FROM BRIDEWEALTH TO DOWRY? A BAYESIAN ESTIMATION OF ANCESTRAL STATES OF MARRIAGE TRANSFERS IN INDO-EUROPEAN GROUPS

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ABSTRACT

Significant amounts of wealth have been exchanged as part of marriage settlements throughout history. Although various models have been proposed for interpreting these practices, their development over time has not been investigated systematically. In this paper we use a Bayesian MCMC phylogenetic comparative approach to reconstruct the evolution of two forms of wealth transfers at marriage, dowry and bridewealth, for 51 Indo-European cultural groups. Results indicate that dowry is more likely to have been the ancestral practice, and that a minimum of four changes to bridewealth is necessary to explain the observed distribution of the two states across the cultural groups.

KEY WORDS

Marriage transfers, dowry, bridewealth, Bayesian MCMC phylogenetic and comparative methods, ancestral states, Indo-European.

INTRODUCTION

Evolutionary interpretation of marriage transfers

Throughout history, money and property have been exchanged as a substantial part of marriage settlements. For many societies these transactions represent more than token offerings, and are often a source of considerable financial stress for the giving family (Gies and Gies 1989, p. 10). In traditional communities of India, Greece and Sicily, for example, brothers have the moral responsibility to help provide their sisters with dowries, although this may delay their own marriage (Caldwell, et al. 1983; Lambiri-Dimaki 1985, p. 173; Schneider 1985, p. 83). In more extreme cases the substantial value of dowries has been linked with the practice of female infanticide (Dickemann 1979; Goody 1990, p. 115; Sudha and Irudaya Rajan 1999). Among the Kipsigis of Kenya the value of bridewealth payments amounts to the third part of an average man's livestock holding (Borgerhoff Mulder 1988, p. 67).

Various models have been proposed for the interpretation of marriage transactions; from an evolutionary perspective they can be viewed as forms of sex-biased parental investment. Parental investment theory posits that it is adaptive for parents to allocate resources among their offspring so as to maximise their own long-term inclusive fitness. As in most animal species, in humans the variance in reproductive success is greater for males than it is for females (Trivers 1972): sons are therefore likely to benefit more than daughters from the investment of wealth. As expected the frequency of forms of male-biased parental investment such as bridewealth is observed to increase with degree of polygyny (Hartung 1982). In monogamous societies, on the other hand, the difference in variance in reproductive success between males and females is greatly reduced, as consequently is the benefit of investing in sons rather than in daughters. In monogamous societies characterised by uneven resource distribution, however, parents can increase their inclusive fitness by securing a high-status husband for their daughters. As expected forms of female-biased parental investment such as dowry are more common in these societies than elsewhere (Gaulin and Boster 1990). Ultimately, bridewealth and dowry represent a means of resource competition for spouses among, respectively, husbands' and wives' families (Gaulin and Boster 1990; Hartung 1982).

Distribution of dowry and bridewealth

Worldwide, bridewealth is a common and widespread practice, whereas dowry is rare and geographically clustered: of the 1267 societies included in the *Ethnographic atlas* (Murdock

1986), 66% are coded as bridewealth and 3% as dowry (Gaulin and Boster 1990); bridewealth is the commonest form of marriage transfer of African, Circum-Mediterranean, East Eurasian and Insular Pacific societies included in the *Ethnographic atlas*, whereas dowry is restricted to Eurasia (Goody 1973, pp. 22-23, 49-50).

Basing their argument on the assumption that the age of a cultural trait is directly proportional to the territory it covers, Jackson and Romney (1973) use cross-cultural data to infer that dowry, with its restricted geographical distribution, is a practice of relatively recent development compared to the more evenly distributed practice of bridewealth. Such an approach, however, corresponds to inferring the past from the distribution of states at the tips of a phylogenetic tree, without taking into account the non-independence of human cultural groups resulting from their historical relationships. This can lead to spurious results, as illustrated in Figure 1.

[Figure 1 approximately here]

In this simple evolutionary scenario, seven hypothetical populations (represented by the tips) descend from a common ancestor (represented by the root) through repeated fission. The trait under investigation, X, can take two states, 0 and 1. Jackson and Romney's (1973) reasoning, based on the distribution of the states at the tips, corresponds to arguing that state 1 must be the ancestral condition because it is more common than state 0 among the descendants. However, it is clear from Figure 1 that the distribution of the states of a trait at the tips of a phylogeny results from the pattern of splitting into sub-populations combined with the pattern of change in the trait. In this example, state 0 represents the ancestral condition, although it is less common than the derived form, state 1, among the descendants.

Phylogenetic comparative analyses of human cultural traits

Given a phylogenetic model of the relationships among a group of taxa, the evolutionary history of one or more traits of interest can be inferred from the distribution of states at the tips of the tree using formal statistical procedures developed in evolutionary biology. In recent years this class of techniques, known as the comparative method (Harvey and Pagel 1991), has been applied to ethnographic and biological data for human societies to characterise the processes underlying the observed patterns of cultural diversity [Mace and Pagel (1994), e.g. Holden and Mace (1997; 2003)]. This approach can be used to complement traditional ones of investigating the past, and is particularly relevant to the study of traits for which historical and archaeological information on the pattern of change is limited.

Comparative analyses are commonly performed on a single phylogenetic tree. Nevertheless, a phylogeny is only a hypothesis for the relationships among a group of taxa, and is rarely known with certainty (Pagel, et al. 2004). Further, the results of comparative analyses are known to depend heavily on the phylogeny used [e.g. Martins and Housworth, (2002)]. Recent developments in tree-building and comparative methods take into account the statistical uncertainty in the estimation of both the phylogeny and the parameters of interest to the comparative question. Building on previous work by Pagel and Meade (2005), we use this approach to reconstruct ancestral states in the evolution of bridewealth and dowry in Indo-European groups. The association of bridewealth with polygyny and of dowry with monogamy holds in Indo-European groups after controlling for the effect of shared phylogenetic history (Fortunato 2004). The evolutionary interpretation of marriage transfers warrants both the opposition of the two practices and the use of phylogenetic comparative methods for the purpose of investigating their evolution.

DATA AND METHODS

Indo-European languages are considered to be one of the two sister groups that form the Indo-Hittite language family, the other consisting of the extinct Anatolian languages, which include Hittite, Palaic, Lydian, Luwian and Lycian (Rexová, et al. 2003; Ruhlen 1991, p. 325). The two most widely accepted hypotheses on the origins of Proto-Indo-Hittite speaking peoples are Gimbutas's (1973) model of expansion of the Kurgan horsemen from the Pontic Steppes beginning *ca*. 6000 BP, and Renfrew's (1987) model of expansion westward from Asia Minor concomitantly with agriculture starting *ca*. 9000 to 8000 BP (Diamond and Bellwood 2003). In accordance with the latter hypothesis, recent estimates by Gray and Atkinson (2003) indicate that the initial split of Proto-Indo-Hittite into Anatolian and Indo-European languages occurred between 9800 and 7800 years BP.

