

## SHORT REPORT

# Investigating mitochondrial DNA relationships in Neolithic Western Europe through serial coalescent simulations

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Recent ancient DNA studies on European Neolithic human populations have provided persuasive evidence of a major migration of farmers originating from the Aegean, accompanied by sporadic hunter-gatherer admixture into early Neolithic populations, but increasing toward the Late Neolithic. In this context, ancient mitochondrial DNA data collected from the Neolithic necropolis of Gurgy (Paris Basin, France), the largest mitochondrial DNA sample obtained from a single archeological site for the Early/Middle Neolithic period, indicate little differentiation from farmers associated to both the Danubian and Mediterranean Neolithic migration routes, as well as from Western European hunter-gatherers. To test whether this pattern of differentiation could arise in a single unstructured population by genetic drift alone, we used serial coalescent simulations. We explore female effective population size parameter combinations at the time of the colonization of Europe 45000 years ago and the most recent of the Neolithic samples analyzed in this study 5900 years ago, and identify conditions under which population panmixia between hunter-gatherers/Early-Middle Neolithic farmers and Gurgy cannot be rejected. In relation to other studies on the current debate of the origins of Europeans, these results suggest increasing hunter-gatherer admixture into farmers' group migrating farther west in Europe.

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## INTRODUCTION

The introduction of farming into Europe around 8600 years ago led to fundamental changes in subsistence strategy and social organization, and left signatures of population turnover.<sup>1–4</sup> It is widely believed that farming spread into Europe from the Aegean along both Mediterranean and Danubian routes.<sup>3,5</sup> Recent archeological<sup>6</sup> and paleogenetic evidence<sup>1,2,4,5,7</sup> indicate a crucial role for migration, with only sporadic hunter-gatherer (HG) admixture into early Neolithic populations, but increasing toward the Late Neolithic.<sup>1,7,8</sup> However, these local inferences still permit spatiotemporal heterogeneity in HG admixture during the Neolithic in continental Europe.

In this context, the mitochondrial DNA (mtDNA) diversity of the Gurgy 'Les Noisats' site, located south of the Paris Basin and dated from 7000 to 6000 years ago, is striking since descriptive analyses<sup>9</sup> indicated affinities not only with early farmers associated with both the Danubian and Mediterranean migration routes but also with European HG. Notably, a relatively lower differentiation between Gurgy and European HG ( $F_{ST} = 0.08$ ) was observed when compared with other published levels of differentiation between Early Neolithic farmers and HG (eg,  $F_{ST} = 0.0923$  (ref. 10);  $F_{ST} = 0.163$  (ref. 2)). This suggests complex admixture pattern between HG and farmer groups to shape Gurgy mtDNA diversity.

Previous mtDNA studies<sup>2,10,11</sup> have used serial coalescent simulations to test for genetic continuity between HG, Neolithic farmers and extant DNA samples from the same geographic region, and regularly concluded in genetic discontinuity between groups. We used a similar approach to address if the observed level of mtDNA differentiation between European HG, Neolithic farmer and Gurgy groups could be obtained under a panmictic population model with various combinations of effective population sizes. Our approach differs in three major aspects from previous studies:<sup>2,10,11</sup> first, we grouped the ancient mtDNA sequences according to subsistence strategy (HG or Neolithic farmers) and Neolithic context (Mediterranean/South-, Danubian/Central- or Gurgy- farmers). Some of the sample groups are consequently contemporaneous and can represent various regions. Second, we did not include modern population sample into the comparison. Third, we extended the effective population size ranges used previously<sup>2,11</sup> toward the lower bound to explore further demographic scenarios.

## MATERIALS AND METHODS

We compiled 282 available ancient mtDNA HVR-I sequences (NC\_012920.1:m.16024\_16380; Supplementary Table S1). Following Rivollat *et al.* 2015, ancient mtDNA data were partitioned into four sample

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groups: (i) Gurgy Les Noisats necropolis (hereafter referred to as 'Gurgy',  $n=39$  sequences), (ii) Neolithic farmers from south Europe (group 'South-F',  $n=56$ , partitioned into four chronological subgroups), (iii) Neolithic farmers from central Europe ('Central-F',  $n=147$ , 5 subgroups) and (iv) hunter-gatherers ('HG',  $n=40$ , 16 subgroups). Chronological subgroups were defined according to both shared geographic location and median calibrated C14 dates (see Figures 1 and 2). As a test statistic that measures the level of population differentiation, we calculated six pairwise  $F_{ST}$  between the four groups (Figure 3) with ARLSUMSTAT version 3.5.1.2.<sup>12</sup>

