Lesson | 03

What Ibn Battuta Didn't See: Plague's Emergence and Focalizations

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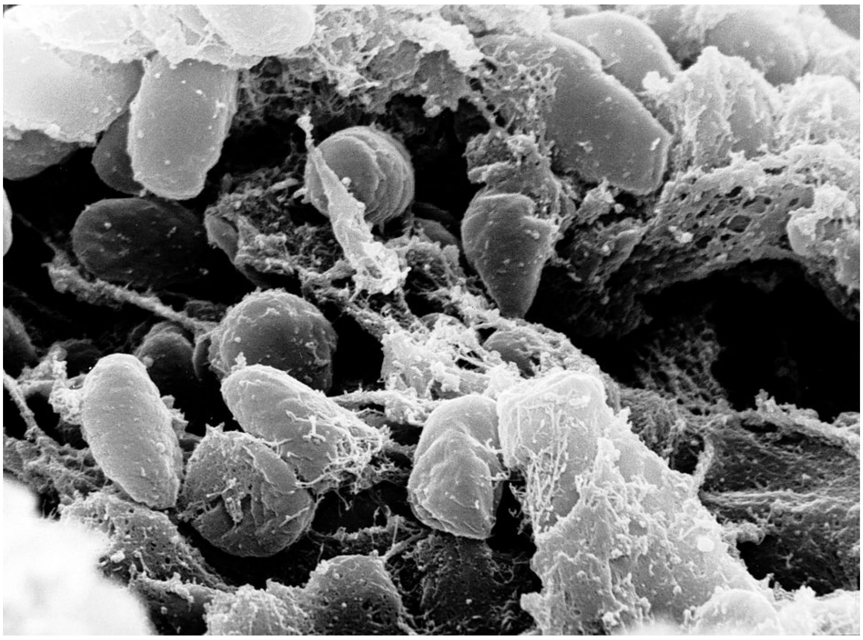
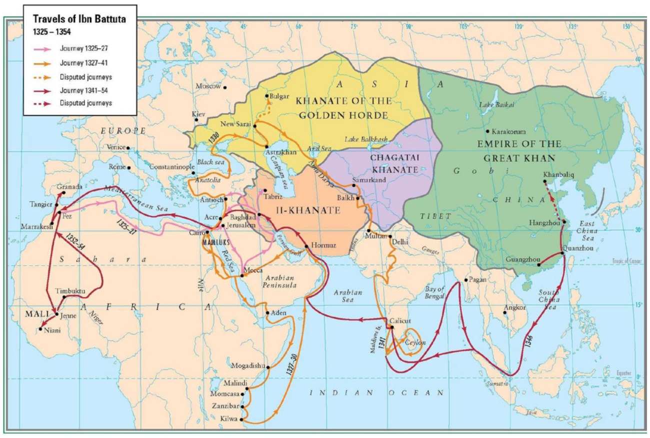


Introduction

In Lesson 1, we learned that in 1332-1333 Ibn Battuta passed through the lands that made up the Chaghadaid Khanate, the Central Asian Mongol realm ruled by the descendants of Chaghatai Khan (1183-1241), the second son of Chinggis Khan. In passing through Samarqand and Balkh before making his way to India, Ibn Battuta would have passed within 1,000 kilometers of the Tian Shan mountains, which likely harbored the strain of the plague (*Yersinia pestis*) ancestral to that involved in the pandemic that we know today as the Black Death. During that first part of his travels, Ibn Battuta said nothing that hinted at the presence of plague in Central Asia.

Yet according to the chronology of the Black Death that has been standard for the past 700 years, and repeated in so many history textbooks, Ibn Battuta *should* have encountered plague, or seen the circumstances that would soon give rise to its proliferation. This is because 1332-1333 is around the same time that one of the most important Middle Eastern writers on the Black Death, the historian Ibn al-Wardi writing in Aleppo in 1349, said that the pandemic began. Ibn Battuta may have actually met Ibn al-Wardi when he visited Aleppo just before witnessing the Plague Prayer in Damascus in July 1348 (discussed in Reading 2). Ibn al-Wardi himself succumbed to the plague in March 1349, but before he died he completed and formally handed on an account of plague's "travels" that claimed it had struck most of the lands that Ibn Battuta journeyed through:

> The plague frightened and killed. It began in the land of darkness. Oh, what a visitor! *It has been current for fifteen years*. China was not preserved from it nor could the strongest fortress hinder it. The plague afflicted the Indians in India. It weighed upon the Sind.[1] It seized with its hand and ensnared even the lands of [the Golden Horde]. How many backs did it break in what is Transoxiana![2] The plague increased and spread further.



