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# How Did the First Humans Perceive the Starry Night? On the Pleiades

Julien d'Huy, Yuri Berezkin

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## How Did the First Humans Perceive the Starry Night? – On the Pleiades

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*Abstract: This study applies phylogenetic software to motifs connected with the Pleiades as identified in Yuri Berezkin's database, The Analytical Catalogue of World Mythology and Folklore. The aim of analysis is to determine which, if any, of the analysed motifs are likely to have spread in conjunction with the earliest migrations out of Africa and to the Americas. The Pleiades analysis is compared to an analysis of Orion motifs.*

Numerous studies have shown that many particular episodes and structural elements of mythological narratives were able to subsist over very long periods of time and that the relations which once existed between peoples separated by time and space can be interpreted through such narrative evidence (e.g. Gouhier 1892; Bogoras 1902; Jochelson 1905; Hatt 1949; Korotayev et al. 2011; Witzel 2012; Berezkin 2013; 2017; Le Quellec 2014). Mainly three types of comparative methods have been used to reconstruct narrative episodes and fragments of the worldview known to people who lived in particular epochs and regions: distribution-based studies, structural studies and phylogenetic approaches. The purpose of the present paper is to show the same by using phylogenetic methods with reference to a specific case. Here, a corpus of motifs will be statistically studied to highlight the evolution of the mythology around the Pleiades. These stars form one of the most frequently and prominently recognized constellations among the hunter-gatherer societies of both hemispheres (Hayden and Villeneuve 2011). According to many authors, including Claude Lévi-Strauss (1971a) and George E. Lankford (2007), beliefs surrounding this constellation are particularly likely to be rooted in a very early period. The mythology of the Pleiades could thus be a good indicator of extremely early long-distance migrations.

### **Comparative Methods**

Before proceeding to the analysis, the comparative method used here will be briefly contextualized in relation to different types of comparative methods that have been used in long-term diachronic studies of mythology. The types of methods will be discussed in terms of myths as narrative plots associated

with mythology and mythological motifs as elements of narrative smaller than a plot. Discussion of the methods reviewed in terms of mythology reflects the focus of the present paper, whereas uses of comparative methods reviewed are not limited to studies of myths and mythological motifs.

### *Areological Approaches*

A method based on the study of the distribution of various myths and mythological motifs to deduce their history and their age can be described as an areological method or areology. Such methods show the clustering of different traits, motifs or versions of the same myth in order to draw conclusions about their history. The basic idea of areological methods is that the geographical distribution of a particular myth or motif is a historical outcome of its spread over time. The formalization of areological methods for the comparative research of myths began already at the end of the 19<sup>th</sup> century, with the Geographical Method of Julius Krohn, which was the foundation of what became known as the (Classic) Historical-Geographic Method (Krohn 1926; see also Frog 2013). Areological methods are often used within a culture or across cultures to consider developments and exchanges that have occurred within a few centuries or a millennium of the documented traditions. On the other hand, an extensive distribution of a narrative across both Eurasia and North America normally suggests a much earlier background to the geographical relation going back to the first human migrations to the New World in the Palaeolithic, because such myths could not otherwise be communicated across these continents until recent centuries in contacts that would not normally account for such distributions of the myth.

For instance, two different Eurasian versions of the Cosmic Hunt show Eurasian–North-American parallels at the level of minor details. According to the first version, the object of the hunt and the hunters are associated with Ursa Major, the Big Dipper or Plough. Three stars of the handle of the Big Dipper are hunters and the dipper itself is an animal; Alcor, a star that appears alongside the star at the end of the Big Dipper’s handle, is a dog or a cooking pot. According to the second version, the object of the hunt and the hunter are associated with Orion. Orion’s Belt represents one or (more typically) three deer, antelopes, mountain sheep or buffaloes; the hunter is Rigel or another star below Orion’s Belt; the hunter’s arrow has pierced the game and is identified either with Betelgeuze or with the stars of Orion’s Head. The correspondences between the Eurasian and the North-American traditions are at a level of detail and complexity that can only be explained by a remote historical relation (Berezkin 2006; 2012; 2017: 73–116, Figures. 21, 25, 26). Remote historical relations have been identified for several myths and motifs, such as the motif of a dog guarding the river of the death (Berezkin 2005), the battle between dwarfs and cranes (Berezkin 2007a; Le Quellec & d’Huy 2017), and diverse narratives surrounding the origin of death (Le Quellec 2015a).

In addition to considering the distribution of single myths or motifs, areal studies can consider the distribution of myths in relation to one another. Two independent studies also show a complementary distribution of myths of the origin of humanity from underground, and of an earth-diver raising dry land from the bottom of the ocean following a succession of dives. Myths of the origin of humanity from underground are concentrated in the southern hemisphere, while the earth-diver myths are concentrated in the northern hemisphere, with few cases where they overlap. Both studies conclude that the narratives had two stages of diffusion: the myths of the origins of human beings followed one or several of the first migrations of homo sapiens out of Africa, after which the earth-diver narratives emerged and were carried in subsequent migrations from Eurasia to Northern America (Berezkin 2007b;

2010; Le Quellec 2014; 2015b). Binary, complementary distribution is found for numerous narratives (Berezkin 2013; Witzel 2012) and corresponds to what we know about the first human migrations.

### *Structural Approaches*

A structural method for historical reconstruction defines a myth as the sum of all its versions. It is always possible to order all the variants of the same myth in a series, forming a group of permutations where the variants are related to one another through a series of transformations. These transformations can include the change of an element into its opposite, like *here* becoming *there* without altering a tale’s abstract structure (Lévi-Strauss 1955).

For example, Claude Lévi-Strauss (1971a: 20) compares a myth of the Greeks and a myth of the Takelma. In both, the raven is sent to remedy the lack of celestial water by means of the only available terrestrial water: a fountain (Greek) or an ocean (Takelma). Owing to greed (Greek: the bird waits for the fruit to ripen) or laziness (Takelma), the bird neglects its mission. As a punishment, the raven will be thirsty during the summer and thus his voice becomes hoarse because of his parched throat. The Greek myth is connected to the eponymous constellation Corvus [Latin ‘Raven’], which marks the end of the dry season. This myth corresponds to a myth from the Xerente people of South America about the origin of Orion and the Pleiades, constellations of summer months in South America that correspondingly mark the beginning rather than the end of the dry season. Similarly, the Blackfoot have a myth very close to that of the Xerente to explain the origin of the Pleiades, heralding a rainy period. Additionally, in North-West America, Raven is often associated with alternating tides, itself often associated with periods of drought and humidity, and of abundance and scarcity. Lévi-Strauss (1971a) concludes that it is not inconceivable that the same myth, transformed through the inversion of one of its elements in relation to the latitude and regional climate, or another myth of the same type, was used to explain the origin of a constellation linked to the dry season in all of these cultures. By comparing these, he asserts that the different versions could ultimately derive from the survival of an ancient myth’s underlying structure.



### *Phylogenetic Approaches*

Phylogenetic classification is a system of classification of species based on the degree of genetic relationship between them. Phylogenetic approaches to myths basically seek to organize relations into a family tree on the biological model. This type of stemmatic method and associated biological metaphor was used for the study of myths already prior to the term 'phylogenetics' in Folklore Studies, known especially through the Classic Historical-Geographic Method with its background in Philology (Krohn 1926; Frog 2013). In *The Tale of Cupid and Psyche* (1955), for example, Jan-Öjvind Swahn used this type of method to examine the transmission of Aarne-Thompson tale-types AT 425 and 428. Today, phylogenetic approaches are being reinvented through the adaptation of software developed for genetic research to studies of culture. Phylogenetic trees are not generated for their own sake: they are considered in relation to current knowledge and theories about the transmission and variation of traditions (Frog 2013). The relationship between language and other aspects of culture such as mythology and religion is now recognized as more complex than has often been assumed in earlier scholarship (Frog, this issue). The spread and transformation of a myth are recognized as separate processes: a myth may first spread and then undergo localized transformations in relation to cultural contacts, social change or difference in the local ecology, or transformation may be integrated into the process of spread itself. Although the processes concerned are obscure in the remote past, they are processes that occur socially and may therefore involve creating relations of sameness and difference with other groups. What spreads may also not be a myth as a stable plot; it may be only a motif, such as that of the sky-woman and of the mysterious housekeeper (d'Huy 2016d), although it is also possible that motifs may be all that remains recognizable in the data from plots that spread in the extremely remote past.

The first to have applied statistical and phylogenetic software to myths and folktales is, to the best of our knowledge, Thomas Abler. Abler used phylogenetic software to classify 41 versions of the Iroquoian myth of the

creation of the world in a 1987 article. Most of the clades in the resulting stemmas or trees were shown to correspond to tribal or national traditions. The idea of using phylogenetic software to classify versions or types of narratives was taken up again by Jun'ichi Oda (2001) and later by Jamie Tehrani (2013). Since 2012, one of the present authors (JdH) has used statistical and phylogenetic tools to explore folktales in a new way. The software construes a synchronic classification of diverse versions of a same myth. Those synchronic relations are organized in a stemmatic hierarchy that suggests the myth's diachronic evolution from a common ancestor. This perspective on diachronic evolution offers the possibility of assessing where the diffusion of a myth may mirror the first human migrations, to quantify the proportion of borrowings and innovations in different branches of its evolution, and to reconstruct first narratives, some going back to the upper Palaeolithic, and potentially even to the era of the first migrations from Africa. This method has been applied to numerous families of myths, and folktales among which may be mentioned the Cosmic Hunt (d'Huy 2012a; 2013b; 2016c), the narrative of Polyphemus (d'Huy 2012b; 2013a; 2015b), the narrative of the perverted message (Le Quellec 2015a) and of the emergence of humanity (Quellec 2015b), narratives linked to Balor-type creatures (Lajoie 2015), the motif of the sky-woman and of the mysterious housekeeper (d'Huy 2016d), and the fight between dwarfs and birds (Le Quellec & d'Huy 2016). Many of these analyses are of the themes but are based on very different corpora (three different databases for the Cosmic Hunt and for Polyphemus), offering a check of results. Results have also been checked by comparing them to what has been found from other non-statistical comparative methods.

