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The peopling of Europe and the cautionary tale of Y chromosome lineage R-M269

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Recently, the debate on the origins of the major European Y chromosome haplogroup R1b1b2-M269 has reignited, and opinion has moved away from Palaeolithic origins to the notion of a younger Neolithic spread of these chromosomes from the Near East. Here, we address this debate by investigating frequency patterns and diversity in the largest collection of R1b1b2-M269 chromosomes yet assembled. Our analysis reveals no geographical trends in diversity, in contradiction to expectation under the Neolithic hypothesis, and suggests an alternative explanation for the apparent cline in diversity recently described. We further investigate the young, STR-based time to the most recent common ancestor estimates proposed so far for R-M269-related lineages and find evidence for an appreciable effect of microsatellite choice on age estimates. As a consequence, the existing data and tools are insufficient to make credible estimates for the age of this haplogroup, and conclusions about the timing of its origin and dispersal should be viewed with a large degree of caution.

Keywords: Y-STRs; R1b1b2-M269; neolithic hypothesis; average squared distance

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1. INTRODUCTION
Since the first attempts to use biological variation in humans to aid our understanding of early human migrations, the peopling of Europe has been a major research focus [1,2]. Following the development of agriculture in the Fertile Crescent some 10,000 years ago [3,4], this technology spread from the Near East westward into Europe, causing a major cultural transition from itinerant hunter–gathering to sedentary farming, which led to dramatic population growth [5,6], during what has become known as the Neolithic transition [7,8]. Within this archaeological framework, debate rages about the relative contributions to modern European populations of the first people of Europe and those who migrated into it with the Neolithic transition, both in terms of their genetic legacy and as to the processes of migration and succession [9–16]. The true scenario is undoubtedly multi-faceted and complex. Both early work on ‘classical markers’ using principal components analysis and more recent studies using the Y chromosome have shown that in Europe, genetic variation is distributed along a southeast–northwest gradient. Such observations have been suggested to support a model of demic diffusion for the Neolithic transition in Europe (i.e. that the spread of agriculture also involved an associated movement of people from the Near East) [2,17–19].

New work [20–22] has addressed the Neolithic transition in Europe by focusing on the main western European Y chromosome haplogroup R1b1b2-M269 (hereafter referred to as R-M269). This lineage had hitherto received little recent attention in this context, although previous work suggested that the broader R-M173 clade (excluding the R1a-M17 sub-lineage) and Haplogroup 1 (derived at chromosome haplogroup R1b1b2-M269 (hereafter referred to as R-M269) European-specific sub-lineage, defined by SNP S127, showing an essentially homogeneous background of microsatellite variation at several different sub-lineage levels, based on a common set of 10 STRs typed across 2000 R-M269 chromosomes.

While acknowledging uncertainty, researchers usually report the age of Y chromosome lineages based on differences between individuals across multiple STRs, often using average squared distance (ASD) or related summary statistics [25,26] as unbiased estimators of coalescence time, \( T \). We investigated how ASD changes in our dataset based on different sets of STRs. Contrary to common belief, estimates of ASD, and therefore \( T \), vary widely when different subsets of STRs are used with the same sample. While recent evidence has increased support for the Neolithic spread of R-M269, we conclude that at the present time it is not possible to make any credible estimate of divergence time based on the sets of Y-STRs used in recent studies. Furthermore, we show that it is the properties of Y-STRs, not the number used per se, that appear to control the accuracy of divergence time estimates, attributes which are rarely, if ever, considered in practise.

2. MATERIAL AND METHODS
(a) Ethics statement
All males sampled gave informed consent following ethical approval by the ethics committees at the various universities where the samples were collected.

(b) DNA samples and genotyping
We assembled a dataset of 2486 R-M269 Y chromosomes from across Europe, the Near East and western Asia, from a total population of 6503, which included both novel and previously published Y chromosomes. To assess the frequency...
distribution of R-M269 and various sub-haplogroups in Europe and Asia, we combined our data with that of Myres et al. [21], which gave a combined set of 4529 R-M269 chromosomes from a total sample of 16298 from 172 different populations (electronic supplementary material, table S1 and figure S1). The frequencies of the following SNPs, whose phylogeny is shown in figure 1, were ascertained: S127/L11 (rs9768076), S21/U106 (rs16981293), S116 (rs34276300), S145/M529 (rs11799226) and S28/U152 (rs1236440). Samples were amplified in a standard PCR reaction and the SNaPshot Multiplex System (Life Technologies Corp., Carlsbad, CA, USA) primer extension protocol was used to provide alternative nomenclature for some SNPs is provided in italics.