We collated the sample of Indo-European cultural groups included in the analyses by matching the speech varieties in Dyen et al.'s (1992) Indo-European linguistic database with cultural data on dowry and bridewealth obtained from ethnographic sources. We then used the linguistic data for these speech varieties to build a statistically justified sample of phylogenetic trees, which we used, combined with the cultural data, to estimate the probability distributions of dowry and bridewealth at ancestral nodes on the trees.

Linguistic data for phylogenetic inference

Dyen et al. (1992) is a database of 95 modern Indo-European speech varieties, including languages, dialects and creoles, available from http://www.ntu.edu.au/education/langs/ielex/IE-DATA1. For each variety the forms of the 200 meanings in the Swadesh list of items of basic vocabulary are recorded and classified into cognate classes according to the criteria of comparative linguistics: two or more meanings are cognate, and are therefore assigned to the same cognate class, if their common origin can be recognised notwithstanding phonological or semantic divergence. The Swadesh list consists of items of cross-culturally universal vocabulary such as pronouns, body parts and numerals, which are less prone to innovation and borrowing than other meanings.

The linguistic data for the speech varieties included in the sample were converted into a matrix. The characters were coded using a binary coding procedure, i.e. each cognate class for the different meanings was treated as a separate character, resulting in 2449 characters for the present dataset; a form belonging to a cognate class was assigned character state ‘1’, ‘0’ otherwise. Data for the extinct Hittite language were added, to be used as the outgroup for rooting the trees. The coded linguistic data were provided by M. Pagel.

Cultural data for reconstruction of ancestral states

We collated the cultural dataset by matching the speech varieties with ethnographic data on dowry and bridewealth derived from Gray’s (1999) revised version of Murdock’s (1986) *Ethnographic atlas*, from the *Encyclopedia of world cultures* edited by Levinson (1994) and from primary ethnographic sources (Table 1). Societies were coded as dowry or bridewealth based on the direction of the parental investment, in keeping with the evolutionary interpretation of marriage transfers: we coded societies in which the bride’s family is expected to give wealth at marriage as dowry, and the ones in which the groom or his family are expected to as bridewealth. Evidence for dowry and bridewealth includes the respective codes for variable 6 (primary mode of marriage) in Gray (1999), and information on the direction of transfers from Levinson (1994) and from the primary sources.

[Table 1 approximately here]

For the sake of comparability across societies, we excluded from the analyses groups for which we found no evidence of either practice, and took the preindustrial pattern for those societies that have recently ceased the traditional practice of marriage transfers [e.g. Nazzari (1991)]. Further, we coded groups with evidence of both dowry and bridewealth as practicing one form or the other based on the prevalent mode of marriage transfer [e.g. we preferred the form in Gray’s (1999) primary mode of marriage code (variable 6) over the one in the alternate mode of marriage code (variable 7)]; these societies are italicised in Table 1. We obtained the necessary data for a total of 52 groups, including the outgroup Hittite; their geographic distribution and form of marriage transfer are shown in Figure 2.

[Figure 2 approximately here]

The cultural information for the extinct Hittite group was taken from the compendium of around 200 clauses known as *The laws*, which dates back to at least the first half of the second millennium BC (Bryce 2002, p. 34). Given that dowry is generally believed to occur in complex state societies with landed property, and that it is state societies that have the earliest written records, using cultural data for the outgroup derived from written sources could be claimed to bias the results in favour of dowry as the ancestral condition [S. Shennan, pers. comm.; e.g. Boserup (1970), Goody (1973; 1976)]. In order to asses the effect of the state of the outgroup on the estimates of ancestral states, we repeated the comparative analyses with the state for Hittite as bridewealth and as 'missing'.

One potential bias in cross-cultural analyses lies in the criterion used to code in discrete categories practices characterised by qualitative and quantitative variation, both within and across societies. In order to assess the robustness of the inferences to coding bias, we repeated the comparative analyses with the state of the fourteen societies with evidence of both forms of transfers as 'missing'. This is a conservative procedure, analogous to restricting the analysis to those groups in which only one practice is present, however it has the advantage of showing the effect of arbitrary coding decisions at the level of individual estimates.

In summary, we performed four sets of analyses: Coding A, following the coding proposed in Table 1; Coding B, as A but with Hittite coded as bridewealth; Coding C, as A but with Hittite coded as 'missing'; Coding D, as A but recoding the groups with evidence of both practices as 'missing'.

Phylogenetic inference from linguistic data

Phylogenetics is the area of biology that deals with estimating the evolutionary history of a group of individuals, populations, species or higher-level taxonomic units, extant or extinct, using morphological and molecular data. In recent years phylogenetic tree-building methods have been applied to linguistic data, based on the assumption that linguistic divergence occurs as the result of the division of speech communities in a process analogous to speciation among isolated biological populations [e.g. Dunn et al. (2005); Gray and Atkinson (2003); Gray and Jordan (2000); Holden (2002); Rexová et al. (2003)].

A phylogeny (or phylogenetic tree) is composed of nodes, which are connected by branches. Terminal nodes (or tips) correspond to the taxa for which the data used to build the tree are available. Internal nodes represent the hypothetical common ancestors of the nodes descending from them; the root of the tree is the node from which all other nodes descend, and thus represents the hypothetical ancestor common to all the taxa. In rooted trees the root is the oldest point of the tree in evolutionary time, and nodes closer to it are older than the ones that descend from them. Outgroups are taxa that are more distantly related to the taxa under investigation (called 'ingroup taxa'), and are used to determine the phylogenetic relationships among them. A hypothetical ancestor plus all the taxa descending from it form a clade (or monophyletic group). Consensus trees are used to summarise the common features of a set of trees; in majority-rule consensus trees, clades that occur in at least a specified proportion of trees are included, and the actual percentage of trees in which a clade is present is shown at each node.

In recent years Bayesian approaches to phylogenetic inference have been proposed for estimating trees and assessing the uncertainty in the reconstructions [e.g. Li et al. (2000); Mau and Newton (1997); Rannala and Yang (1996); Yang and Rannala (1997); Larget and Simon (1999); Huelsenbeck and Ronquist (2001)]. Bayesian inference is a statistical framework based on the posterior distribution (or simply 'the posterior') of hypotheses of interest, which is obtained by combining their prior distribution with information about them contained in the data (their likelihood). The distribution of prior probabilities is specified by the investigator to incorporate any *a priori* belief about the phenomenon under study without reference to the data. Since analytical computation of the posterior is only feasible for problems involving a limited number of parameters, numerical methods such as Markov chain Monte Carlo (MCMC) algorithms are used to approximate complicated ones. The underlying idea is to simulate a random walk across parameter space, i.e. the universe of possible hypotheses, and periodically sample values. The sample of hypotheses generated from the posterior distribution is used to approximate their posterior probabilities, and all subsequent inferences are based on this sample (Larget and Simon 1999; Lewis 2001).