Of course, myths are not genes, and software borrowed from biology can only provide a tool to organize myths (Abler 1987; d'Huy 2012a), traditions (d'Huy 2015a; da Silva & Tehrani 2016) or motifs (d'Huy 2016a) as data. If we accept that the more common features shared by two traditions or myths, the more likely they are to be related, then it is also possible to build diachronic 'trees' of myths or oral traditions that are considered to be most likely related owing to the number and

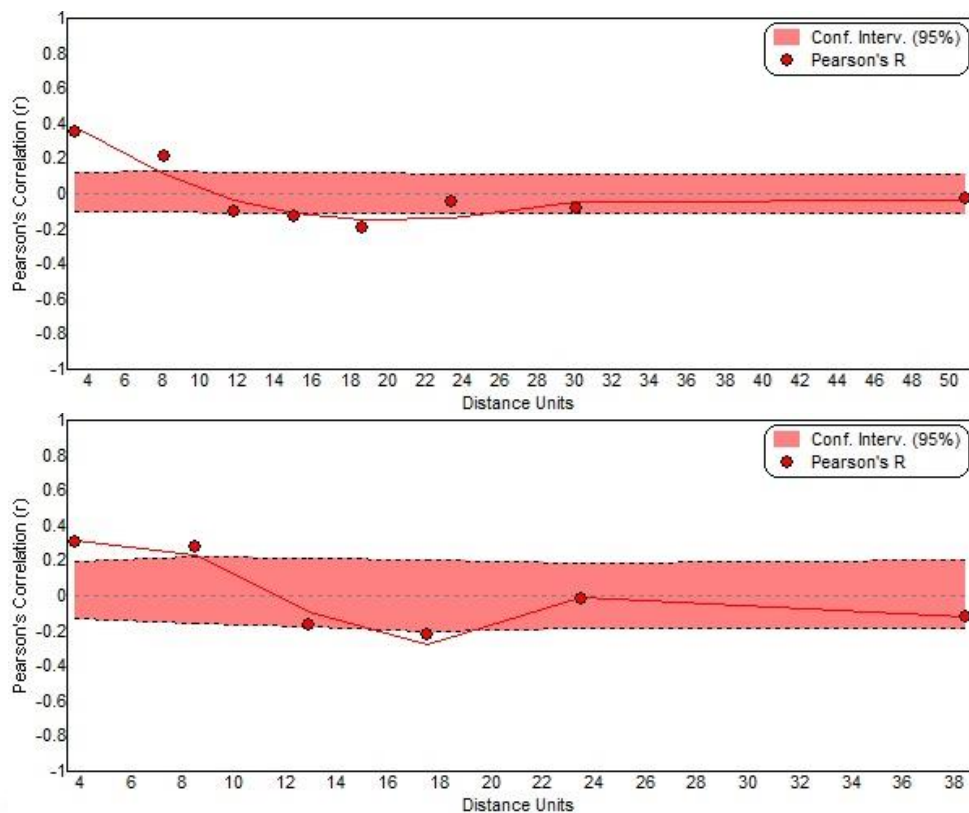


Figure 1. Mantel correlogram from the Lankford's dataset (the Mantel correlogram separates the geographic space into sequential distance classes to identify the changes in the strength of correlation with the distance). Spatial correlogram plot showing correlation coefficient between individual traditions' Jaccard distance values and geographical distance. The bootstrapped 95% confidence error bar is also shown. 1a. Ethnic groups exhibiting three or more motifs (24 ethnic groups; Global Pearson's  $r$ , which measures the linear correlation between two variables  $X$  and  $Y$  and has a value between  $+1$  as a total positive linear correlation and  $-1$  as a total negative linear correlation;  $0$  is absence of a linear correlation.:  $0.176$ ); 1b. Ethnicities exhibiting four or more motifs (15 ethnic groups; Global Pearson's  $r$ :  $0.3$ ).

complexity of their shared features. Note that whatever the distance between two versions or traditions of the database is, the shared features should be sufficiently numerous to make random proximity impossible. The phylogenetic message present in the database should also be checked, for example with alternative methods or different data sets.

### Grounds for the Study

As noted above, beliefs connected with constellations have been considered likely to be historically enduring even if they undergo transformations over time, making them particularly interesting for long-term diachronic study. To test this hypothesis, we used Lankford's (2007: 263–264) table 11.1 "Occurrences of major motifs and subtypes", which identifies the presence or absence of the eighteen star-related beliefs he identified among North American cultures (Eurasian cultures in the table were not considered).

These were taken as data without prior clustering. Using Berezkin's database, geographical locations were identified for each linguistic-cultural group where relevant motifs have been found. A Mantel test (Jaccard's coefficient matrix, 10,000 permutations) was applied to this data using SAM v.4.0 (Rangel et al. 2010). First, only the 24 ethnic groups with at least three of the eighteen motifs were analyzed to avoid sample bias: some of these cultures have been studied much more than others, which may account for 'gaps' in certain mythologies where only one comparable type was found. Then, for the same reason, only the 15 ethnic groups with at least four of the eighteen motifs were studied. Question marks in Lankford's table have been treated as absence and a Jaccard coefficient matrix has been used. Robert M. Ross and Quentin D. Atkinson (2016) have examined the effect of distance in folktale inventories of 18 hunter-gatherer cultures of Siberia, Alaska, Canada,

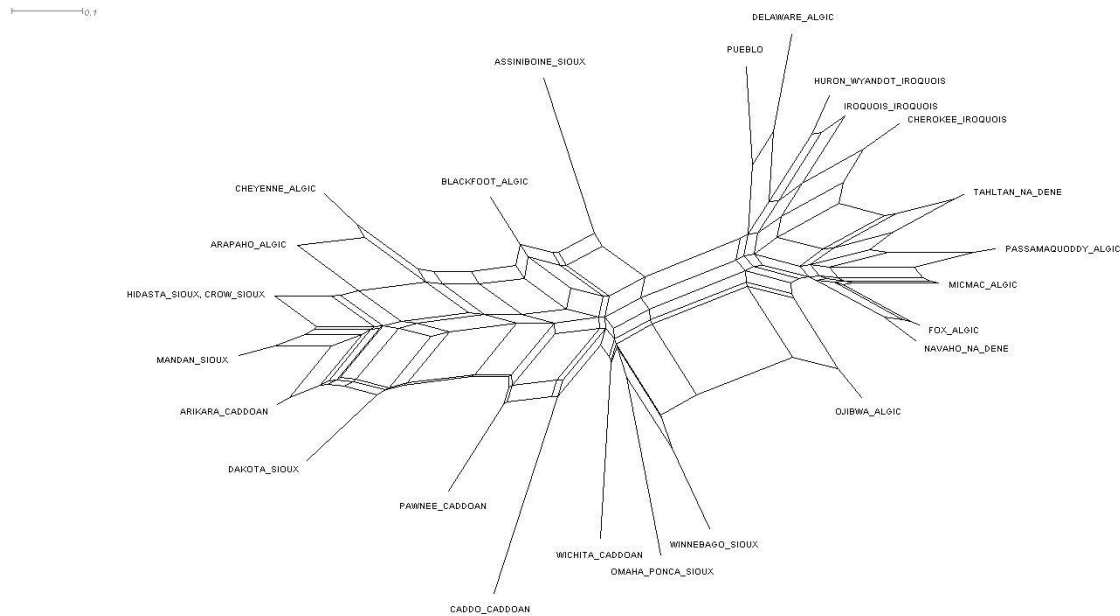


Figure 2a. NeighborNet based on the Jaccard folktales distance matrix for the 24 ethnic groups in Lankford's dataset exhibiting three or more motifs. Box-like structures indicate a conflicting signal (i.e. suggesting similar independent inventions, borrowings).

and Greenland, spread across 6000 kilometers. They found that linguistic relatedness and geographic proximity were independent factors in predicting shared folktales, calculating that geographical distance is related to 25.50% of variance in the inventories. In Lankford's data, geographical distance appears related to only 3.09% of the variance in the first dataset ( $p=0.004$ ), and 9% ( $p=0.002$ ) in the second (Figure 1a–b). In other words, geographical distribution does not seem to be a significant factor in which groups share motifs. This result is far lower than in Ross and Atkinson's study, which is a potential indicator that the distribution of relevant motifs is an outcome of their longer history rather than attributable to recent contacts between adjacent populations and their networks. This preliminary finding is a potential indicator of the greater endurance of star-related beliefs among hunter-gatherer cultures. Similar conclusions have been reached in studies of d'Huy (2015a) and da Silva and Tehrani (2016), although these must be regarded with caution because their datasets were based on the Aarne–Thompson–Uther tale-type index, which is inadequate for such analyses (see Berezkin 2015; d'Huy et al. 2017). The small dataset and the large geographic distances between the groups serve as a reminder that caution is needed when attempting to interpret

this data. Nevertheless, the analysis of data by George Lankford suggests strong connections in star-beliefs across North American cultures that would at least be consistent with deep historical roots in these traditions.