(c) Analysis
Maps of SNP frequencies were displayed using ArcMap GIS (v. 9.2; ESRI). Interpolation was performed using the inverse distance weighting procedure. Latitudes and longitudes for all populations were based on the highest-resolution sampling centre associated with the samples and are shown in electronic supplementary material, table S1.

The R statistical package [32] was used to calculate the median STR variance (the variance in the number of repeats within a locus averaged across all loci) between all individuals within a population following 1000 bootstrap replicates with replacement over individuals. Regression analysis was performed in R to compare average STR variance with latitude and longitude for the R-M269, R-M269(xS127) and R-S127 haplogroups.

We investigated how ASD estimates change within our sample when using different combinations of STRs based on two separate criteria: mutation rate, \( \mu \); and observed linearity, \( \theta(R) \) (table 1). We used the observed \( \mu \) calculated recently [33] to rank the 15 STRs on a scale of speed, and separately calculated ASD based on the seven fastest and seven slowest rates (electronic supplementary material, table S4). Our second criterion was based on the estimated duration of linearity, \( D \), of different groups of STRs. Duration of linearity is an estimate of the divergence time after which ASD ceases to increase linearly with time. For STRs mutating under a strict stepwise model, Goldstein et al. showed that ASD initially increases linearly with time, but that this linearity is constrained by the maximum number of repeats an STR can take, \( R \) [26]. \( D \) is approximated using \( \theta(R) \) (which is a simple transformation of \( R \) and \( \mu \)) and the effective population size (Ne) (eqns 3 and 4 in [26]). Greater values of \( \theta(R)/2\mu \) yield increased estimates of \( D \). Using STRs with greater values of \( \theta(R)/2\mu \) should allow linearity to be assumed further into the past, and ASD calculated from these STRs should be less likely to be underestimated as a result of saturation. Table 1 and electronic supplementary material, table S4 show the different groups of STRs used and associated values of \( \mu \), \( R \), \( \theta(R)/2\mu \) and ASD.

To check that any differences in time to the most recent common ancestor (TMRCA) estimation are not specific to methods based on ASD, we used BATWING [35] on the HGDP Bedouin population for which a greater number of Y-STRs (n = 65) were available [36]. We compared four different sets of STRs with varying degrees of duration of linearity estimates (electronic supplementary material).

3. RESULTS
To investigate the origins of the R-M269 lineage in Europe, we analysed a large dataset of 4529 R-M269 chromosomes (2486 of which have not previously been published at such detailed resolution) from several populations across Europe, the Near East and western Asia (electronic supplementary material, figure S1 and table S1). Within Europe, we observed a northwest–southeast frequency cline for R-M269, similar to those observed previously [10,11,37], from high frequencies in western Europe to lower frequencies in the east. Within haplogroup R-M269 we genotyped a newly characterized SNP, S127 (equivalent to L11), for which the distribution in Europe and the Near East, together with that of R-M269 and R-M269(xS127), are shown in figure 2. The distributions of R-M269 and R-S127 are broadly consistent with the original haplotypes of Weale et al. [21], which gave a combined set of 4529 R-M269 chromosomes from a total sample of 16298 from 172 different populations (electronic supplementary material, table S1 and figure S1). The frequencies of the following SNPs, whose phylogeny is shown in figure 1, were ascertained: S127/L11 (rs9768076), S21/U106 (rs16981293), S116 (rs34276300), S145/M529 (rs11799226) and S28/U152 (rs1236440). Samples were amplified in a standard PCR reaction and the SNaPshot Multiplex System (Life Technologies Corp., Carlsbad, CA, USA) primer extension protocol was used to characterize the allele present at each SNP loci. All primers are listed in the electronic supplementary material.

For the majority of the individuals typed in this study (2289), the following 10 STRs were available: DYS19; DYS389I; DYS389b (subtracting the alleles scored at DYS389I from the DYS389II locus); DYS390; DYS391; DYS392; DYS393; DYS437; DYS438; and DYS439, either being previously published or having been typed by ourselves using the Yfiler kit (Life Technologies Corp., Carlsbad, CA, USA) primer extension protocol was used to characterize the allele present at each SNP loci. All primers are listed in the electronic supplementary material.

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Table 1. Fifteen Y-STRs with mutation rates, range of alleles and estimate of duration of linearity. All STRs investigated in this study are shown with their mutation rates ($\mu$), estimated from Ballantyne et al. [33], and range of observed alleles, $R$, with 95% CI is taken from the YHRD [34]. $\theta(R)/2\mu$ is an estimate of the duration of linearity of an STR (see §2).