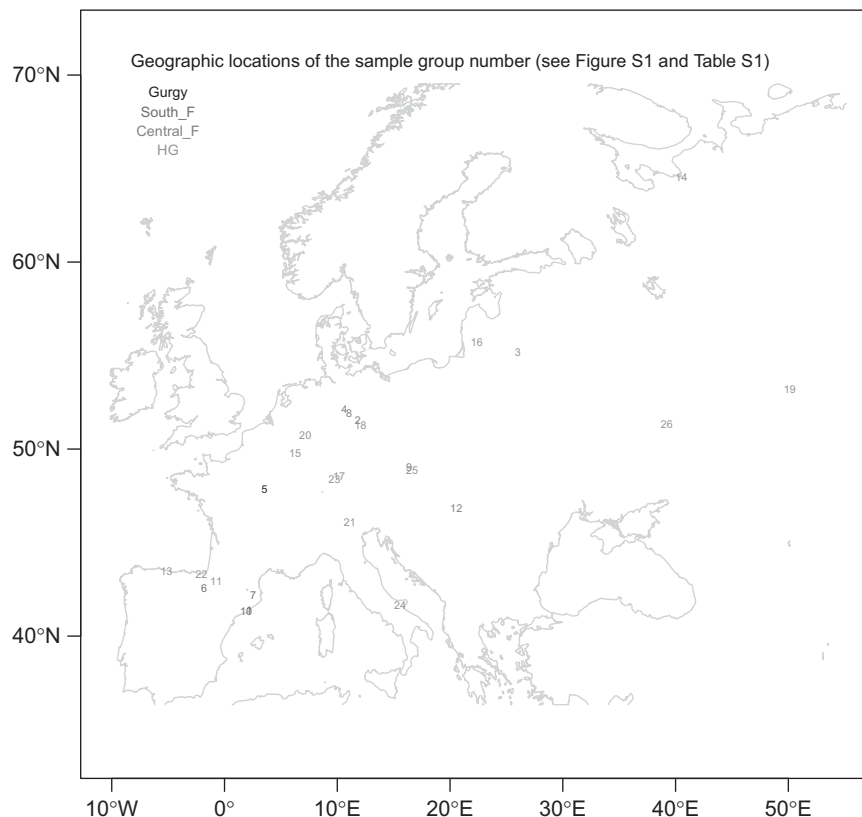
Following previous studies,<sup>2,11</sup> we performed serial coalescent simulations under a single panmictic population model with two demographic events: an initial colonization of Europe 45 000 years ago of female effective population size  $N_{UP}$ , followed by exponential growth or decline to the Neolithic transition in Western Europe 5900 years cal. BP of female effective population size  $N_N$ . Before  $N_{UP}$ , we assume an ancestral female effective population size  $N_A$  of 5000, derived from the commonly used long-term effective human population size of 10 000 individuals outside Africa<sup>13</sup> and assuming a 1:1 female to male ratio. We explored 50 values for  $N_{UP}$  ranging from 1 to 5000 and 50 values for  $N_N$  ranging from 10 to 100 000 (Supplementary Table S2). We generated 50 000 mitochondrial genealogies of ancient HG and farmer sequences using fastsimcoal version 2.5.1 (ref. 12) under each of the 2500  $N_{UP}$ - $N_N$  combinations (Supplementary Table S2). We used a fixed mutation rate of  $5 \times 10^{-6}$ /bp/generation,<sup>15</sup> assuming a 25 years generation time. These simulated genealogies were used to compute expected pairwise  $F_{ST}$  values for the six sample comparisons (Figure 2). We recorded the proportion of

simulated  $F_{ST}$  values that were greater than those observed per  $F_{ST}$  and parameter combination (Figure 3).