The posterior probability of a tree is the probability of the tree conditional on the data, and can be interpreted as the probability that the tree is correct (Huelsenbeck, et al. 2001). An MCMC algorithm commonly used for Bayesian phylogenetic inference is the Metropolis-Hastings algorithm (Hastings 1970; Metropolis, et al. 1953). In Bayesian inference of phylogeny, each state in parameter space includes the tree topology and associated parameters such as branch lengths and parameters of the model of evolution. The MCMC sampler is constructed to converge to the posterior distribution of trees. The distribution of the states sampled by the Markov chain after it reaches convergence closely approximates the posterior distribution, and the proportion of the time that any state, i.e. tree topology and associated parameters, appears in the sample is a valid approximation of its posterior probability. The percentage of trees in the sample in which a node appears represents its Bayesian posterior probability, and is indicated as $p(n)$. If, for example, the Romance speech varieties form a monophyletic group in 97% of the trees in the sample, the probability that they are a monophyletic group is $p(n) = 0.97$, given the data and the model of evolution (Felsenstein 2004, p. 292). Pagel and Meade (2005) give a formal introduction to Bayesian phylogenetic inference from linguistic data.

We performed the tree-sampling on the linguistic data for the 52 speech varieties using Pagel and Meade's (2004) Bayesian MCMC sampling program *BayesPhylogenies*, available from http://sapc34.rdg.ac.uk/meade/Mark. We used Hittite as the outgroup in all analyses, uniform prior probabilities (i.e. all tree topologies and parameters of the model of evolution were considered *a priori* equally probable), and allowed the different meanings to evolve at different rates by letting rates vary according to a gamma distribution with four categories.

In order to ensure the near-independence of successive sampling events, we started the chain from a random tree. The chain added a tree (and associated parameters) to the sample every 10000 iterations, and its behaviour over time was examined by plotting the log-likelihoods of successive sampling events against iteration. As the chain was started from a random seed, the log-likelihood values increased steadily until convergence was reached; at convergence, the log-likelihoods fluctuated around a specific value. The stage before convergence is reached is referred to as 'burn-in period'; we discarded the corresponding trees from the sample. We estimated the degree of autocorrelation among successive trees in the converged sample by calculating the autocorrelation coefficient *r* (program provided by A. Meade). To ensure that the chains converged to the same region of the universe of possible trees, as indicated by average log-likelihood values and posterior probabilities of nodes on the consensus trees, we repeated this procedure ten times for each of the two models implemented by *BayesPhylogenies* for the analysis of binary data (see below), each time starting from a different random tree. All chains were run for between $10*10^6$ and $20*10^6$ iterations, with burn-ins of between $5*10^6$ and $10*10^6$ iterations.

Under the simpler model available for the analysis of binary data (time-reversible, M1P), the rates of gain of the trait (a change from state 0 to state 1) are equal to the rates of loss of the trait (a change from state 1 to state 0); under the directional model (non time-reversible, M2P), the rates of gain and loss are allowed to differ. Since the M2P model has an extra parameter compared to the M1P model, the chains may sample from slightly different regions of the universe of possible trees (M. Pagel, pers. comm.). Although both models retrieved the commonly recognised elementary Indo-European groups, the consensus trees differed in their deep splits. The log-likelihoods for sampled trees varied, at convergence, around means of -19272.40 and -19224.45 for the M1P and M2P models, respectively. Despite the significant improvement in the likelihood for M2P samples compared to M1P samples, we present the results obtained with a sample of 1000 trees generated under the M1P model, because the topology of the trees in the M1P samples is more in keeping with the outcome of previous analyses of the linguistic dataset (e.g. Gray and Atkinson 2003). Results of the comparative analyses for a sample of 650 trees generated under the M2P model are largely consistent with the ones we present here.

Reconstruction of ancestral states from cultural data

Pagel et al. (2004) and Pagel and Meade (2005) describe methods for testing comparative hypotheses across a sample of trees, which take into account the uncertainty in reconstruction of both the phylogeny and of the evolutionary scenario derived from the comparative data. They are implemented by the program *BayesMultiState*, available from http://www.rubic.rdg.ac.uk/meade/Mark.

Pagel et al. (2004) focus on the issue of reconstructing ancestral states. They propose the use of a continuous-time Markov model to describe the evolution of the trait of interest along the branches of a phylogeny. Under this model, a binary trait can evolve repeatedly between its two possible states in any of the branches of a tree. The trait ‘marriage transfer’, for example, can evolve repeatedly between its two states B (bridewealth) and D (dowry) along the branches of a phylogeny. The parameters q_{BD} and q_{DB} measure the instantaneous rate of change from bridewealth to dowry and from dowry to bridewealth, respectively, and are used to define the probability of these changes (Pagel 1994; 1999). Their posterior probability distribution can be approximated from the sample of trees and from the comparative data using a Markov chain that periodically samples values, following the Metropolis-Hasting algorithm.

The chain can also be used to estimate the posterior probability distribution of states D and B at internal nodes. Given that different nodes will be present on different trees in a sample, the estimated posterior probabilities at node n are denoted as $p(D \mid n)$ for state D and $p(B \mid n) = 1 - p(D \mid n)$ for state B, indicating that they are derived only from those trees in the sample in which node n is present. The probability of a tree having a node and of that node adopting states D or B, $p(D)$ or $p(B)$, can be approximated by multiplying the estimated posterior probability of state D or B, $p(D \mid n)$ or $p(B \mid n)$, by the probability that node n exists, $p(n)$, as estimated from the tree-sampling procedure above, that is $p(D) = p(D \mid n) * p(n)$ or $p(B) = p(B \mid n) * p(n)$. The sum of the combined probabilities of the two states equals the node's posterior probability, $p(D) + p(B) = p(n)$, whereas the remainder of the probability, 1-$p(n)$, corresponds to the probability that the node does not exist. In other words, by combining information on the uncertainty about the existence of a node with information on the uncertainty in the estimate of the ancestral state, this approach limits the confidence that can be placed in the reconstruction of an ancestral state if the node is itself uncertain (Pagel, et al. 2004).

We performed the comparative analyses using *BayesMultiState* on the sample of 1000 trees and the marriage transfer data for the 52 cultural groups. We restricted the parameters q_{BD} and q_{DB} to take equal values, as this did not cause a significant reduction in the likelihood. The Markov chain used uniform prior probabilities, and was run for $10*10^6$ iterations, with a burn-in period of 10000. This ensured that the chain visited each tree in the sample repeatedly; we ensured that the chain reached convergence as described above for the tree samples. The chain started from a random tree, and sampled parameters every 100 iterations. The proposal mechanism responsible for changing the parameters at every iteration was set to 10, which resulted in an average 24.9% of the proposed changes being accepted between two sampling events for Coding A, 30.0% for Coding B, 26.3% for Coding C and 31.8% for Coding D. Each set of parameters and associated tree sampled were used to estimate the posterior probabilities of states D and B, $p(D \mid n)$ and $p(B \mid n)$, at internal nodes. The combined probabilities $p(D)$ and $p(B)$ were obtained as described above; values ≥ 0.70 were arbitrarily taken as the reconstruction for a state at a node as being certain.

RESULTS

Phylogenetic tree sample

The autocorrelation coefficient for the 1000 trees sampled by the Markov chain after it reached convergence was $r = - 0.002$, indicating the near-independence of successive sampling events. Figures 3 and 5 show the majority rule consensus tree of the sample, including clades present in more than 50% of the trees and other compatible groupings. The number of trees, out of a hundred, in which a node appears is reported above each node, and represents its posterior probability $p(n)$.