Further perspective on this data is provided by a NeighborNet (Jaccard; Bryant & Moulton 2004) analysis constructed with *Splitstree* 4.14.4. (Huson & Bryant 2006) in order to visualize specific relationships among traditions of the linguistic-cultural groups (Figure 2a–b). The network shows a low mean delta score (0.32 for the first database; 0.23 for the second). In general the closer to zero the delta score is, the more the data will exhibit a straightforward stemmatic tree. These scores can be compared to the mean delta-score of the principal language families of the world. These language families are generally accepted as analysable in tree-like relations, and the mean delta score within these language families has been calculated by Søren Wichmann et al. (2001) as 0.31. Comparison with the scores reflected in Figure 2a–b suggests that the transmission of these mythological traditions is more tree-like than for many language families. Moreover, the NeighborNet analysis shows a low correlation between the mythologies and language family. Such low correlation presents the possibility of mythological substrate influence which

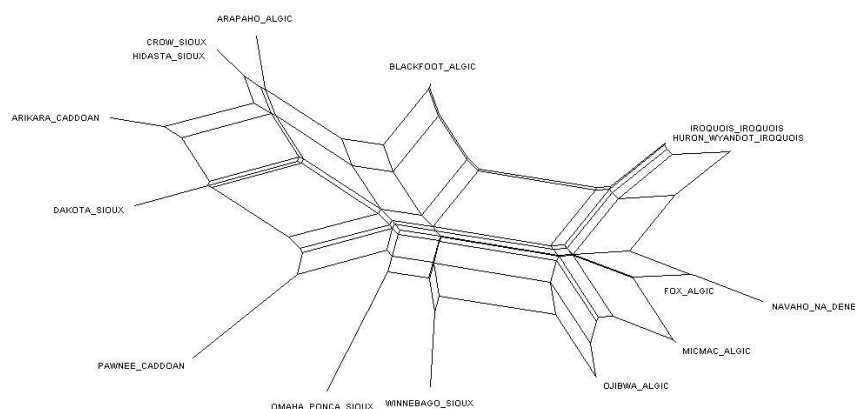


Figure 2b. NeighborNet based on the Jaccard folktale distance matrix for the 15 ethnic groups in Lankford's dataset exhibiting four or more motifs. Box-like structures indicate a conflicting signal (i.e. suggesting similar independent inventions, borrowings).

antedates the spread of the language families (cf. also Frog, this issue, on the spread of Proto-Sámi). Geographical distance appears as a strikingly low factor in the Mantel tests, suggesting that contacts between groups have not been significant in the distribution of these traditions. This observation, coupled with the common 'Amerindian' nature of the myths, makes a hypothesis of recent changes owing to contact networks improbable. Although further research is needed, the low correlation of motifs with language family make it seem more probable that these elements of star-related mythology have largely survived historical changes in culture and language, potentially going back to the first inhabitants of the continent. Although these findings remain tentative owing to limitations of the corpus analysed, mythology of the stars seems to be particularly well suited to phylogenetic analysis for long-term perspectives on the history of motifs, potentially extending back into the Palaeolithic.

### Material

The databases used in this paper were built from a database developed by Yuri Berezkin. This database, available in Russian on <http://ruthenia.ru/folklore/berezkin>, was consulted in October 2017. The Analytical Catalogue of World Mythology and Folklore consists of ca. 55,000 summaries of narratives and descriptions of mythological ideas among ca. 1500 large and small ethnic groups combined

into almost 1000 traditions, mostly on the basis of language. Most of the texts in the database were recorded between 1850 and 1980.

Such narratives easily pass the test of a certain degree of distortion due to translation, which affects their linguistic surface but not their structure. Indeed, according to Lévi-Strauss (1958: 232), the signification of a text is preserved even through the worst translation. The basic content of stories is easily translated, for which elementary command of the corresponding language is usually sufficient.<sup>1</sup> What is impossible to translate – people's attitude towards the stories and their feelings when they hear them – are studied by another discipline: cultural anthropology. Furthermore, Yuri Berezkin classifies narratives at a high level of abstraction, which reduces the probably of impacts from translation on the encoding of mythological motifs. Such a classification system avoids dealing with elements that may be deformed, such as surface details of narration. Within a corpus of this size and at such a level of abstraction, issues of the 'quality' of individual sources and their translation do not present significant methodological problems in quantitative analysis.

The mythological motifs selected in Berezkin's database are cultural elements subject to replication. There is no evidence in the database that all the motifs studied have the same history. On the contrary, each motif seems to have a distribution area of its own.

Figure 3a.  
Cultural regions of Africa, Eurasia,  
Australia and the Pacific according to the  
work of Yuri Berezkin.



This avoids a vicious circle: a perfect homogeneity of the data could have explained the existence of general trends: but if such trends were to be found here, they would be attributable to data selection.

For the current paper, all the units where the Pleiades appeared in the summary of a motif were added to the dataset. The delimitation of the field is thematic and relationships between motifs is not presupposed, but rather needs to be demonstrated (see below). This leaves 21 motifs listed here according to Berezkin's motif system, as listed in Table 1:

Table 1. The 21 motifs according to Berezkin's motif system analysed in the current paper.

1. B42K In the Cosmic Hunt tale, either hunters or game are identified with the Pleiades.
2. B47 In former times or presently, the Pleiades or other group of stars produced or produce severe cold until the present.
3. B47A A cow steps on the stars of the Pleiades, which were a dangerous being that lived on the earth. Part of these stars slip through its split hoof.
4. B59 A group of people (usually children, brothers or sisters) play, dance, ascend to the sky and turn into the Pleiades or another compact constellation.
5. B60 Children come into conflict with their parents who do not pay enough attention to them, condemn their sexual behaviour, do not give them enough food, clothes, etc.; the children abandon their parents, become birds, bats, atmospheric phenomena, or stars (usually the Pleiades).
6. I94 The Pleiades are a sieve, holes in the firmament, etc.
7. I95 The Pleiades are a sieve to process agricultural products.
8. I98A The Pleiades are a brooding hen, a hen with its chicks, chickens.
9. I98B The Pleiades are wild ducks, a nest or eggs of wild ducks.
10. I98c The Pleiades are a flock of birds.
11. I99 The Pleiades are a group of boys, lads, men, or a group of different people, but predominantly males.
12. I100 The Pleiades are a group of girls or women (with children).
13. I100A The Pleiades are a woman with her children.



Figure 3b. Cultural regions of the Americas according to the work of Yuri Berezkin.

- 14.I100C God transformed man into cuckoo, his wife and children into the Pleiades.
- 15.I108 The Pleiades are one anthropomorphic person, not several persons.
- 16.I114 Ursa Major and the Pleiades are described in the context of one and the same tale, Ursa Major being associated with men and the Pleiades with women.
- 17.115 Orion and the Pleiades are described in the context of one and the same tale.
- 18.115A Orion and the Pleiades are opposed as a man or men and a woman or women. Usually Orion is male.
- 19.I122 The Pleiades are a nest, a swarm of insects.
- 20.I130 Orion, the Pleiades, Ursa Major or Ursa Minor are a hunting or fishing net.
- 21.M50 A man (usually Coyote) tries to join a group of persons who are or become stars (usually the Pleiades) but suffers a reversal. He pursues the stars to have sexual contact with them or to be re-integrated with members of his family.

To avoid bias in the documentation of cultural areas (on units used in this analysis, see below), only those cultural areas possessing more than six relevant motifs (more than 1/4 of the all motifs considered) were retained.

The level of analysis chosen for the database is the cultural area, according to Berezkin's division of the world into a series of areas on the basis of general culture (Figure 3a–b). Obvious long-distance borrowings were already excluded from the database. The

cultural unity of each area may maintain consistent boundaries with its neighbours, with a significant part of variation that occurs between areas, significant area-internal similarity, and a decrease of the probability of short-distance borrowings. Accordingly, structural (Lévi-Strauss 1971b) and phylogenetic (Ross et al. 2013) methods show a strong effect of ethnolinguistic and cultural boundaries on the distribution of myths and the folktales. Additionally, in traditional societies, the mythological motifs used in the current database are believed to be 'true'; they are consequently less easily and rapidly borrowed than for folktales.

A dataset of individual ethnic groups was also created to check the results. Only ethnic groups with at least four motifs were retained (five or six motifs eliminates too many ethnic groups to make the corpus significant).

To sum-up, the dataset used is not based on a predefined idea of genealogy. It also has to be noted that the obtained results will be easily be falsifiable by establishing new datasets.

### Method

Each cultural area was coded by a series of 1s and 0s according to the presence or the absence of each studied motif. This produced columns of binary codes for every cultural area. Uncertainty in the presence or absence of a motif was coded with a question mark. 'Absent' does not mean that the motif never

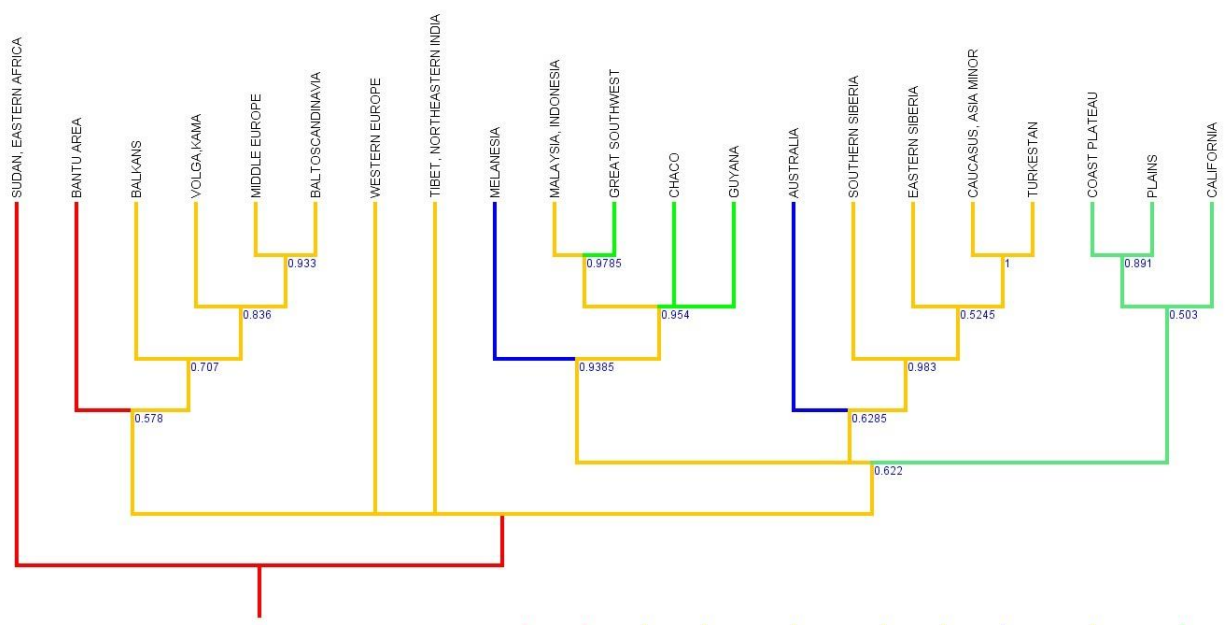


Figure 4. Tree based on Pleiades motifs in the database of Yuri Berezkin according to cultural area.