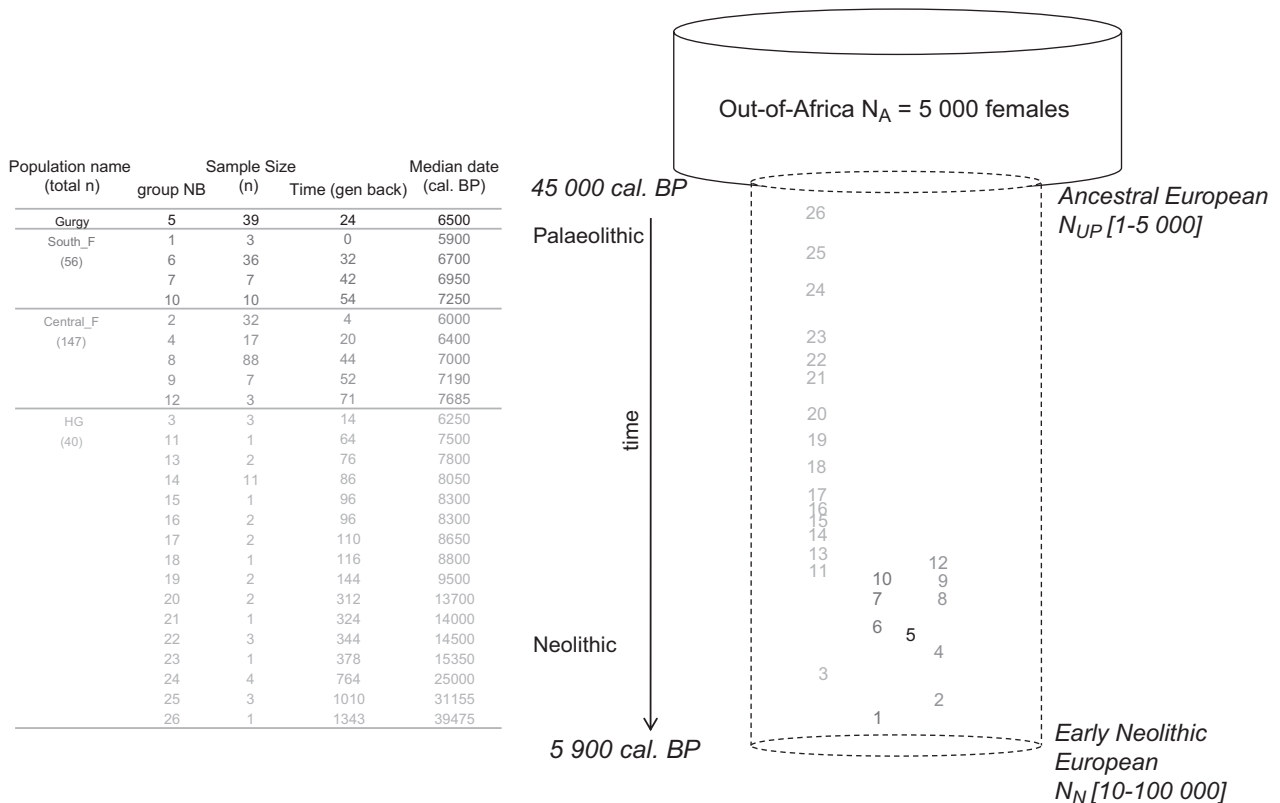
We also tested if the six observed pairwise  $F_{ST}$  values as well as eight within sample group statistic values (number of segregating sites and of pairwise differences) could be recovered from simulations under this simple model by performing an approximate Bayesian computation (ABC)-related approach<sup>16</sup> (see details in SI). We used the rejection algorithm of the 'abc' package<sup>17</sup> available in R to retain the parameter combinations that generated simulated pairwise  $F_{ST}$  the closest to the six observed values. Even though we provide some effective population size estimates, we caution against over-interpretation since there is likely insufficient information in the data to make precise estimates.

## RESULTS AND DISCUSSION

Analyses indicate that for the six pairwise population group comparisons, some  $N_{UP}$ - $N_N$  combinations can result in simulated differentiation greater than the one observed (gray area on Figure 3). Notably, results show that we cannot reject the possibility that European HG, South-F, Central-F and Gurgy were sampled from a single panmictic population. Whereas these results may appear to contrast with previous studies that have used serial coalescent simulations to address local mtDNA population continuity between diachronic HG and farmers samples,<sup>2,11</sup> we highlight that our analyses do not address 'population continuity' as defined in these studies. The grouping of diachronic



**Figure 1** Geographic locations of the sites sampled for ancient mtDNA in the current analysis. 1 refers to the most recent sample group in the gene genealogy and 26 to the most ancient. Groups were categorized based on common median C14 dates, archeological context and geographic location; one group can consequently be sampled from more than one geographic location; for those groups with more than one location, only the location of the largest sample size group is displayed on the map (details in Figure 2 and Supplementary Table S1).