The topology confirms the commonly recognised elementary Indo-European groupings (Albanian, Iranian, Indic, Slavonic, Celtic, Germanic, Romance), which were all recovered as monophyletic with high posterior probabilities [$p(n) = 0.96$ for Indic; $p(n) = 1$ for all other clades]. Previously suggested higher groupings such as Indo-Iranian and Balto-Slavonic were also recovered with $p(n) = 1$. Some of the groupings both above and below this level were recovered with lower posterior probabilities, however resolution of higher level relationships among the elementary Indo-European groups has proven a difficult task using both classical comparative linguistic and computational phylogenetic methods (e.g. Gray and Atkinson 2003; Rexová, et al. 2003; Ruhlen 1991). In general, the gross topology is compatible with widely accepted hypotheses on the historical relationships among Indo-European groups. The following discussion on the phylogenetic context of the evolution of marriage transfers in Indo-European groups refers to the topology of the consensus tree, although the topology of individual trees in the sample will differ from it.

Reconstructed ancestral states

Values of the combined probabilities $p(D)$ and $p(B) \geq 0.70$ were arbitrarily taken as the reconstruction for a state at a node as being certain. In the consensus trees shown in Figures 3 and 5, nodes with $p(D) \geq 0.70$ are in black, nodes with $p(B) \geq 0.70$ are in white, and nodes with combined probabilities < 0.70 for both states are indicated by dashed lines.

Figure 3 shows the estimated ancestral states obtained for Coding A. Results indicate that dowry is more likely to have been the ancestral practice for the Indo-European groups [node indicated by the asterisk: $p(n) = 1.00$; $p(D \mid n) = p(D) = 0.97 \pm 0.04$, range: 0.53 – 1.00; $p(B \mid n) = p(B) = 0.03 \pm 0.04$, range: 0.00 – 0.47]. The pattern of reconstructed states suggests that dowry was retained throughout most of the tree, and that a minimum of four changes from dowry to bridewealth is necessary to explain the distribution of the two states at its tips. These changes are indicated by the arrows in Figure 3; the probabilities of the two states for the respective nodes are reported in Table 2.

[Figure 3 and Table 2 approximately here]

The panels in Figure 4 show the estimated distributions of posterior probabilities of the two states at the root, obtained for Coding A – D; mean values are reported in Table 3. Results indicate dowry as more likely to have been the ancestral state at the root for Coding A, C and D; for Coding B, the combined probabilities of both states < 0.70.

[Figure 4 and Table 3 approximately here]

Results also indicate that alternative coding of the outgroup (Coding B and C), negligibly affected the estimation of ancestral states at other nodes (Table 3). Results for Coding D are presented in Figure 5, in which the societies coded as ‘missing’ are italicised. This coding affected the estimation of ancestral states for the Albanian, Indic and Iranian clades, in which all or many of the groups were coded as 'missing'. Results also suggest that a change from the ancestral condition of dowry to bridewealth is likely to have occurred at the base of the Indo-Iranian clade [$p(n) = 1.00$; $p(D \mid n) = p(D) = 0.27 \pm 0.11$, range: 0.01 – 0.66; $p(B \mid n) = p(B) = 0.73 \pm 0.11$, range: 0.34 – 0.99]. The estimation of the ancestral states for the node where the split between the Romance, Germanic, Celtic and Slavonic from the remaining clades occurs was also marginally affected [$p(n) = 0.76$; $p(D \mid n) = 0.89 \pm 0.07$, $p(D) = 0.67$, range: 0.50 – 1.00; $p(B \mid n) = 0.11 \pm 0.07$, $p(B) = 0.08$, range: 0.00 – 0.50]. The inference that dowry is more likely to have been the ancestral practice for the Indo-European groups was however not affected [node indicated by the asterisk: $p(n) = 1.00$; $p(D \mid n) = p(D) = 0.95 \pm 0.06$, range: 0.50 – 1.00; $p(B \mid n) = p(B) = 0.05 \pm 0.06$, range: 0.00 – 0.50]

DISCUSSION AND CONCLUSIONS

Kinship and marriage practices have left only fragmentary information about their evolution in the historical and archaeological records. Consequently their analysis has largely been synchronic, both across and within societies, rather than diachronic [e.g. Goody (1983, pp. 240-261)]. The belief that dowry results from a shift towards higher civilisation can be dated back to Aristotle (Hughes 1985, p. 15), and many scholars dealing with the nature of marriage transactions have assumed some long-term progression from bridewealth to dowry (Goody 1983, p. 240). However, the evidence supporting such a shift is, for the most part, anecdotal, and this widespread assumption possibly stems from the lack of principled and systematic investigation of the development of the practices over time (Goody 1983, p. 261). In this paper we use Bayesian MCMC phylogenetic and comparative methods to reconstruct the evolutionary history of marriage transfers in Indo-European groups. Results indicate that dowry is more likely to have been the ancestral practice, and that a minimum of four changes to bridewealth is necessary to explain the observed distribution of the two states across the cultural groups. Further analyses confirm the robustness of these inferences to potential coding biases. Nevertheless, alternative evolutionary scenarios cannot be excluded, because state reconstructions at some nodes are not certain, and because under the model of evolution implemented a trait is allowed to evolve repeatedly between its two possible states in any branch of a tree.

Results also indicate dowry as more likely to have been the ancestral state at the root; even coding the outgroup Hittite as bridewealth fails to retrieve this state as the ancestral condition at the root. This finding is in line with Gurney's (1975) and Bryce's (2002) interpretation of Hittite marriage transfers. Legal and religious texts, from the Code of Hammurabi to the Bible, from Old Babylonian myths to ancient Egyptian records, suggest that bridewealth was the legally required marital transaction for most of the historic peoples of the Mediterranean; simultaneous giving to brides of dowry was however known to the ancient Assyrian, Babylonian, Hebrew and Sumerian civilisations, as early as in the third and second millennia BC. The available evidence suggests that bridewealth invariably disappeared, often to be replaced by dowry, as these ancient Mediterranean societies grew and prospered (Goody 1990; Hughes 1985; Kaplan 1985b). Hittite marriage was accompanied by *kusata*, a symbolic gift from the groom to the bride's family generally referred to as 'brideprice', and by *iwaru*, a substantial dowry provided to the bride by her father, often a share of the family estate (Bryce 2002, p. 120; Gurney 1975, p. 100). However, both Gurney (1975, p. 100) and Bryce (2002, p. 120) express reservations about viewing *kusata* as bridewealth. *Kusata* marriage was of particular importance in the formalisation of unions between slave and free, and was required in order for the free partner to retain free status. This was in the slave partner's best interest, given that the descendants of mixed marriages also acquired free status. The fact that *kusata* was given by a male slave marrying a free woman, and by the father of the bride when a free man married into a slave family supports this interpretation of the practice (Bryce 2002, pp. 121-124).

