Human ancient DNA analyses reveal the high burden of tuberculosis in Europeans over the last 2,000 years

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Summary

Tuberculosis (TB), usually caused by Mycobacterium tuberculosis bacteria, is the first cause of death from an infectious disease at the worldwide scale, yet the mode and tempo of TB pressure on humans remain unknown. The recent discovery that homozygotes for the P1104A polymorphism of TYK2 are at higher risk to develop clinical forms of TB provided the first evidence of a common, monogenic predisposition to TB, offering a unique opportunity to inform on human co-evolution with a deadly pathogen. Here, we investigate the history of human exposure to TB by determining the evolutionary trajectory of the TYK2 P1104A variant in Europe, where TB is considered to be the deadliest documented infectious disease. Leveraging a large dataset of 1,013 ancient human genomes and using an approximate Bayesian computation approach, we find that the P1104A variant originated in the common ancestors of West Eurasians ~30,000 years ago. Furthermore, we show that, following large-scale population movements of Anatolian Neolithic farmers and Eurasian steppe herders into Europe, P1104A has markedly fluctuated in frequency over the last 10,000 years of European history, with a dramatic decrease in frequency after the Bronze Age. Our analyses indicate that such a frequency drop is attributable to strong negative selection starting ~2,000 years ago, with a relative fitness reduction on homozygotes of 20%, among the highest in the human genome. Together, our results provide genetic evidence that TB has imposed a heavy burden on European health over the last two millennia.

Infectious diseases have been the leading cause of mortality since the origin of modern humans in Africa and throughout their subsequent dispersals around the world. 1–5 Tuberculosis (TB [MIM: 607948]) is considered to be the deadliest infection of the common era, with more than one billion deaths over the last 2,000 years,6–8 and still responsible for more than 1.5 million deaths annually according to the WHO. The human genetic basis of TB susceptibility has remained elusive until the turn of the 21st century, when two rare inborn errors of immunity, autosomal-recessive interleukin-12 receptor b1 (IL-12Rb1) and tyrosine kinase 2 (TYK2) deficiencies, were identified in children with severe TB.9,10 It was only in 2018 that the first common, monogenic predisposition to TB was identified. Homozygotes for the TYK2 (MIM: 611521) P1104A polymorphism (rs34536443) were found to be at higher risk of developing clinical forms of TB, due to the selective disruption of IL-23-dependent antimycobacterial IFN-g immunity, underlying a recessive trait.11 A subsequent study revealed an enrichment in P1104A homozygotes among TB cases of a case-control cohort from the United Kingdom, where the allele is most prevalent today (4%).7 The frequency of P1104A, together with its high penetrance for TB in the homozygous state (>0.8),11 suggests that about 1/600 British individuals would develop TB during their lifetime because of the mutation, if TB were still highly endemic in Europe.

Pathogen-imposed selective pressures have been paramount during human evolution.2,4,5 Over the last decade, population genetic studies have documented strong, distinct selection signatures among host defense genes, helping to delineate immunological mechanisms of major importance.12 and supporting the notion that microbes have had an overwhelming impact on human genome diversity.4,5 While several studies have provided insight into the periods when malaria has exerted pressure on humans,13–17 little is known about the historical burden of other infectious diseases associated with past epidemics. Yet, TB appears to have been more lethal than malaria in the common era,6 making it a stronger selective pressure in endemic regions. Recent evidence based on mycobacterial ancient DNA (aDNA) suggests a Holocene dispersal of M. tuberculosis <6,000 years ago (ya),18,19 a time frame that coincides with the growth of agricultural communities and anthropogenic environmental changes, which may have favored infectious disease transmission.20

To investigate the historical burden of TB in humans, we sought to reconstruct the evolutionary history of the TYK2 P1104A variant. Indeed, this mutation, in the homozygous state, underlies the only known common, monogenic predisposition to TB.7,11 Moreover, TYK2 P1104A does not affect the risk for other infectious diseases except, to a milder degree, rare cases of infection by environmental mycobacteria in otherwise healthy individuals.11 Whereas

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disease-protective variants may rapidly increase in frequency owing to positive Darwinian selection. Disease-risk alleles are expected to evolve under strong negative selection and be gradually purged from the population. Because negatively selected variants have become rare, very rare, or even extinct, they are harder to study using genetic data from modern human populations. However, with the increasing availability of genomes from ancient individuals, direct measurements of the intensity of selection are now possible, as significant increases or decreases of allele frequencies can be captured with aDNA from time transects. Thus, the study of the P1104A variant offers an unprecedented opportunity to shed light on the evolutionary history of a deadly human disease such as TB.

