Hypotheses

Shifting Paradigms in Black Death Chronologies

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After decades of doubt about the nature of the disease that caused the Black Death, the identification in 2011 of *Yersinia pestis* in a 14th-century London cemetery – and, most importantly, the revelation of its genetic proximity to current forms of the bacterium – closed that (sometimes harsh) debate, and demonstrated beyond all doubt the main role of paleogenomics in the future studies of historical epidemics, especially plague. However, the role of historians has not diminished with the arrival of this new protagonist in the field of disease history. On the contrary, the need for on-going multidisciplinary dialogue has become undeniable and mandatory, if the ultimate goal is effectively to advance knowledge about historical epidemic phenomena.

As historians, we are builders of narratives that aim to reconstruct past events, processes and dynamics, explaining and understanding them. Throughout our academic training, we are presented with dominant narratives, and we are prepared to understand them and their origin. However, and although we are prepared to, frequently we fear challenging those classic, crystalized narratives that offer us a comfortable, widely and long accepted framing for the entire big picture.

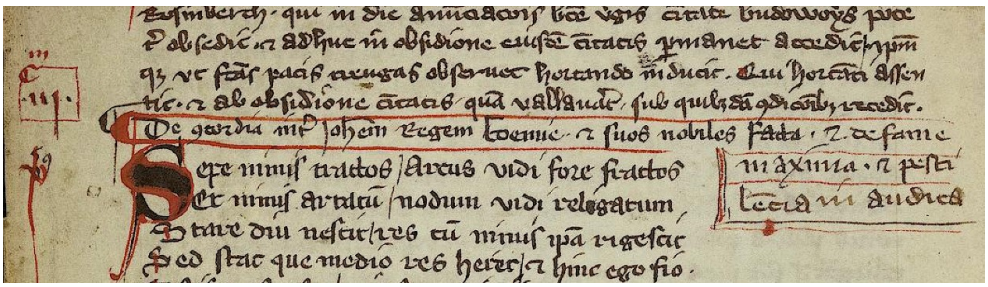
The Black Death paradigm is a perfect example. A massive, transcontinental, proto pandemic series of outbreaks of plague 'invades' the Mediterranean and Europe in the 1340s for the first time in centuries, inaugurating the Second Pandemic cycle that would last in those regions until the first decades of the 19th century. Both historians and scientists have accepted this classical historiographical narrative, even as genetics has made entirely new perspectives on the pandemic possible. Nevertheless, historians must apply their method and challenge accepted narratives when data support a completely different scenario. New paleogenomic data suggest that regional outbreaks of plague occurred in Europe before the beginning of the Black Death. And, surprisingly, these data shed new light on a group of very puzzling historical testimonies and support that plague did indeed ravage some European areas before 1346. But why, if this is so obvious now, has nobody seen these phenomena before?

In a talk on 16 May at the University of Erfurt, we presented our most recent findings about pre-Black Death episodes of plague in western Europe. Since the initial 2011 findings from the London cemetery, a variety of subsequent paleogenomics studies have retrieved additional genomes of *Yersinia pestis* from European gravesites. (Another study was announced days after the talk, in fact, and more will most certainly continue to appear.) Consistently, every single one of these European studies shows that a single main lineage of *Y. pestis*, Branch 1, entered western Eurasia in the late Middle Ages. These (along with Branches 2, 3, and 4, which remain in Asia) are all part of what we now call the Second Plague Pandemic.

Traditionally, it is assumed that the Black Death—the catastrophic outbreak of plague that can be dated precisely to the years 1346 to 1351 (or 1353 according to some timelines) and described by Boccaccio and so many other medieval witnesses—was the first time plague entered Europe since the Justinianic Plague had faded from the scene in the 8th century. The assumption that the 14th century saw a *new* wave of plague has been entirely supported by more than a decade of paleogenomic studies. Again, these are all Branch 1 lineages, part of the "Big Bang" of plague proliferation in Central Asia that preceded the Black Death.

But the two most recent paleogenomics studies have now provided data to support an inference already proposed by historians several years ago: that is, that plague's late medieval dissemination out of Central Asia began not in the 14th century, but already in the 13th century. Documentary evidence that plague was present in northern China in the early 13th century, combined with evidence that plague was involved in the Mongol incursions into the Middle East in the 1250s, has already brought plague across Eurasia to the edge of the Mediterranean.