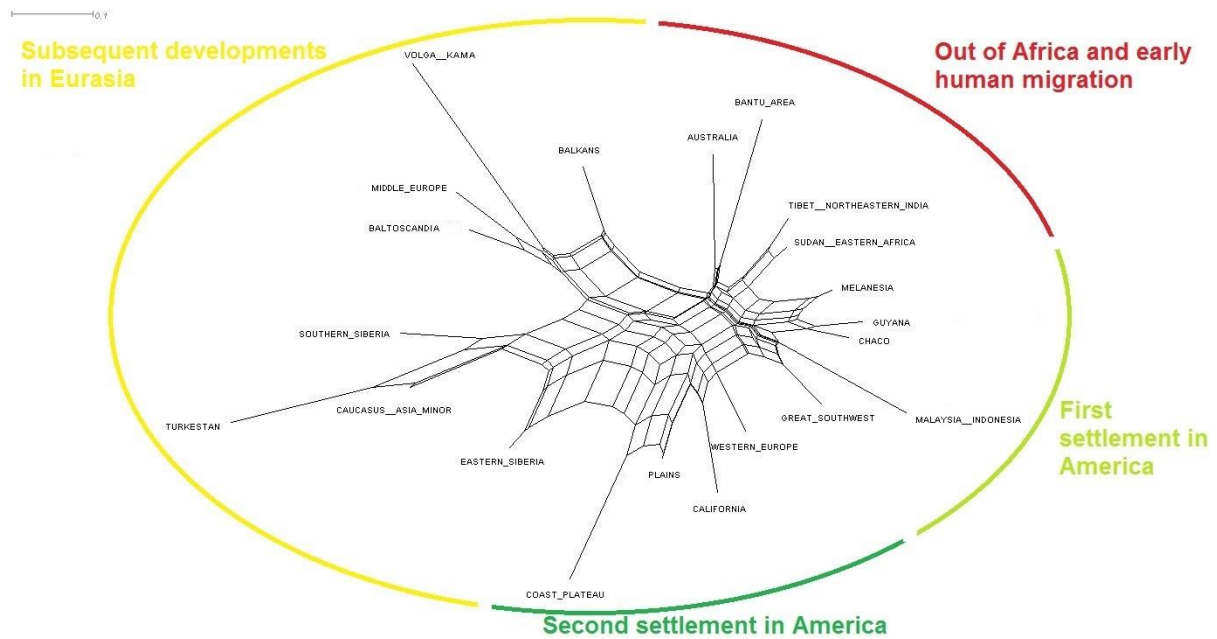


Figure 5. NeighborNet based on Pleiades motifs in the database of Yuri Berezkin according to cultural area. The clusters were defined on the results obtained from the phylogenetic tree.

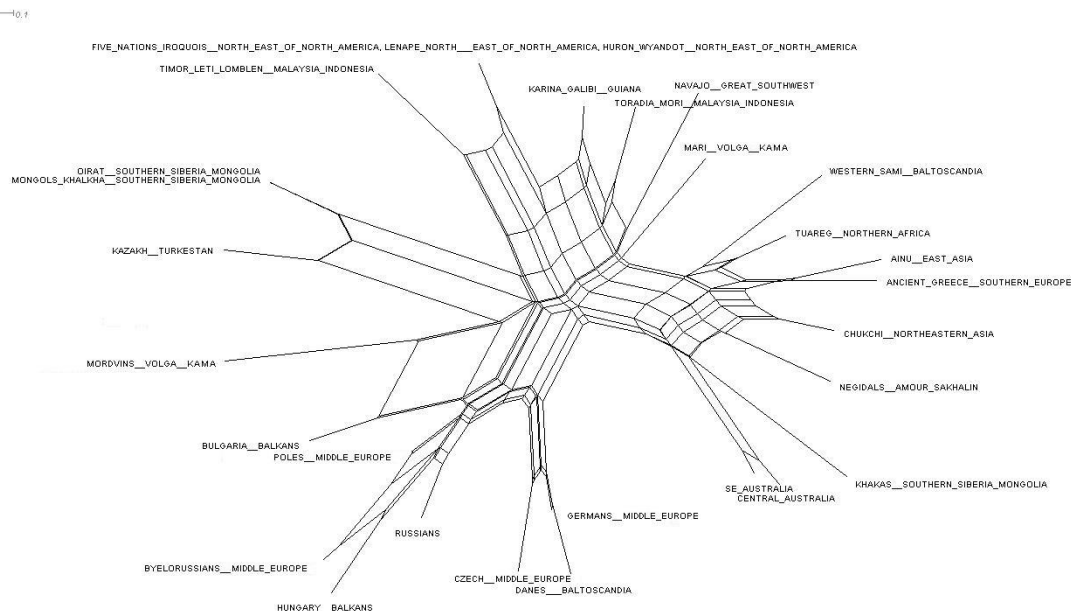


Figure 6. NeighborNet based on Pleiades motifs in the database of Yuri Berezkin according to cultural groups.

existed in that tradition, only that it has not been documented there or otherwise has not been recorded in Berezkin's database. This issue was a motivation for a two-level analysis by both ethnic groups and cultural areas.

*Mesquite* 3.2 (Maddison and Maddison 2017) was then used to construct the 1000 most parsimonious trees for the character matrix (method SPR) to address phylogenetic uncertainty and only those clades present in more than 0.50 of the reconstructed trees (Figure 4). This tree represents the branching history of descent linking traditions. It should be noted that a tree can only establish an

extremely simplified evolutionary model of myths.

Another approach – the creation of networks, used for the first time in comparative mythology in 2012 (d'Huy 2012b; 2013a–c; Ross et al. 2013) – can visually report borrowings between versions and/or common independent inventions. From the same data that permits the construction of the tree, it is possible to create a NeighborNet (Figure 5; Jaccard) with *Splitstree* 4.14.4 as above. In such a network, boxes indicate common features between taxa that seem not to be



inherited phylogenetically, or, in our case, borrowings or independent inventions.

To check the previous results, another NeighborNet was built from 29 individual ethnic groups and the same motifs previously used from Berezkin's database (Jaccard; Figure 6). To keep the maximum number of linguistic-cultural groups, only those with more than three of the relevant motifs were retained.

### Results and Discussion

The first point to address is the unity of the corpus and the existence of a phylogenetic signal.

About the NeighborNet, the average delta score of the network built from cultural areas (0.40) and from individual ethnic groups (0.37) show a relatively low, yet existing, tree-like message, comparable to what Russell D. Gray et al. (2010) obtained for Austronesian (0.44) and Indo-European (0.4) language families using typological data, i.e. structural and functional features of many languages.

The delta score ranges from 0 to 1; it equals zero if the data are well-fitted to the tree. The LSFit, expressed as a percentage, shows how accurate the correspondence between the pairwise distances in the graph and the pairwise distances in the matrix are. The fit of the data to the NeighborNet network (Saitou & Nei 1987; Gascuel 1997; Uncorrected\_P: 98.18; Jaccard: 98.11; calculated with *Splitstree* 4.14.4) is better than its fit to a bio Neighbor-joining tree (Uncorrected\_P: 95.8; Jaccard: 95.74; Figure 7). Consequently, the data fit better with a reticulating network than with a tree. However, there is a small difference between the two LSFit, which indicates that the data also corresponds well to a tree.

Concerning the tree, from a mathematical point of view, it is possible to calculate the Retention Index (RI) to measure the amount of homoplasy (i.e. parallel evolution, including convergence) but also how well synapomorphies (shared ancestry between a pair of character or trait states) explain the tree. It is calculated as  $(h - s) / (h - m)$ , where  $h$  is the maximum number of changes on a tree,  $s$ , the number of changes on the tree and  $m$ , the minimum number of changes in the dataset. The RI must be the highest possible (close to 1).

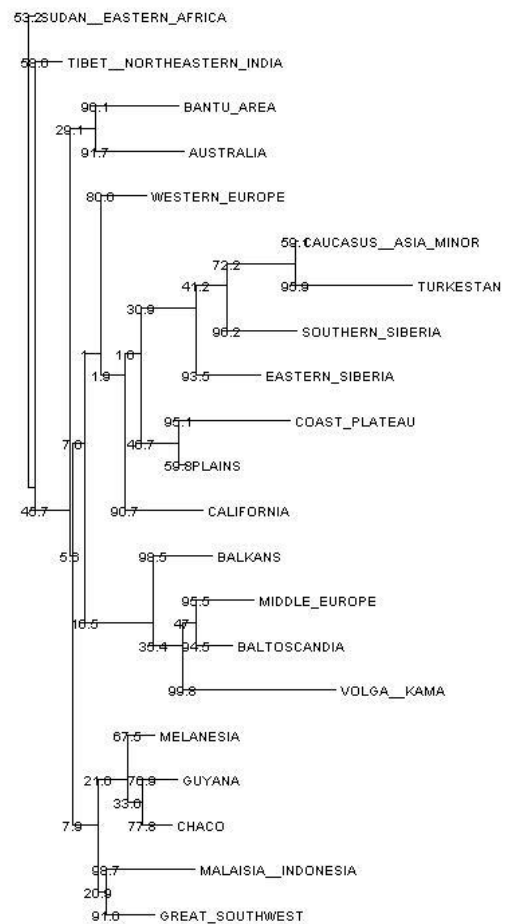


Figure 7. Bio Neighbor-joining (Jaccard) based on the database of Yuri Berezkin according to cultural areas (bootstrap: 10.000).