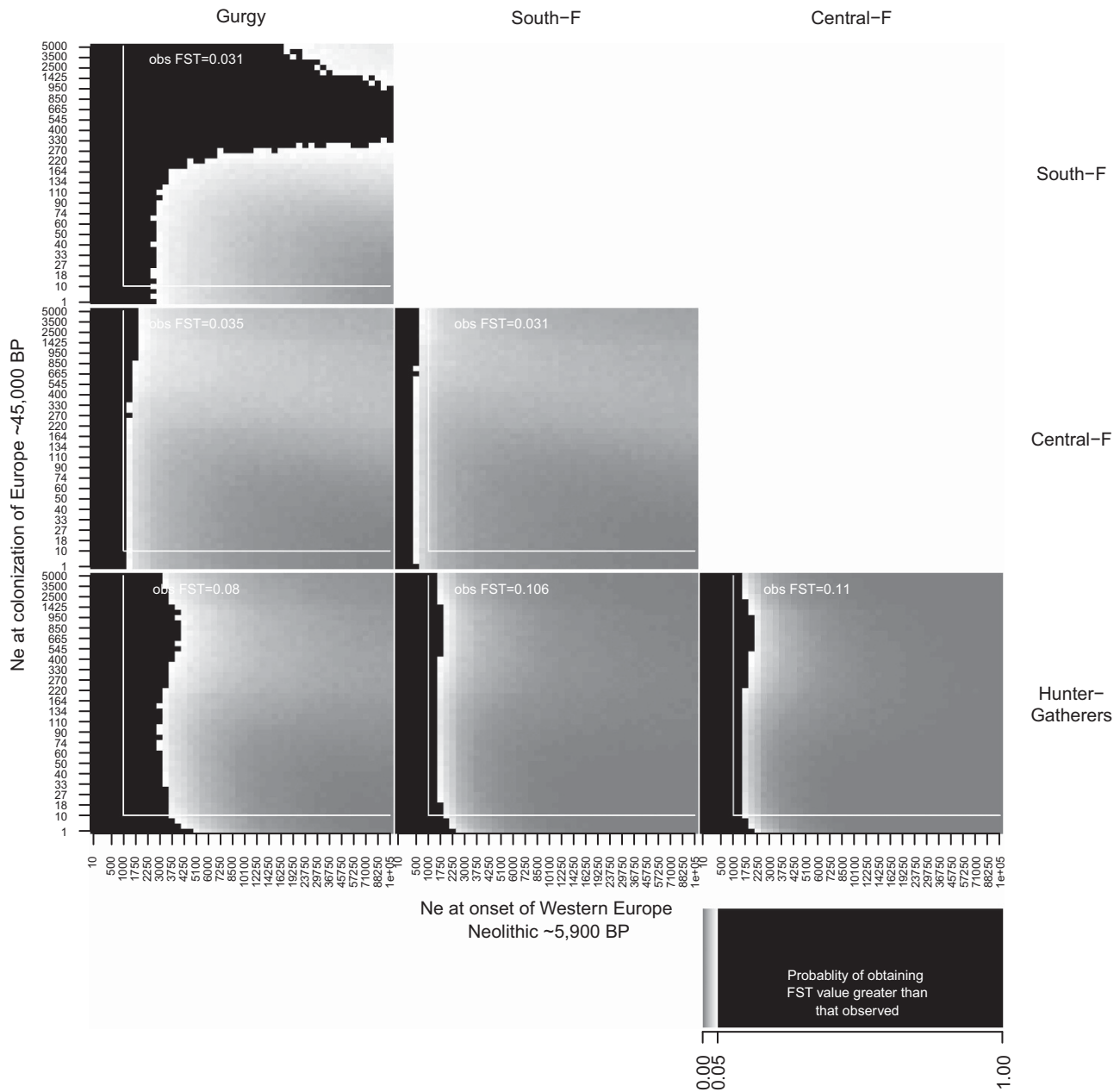
**Figure 2** Demographic model simulated with the serial coalescent. Time is the median calibrated C14 years before present (cal BP) backward in time from ‘t0’ and expressed in generations. ‘t0’ refers to 5900 years cal. BP, the median C14 date of the youngest ancient mtDNA sample. Groups are numbered backward in time from the most recent to the most ancient. The dashed cylinder shows constant population size between  $N_{UP}$  and  $N_N$ , but the simulated population can undergo expansion or decline depending on the combinations of these parameter values.