And now we can ask: did it go further? The answer, to judge from the publication of new *Y. pestis* genomes from Denmark, and from a new phylogenetic analysis based on later French genomes, is YES. We will be laying out our reasoning in another setting, arguing that rigorous attention to *dating* the phenomena recorded in cemetery depositions and genomic phylogenies shows that at least two already-published genomes were not part of the Black Death transmission of plague in the 1340s, but should instead be associated with "mortality" events in prior decades, perhaps as early as the 1310s. We have chanced upon these new insights because, as historians, we are engaged on work that documents specific *datable events* that, once examined closely, can be shown to describe epidemiological situations compatible with manifestations of plague. The genomes confirm our analyses.



This chapter heading from the Zbraslav Chronicle (Chronicon Aulae Regiae) by Peter of Zittau (Žitava) reads 'On the concord made between John, King of Bohemia and his nobles, and on the great famine and

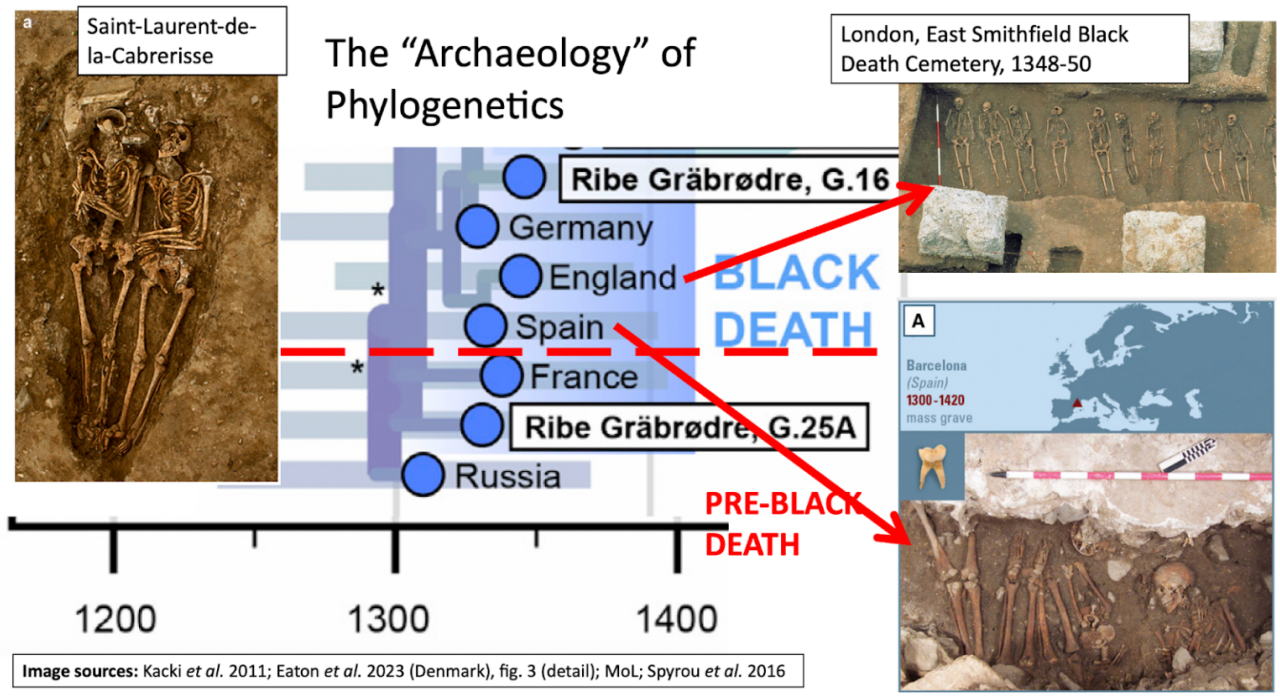
unheard of pestilence'; it refers to events in 1317-18. Source: Vatican, BAV, MS Pal. Lat. 950, f. 5v (detail)Vatican, BAV, MS Pal. Lat. 950, f. 5v (detail)

Here is just one of those events.