Cross-cultural analyses of marriage transfers have been hindered by awareness of the fact that dowry and bridewealth are not opposite or opposed practices, and by their degree qualitative and quantitative variation within and across groups (Goody 1973, p. 1; Hughes 1985, p. 15, p. 40). The approach we use in this paper circumvents these issues by grounding the distinction between dowry and bridewealth on an evolutionary model based on the tenets of parental investment theory and supported by empirical data, and by assessing the effects of arbitrary coding decisions on the inferences made. Further, by explicitly incorporating information on the phylogenetic relationships among the groups, on the uncertainty in their estimations and on the estimation of the parameters of interest to the comparative question, this approach largely improves on previous attempts to infer historical information from cross-cultural data, offering a promising tool for systematically investigating the diachronic development of cultural practices.

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BIOGRAPHICAL NOTES

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Table 1 Form of marriage transfer of cultural groups associated with 51 Indo-European speech varieties and with Hittite.

Map legend[a]	Speech variety[b]	Ethnonym[c]	Marriage tranfer	Source
1	Afghan	*Pushtun, Pathan*	Bridewealth	Gray (1999); Levinson (1994)
-	Afrikaans	Boers	Dowry	Gray (1999)
2	Albanian G	*Gheg*	Bridewealth	Gray (1999)
3	Albanian T	*Tosk*	Bridewealth	Goody (1990); Hasluck (1954); Levinson (1994)
4	Armenian Mod	Armenians	Dowry	Gray (1999); Levinson (1994)
5	Baluchi	Baluchi	Bridewealth	Levinson (1994)
6	Bengali	*Bengali*	Dowry	Gray (1999)
-	Brazilian	Brazilians	Dowry	Nazzari (1991)
7	Breton List	Bretons	Dowry	Brékilien (1966)
8	Bulgarian	*Bulgarians*	Dowry	Genchev (1988); Goody (2000); Levinson (1994)
9	Byelorussian	Byelorussians	Dowry	Gray (1999)
10	Catalan	Catalans	Dowry	Casey (1999); Levinson (1994)
11	Czech	Czechs	Dowry	Gray (1999)
12	Dutch List	Dutch	Dowry	Goody (2000); Wijsenbeek-Olthuis (1996)
13	English ST	English	Dowry	Goody (1983)(2000)
14	French	French	Dowry	Goody (2000)
15	German ST	Germans, Tiroleans	Dowry	Kaplan (1985a); Levinson (1994)
16	Greek MD	Greeks	Dowry	Gray (1999); Goody (1990); Lambiri-Dimaki (1985); Levinson (1994); Sant Cassia and Bada (1991)
17	Gujarati	*Gujarati*	Bridewealth	Gray (1999)
18	Icelandic ST	Icelanders	Dowry	Gray (1999)
19	Irish B	Irish	Dowry	Gray (1999)
20	Italian	Italians, Sicilians	Dowry	Goody (1976; 2000); Levinson (1994); Schneider (1985)
21	Kashmiri	*Pandits of Kashmir*	Dowry	Levinson (1994); Tambiah (1973)
22	Khaskura	*Nepali*	Dowry	Levinson (1994)
23	Lahnda	*Punjabi*	Dowry	Levinson (1994)
24	Lithuanian O	Lithuanians	Dowry	Gray (1999); Levinson (1994)
25	Macedonian	Slav Macedonians	Dowry	Levinson (1994)
26	Marathi	Maratha	Bridewealth	Levinson (1994)

27	Nepali List	*Nepali*	Dowry	Levinson (1994)
28	Ossetic	*Ossetes*	Bridewealth	Gray (1999); Levinson (1994)
29	Panjabi ST	*Punjabi*	Dowry	Gray (1999); Levinson (1994)
-	Pennsylvania Dutch	Mennonites	Dowry	Levinson (1994)
30	Persian List	Iranians	Bridewealth	Gray (1999)
31	Polish	Kashubians	Dowry	Levinson (1994)
32	Portuguese ST	Portuguese	Dowry	Cutileiro (1971); Gallop (1961)
33	Russian	Russians	Dowry	Gray (1999)[d]; Goody (2000); Levinson (1994)
34	Sardinian C	Sardinians	Dowry	Oppo (1990); Goody (2000)
35	Serbocroatian	Croats, Serbs	Dowry	Gray (1999); Levinson (1994)
36	Singhalese	Kandyan, Sinhalese	Dowry	Gray (1999); Levinson (1994); Tambiah (1973)
37	Slovak	Slovaks	Dowry	Levinson (1994)
38	Slovenian	Slovenes	Dowry	Levinson (1994)
39	Spanish	Spanish	Dowry	Goody (1973; 2000)
40	Swedish List	Swedes	Dowry	Levinson (1994)
41	Tadzik	Tajik	Bridewealth	Levinson (1994)
-	Takitaki	Saramaka	Bridewealth	Gray (1999)
42	Ukrainian	Ukrainians	Dowry	Gray (1999); Levinson (1994)
43	Vlach	Sarakatsani	Dowry	Levinson (1994)
44	Wakhi	Pamirians	Bridewealth	Levinson (1994)[e]
45	Walloon	Walloons	Dowry	Alter (1988); Gray (1999)
46	Waziri	*Pushtun, Pathan*	Bridewealth	Gray (1999); Levinson (1994)
47	Welsh N	Welsh	Dowry	Rees (1950)
48	Hittite	*Hittites*	Dowry	Bryce (2002); Gurney (1975)

[a] Refers to Figure 2; Afrikaans, Brazilian, Pennsylvania Dutch and Takitaki shown in inset.

[b] Derived from Dyen et al. (1992, pp. 99-101); in cases where more than one speech variety could be associated with the same cultural group, the first one in the list was arbitrarily selected. Hittite added as the outgroup.

[c] Groups in italics are the ones with evidence of both practices, coded as ‘missing’ for Coding D.

[d] Gray (1999) has ‘reciprocal gift exchange’ as primary mode of marriage (variable 6), and dowry as alternate mode (variable 7).

[e] Levinson (1994) specifies that although there is no formal payment of bridewealth, the family of the groom spend a considerable amount to provide the couple with all necessities.

Table 2 Probabilities of the two states at the nodes indicated by the arrows in Figure 3

Clade	$p(n)$	$p(D \mid n)$ ± sd (range)	$p(D)$	$p(B \mid n)$ ± sd (range)	$p(B)$
Albanian	1.00	0.00 ± 0.00 (0.00 – 0.05)	0.00	1.00 ± 0.00 (0.95 – 1.00)	1.00
Iranian	1.00	0.01 ± 0.01 (0.00 – 0.27)	0.01	0.99 ± 0.01 (0.73 – 1.00)	0.99
Indic	1.00	0.00 ± 0.00 (0.00 – 0.10)	0.00	1.00 ± 0.00 (0.90 – 1.00)	1.00
Germanic	0.99	0.60 ± 0.07 (0.31 – 0.80)	0.59	0.40 ± 0.07 (0.20 – 0.69)	0.40

Table 3 Probabilities of the two states at the root and relative mean differences for Coding A – D

Coding[a]	$p(D \mid n)$ ± sd[b] (range)	$p(B \mid n)$ ± sd[b] (range)	Mean difference [c] ± sd (range)
A	0.99 ± 0.02 (0.59 – 1.00)	0.01 ± 0.02 (0.00 – 0.41)	--
B	0.44 ± 0.26 (0.00 – 0.99)	0.56 ± 0.26 (0.01 – 1.00)	0.00 ± 0.00 (0.00 – 0.01)
C	0.89 ± 0.08 (0.50 – 1.00)	0.11 ± 0.08 (0.00 – 0.50)	0.01 ± 0.01 (0.00 – 0.04)
D	0.87 ± 0.09 (0.50 – 1.00)	0.13 ± 0.09 (0.00 – 0.50)	0.12 ± 0.23 (0.00 – 0.86)

[a] A: as shown in Table 1; B: as A but with Hittite coded as bridewealth; C: as A but with Hittite coded as ‘missing’; D: as A but recoding groups with both practices as ‘missing’.