We therefore examined the frequency trajectory of P1104A over the last 10,000 years of European history, by screening a collection of 1,013 genomes that cover a time transect from the Mesolithic period to the Middle Ages (Figure 1A; Table S1). We partitioned the aDNA data into seven epochs and incorporated data from present-day populations (supplemental material and methods). The P1104A variant, which we found to be the result of a single mutational event (Figure S1), appeared for the first time in our dataset during the early Neolithic (0.00–0.10); Table S3), highlighting the marked impact of the aforementioned migratory events on the frequency of a large fraction of genomic variants, including P1104A. Furthermore, simulated neutral variants closely matched observed frequency distributions of non-coding variants for all epochs (Figure S3), indicating that the demographic model used—present-day Europeans are a mixture of Mesolithic hunter-gatherers, Anatolian Neolithic farmers, and Eastern steppe-related groups—well reproduces the neutral patterns of European diversity.

We next investigated the evolutionary forces that could have provided a fitness advantage opposed to that attributable to TB infection, the general late onset manifestation of autoimmune and inflammatory disorders makes unlikely the occurrence of a large counteractive effect. Together, our results provide robust evidence that the frequency decrease of P1104A since the Bronze Age explained both the observed aDNA. In doing so, considering the aforementioned large prior assumptions, we obtained simulated frequency trajectories that closely reproduce that of P1104A, similarly to other genome-wide variants (Figure S2). We also noted a similar, or higher, increase in frequency as that observed for P1104A until the Bronze Age for more than 20% of other aDNA variants within the uncertainty frequency interval of P1104A in the Mesolithic (0.00–0.10); Table S3), similarly to other genome-wide variants at the end of the Bronze Age explained both the observed aDNA and modern data only if s > 0.1. Furthermore, the frequency decrease after the Bronze Age was observed in
the trajectories of 25% of the best fitting simulated deleterious variants \( (s < \mu[0–1] \text{ and } T_{\text{onset}} < 500–10,000); \) supplemental material and methods), relative to only 1% of the best fitting simulated neutral variants \( (OR = 33, 95\% \text{ CI} = [5–240], \ p < 10^{-10}; \) Figure S5B; Table S4). These observations collectively support a history of negative selection driving the evolution of the TB-risk P1104A variant after the Bronze Age.

To quantify the degree of deleteriousness of TYK2 P1104A during European history, we verified that allele frequency trajectories were informative to assess negative selection, and, encouragingly, we observed a strong positive correlation between drops in allele frequencies and \( s \) values (Figure S6A). We first hypothesized that negative selection started with the arrival of agriculture in Europe,20 a period that includes the upper bound estimation for the most recent common ancestor of the \( M. \) tuberculosis complex \( /C6,000 \text{ ya.}^{18,19} \) However, such an early onset of selection \( (T_{\text{onset}} = 10,000) \) was clearly rejected by our simulations (Hotelling’s T-squared test \( p = 5.4 \times 10^{-4} \); Figure S6B; supplemental material and methods; Table S4), as no simulated variants were able to reproduce the frequency increase of P1104A until the Bronze Age.