Fifteen years before the Black Death, a drought-induced grain shortage occurred throughout much of southwestern Europe. Called *anos maos* in Galician-Portuguese ("the bad years") and *lo any mal primer* in Catalan ("the first bad year"), the period of grain shortages in the fall and winter of 1333-34 was followed by episodes of severe mortality. In fact, through an exhaustive study of wills from Catalonia during the first half of the 14th century, the economic historian Joan Maltas i Montoro has documented three distinct periods of excess mortality in Catalonia prior to 1348: 1306-8, 1323-24, and 1333-34. Although long assumed to be the result of malnutrition, these periods of excess mortality may have been caused by an epidemic disease. Documentary sources — such as the *Petit Thalamus*, which includes a chronicle of the city of Montpellier (Mediterranean France), and the *Livro da Noa*, produced at the Monastery of the Holy Cross in the city of Coimbra (Portugal)—show the effects on both sides of the Pyrenees. Sources describe not simply sudden deaths (in one case, in the space of 3-4 days), but also disrupted burial practices and even mass graves, on a scale that archaeologists normally associate with plague outbreaks.

Ideally, one would like corroborating evidence to tie genomes, documentary evidence, and archaeological sites together. While fragments of *Y. pestis* were retrieved from the rural French site of Vilarnau in 2008, those remains cannot be dated within less than a 200-year window. More promising is L'Esquerda da Roca, a suburb of the Catalan town of Vic, whose archives have helped document repeated mortality events in the 14th century, including the *mal any primer* of 1333-34. aDNA testing for *Y. pestis* has thus far been inconclusive for the two layers of mass graves at L'Esquerda da Roca. However, radiocarbon dating of a multiple burial in the earlier deposition yields a mean date of "1333" (cal AD 1301-1368 61.20%). Importantly, this earlier outbreak is characterized by "household" mortalities: that is, two or three individuals who died at the same time and were buried together. Black Death sites, in contrast, are more apt to have mass burials, sometimes with dozens of people at a time.

Right now, the best combination of genetic and archaeological evidence comes from a rural site in Occitania very close to the Pyrenees, Saint-Laurent-de-la-Cabrerisse. Excavated in 2007, the site yielded three "multiple" burials: that is, two to five individuals in a single grave, perhaps a household unit who all died at the same time. One of these individuals, labeled SLC1006, yielded enough *Y. pestis* genetic material to reconstruct its genomic profile.



And that profile places it phylogenetically at an earlier stage of evolution than the genomes involved in the Black Death outbreak of the 1340s. Moreover, SLC1006's "gravemate" was radiocarbon-dated to cal AD 1279-1389, which yields a mean date of 1334. Neither the genome nor the radiocarbon-dating provide an exact calendrical date for this outbreak at Saint-Laurent-de-la-Cabrerisse. But the historical context aligns with everything we are learning about the "famine" situation in southwestern Europe in the 1330s.

Both sides of the Pyrenees are rich in documentary records and archaeological sites that might be investigated for pre-Black Death mortality events. And given that the western Mediterranean region occasionally shipped grain to northern Europe when there was need, exploration of parallel histories in northern Europe may help identify the circumstances that brought what appears to be an even earlier strain (found in the G.25A genome) to Denmark. Given *Y. pestis*' proposed effects on human immune profiles, determining whether plague exposure may have happened in Europe earlier than 1348 has major implications for science, not just history.

In short: we do not believe there is any longer a question whether the first outbreaks of plague occurred in Europe before the onset of the Black Death. Now that the paradigm of the Black Death's chronology has shifted, the question should focus on when, where and in what way. We are not saying that all major mortality events in Europe between 1250 and 1346 were unidentified plague outbreaks. We are saying that plague was already present, and may have occurred at the same time as other phenomena that caused mortality crises, such as famines, other epidemic diseases, and episodes of violence, without reaching a scale that made people become aware of its singularity, as occurred with the Black Death and later outbreaks.

Now that rigorous methods are being developed to test the evidence and dating methods of different disciplines against one another, we need no longer revert to careless inferences. The increasing enrichment of *Yersinia pestis*' phylogenetic tree will allow us to gradually confirm additional pre-1346 outbreaks. And careful epidemiological tracking using alternate sources has been shown to be viable, even in the absence of confirmatory aDNA. It is a necessary turning point; although unimaginable only a few years ago, we need to accept the evidence, promote multidisciplinary collaboration and join forces to bring us closer to the reality of the past, even when it changes everything we believed for decades.