[b] For the root $p(n) = 1.00$, i.e. in all cases $p(D \mid n) = p(D)$ and $p(B \mid n) = p(B)$.

[c] Obtained from the absolute values of the differences between the estimates of $p(D \mid n)$ and $p(B \mid n)$ at nodes other than the root for Coding A and the same estimates for Coding B – D.

FIGURE CAPTIONS

Figure 1. Hypothetical phylogenetic tree showing the relationships among seven taxa and the distribution of the two possible states of trait X.

Figure 2. Geographical distribution and form of marriage transfer of cultural groups associated with 51 Indo-European speech varieties and with Hittite. Legend as indicated in Table 1. Map not to scale.

Figure 3. Majority rule consensus tree of the 1000 trees sampled from the converged Markov chain for 51 Indo-European speech varieties and the outgroup Hittite. Branch lengths were fitted as the maximum likelihood values obtained from applying the HKY + Γ model with four rate categories. Groups in black practice dowry, the ones in white bridewealth. Probabilities of the two states at the nodes were obtained using Coding A: $p(D) \geq 0.70$ are indicated by nodes in black, $p(B) \geq 0.70$ by nodes in white, $p(D)$ and $p(B)$ both < 0.70 by dashed nodes.

Figure 4. Estimated distribution of posterior probabilities of bridewealth $[p(B \mid n)]$ and dowry $[p(D \mid n)]$ at the root for Coding A – D.

Figure 5. The consensus tree in Figure 3 with the probabilities of the two states obtained using Coding D. As in Figure 3, groups in black practice dowry, the ones in white bridewealth; $p(D) \geq 0.70$ are indicated by nodes in black, $p(B) \geq 0.70$ by nodes in white, $p(D)$ and $p(B)$ both < 0.70 by dashed nodes.