Figure 1. Evolutionary history of the TB-associated TYK2 P1104A variant
(A and B) European frequency trajectory for the TYK2 P1104A variant over the last 10,000 years for (A) bins of 1,000 years and sliding windows of 500 years or (B) seven (pre-) historical European epochs and current times. The red and blue horizontal dashed lines indicate a frequency of 10% and 0%, respectively. Uncertainty of the frequency estimation is indicated by a gray colored area, representing the normal approximation of the 95% binomial proportion CI. Large uncertainty for older times is due to small sample sizes. For each bin, at least one carrier was assumed to obtain uncertainty estimates.
(C) Geographical distribution of the TYK2 P1104A allele by country (using today’s political borders), across all defined epochs. Colors indicate frequency estimations by country, from 0 (yellow) to 0.5 (blue). Grey indicates unavailable data. Number of P1104A carriers is indicated with its respective number on each country. Sample sizes for countries with non-zero counts (Table S1) are the following:

- Early/Late Neolithic: Austria \( (n = 7) \), Bulgaria \( (n = 21) \), Croatia \( (n = 10) \), Czech Republic \( (n = 8) \), Denmark \( (n = 1) \), Estonia \( (n = 1) \), France \( (n = 4) \), Greece \( (n = 9) \), Hungary \( (n = 51) \), Ireland \( (n = 4) \), Italy \( (n = 11) \), Latvia \( (n = 20) \), Lithuania \( (n = 8) \), Luxembourg \( (n = 1) \), Macedonia \( (n = 1) \), Norway \( (n = 1) \), Poland \( (n = 32) \), Portugal \( (n = 11) \), Romania \( (n = 3) \), Russia \( (n = 10) \), Serbia \( (n = 14) \), Spain \( (n = 57) \), Sweden \( (n = 11) \), Turkey \( (n = 22) \), UK \( (n = 46) \), Ukraine \( (n = 27) \), Bronze Age: Bulgaria \( (n = 2) \), Croatia \( (n = 2) \), Czech Republic \( (n = 46) \), Denmark \( (n = 2) \), Estonia \( (n = 7) \), France \( (n = 6) \), Germany \( (n = 58) \), Hungary \( (n = 17) \), Ireland \( (n = 1) \), Italy \( (n = 8) \), Lithuania \( (n = 4) \), the Netherlands \( (n = 10) \), Poland \( (n = 15) \), Portugal \( (n = 2) \), Russia \( (n = 2) \), Spain \( (n = 33) \), Sweden \( (n = 7) \), Switzerland \( (n = 1) \), Turkey \( (n = 5) \), UK \( (n = 75) \); Iron Age: Bulgaria \( (n = 1) \), Croatia \( (n = 1) \), Czech Republic \( (n = 1) \), Estonia \( (n = 3) \), Hungary \( (n = 5) \), Italy \( (n = 6) \), Latvia \( (n = 8) \), Moldova \( (n = 4) \), Russia \( (n = 2) \), Spain \( (n = 12) \), UK \( (n = 1) \); Middle Ages: Czech Republic \( (n = 1) \), Finland \( (n = 4) \), Germany \( (n = 5) \), Hungary \( (n = 30) \), Iceland \( (n = 9) \), Italy \( (n = 89) \), Moldova \( (n = 2) \), Russia \( (n = 3) \), Serbia \( (n = 1) \), Slovakia \( (n = 1) \), Spain \( (n = 32) \), Sweden \( (n = 13) \), UK \( (n = 12) \).
Age. Conversely, when allowing the onset of selection to vary across the last 10,000 years, using the former large priors ($T_{\text{onset}} \sim \mathcal{U}[500–10,000]$ ya and $s \sim \mathcal{U}[0–1]$), our best simulations did not significantly differ from P1104A (i.e., the simulation set was not rejected; Hotelling’s T-squared test $p = 0.09$) and revealed that scenarios with recent onsets of negative selection were those best fitting the data (Figure S6B).