According to Charles L. Nunn et al. (2010), a high RI (for example, greater than 0.60) usually indicates a low horizontal transmission (including borrowings, total or partial, from nearby societies) and an essentially vertical sense of inter-generational transmission. The applicability of these findings to our database is justified because the areal diffusion of studied motifs is very largely or wholly independent of one another. Here, the RI of the tree is 0.56. Such results indicate that most of the motifs are synapomorphic character states, providing evidence of grouping and that they share a common history. The obtained tree indicates general trends of diffusion, and not the sense of diffusion or the evolution of each feature taken individually.

Using SAM v.4.0 (Rangel et al. 2010), Mantel test was applied to the Eurasian ethnic groups ( $n > 3$ ; data and geographical locations found in Berezkin's database, Jaccard's coefficient matrix, 10.000 permutations) to individual ethnic groups to test the

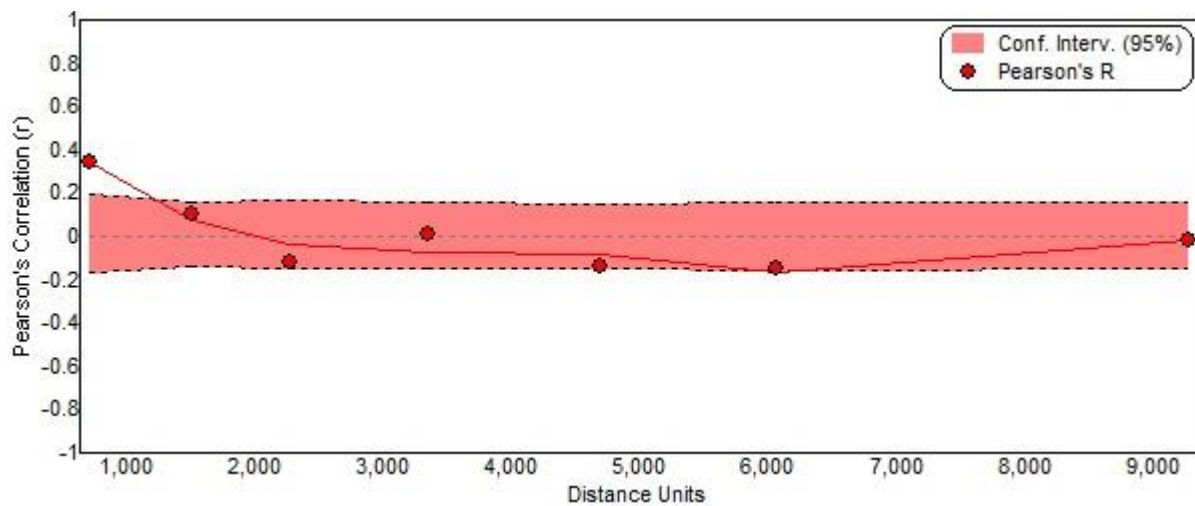


Figure 8. Mantel correlogram of Pleiades motifs in the database of Yuri Berezkin according to ethnic groups.

phylogenetic message. According to the previous results, the geographic distance explains 4.4% of the variance (global Pearson's  $r$ : 0.211;  $p=0.021$ ), which could imply a strong phylogenetic message (Figure 8). Such a result may be due to the disappearance of some motifs over time, but it reduces the likelihood of a recent diffusion of the motifs and supports the interpretation of a vertical transmission.

The tree in Figure 4 suggests a common branching tree of descent for traditions around the globe. Relations in this tree group in broad geographical areas that correlate well with knowledge of the earliest migrations of human populations and the developments that make Eurasia a distinctive cultural area. The tree can be readily interpreted as suggesting that mythology connected with the Pleiades was established already in Africa, whence it spread with the first human migrations. It also appears to reflect two waves of migration into the Americas. The first of these would seem to have originated from or to have also spread into Southeastern Asia (Melanesia) and also dispersed across North and South America, although its traces are found mainly in the south part of North America and in South America (Great Southwest, Chaco, Guyana). The second wave of migration, doubtless Palaeolithic, probably spread from somewhere in northern Eurasia (see Figure 5) and impacted especially North America (Coast Plateau, Great Plains, California). The first wave, with extensions deeper into inner Africa, Eurasia and America, is probably the older

one, while the second would have partially superseded the first in many regions. The two waves of migrations into the Americas have been confirmed by recent genetic data (e.g. Kashani et al. 2012; Raghavan et al. 2014; Skoglund et al. 2015) and diverse studies in comparative mythology have revealed differences in the mythology correlated with each wave (e.g. Korotayev et al. 2011; Berezkin 2013; Le Quellec 2014; 2015b; d'Huy 2012a; 2016b; 2016d; 2017a). The Eurasian grouping of Figure 4 would show an independent development from Eurasian areas, probably due to the reconquest of these lands after the last Glacial Maximum.

The phylogenetic analysis of motifs in Figures 4 and 5 can be compared with that of ethnic groups in Figure 6 as in Table 2. Figure 6 is constructed from a less extensive dataset (only ethnic groups with four or more relevant motifs), so it is probably less reliable. This would explain the presence of a cluster of ethnic groups not found in figures 4 and 5.

The global structure of the tree, from the initial migrations out of Africa to the settlement of the Americas, is also found in other trees built from radically different datasets, such as motifs connected with the myths of the serpent (d'Huy 2016a), the Milky Way (d'Huy 2017b), or with matriarchy and the origin of fire (d'Huy 2017c). This model of diffusion is also broadly supported by the work of Yuri Berezkin (2013) and Jean-Loïc Le Quellec (2014; 2015b). Correspondence between the resulting trees and what we know about first human migrations is hardly a

Table 2. Summary comparison of information in Figures 4–7.

	Tree (cultural areas; Figures 4 and 7)	NeighbourNet (cultural areas; Figure 5)	NeighbourNet (individual ethnic groups; Figure 6)
<i>Out-of-Africa</i>	(Bantu area), Australia	Bantu area, Australia	SE Australia, Central Australia (Australia)
<i>Two waves of migrations from Asia to America</i>	Two different clusters: Melanesia, Guyana, Chaco, Malaysia-Indonesia, Great Southwest + Coast-Plateau, Plains, California	Two different clusters: Melanesia, Guyana, Chaco, Malaysia-Indonesia, Great Southwest + Coast-Plateau, Plains, California	Five Nations – Iroquois, Lenape, Huron, Wyandot (Northeastern of North America), Karina Galabi (Guiana), Toradia, Mori, Timor, Leti, Lomblen (Malaysia-Indonesia), Navajo (Great Southwest)
<i>Independent Eurasian development</i>	Balkans, Volga – Kama basin (i.e. Volga – Perm), Middle Europe (Eastern and Western Slavs), Baltoscandia	Balkans, Volga – Kama basin (i.e. Volga – Perm), Middle Europe (Eastern and Western Slavs), Baltoscandia	Bulgaria, Hungary (Balkans), Mordvins (Volga – Kama basin), Russian, Poles, Byelorussians, Czech, Germans (Middle Europe), Danes (Baltoscandia)
<i>Independent Eurasian development</i>	Southern Siberia, Turkestan, Eastern Siberia, Caucasus, Asia Minor	Southern Siberia, Turkestan, Eastern Siberia, Caucasus, Asia Minor	Mongols Khalkha, Oirat (Southern Siberia, Mongolia), Kazakh (Turkestan)
<i>Correspondance not found</i>			Khakas (Southern Siberia, Mongolia), Chukchi (Northeastern Asia), Ainu (Eastern Asia), Negidals (Amur, Sakhalin), Ancient Greece (Southern Europe), Tuareg (Northern Africa), Western Sami (Baltoscandia)

surprise. Indeed, a significant correlation between the distribution of certain motifs and the distribution of certain genes has been highlighted by Andrey Korotayev and Daria Khalitourina with Yuri Berezkin (2011). In addition, the low correlation between the relationships of a set of narrative-types (in the form of an oral tradition belonging to a given population) and the geographical distance separating these populations is an indicator of an essentially vertical distribution of the oral narratives (see above).

### **Methodological Considerations for Reconstruction**

Once the tree in Figure 4 is established, it becomes possible to statistically reconstruct what the earliest mythology was that spread at the time of migrations out of Africa process. The method of reconstruction chosen here is the

maximum likelihood method (d’Huy 2012a; 2015a; da Silva & Tehrani 2016). This method calculates the most probable ancestral states at each node of the tree that, within a model of evolution, would produce the observed evidence, allowing states at all other nodes to vary. Use of this method leads to certain methodological concerns that require discussion.