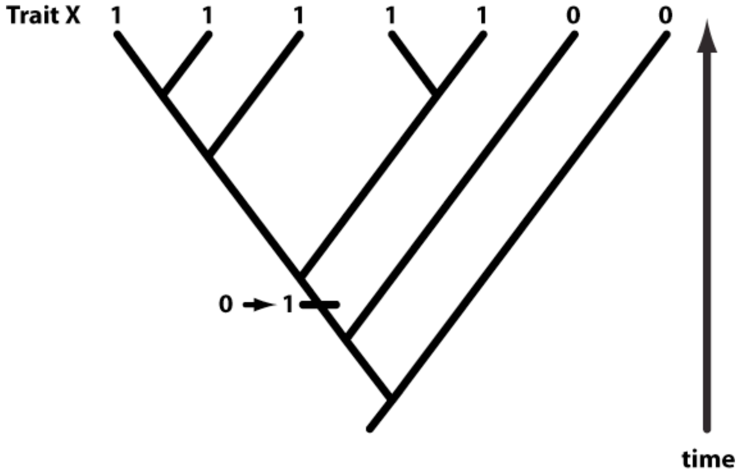


Figure 1

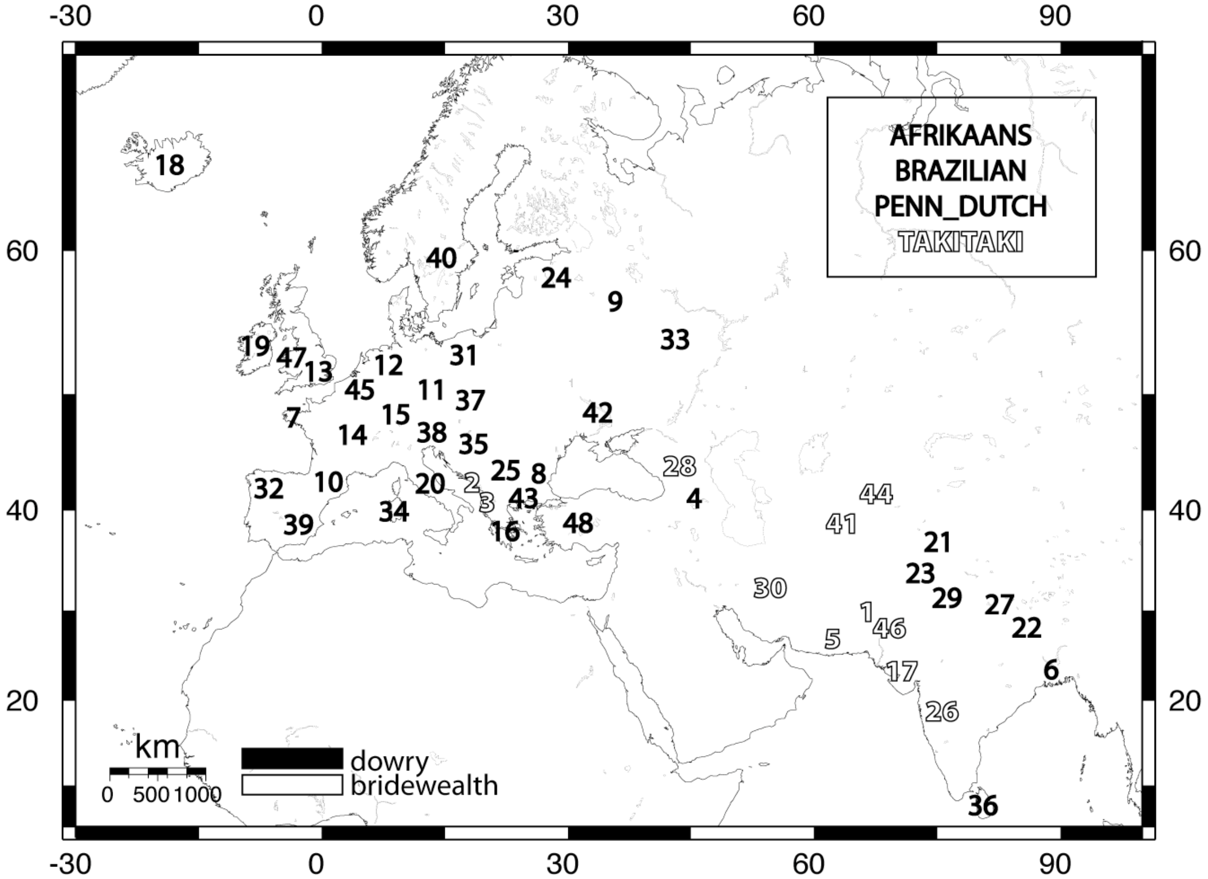
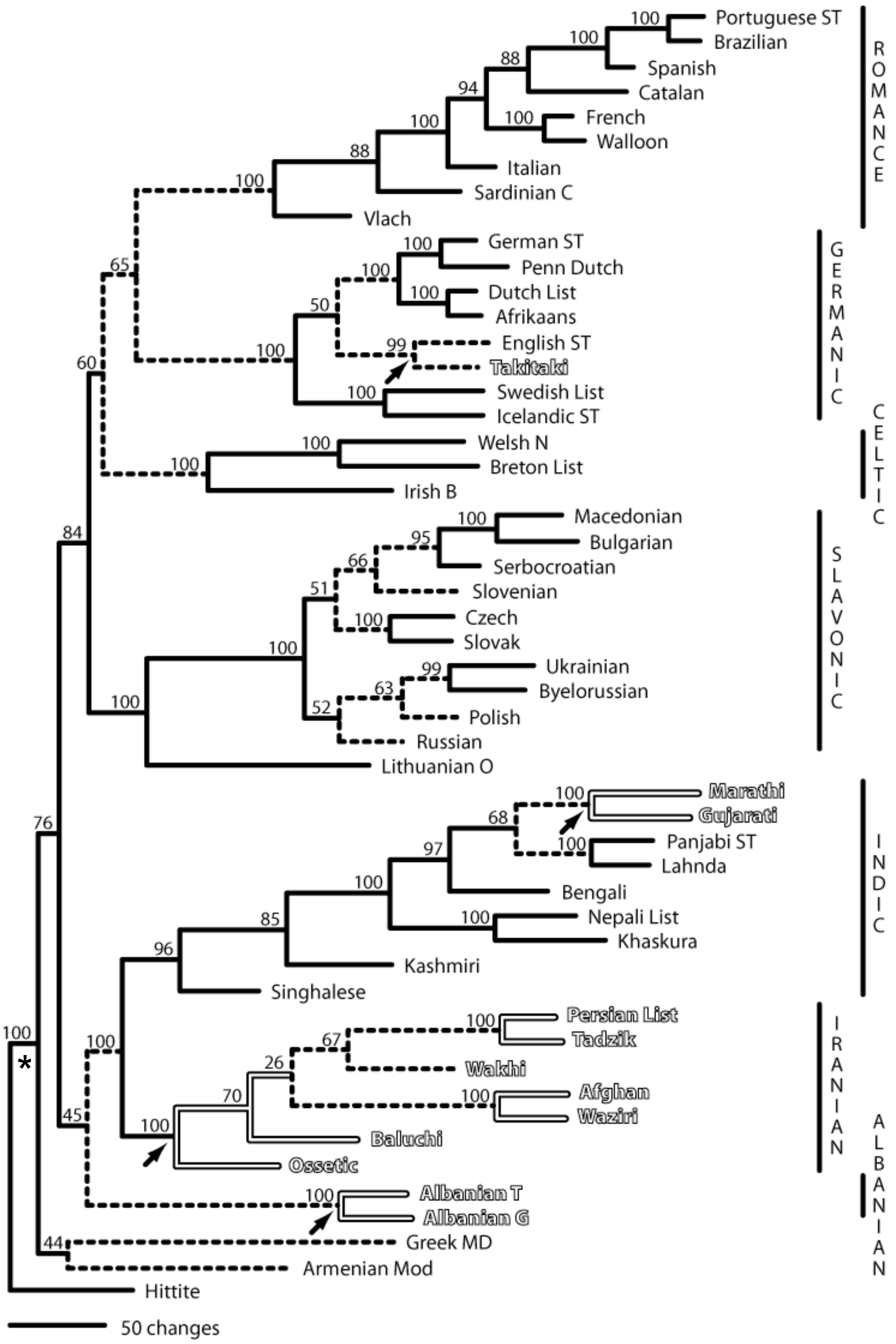


Figure 2


100
Portuguese ST
Brazilian
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Spanish
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Catalan
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French
Walloon
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Italian
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Sardinian C
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Vlach
ROMANCE
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German ST
Penn Dutch
100
100
Dutch List
Afrikaans
50
99
English ST
Takitaki
65
100
100
Swedish List
Icelandic ST
GERMANIC
60
100
Welsh N
100
Breton List
Irish B
CELTIC
84
100
Macedonian
Bulgarian
95
66
Serbocroatian
Slovenian
51
100
Czech
Slovak
100
99
Ukrainian
Byelorussian
63
100
52
Polish
Russian
Lithuanian O
SLAVONIC
100
Marathi
Gujarati
68
100
Panjabi ST
Lahnda
97
100
Bengali
85
100
Nepali List
Khaskura
96
Kashmiri
Singhalese
76
100
Persian List
Tadzik
67
Wakhi
26
100
Afghan
Waziri
70
100
Baluchi
Ossetic
IRANIAN
100
45
100
Albanian T
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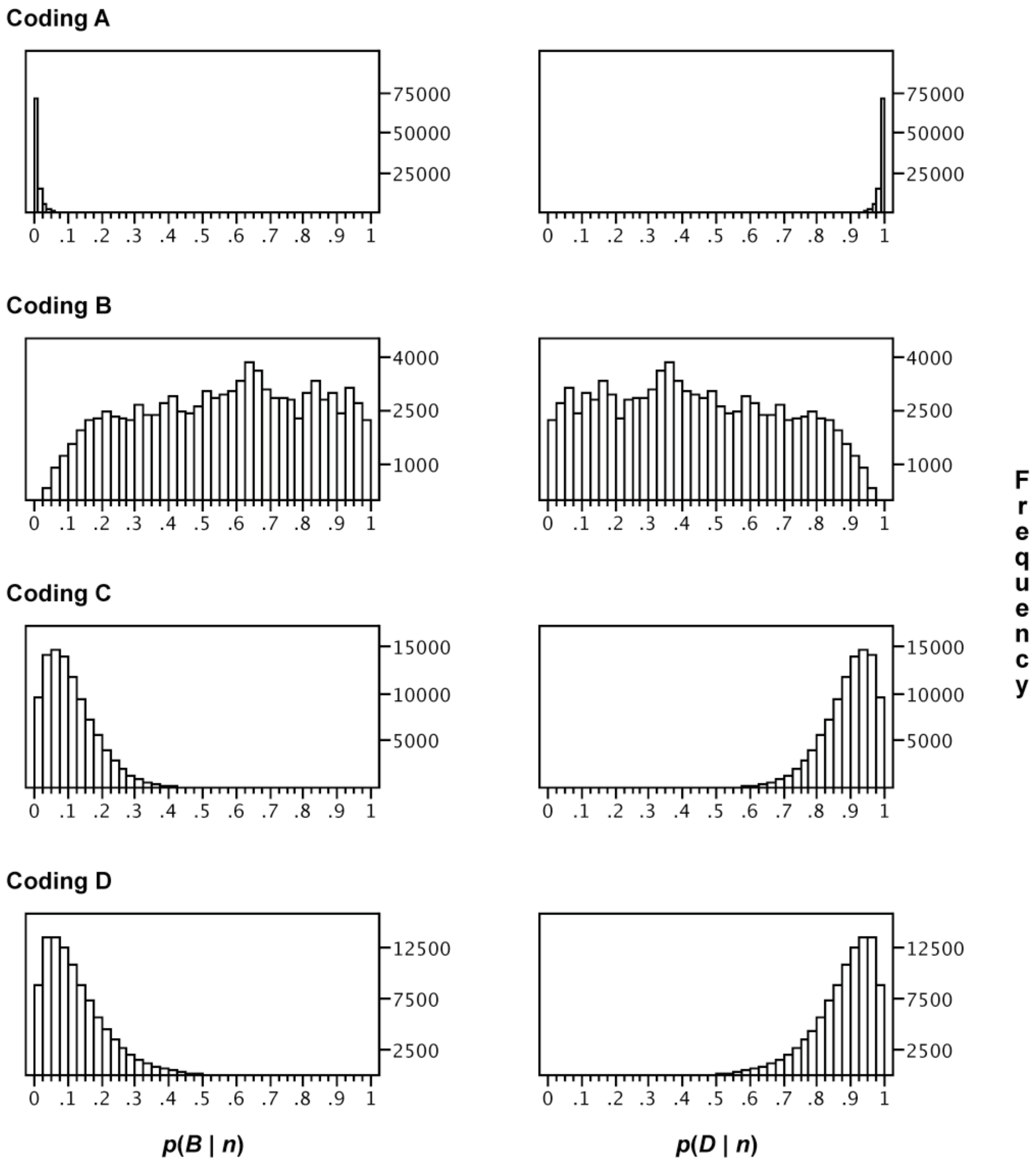
*
44
Greek MD
Armenian Mod
Hittite
50 changes
INDIC