To explain the strongest frequency increase and decrease for P1104A, we modeled allele frequencies of K = 5 ancient populations (Late Neolithic, Bronze Age, Iron Age, and Middle Ages) and present-day Europeans, and assumed large priors for model parameters (supplemental material and methods, Table S3). We found that negative selection on P1104A homozygous carriers started 1,937 ya (95% CI [500–7,912]), with a selection coefficient of 0.21 (95% CI [0.06–0.82]) (Figures 3A–3C). This onset of selection is consistent with a neutral evolution for the allele until the Bronze Age, suggesting that drift and admixture are sufficient to explain the increase of P1104A frequency until this epoch. These estimations should not be biased owing to reading mapping bias of the reference allele in the ancient genome dataset, given that 1104A is the alternative allele (supplemental material and methods). Furthermore, parameter estimation was found to be robust to the choice of the summary statistics used, with the 95% CIs of the estimates including the true simulated value 93% of the time (Figures S6C and S6D). Although our analysis showed that the more recent the onset of selection was the closer the frequency trajectory estimation was to the empirical data (Figure S6A), the fit was found to be similar within the last ~2,000 years (Figure 3B), consistent with our estimation. With respect to the selection coefficient, the posterior distributions of $s$ were shifted to 1 as $T_{\text{onset}}$ became closer to 0, and the general posterior distribution for the strength of negative selection was similar to that of onsets of selection occurring between 1,000 and 3,000 ya (Figures 3A and 3C). Importantly, consistent ABC estimates of the strength and the onset of selection were found when either excluding the Iron Age, i.e., the epoch with smallest sample size ($\hat{s} = 0.19; 95\% = [0.03–0.83]; T_{\text{onset}} = 1,670$ ya; 95% CI = [500–8,388] ya) or when using the whole European frequency trajectory, i.e., from the Paleolithic to the present ($\hat{s} = 0.21; 95\% = [0.04–0.84]; T_{\text{onset}} = 1,567$ ya; 95% CI = [500–8,367]).

Using the same approach, we estimated the selection coefficient of another mutation, TYK2 I684S, a missense variant that is neither in linkage disequilibrium with P1104A nor associated with TB risk, and found values that were compatible with neutrality ($\hat{s} = 0.02; 95\%$ CI [0–0.19]; Figures S7A and S7B). Thus, our analyses support the notion that, despite the reported protective effects of P1104A against some immune-related disorders, TB has exerted pressure on the TYK2 P1104A variant over the last ~2,000 years, with a 20% relative fitness reduction for homozygotes at each generation since.

Finally, we sought to apply the same approach to reported pathogenic variants, by cross-matching the ClinVar database with aDNA variants present in our cohort that fall into the uncertainty range of P1104A in the Bronze Age ([0.04–0.10], Figure 1B). Among the resulting three variants with a “pathogenic” clinical significance annotation, only one (HFE C282Y [MIM: 613609]) presents a frequency decrease across the last four epochs. HFE C282Y is a known disease-causing variant underlying hemochromatosis, an autosomal-recessive autoimmune disease (HFE1 [MIM: 235200]) that impairs mineral metabolism, which can affect the growth and clearance of intra- and extra-cellular pathogens. HFE C282Y reached its maximum frequency, of
nearly 10%, during the Middle Ages and then decreased to its present-day frequency of 4%. Consistent with our expectations, we found a similarly strong selection coefficient of $s = 0.20$ (mode $= 0.22$; 95% CI $[0.03–0.76]$; Figure S7B), and an onset of negative selection during the Middle Ages (mode $= 724$ ya; 95% CI $[500–7,508]$).

A potential limitation of our approach, which is inherent to most aDNA studies, is genetic discontinuity due to large population replacements or to sampling bias for geographical locations.35 For example, different sampling proportions from northern and southern Europeans across epochs may result in genetic discontinuity in our dataset, given that the former present higher Eastern steppe ancestry than the latter after the Bronze Age.36 We thus repeated our ABC setup for northern and southern Europeans using a geographical division,37 designed to distinguish high and low levels of Steppe ancestry (Figure S8). Despite much lower sample sizes, we found evidence for negative selection in both northern ($s = 0.24$; 95% CI: [0.02–0.87]) and southern ($s = 0.13$; 95% CI: [1.6 x $10^{-4}$–0.81]) European homozygotes, with a slightly left-shifted posterior distribution in southern Europe, where the sample size is more limited (Figure S9). We also found, using factor analysis,38 that P1104A carriers scattered throughout European sub-structured populations, across all epochs after its introduction to Europe (Figure 4).