First, the tree is generated through the analysis of all 21 motifs listed in Table 1, following which individual motifs are traced on the tree. The tree thus becomes treated as having objective and uniform validity for all the analysed motifs while being independent of any one of them. Faced with this problem, Sara Graça da Silva and Jamshid J. Tehrani (2016) came up with the ingenious solution of taking an undisputed tree of the genetic relations between Indo-European languages and then analysing tale-types documented in those

*Table 3. Likelihood of the data under the Markov k-state 1 parameter and the symmetrical Markov k-state 2 parameter models. The asymmetrical Markov k-state 2 parameter model has a higher likelihood than the Mk1 model; however, most of the time, the first model does not support the probability significantly more than the second. Note that a motif reconstructed for the migration out of Africa possess a much higher rate of change from state from 0 to 1 than for the rate of change from 1 to 0 (with the exception of I115A).*

	Asymmetrical Markov k-state 2 parameter model			Markov k-state 1 parameter model		2*ln(likelihood ratio) of asymmetrical vs symmetrical model (assuming chi-square 1 d.f.)
	Forward rate (0=>1)	Backward rate (1=>0)	LogL	Rate	LogL	
B42K	0.338	1.095	-11.484	0.158	-12.617	2.265 (p=0.132)
B47	0.104	0.092	-10.762	0.103	-10.767	0.010 (p=0.917)
B47A	1.410	13.400	-6.604	0.065	-8.223	3.238 (p=0.071)
B59	0.024	0.065	-5.042	0.029	-5.232	0.378 (p=0.538)
B60	0.050	0.084	-7.550	0.062	-7.625	0.150 (p=0.698)
I94	0.068	0.065	-8.162	0.067	-8.163	0.001 (p=0.97)
I95	0.065	0.077	-8.157	0.067	-8.166	0.017 (p=0.893)
I98A	0.124	0.265	-12.111	0.163	-12.552	0.882 (p=0.347)
I98B	0.063	0.149	-8.041	0.066	-8.218	0.355 (p=0.551)
I98S	1.418	13.479	-6.604	0.063	-8.284	3.3609 (p=0.066)
I99	12.170	2.028	-8.612	0.105	-10.684	4.143 (p=0.041)
I100	13.193	2.198	-8.612	0.104	-10.694	4.164 (p=0.041)
I100A	0.259	0.417	-13.505	0.257	-13.763	0.516 (p=0.472)
I100C	0.028	0.141	-4.815	0.030	-5.203	0.776 (p=0.378)
I108	15.122	2.520	-8.612	0.105	-10.684	4.144 (p=0.041)
I114	0.098	0.351	-9.300	0.103	-10.012	1.424 (p=0.232)
I115	0.152	0.107	-10.551	0.108	-10.593	0.084 (p=0.770)
I115A	0.083	0.201	-11.923	0.172	-12.309	0.772 (p=0.379)
I122	0.036	0.167	-7.44	0.063	-8.281	1.680 (p=0.194)
I130	0.805	16.102	-4.020	0.029	-5.232	2.425 (p=0.119)
M50	0.416	0.445	-14.399	0.425	-14.407	0.017 (p=0.896)

languages against that tree. A major risk in adopting this method is that approximations can be built on approximations. In their case, da Silva and Tehrani seek to establish the tales with continuity from the beginning of the Indo-European diffusion. However, the stemma of Indo-European used (da Silva & Tehrani 2016: Figure 2) is both ideal and its regular progressive branching of language families is far from certain; the stemmatic relations of languages within its branches also appear inaccurate, mixing West Slavic languages like Polish with East Slavic languages like Russian, and so forth.<sup>2</sup> Although assessing data against an independent tree is ideal, assessment

becomes conditional on the validity of that tree, which may itself be problematic. Such a method is also limited in applicability by the time-depth of the available trees: the histories of language families can be traced back no more than several thousand years, which is only a small percentage of the time since the first migrations from Africa. Here, it is considered best, though not ideal, to reconstruct the motifs present in the past by using the tree constructed from sets of related motifs, provided that the reconstructed motifs can be verified using other methods. The reconstruction of the earliest presence or absence of motifs depends on the structure of

the tree. Even if the structure of the tree in Figure 4 seems very strong, it remains necessary to move forward with caution. Another methodological issue is that phylogenetic software always organizes data in a single tree. Consequently, even if the researcher includes data not genetically related, the software will organize this into a single tree. This problem is compensated by the retention index (RI) and the delta score, which are indicators of whether or not the tree represents the evolutionary history of most of its constituent motifs. A third shortcoming of phylogenetic reconstruction methods is their dependence on the structure of the tree, and thus in the choice of the root – i.e. what is considered the earliest split. Estimating phylogenies and ancestral states is not a trivial problem and the necessary precautions need to be taken.

Table 4. Reconstructed motifs with a probability of >75%. Dark gray rows: calculation of Markov k-state 1 parameter; light grey rows: calculation of Asymmetrical Markov k-state 2 parameter:

- A. Out-of-Africa (Sudan + Melanesia, Chaco, Malaysia, Great Southwest). First result: root = Sudan – Eastern Africa; second result: root = Bantu area.
- B. First migration in America (Melanesia, Chaco, Malaysia, Great Southwest). Root: Sudan – Eastern Africa.
- C. Second migration in America (California, Coast Plateau, Great Plains). Root: Sudan – Eastern Africa.

Motif	Migrations		
	A	B	C
B60		96.95	96.78
		98	97.9
I99	98.89   47.33	99.86	99.85
	85.71   76.79	85.71	85.71
I100	98.92   98.68	99.87	98.9
	85.71   85.71	85.71	85.71
I108	98.9   98,66	99.87	98.89
	85.71   85.71	85.71	85.71
I115	98.83   98,68	99.74	88.26
	98.45   98.17	99.40	83.79
I115A	93.1   93.15	96.74	
	97.73   97.02	99.40	
M50			81.65
			81.33

For a motif to be inferred to have continuity from the first migrations out of Africa, it must be able to be reconstructed at the root of the tree, whether the tree is rooted on Bantu or Eastern Africa. Indeed, a different rooting changes the structure of the tree and consequently the likelihood for a particular motif to be reconstructed at the root. The possibility of migration from Eurasia back into Africa could also potentially interfere with the data. In order to compensate for this, the relevant motif should also exhibit continuity through clades in the South Amerindian areas and Melanesia. In contrast to a distribution analysis, the reconstruction of historical presence or absence of motifs is probabilistic and depends on the evolutionary history of the majority of them. The reconstruction must be conclusive with the two likelihood models implemented in Mesquite. Likelihoods under a Markov k-state 1 parameter model and under an Asymmetrical Markov k-state 2 parameter model are compared in Table 3. The reconstruction must also exhibit more than a seventy-five percent probability in the assessments in Table 4. Besides, every feature must be confirmed by using at least another method used in comparative mythology.

### Reconstruction

From the calculations in Table 4, four motifs can be reconstructed as likely to have existed and spread with the earliest migrations out of Africa:

Table 5. Four motifs reconstructable to the earliest migrations from Africa.

- I100 The Pleiades are a group of girls or women (with children).
- I108 The Pleiades are one anthropomorphic person, not several persons.<sup>3</sup>
- I115 Orion and the Pleiades are described in context of one and the same tale.
- I115A Orion and the Pleiades are opposed as a man or men and a woman or women. Usually Orion is male.<sup>4</sup>

The reconstruction of these four motifs is consistent with earlier studies. For example, Brian Hayden & Suzanne Villeneuve state:

the Pleiades are almost always viewed as a group of individuals and are one of the most



Figure 9. Distribution of motif I115A: Orion and the Pleiades are opposed as a man or men and a woman or women. Usually Orion is male.

frequently mentioned star clusters [in the world]. [...] Their importance cross-culturally strongly suggests that they would have been similarly notable in the past. (Hayden & Villeneuve 2011: 342.)

Mentioning two Australian tribes, Edwin N. Fallaize also notes that “The almost unvarying association of the Pleiades with women among different races is remarkable” (1922: 64). According to Yuri Berezkin, the identification of Orion and the Pleiades with characters of different sex, Orion often appearing in the role of men or groups of men, and the Pleiades as a woman or group of women, is widespread (Figure 9), and, in any case, is more popular than the opposite variant, in which the Pleiades pursue Orion. Moreover, the sexual opposition between the Pleiades and Orion, although it occurs on different continents, is absent in the main part of Eurasia: the irregular distribution of the image of Orion as a man, and the Pleiades as women can be considered as an argument that likely emerged among pre-

migration populations in Africa (Berezkin 2017: 20-24).

#### **Orion Mythology as a Test**

To test these results, the database of Berezkin has been used to study all the motifs linked to Orion, listed in Table 6:

Table 6. Motifs connected with Orion in Berezkin’s database.

1. B42H The game of the Cosmic Hunt tale is identified with Orion’s Belt.
2. B42h1 In the Cosmic Hunt, an arrow pierced the animals of Orion’s Belt.
3. B42N The constellation Orion or Orion’s Belt is identified with only one male person, usually with a warrior or hunter.
4. B42R The three stars of Orion’s Belt are three persons or animals who pursue each other.
5. I95A Orion is a balance, scales.
6. I95B Orion is a shoulder-yoke.
7. I95C Orion is a staff.
8. I110A Orion (rare: another constellation) is a plough, associated with breaking ground.