Figure 3


Coding A
75000
50000
25000
0
.1
.2
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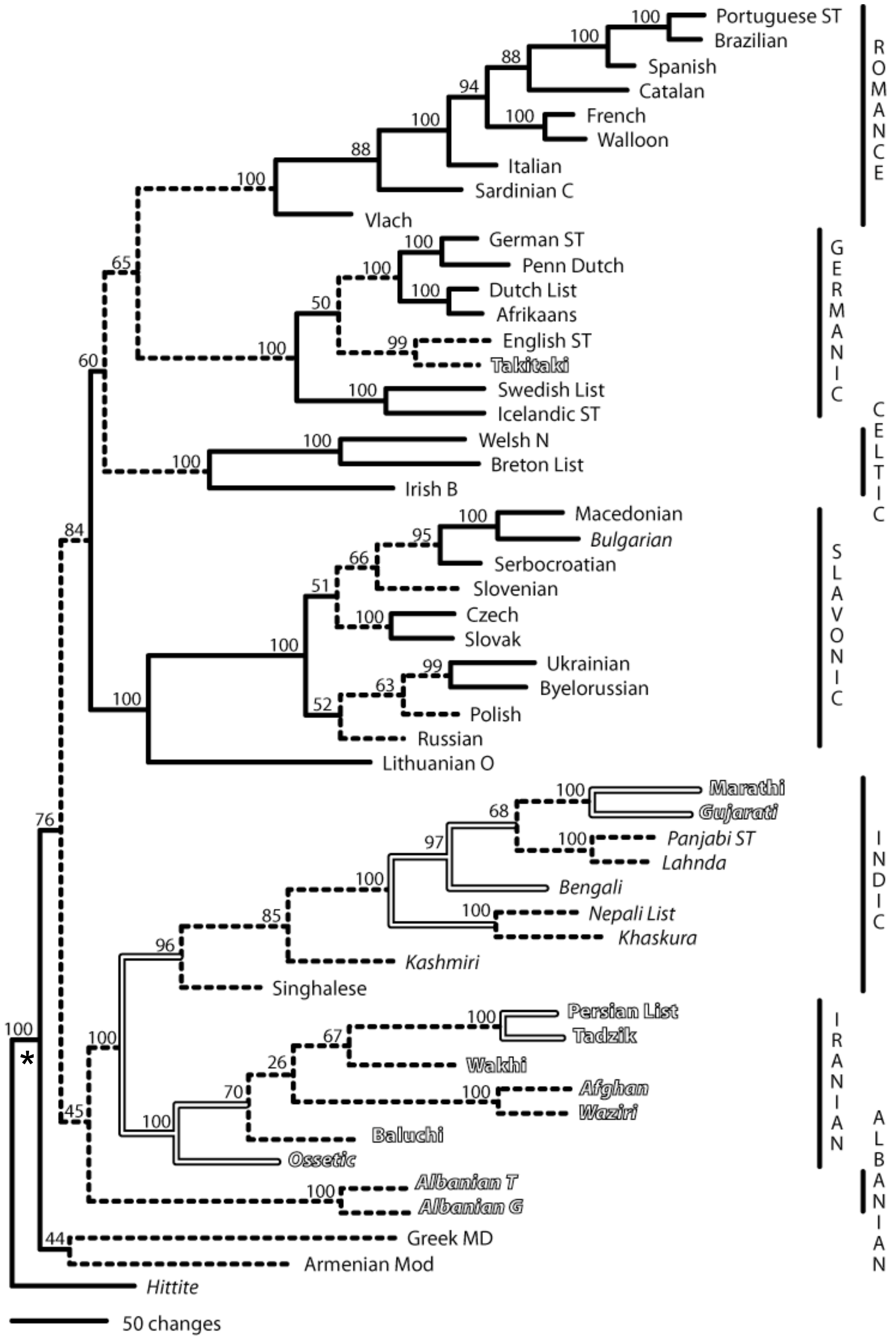
.4
.5
.6
.7
.8
.9
1
Coding B
4000
2500
1000
Coding C
15000
10000
5000
Coding D
12500
7500
2500
Frequency
$p(B \mid n)$
$p(D \mid n)$

Figure 4


100 Portuguese ST
Brazilian
100 Spanish
88 Catalan
94
100 French
Walloon
100 Italian
88 Sardinian C
100 Vlach
ROMANCE
100 German ST
Penn Dutch
100 Dutch List
Afrikaans
100
50
99 English ST
Takitaki
65
100
100 Swedish List
Icelandic ST
GERMANIC
60
100 Welsh N
100 Breton List
Irish B
CELTIC
100 Macedonian
Bulgarian
95 Serbocroatian
66 Slovenian
51
100 Czech
Slovak
100
99 Ukrainian
Byelorussian
63 Polish
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100 Panjabi ST
Lahnda
97 Bengali
100 Nepali List
Khaskura
85 Kashmiri
96 Singhalese
INDIC
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100 Persian List
Tadzik
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100 Afghan
Waziri
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100 Ossetic
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Albanian G
ALBANIAN
44 Greek MD
Armenian Mod
100
*
Hittite
50 changes

Figure 5