<table>
<thead>
<tr>
<th>Y-STR</th>
<th>$\mu$</th>
<th>$\mu(2.5)$</th>
<th>$\mu(97.5)$</th>
<th>$R$</th>
<th>$\theta(R)/2\mu$</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS448</td>
<td>0.00394</td>
<td>0.000141</td>
<td>0.00211</td>
<td>11</td>
<td>25.381</td>
</tr>
<tr>
<td>DYS392</td>
<td>0.00097</td>
<td>0.00143</td>
<td>0.00323</td>
<td>15</td>
<td>19.244</td>
</tr>
<tr>
<td>DYS438</td>
<td>0.00056</td>
<td>0.00137</td>
<td>0.00318</td>
<td>12</td>
<td>12.465</td>
</tr>
<tr>
<td>DYS390</td>
<td>0.00152</td>
<td>0.00352</td>
<td>0.00409</td>
<td>13</td>
<td>9.211</td>
</tr>
<tr>
<td>DYS393</td>
<td>0.00211</td>
<td>0.00621</td>
<td>0.005</td>
<td>12</td>
<td>5.648</td>
</tr>
<tr>
<td>DYS439</td>
<td>0.00384</td>
<td>0.00163</td>
<td>0.00754</td>
<td>15</td>
<td>4.861</td>
</tr>
<tr>
<td>DYS437</td>
<td>0.00153</td>
<td>0.00354</td>
<td>0.0041</td>
<td>9</td>
<td>4.357</td>
</tr>
<tr>
<td>DYS635</td>
<td>0.00385</td>
<td>0.00163</td>
<td>0.00755</td>
<td>14</td>
<td>4.221</td>
</tr>
<tr>
<td>DYS456</td>
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<td>0.00235</td>
<td>0.00897</td>
<td>14</td>
<td>3.289</td>
</tr>
<tr>
<td>DYS389II</td>
<td>0.00383</td>
<td>0.00161</td>
<td>0.00749</td>
<td>12</td>
<td>3.111</td>
</tr>
<tr>
<td>DYS391</td>
<td>0.00323</td>
<td>0.00126</td>
<td>0.00665</td>
<td>10</td>
<td>2.554</td>
</tr>
<tr>
<td>DYS458</td>
<td>0.00836</td>
<td>0.0048</td>
<td>0.0134</td>
<td>14</td>
<td>1.944</td>
</tr>
<tr>
<td>DYS19</td>
<td>0.00437</td>
<td>0.00198</td>
<td>0.00823</td>
<td>10</td>
<td>1.888</td>
</tr>
<tr>
<td>Y-GATA-H4</td>
<td>0.00322</td>
<td>0.00128</td>
<td>0.00662</td>
<td>8</td>
<td>1.630</td>
</tr>
<tr>
<td>DYS389I</td>
<td>0.00551</td>
<td>0.00272</td>
<td>0.00974</td>
<td>8</td>
<td>0.953</td>
</tr>
</tbody>
</table>

overlapping, but the frequency of R-S127 drops off around the Balkans, reaching extremely low values further to the east and outside of Europe. Conversely, R-M269(xS127) shows higher frequencies in eastern populations. Frequency maps showing three geographically localized R-S127 sub-haplogroups (R-S21, R-S145 and R-S28) are shown in figure 3.

We next calculated STR diversity for each population for the whole R-M269 lineage, and for the R-S127 and R-M269(xS127) sub-haplogroups, and investigated the relationship between average STR variance and longitude and latitude in exactly the same fashion as Balaresque. We provide estimates of uncertainty for these values by bootstrapping over individuals, and report the median of the observed variance values and its 95 per cent CI (figure 2). We normalized latitude and longitude, and performed a linear regression between these values and the median microsatellite variance for the three R-M269 sub-haplogroups. We found no correlation with latitude (data not shown) and, contrary to Balaresque, we did not find any significant correlation between longitude and variance for any haplogroup.

The Balaresque dataset presents genotype data only to the resolution of SNP R-M269. Our results show that the vast majority of R-M269 samples in Anatolia, approximately 90 per cent, belong to the R-M269(xS127) sub-haplogroup. Removing these Turkish populations from the Balaresque data and repeating the regression removes the significant correlation ($R^2 = 0.23$, $p = 0.09$; details in the electronic supplementary material and figure S2). These populations are therefore intrinsic to the significant correlation.