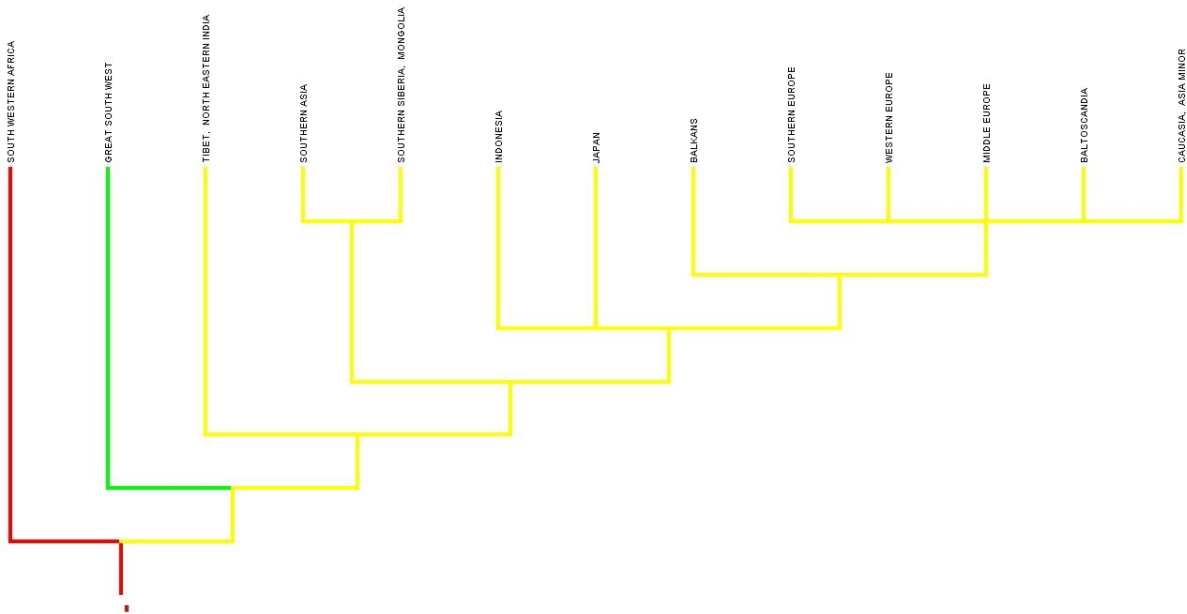


Figure 10. Tree of Orion motifs based on the database of Yuri Berezkin by cultural region.

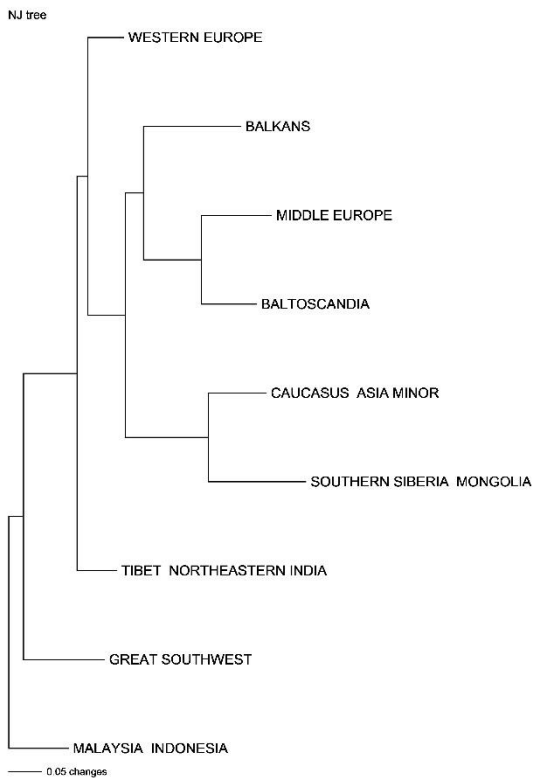


Figure 11a. Bio Neighbor-joining based on the common Pleiades motifs by cultural region.

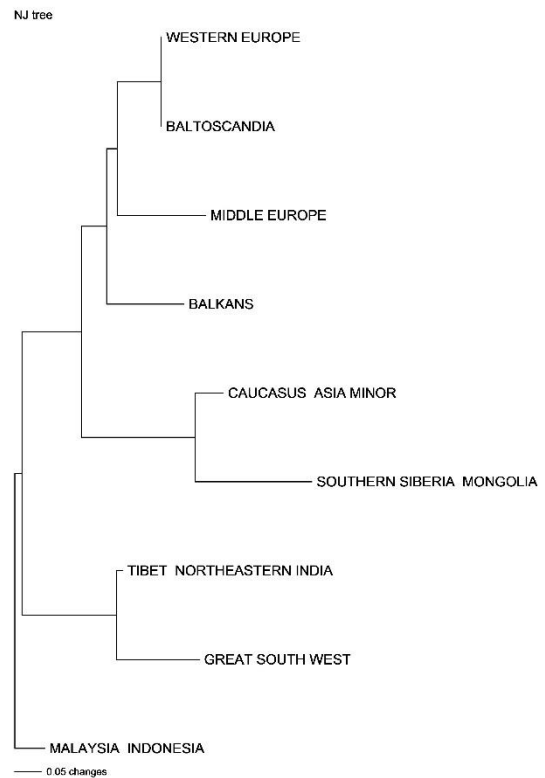


Figure 11b. Bio Neighbor-joining based on the common Orion motifs by cultural region.

9. I110B Orion(’s Belt) is (three) mowers or agricultural tools related to mowing and harvesting.
10. I115 Orion and the Pleiades are described in the context of one and the same tale.

11. I115A Orion and the Pleiades are opposed as a man or men and a woman or women. Usually Orion is male.
12. I130 Orion, the Pleiades, Ursa Major or Ursa Minor is a hunting or fishing net.

These 12 motifs have been converted into a binary dataset (uncertainty with question mark), and, given the low number of motifs used, only areas with more than four motifs (1/3 of the totality) have been retained. The consensus tree in Figure 10 (1000 trees, method SPR, RI: 0.6) is artificially rooted in Southwest Africa. To compare the tree of Figure 10 with the tree of Figure 4, it is possible to reduce the two matrices (Pleiades and Orion) to the cultural areas where both are attested – i.e. Western Europe, Tibet / Northeastern India, Malaysia / Indonesia, the Balkans, Central Europe, Baltoscandia, the Caucasus / Asia minor, Southern Siberia, the Great Southwest. Using PAUP 4.0a152, two bio Neighbor-Joining trees based on the Pleiades (RI: 0.536), shown in Figure 11a) and on Orion (RI: 0.591) in Figure 11b) datasets were constructed: only the cultural areas common to the two corpus were retained. The proximity of the two trees is obvious, only one area varies position across the two trees.

The motifs reconstructed both at the root of the tree (Figure 10) and on the basis of the Great Southwest (from the first migration to the Americas?) are B42H (probability at the root of the tree: Mk1: 97.96%; Asymm. 2 param.:98.24%), B42N (90.78% | 81.90%), I115 (75.38% | 73.49%) and I115A (97.96% | 97.72%). When taking into account the whole of Berezkin's database, these motifs, with the exception of B42H, have been found in at least two of the four Sub-Saharan areas (i.e. Southwestern Africa, the Bantu Area, the Western Area, the Eastern Area) and in Australia. These findings support a Sub-Saharan origin of the motif of Orion as a man following the Pleiades as a woman.

### ***The Pleiades–Orion Opposition***

The opposition between Orion and the Pleiades brings us back to one of the intuitions of Lévi-Strauss (1964). He proposed the existence of a significant worldwide correlation and opposition between Orion and the Pleiades, both in terms of the simultaneous presence or absence of the constellations and in terms of the discontinuous and well-articulated system of Orion as opposed to the continuous and inarticulate set of stars of the Pleiades. Following this second opposition, the couple

Orion–Pleiades becomes a significant expression of seasonal alternation (summer / winter, dry / rainy season, work / leisure, abundance / scarcity, etc.). Is it possible to test Lévi-Strauss' hypothesis? Such structural opposition requires correlation within an individual culture, which means the analysis would have to assess co-occurrence of contrast. The problem is that the opposition between a single Orion and a plural Pleiades can take many forms: the constellation of the Pleiades can represent several men, several women, several children, several birds, etc.; the constellation of Orion can represent a single man, a single stick, etc. It is therefore impossible to correlate precisely the evolution of the two opposing terms on the whole tree, because they can take different values: this structural opposition must be reconstructed at each node. It is therefore impossible to answer this question given the current state of the database. However, the facts that the opposition of Orion as male and the Pleiades as female is not universal (Berezkin 2017: 23) and that the motif is not reconstructed at the root of the northern Amerindian clade (see below) speaks against such a structural opposition.

### ***Diffusion of the First Narratives and Founder Effects***

If the reconstructed motifs I100, I108, I115 and I115A existed at the time of the exit from Africa, it is likely that they were carried by the men during those first migrations. Under these conditions, it should be possible to reconstruct a tree similar to the one in Figure 4 on the basis of only these four motifs. The results obtained using Mesquite are insufficient for such a reconstruction due to the small number of items used (only four motifs!) To solve this problem, a majority-rule consensus tree was constructed using a heuristic search implemented in PAUP 4.0a152 (parsimony; Swofford 2002). Figure 12 shows the results of applying this method to the full dataset yielding a consensus of 35 trees with an RI of 0.588, which is high enough to suggest a good proportion of vertical transmission, and a delta score of 0.40. Figure 13 shows the results of this method applied to the adjusted dataset (i.e. only I100, I108, I115 and I115A), yielding a



consensus of 9 trees: the RI increases to 0.889 while the delta score decreases to 0.20. These results suggest the existence of a primitive group of traits transmitted *en bloc* in connection with the initial migrations out of Africa with a low amount of homoplasy.

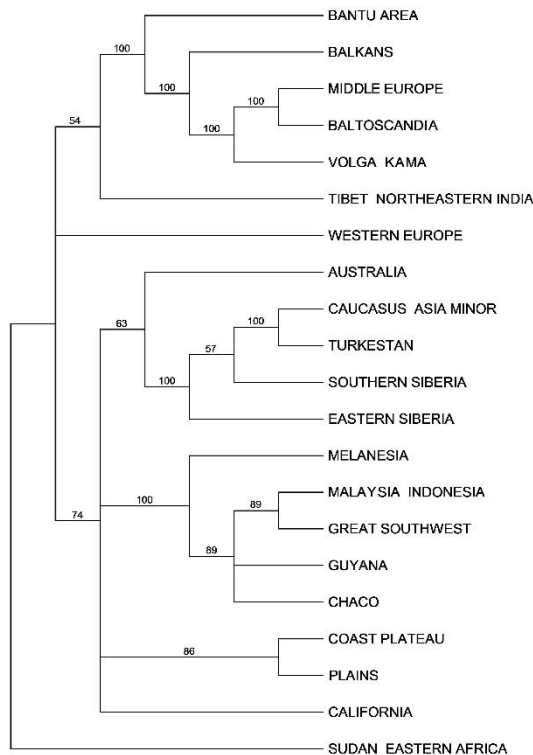


Figure 12. Parsimony tree (heuristic search) based on Pleiades motifs in the database of Yuri Berezkin based on cultural areas.