samples may artificially reduce the level of differentiation that would be observed in case of significant mtDNA population structure. This grouping none-the-less allows us to investigate the genetic relationships between set of lineage samples associated with specific archeological Neolithic contexts.

We confirmed that our panmictic population model generated simulated between and within population group diversity values close to the observed using an ABC-rejection algorithm (see SI and Supplementary Figure S1). The 95% credible intervals estimated from the retained simulations are (5–3500)  $N_{UP}$  females and (200–7750)  $N_N$  females. These estimates concur with the observation that the parameter space for which a panmictic population model may hold is rather narrow (Figure 3). Most  $N_N$  values tested and compatible with the level of mtDNA differentiation observed are relatively low (10–200 females for the South-F and Central-F comparison, Figure 3). Noteworthy, some  $N_{UP}$ – $N_N$  combinations imply a population decline that clearly contrasts with previous studies based on modern DNA data, which have inferred female effective population size growth in Europe during the Holocene.<sup>18</sup> However, we were not constrained to simulate population expansion, since we did not consider modern DNA data in our analyses. Moreover, a Holocene population decline in Europe corroborates recent Y chromosome data<sup>18</sup> and various archeological evidence support demographic fluctuation of Neolithic populations.<sup>19,20</sup>

Our results indicate that a simple panmictic population model can account for the mtDNA differentiation observed between European HG and Early/Middle Neolithic farmers; a larger proportion of the HG–Gurgy explored parameter space failed to reject panmixia. This result suggests increasing HG admixture into farmers’ group migrating farther west in Europe. Similarly, we note that a larger proportion of the explored parameter space fails to reject panmixia when comparing Gurgy and South-F than when comparing Gurgy and Central-F. Thus, our results seem to support Gurgy as the most ancient Neolithic sample studied so far with appreciable admixture between pre-Neolithic HG and Early/Middle Neolithic farmers from both streams of Neolithization in Europe (with a suspected higher participation of Mediterranean farmers).

As with any model, the one we test here has a few assumptions that may not hold, for example,  $N_A$  of female to male ratio of 1 (ref. 18) and no population structure in any of the four groups.<sup>5</sup> Moreover, the panmictic population model proposed would need to be compared against alternatives (eg, ref. 11). Such a simple panmictic population model nevertheless lays the ground for building more complex ones.<sup>17</sup> Notably, a serial coalescent approach coupled with ABC would allow estimation of the possible contribution of each of the three population groups (HG, Mediterranean and Central Europe farmers) in shaping Gurgy mitochondrial diversity.



**Figure 3** Probability of obtaining simulated  $F_{ST}$  value greater than that observed for the six pairwise population groups compared (see text for details). Corresponding observed pairwise  $F_{ST}$  are shown in the top left corner of each grid. The  $50 \times 50$  grids show values of assumed effective population size  $N_N$  on the x-axis and values of parameterized  $N_{UP}$  on the y-axis (note that 25 values are shown on each axis for clarity, see Supplementary Table S2). The top right area delimited by vertical and horizontal black lines outline  $N_N$  and  $N_{UP}$  ranges, respectively, used in comparable studies.<sup>2,11</sup> Gray shows proportions of observed  $F_{ST}$  greater than observed (proportion  $> 0.05$ ), for which panmixia cannot be rejected. Color-scale represents significance level from blue (proportion lower or equal to 0.05) to red (proportion close to 0). Proportions were obtained over 50 000 simulated pairwise  $F_{ST}$  per combination of  $N_N$  and  $N_{UP}$  value. A full color version of this figure is available at the *European Journal of Human Genetics* journal online.

**CONFLICT OF INTEREST**

The authors declare no conflict of interest.

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