We observed that the Irish haplotypes used in the Balaresque analysis had a very low STR variance (0.208) compared with those included in our analysis (0.35; originally published by Moore et al. [38]). Balaresque used a sample of Irish haplotypes downloaded from the online Ysearch database (http://www.ysearch.org). To test if the Ysearch haplotypes were representative of the Irish R-M269 of Moore et al. [38], we independently resampled the Moore et al. dataset 10 000 times, selecting sub-samples of 75 haplotypes from which we estimated the variance using the same nine STRs used in the Balaresque paper (detailed methodology and justification can be found in the electronic supplementary material). The median variance of these 10 000 replications was 0.354 with a 95 per cent CI of (0.285–0.432). When we repeated the regression analysis with this different variance estimate, the correlation was no longer significant ($R^2 = 0.09$, $p = 0.19$).

Microsatellite-based ASD has been shown to increase linearly with time [26] and has been used as an unbiased estimator of mean coalescence time, given that it approximates to $2\mu T$ [21,25,39]. It would be expected that using different sets of STRs should not dramatically alter the estimation of $T$: as $\mu$ changes, ASD should similarly change, with $T$ staying constant. Table 1 shows estimates of the duration of linearity based on observed mutation rates estimated recently [33] and range estimated from the YHRD [34]. The ASD for R-S127 was calculated by comparing the 15 STR haplotypes of its two major sub-haplogroups, R-S21 (141 chromosomes) and R-S116 (717; electronic supplementary material, table S3). Figure 4a is a plot of $T$ (estimated as ASD/2$\mu$) for several different sets of STRs with different characteristics (electronic supplementary material, table S4).

To further explore the correlation between $T$ and STR selection, we calculated $T$ in the same way as described above based on chromosomes belonging to the two deepest branches of the Y chromosome phylogeny, AxA1 and B [40] (figure 4b; electronic supplementary material, table S4). As a comparison, ASD calculated from the same STR subsets is shown for the R-S127 on the same plot.

4. DISCUSSION

Here, we have confirmed with the broadest analysis to date that the spatial distribution of Y chromosome haplogroup M269 can be split by R-S127 into European and western Eurasian lineages. Contrary to the results of Balaresque, we see no relationship between diversity
and longitude (figure 2) for R-M269. The presence of two sets of populations in the Balaresque paper appears to be causal to the observed relationship: the underestimated diversity of the Irish population and the inclusion of the Turkish chromosomes, the majority of which potentially belong to the non-European clade R-M269(xS127). When these elements are properly taken into account, jointly or independently, the correlation no longer exists. This correlation is the central tenet to the hypothesis that R-M269 was spread with expanding Neolithic farmers.

Morelli et al. [22] (hereafter ‘Morelli’) found STR motifs that split R-M269 into eastern and western lineages. We observed that 71 per cent of the Myres et al. R-M269(xS127) chromosomes for which STR information is available have the eastern motif (DYS393-12/DYS461-10), while 80 per cent of the R-S127 chromosomes of Myres et al. have the western

Figure 2. Frequency distributions and variation of Y chromosome haplogroups R-M269, R-S127 and R-M269(xS127) in Europe. The three panels show contour maps based on the frequencies of the different haplogroups found across Europe and western Asia: (a) R-M269, (b) R-S127 and (c) R-M269(xS127). The maps on the left are based on the frequencies of the SNPs in all populations marked on the map (data in electronic supplementary material, table S1 and figure S1). The graphs on the right show the relationship between longitude and bootstrap variance based on 10 STRs for all populations with at least 10 individuals carrying that SNP. The $R^2$ and associated p-values are shown for the correlations in the graphs. The population codes are detailed in table 1 and electronic supplementary material, table S1.
Dating of Y chromosome lineages is notoriously controversial [25,41–44], the major issue being that the choice of STR mutation rate can lead to age estimates that differ by a factor of three (i.e. the evolutionary [25] versus observed (genealogical) mutation rates [33,45]). Interestingly, despite the fact that Myres et al. and Balaresque used different STR mutation rates and dating approaches, their TMRCA estimates overlap: 8590–11 950 years using a mutation rate of $6.9 \times 10^{-4}$ per generation, and 4577–9063 years using an average mutation rate of $2.3 \times 10^{-3}$, respectively. Separately, Morelli calculated the TMRCA based only on Sardinian and Anatolian chromosomes, and estimated the R-M269 lineage to have originated 25 000–80 700 years ago [22], based on the same evolutionary mutation rate [25,41] as Myres et al.

