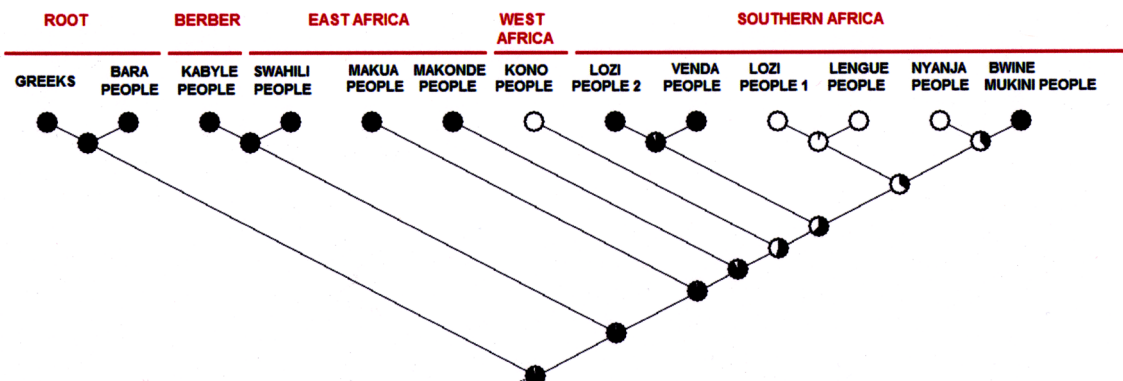


Figure 2. Ancestral reconstruction of the mytheme ‘the sculptor is a human being’ using maximum likelihood.

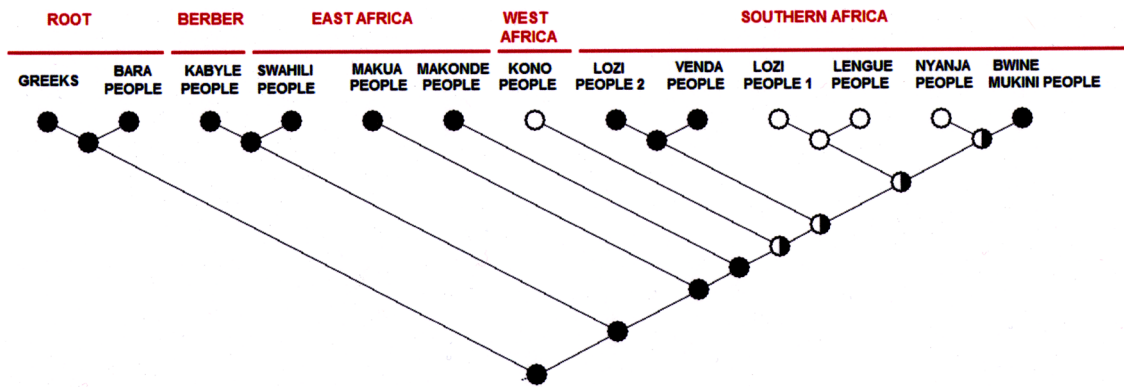


Figure 3. Ancestral reconstruction of the mytheme 'the sculptor is a human being' using parsimony.

being'. For each mytheme, both maximum likelihood and parsimony reconstructions were similar. Maximum likelihood reconstruction with model Mk1 was the following tale: a man makes a wooden statue from a tree-trunk; he or another man clothes it; the statue is seen as a real person and it becomes alive, thanks to another person. A fundamental detail was added with parsimony reconstruction: a man falls in love with the statue. So the protomyth is reconstructed as simplified version of the descendant versions. Of course, it is important to remember that the protomyth is likely to be as rich in complexity as the versions upon which the reconstruction is based.

The protomyth can itself be used to make inferences about the behaviour of its Saharan speakers. It informs us about what they were communicating and documents evidence for a strong belief in the possibility for an image to come to life (as documented by archaeological evidences: d'Huy 2009; d'Huy and Le Quellec 2009; Le Quellec 2012).

The phylogenetic model used in this paper integrates archaeological, mythological and genetic data. It allowed us to make inferences about human migrations; test the impact of mythological borrowings between neighbouring tribes; and reconstruct ancestral states of a mythological family with quantification of confidence and implication in the rock art interpretation.

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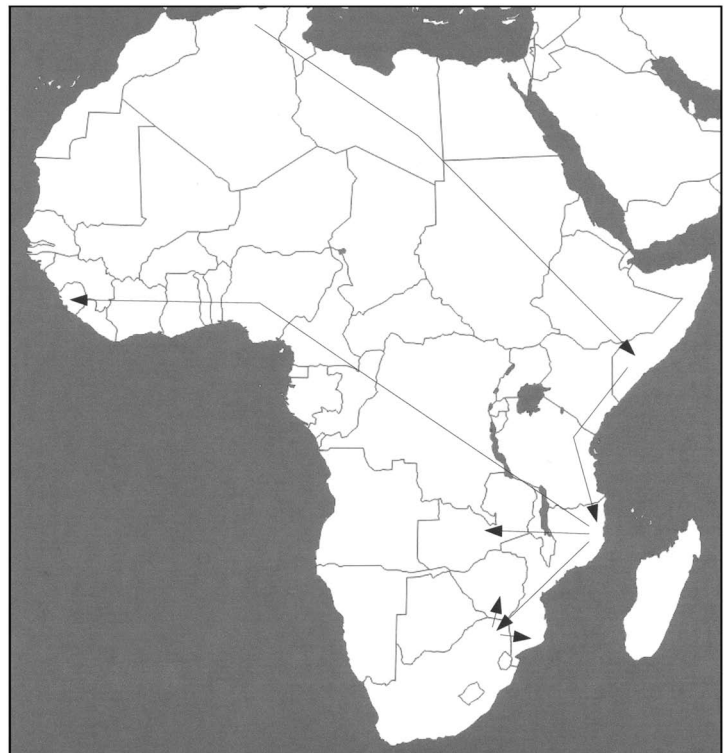


Figure 4. Phylogeography of the Pygmalion myths expansion. Locations of cultures are connected with the phylogenetic tree.

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