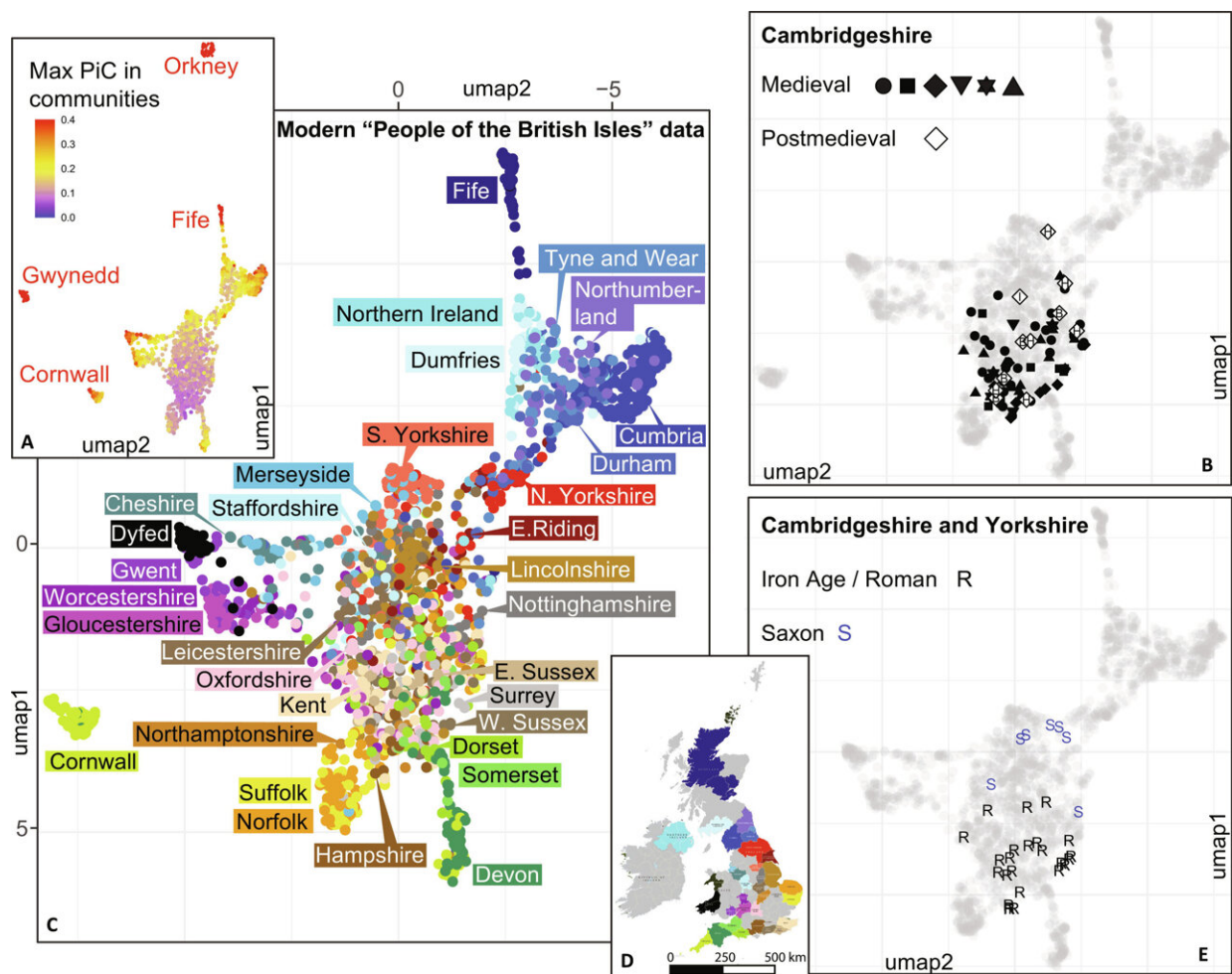


Genetic study offers little evidence of Black Death having selective impact on genetic variation in England

January 18 2024, by Bob Yirka



UMAP plot of individual connectedness among modern and ancient genomes from Britain. (A) Density of maximum PiC score values per individual in one of the extracted communities. (B) UMAP coordinates of the medieval and

postmedieval genomes ($> 0.2\times$ coverage) from Cambridgeshire. (C) Individual connectedness among modern genomes of the "People of the British Isles" project based on PiC scores of 20 significant communities with more than 10 members extracted from the combined data with the Louvain method (unsupervised cluster analysis). (D) Map showing the color codes by counties for the modern genomes used in the UMAP plot A. (E) UMAP coordinates of the Iron Age/Roman and Saxon period genomes. Credit: *Science Advances* (2024). DOI: 10.1126/sciadv.adi5903

A team of archaeologists, geneticists and pathologists affiliated with a host of institutions across Europe, working with one colleague from the U.K. and another from the U.S., has found little evidence of the Black Death causing genetic variants to arise in affected populations.

In their study, [reported](#) in the journal *Science Advances*, the group compared the genes of people living before and after the [plague](#) in the same area to see if they could find any [genetic changes](#).

The Black Death was a plague (caused by *Yersinia pestis*, a bacteria carried by wild rodents) that affected people living in Europe and parts of Africa and Asia in the middle of the 14th century. Researchers believe the plague killed approximately 25 million people, with some countries seeing 65% of their population lost.

Because of the duration of the plague and the large number of deaths, some in the infectious community have suggested genetic variations may have arisen, giving some people more protection against infection. In this new effort, the research team tested this theory by conducting a genetic study of people living in Cambridgeshire, England, over the years 1000 to 1850, comparing the genetic profiles of 275 people who lived in the county both before the plague arrived and after it had dissipated to see if they could spot any changes.

To ensure the integrity of their samples (retrieved from cemeteries), the researchers used genetic samples from people from all walks of life living around the county. This provided new insights into the social makeup of the county, including relatedness between groups. They also found introductions into the population from migrants from several Nordic countries. What they did not find was any [genetic variation](#) that might be attributed to the Black Death.

The research team points out that their work does not rule out the possibility of the plague having some selective impact, it only suggests that if it did happen, it was likely in ways that they were not able to identify, such as via multiple pathways—or that it happened in other populations.

More information: Ruoyun Hui et al, Genetic history of Cambridgeshire before and after the Black Death, *Science Advances* (2024). [DOI: 10.1126/sciadv.adi5903](https://doi.org/10.1126/sciadv.adi5903)

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