The tree in Figure 13, rooted on Eastern Africa, is not exactly identical to that in Figure 12. The differences could be explained by the small number of traits used to construct it, which makes it less reliable. According to the tree in Figure 13, the first migration, shortly after the migration out of Africa, would have spread the proto-folklore of the Pleiades along the Southern Asian coast as far as South America as well as along the southern Asian coast. The second migration, in its turn, presumably spread from northern Eurasia and diffused into North America, possibly in multiple waves with a serial founder effect. A serial founder effect hypothesis could explain this diffusion of the Palaeolithic mythology generally with respect to the topology of the tree and what we know about the earliest human migrations (see also d’Huy 2017c). According to this hypothesis, at each step of geographical

expansion, populations may carry only a subset of the mythological diversity from previous migrations along with new motifs or myths, increasing the mythological differentiation between them and from the previous settlement (for an empirical analysis of a mythological founder effect and an earlier formulation of the hypothesis, see d’Huy 2013d).

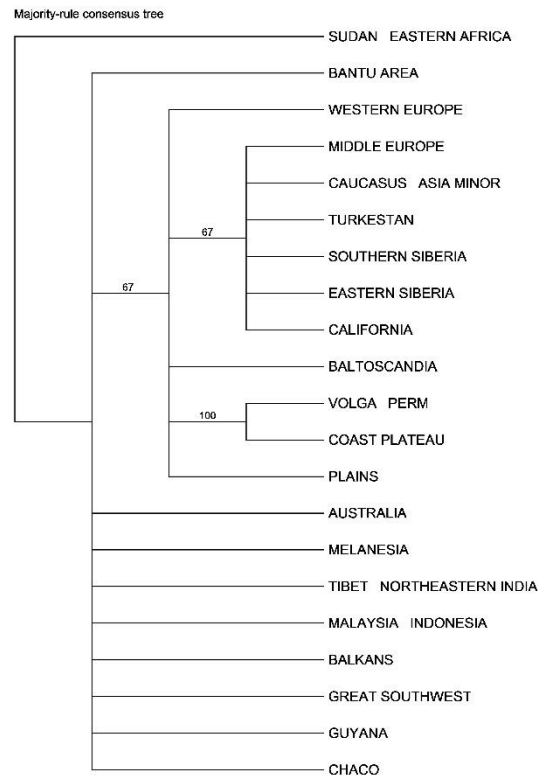


Figure 13. Parsimony tree (heuristic search) based on the adjusted dataset of Pleiades motifs in the database of Yuri Berezkin: cultural areas.

### A Reconstruction of Variation in Spread

In order to test the reliability of the results and of the structure of the tree in Figure 4, and the reliability of an inherited opposition between the Pleiades and Orion, a reconstruction of the patterns present at several nodes/steps following the migration from Africa is developed here. This reconstruction is then compared with the results obtained by other comparative methods.

People who lived somewhere in Southeast Asia contributed to the mythology of both very early Australian and Melanesian and – today essentially southern – Amerindians. This diffusion was already mathematically demonstrated by using comparative and phylogenetic tools, e.g. for the motifs of the

sky-woman and the mysterious housekeeper originating in this area (similar conclusions about this folktale have been drawn using different approaches in Hatt 1949: 101–102, 107; Berezkin 2013: 178–179; d’Huy 2016d), or by using multivariate statistics (Korotayev et al. 2011). The possibility that some of these features may have earlier been established in Africa as well and subsequently disappeared under innovations cannot be overlooked, yet this remains difficult to either corroborate or refute. The most parsimonious hypothesis nevertheless remains an origin of such motifs subsequent to the initial migrations out of Africa.

In Table 4, the four motifs reconstructed for the earliest migrations from Africa in Table 5 are complemented by two additional motifs reconstructable with a probability higher than 75%, at the root of the two Amerindian clusters in Figure 4 (south Amerindian cluster: the Great Southwest, Chaco, Guyana + Malaysia; and the north Amerindian cluster: the Coast Plateau, California, the Great Plains): B60 (Children come into conflict with their parents who do not pay them enough attention, condemn their sexual behavior, do not give them enough food, clothes, etc; children abandon their parents, become birds, bats, atmospheric phenomena, or stars (usually the Pleiades)), and I99 (The Pleiades are a group of boys, lads, men, or a group of different people but predominantly males). This implies that these motifs probably existed before the first settlement in the Americas.

I115A (Orion and the Pleiades are opposed as a man or men and a woman or women. Usually Orion is male) has only been reconstructed at the root of the south Amerindian cluster. This may be due to a cultural survival of the first settlement in the Americas, replaced in North America by other people and other motifs. This would indicate that the opposition of the Pleiades = several people versus Orion = one person is not logical (or should be found reconstructed at the base of North American cultural areas) but probably inherited.

According to William B. Gibbon (1972: 243), “the two motifs [...] – dancing [note: people] and the women – must have been part of one original legend, which began in the Old

World and was perpetuated in the New.” A motif very close to the dancing motif – B59 (A group of people (usually children, brothers or sisters) play, dance, ascend to the sky and turn into Pleiades or other compact constellation) – has not been reconstructed because it is not present in the cultural areas retained for the Americas. This shows a limitation of the method, which requires an extensive corpus, but it does not refute it. However, the motif of the dancers is even closer to the Dancing children myth (B60); the large distribution area of this myth, from North to South America, suggests a significant time depth (Lankford 2007: 175, 180). According to Lévi-Strauss, the tradition relating to an astronomical triad composed of two minor terms symmetrically framing a major term, the one ascribing the origin of the Pleiades to seven characters who ascend into the sky and are, more often than not, greedy or hungry children are “two independent transformations which presumably emerged from the same basic material” (Lévi-Strauss 1968: 39). The reconstructed motifs corresponding to the first settlement of Americas seem to be corroborated by other analyses, which make it possible to corroborate the overall structure of the tree, raising the question of whether it is possible to do this at the level of other nodes.

As discussed above, certain motifs seem to have arrived in North America with a later migration, doubtless Palaeolithic, coming from Northern Eurasia. Such a migration has been shown to be relevant to the history of a number of mythic motifs in earlier studies using different independent approaches, for instance concerning Polyphemus’ narratives (areological approach: Berezkin 2007a; multivariate statistics’s approach: Korotayev et al. 2011; phylogenetic approach: d’Huy 2012b; 2013a; 2015b). Many previously reconstructed motifs probably arrived twice or more into the Americas, in different forms, as it has seems to have been the case for other families of myths, such as the Cosmic Hunt (Berezkin 2006; 2012; d’Huy 2016c) or the motif of the flood and the separation of the earth from the sky (d’Huy 2017a).

In the case of Berezkin’s database, motif M50 (A man (usually Coyote) tries to join a group of persons who are or become stars

(usually the Pleiades) but suffers a reversal. He pursues the stars to have sexual contact or to be reintegrated with members of his family) is only reconstructed on the basis of the northern Amerindian cluster. To my knowledge, no structural or areological study was interested in the distribution of this motif at the global level, which prevents a corroboration of this reconstruction. This result also does not corroborate or refute previous results. Motif I15A is not reconstructed for this migration.

### Conclusion

In summary, computational phylogenetic methods are powerful tools to study the evolution of mythology. They supplement traditional comparative methods, can measure the phylogenetic message and its uncertainty (retention index, bootstrap, delta-score), test different evolutionary models (transmission by distance versus inherited motifs), the existence of a package or myths or motifs that have spread *en bloc*, and allow the result to be tested in a scientific and rigorous manner. Additionally, phylogenetic methods allow the statistical reconstruction of ancient states of mythology.

The study described here shows that the motifs connected with the Pleiades and the stars are more frequently inherited than borrowed from close neighbours. A core tradition of motifs can be statistically reconstructed as spreading at the time of the migrations out of Africa, at the same time as other set of motifs (e.g. myths of: the origin of humanity from underground, the serpent, matriarchy, the origin of fire, the Milky Way, Orion, etc.). This core tradition remains very stable, yet also integrates peripheral motifs that were more easily exchanged and borrowed.

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### Notes

1. Additionally, most of the texts are published in translation and no one (even people who easily read in 30 or 50 languages) can read in 1000 languages.
2. Their study is further made problematic by reliance on the Aarne–Thompson–Uther tale-type index for constructing their data-set, which is not a suitable resource for such investigations (Berezkin 2015; d'Huy et al. 2017), making their conclusions conditional on the representativeness of that data.
3. Motif I108 may seem to be mutually exclusive of the other motifs in identifying the Pleiades as a singular rather than plural entity. Nevertheless, this can be easily accounted for. It is extremely unlikely that a unique culture was at the origin of each diffusion. More likely, there was a pre-existing socially structured mythology within a given geographical area that would be diffused in conjunction with the migrations. Such a general mythology does not preclude the existence of opposing beliefs embedded in the same symbolic system: for instance, the general idea that the Pleiades is female versus Orion as male can take the form of the Pleiades as either many people or only one person. Broadly speaking, the search for an origin of human mythology is not incompatible with the idea of an original diversity, but this diversity, which was probably significant within an area the size of Africa, was inevitably reduced by the phenomenon of bottlenecks.
4. However, note that the motif I99 (The Pleiades are a group of boys, lads, men, or a group of different people but predominantly males) has also been reconstructed using the Asymmetrical Markov k-state 2 parameter model that may be the most suitable model for this motif (see Table 3). Yet the reconstruction is not corroborated by the Mk1 method, and this reconstruction could be invalid.

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