In addition, ancestry proportions were similar between P1104A carriers and the rest of the dataset at each epoch (Table S1). Notably, the observed ancestry shift between Bronze Age and present-day samples (from 0.29 to 0.36 for the whole dataset [Table S3], representing a 24% relative increase, and from 0.23 to 0.39 for P1104A carriers [Table S1]) does not, on its own, explain the frequency decline of the allele after the Bronze Age (from 0.074 to 0.029, representing a 61% relative decrease). Yet, we performed an ABC estimation accounting for ancestry variation across epochs (supplemental material and methods). Using the estimated Anatolian ancestry of our dataset at each epoch from the Late Neolithic onward, we estimated very similar values for the strength and onset of negative selection for $TYK2$ P1104A at the pan-European level ($s = 0.27$; 95% CI: [0.08–0.93]; $T_{onset} = 2,045$ ya; 95% CI [500–8,690]; Figures S10A and S10B). Similarly, we found comparable estimations for northern and southern Europeans ($s = 0.26$; 95% CI [0.06–0.83]; $T_{onset} = 1,046$ ya; 95% CI [500–6,934]; Figures S10C and S10D); and $s = 0.24$; 95% CI [0.02–0.85]; $T_{onset} = 3,229$ ya; 95% CI [500–8,963]; Figures S10E and S10F, respectively). Conversely, we found no evidence of selection for $TYK2$ I684S ($s = 0.02$; 95% CI: [0–0.69]), as expected, and a weaker signal of negative selection for $HFE$ C282Y ($s = 0.12$; 95% CI: [0–0.76]). Collectively, these findings suggest that the observed frequency drop of P1104A after the Bronze Age is not due to major geographical and/or temporal differences in ancestry components in our aDNA dataset, but instead to the action of natural selection. Moreover, when re-estimating the age of P1104A without modern data from Middle Easterners and Central Asians, as they are not entirely representative of ancestral Anatolian farmers and steppe herders, respectively,39,40 we obtained almost identical results (mode $= 30,303$ ya; 95% CI [23,113–60,273]).

Figure 3. Estimation of the onset and strength of negative selection driving the evolution of $TYK2$ P1104A
(A) Joint (as a 2D density plot) and individual (as purple densities) posterior distributions for the onset (in thousands of years) and the strength of negative selection ($s$) for $TYK2$ P1104A, based on the best fitting simulations with variable onset of selection, using European summary statistics from the Late Neolithic epoch onward (10,000,000 simulations). CI boundaries are shown with dashed black lines. (B) Distribution of the weighted Euclidean distances between the best fitting simulations and the observed data, under the proposed demographic model, for (from right to left) $3,000 < T_{onset} \leq 4,000$, $2,000 < T_{onset} \leq 3,000$, $1,000 < T_{onset} \leq 2,000$, or $500 < T_{onset} \leq 1,000$. (C) Posterior distributions for the $TYK2$ P1104A’s negative selection coefficient, based on the best fitting simulations with variable onset of selection, for the same groups of onsets of selection as in (B) using the same color code.
than 3,000 ya, are represented by gray dots.

We anticipate that the same population genetics framework could be used to delineate other human genetic variants, of yet unknown function, that have drastically decreased or increased in frequency across time due to microbial pressure. Thus, adopting an evolutionary approach represents a promising alternative to investigate the genetic sources of present-day disparities, between individuals and populations, in susceptibility to infection.

Data and code availability

Pseudo-haploid ancient and modern genome data are available at https://reich.hms.harvard.edu/allen-ancient-dna-resource-aadr-downloadable-genotypes-present-day-and-ancient-dna-data (V42.4: March 1, 2020 release). Code to perform ABC estimations from simulated frequency data are available at https://github.com/h-e-g/SLiM_aDNA_selection.

Supplemental Information

Supplemental Data can be found online at https://doi.org/10.1016/j.ajhg.2021.02.009.

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Declaration of Interests

The authors declare no competing interests.

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Web resources

OMIM, https://www.omim.org/
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