In seeking to find a suitable set of STRs with which to estimate the average coalescence time, $T$, of sub-haplogroup R-S127, we have shown that not all STRs are of equal use in this context. We concentrated on estimating the duration of linearity, $D$, using different sets of STRs. Our analyses suggest that the $D$ of an STR is key to its ability to uncover deep ancestry. Duration of linearity refers to the length of time into the past over which ASD and $T$ continue to be linearly related for a specific STR. Goldstein et al. [26] showed that $D$ is affected by two properties of the STRs used to calculate ASD: the mutation rate and range of possible alleles that the STR can take. When we manipulated our choice of STR marker based on $u(R)/2m$ (a surrogate for $D$; table 1), we found that different sets of STRs gave different values for $T$. It is clear, then, that coalescence estimates explicitly depend on the STRs that one uses.

Our analysis confirms that this phenomenon is not specific to the R-M269 haplogroup nor to methods using ASD. Figure 4b shows that STRs with high $D$ produce larger estimates of $T$. What is clear is that estimates of $T$ implicitly depend on the STRs that are selected to make this inference. Using BATWING on an HGDP population for which 65 Y-STRs are available, we have shown that the median estimate of TMRCA can differ by over five times when STRs are selected on the basis of the expected duration of linearity (electronic supplementary material, figure S4). While researchers take into account STR mutation rates when estimating divergence time with ASD, commonly used STRs do not have the specific attributes that allow linearity to be assumed further into the past. The majority of haplogroup dates based on such sets of STRs may therefore have been systematically underestimated.

5. CONCLUSION

The distributions of the main R-S127 sub-haplogroups, R-S21, R-S145 and R-S28, show markedly localized concentrations (figure 3). If the R-M269 lineage is more recent in origin than the Neolithic expansion, then its current distribution would have to be the result of major population movements occurring since that origin. For this haplogroup to be so ubiquitous, the population carrying R-S127 would have displaced most of the populations present in western Europe after the Neolithic agricultural transition. Alternatively, if R-S127 originated prior to the Neolithic wave of
expansion, then either it was already present in most of Europe before the expansion, or the mutation occurred in the east, and was spread before or after the expansion, in which case we would expect higher diversity in the east closer to the origins of agriculture, which is not what we observe. The maps of R-S127 sub-haplogroup frequencies for R-S21, R-S145 and R-S28 show radial distributions from specific European locations (figure 3). These centres have high absolute frequencies: R-S21 has a frequency of 44 per cent in Friesland, and R-S28 reaches 25 per cent in the Alps; and in the populations where they are at the highest frequency, the vast majority of R-S127 belong to that particular sub-lineage. For example, half of all R-M269 across southern Europe is R-S28-derived, and around 60 per cent of R-M269 in Central Europe is R-S21-derived. At the sub-haplogroup level, then, R-M269 is split into geographically localized pockets with individual R-M269 sub-haplogroups dominating, suggesting that the frequency of R-M269 across Europe could be related to the growth of multiple, geographically specific sub-lineages that differ in different parts of Europe.

A recent analysis of radiocarbon dates of Neolithic sites across Europe [46] reveals that the spread of the Neolithic was by no means constant, and that several ‘centres of renewed expansion’ are visible across Europe, representing areas of colonization, three of which map intriguingly closely to the centres of the sub-haplogroups foci (electronic supplementary material, figure S3). Future work involving spatially explicit simulations, together with accurate measures of Y chromosome diversity, are needed to investigate how the current distribution of sub-haplogroups may have been produced. In this context, recent work by Sjödin & François [47] rejected a Palaeolithic dispersion for R1b-M269 using spatial simulations based on the dataset of Balaresque. Nevertheless, we note that additional work is still necessary as these authors were not aware of the limitation of the Balaresque dataset presented here, and did not fully explore the impact of the different molecular characteristics of the investigated loci on their analysis.

Age estimates based on sets of Y-STRs carefully selected to possess the attributes necessary for uncovering deep ancestry (for example, from the almost 200 recently characterized here [33]), and from whole Y chromosome
sequence comparisons, will provide robust dates for this haplogroup in the future. For now, we can offer no date as to the age of R-M269 or R-S127, but believe that our STR analyses suggest the recent age estimates of R-M269 [20] and R-S116 [21] are likely to be younger than the true values, and the homogeneity of STR variance and distribution of sub-types across the continent are inconsistent with the hypothesis of the Neolithic diffusion of the R-M269 Y chromosome lineage.

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