Map of Ibn Battuta's travels.

Key Terms:

Tian Shan mountains

Ibn al-Wardi

Ibn al-Khatib

Ibn Khatima

"Quick Transit Theory"

Phylogeny and phylogenetic trees

Polytomy

"Big Bang"

Issyk Kul

Mongol realm

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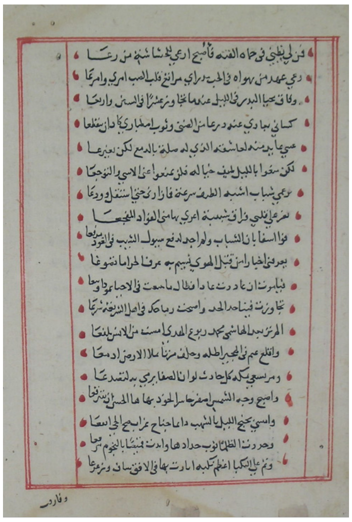
1. A region in northwest India.
2. "Transoxiana" is a classical term to refer to the lands beyond the Oxus River in Central Asia, corresponding to modern-day Uzbekistan, Tajikistan, Kazakhstan, Turkmenistan and Kyrgyzstan.



Ibn al-Wardi’s maqama on plague.

> It attacked the Persians, extended its steps toward the land of the Khiṭai,[3] and gnawed away at the Crimea. It pelted Rum [Byzantium] with live coals and led the outrage to Cyprus and the islands. The plague destroyed mankind in Cairo.[4]

Similar to Ibn al-Wardi’s precise dating of the pandemic’s commencement, a writer in al-Andalus (Islamic Iberia), Ibn al-Khatib (d. 1374), whom we know met Ibn Battuta when he visited Granada in 1350, also says that this “universal plague” dated to 1333-1334. He vividly recounted how “it was created by many corpses that were the result of war in these areas [northern China], which decayed after a fire in that country, which devastated plants and trees over a period of around ten days.”[5]

Here we have the crux of our problem as historians: two of our earliest sources, Ibn al-Wardi in Aleppo and Ibn al-Khatib in Granada—writing at almost the same time at opposite ends of the Mediterranean, one or both of whom can be tied directly to Ibn Battuta—have given us an explicit timeframe for the pandemic. Yet it seems to make no sense. Biologically, it stretches all plausibility that a bacterial disease that must have cycled continuously through thousands of rodent populations (and perhaps many millions of insect vectors) could have moved across close to 9,000 miles of the Eurasian expanse in just 15 years *and* immediately established environmental foci that would persist for centuries thereafter. There were, after all, no airplanes in the 14th century. If it was so easy for plague to travel so far, so fast, why hadn’t it done so before?

If, however, we engage seriously with both our medieval sources and our modern evidence of plague’s biology, a different narrative falls into place. Instead of *one single* pandemic wave proliferating out of one source (be it a battlefield of rotting corpses, a fire-scarred landscape, or high in the Tian Shan mountains), the crisis of the mid-14th century should be seen as arising out of *multiple* plague reservoirs that had already been seeded in Afro-Eurasia in the previous century. What 14th-century observers saw as a *universal* plague was indeed universal. What none of these observers could see, however, or even conceive of in their contemporary frameworks for understanding epidemics, was that beyond local circuits of maritime trade, the “universality” of plague was due, not to new arrivals of the disease descending across vast landscapes all at once, but to the fact that regional reservoirs had already been embedded across the Afro-Eurasian landscape. Now, under pressure from a shifting climate, they were all erupting at once.

In fact, yet another contemporary observer, Ibn Khatima (d. 1369), a poet, historian, and grammarian in Almería (in present-day southern Spain), writing

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[3] The “Khitai” refers to the realm of the Qara Khitai, who occupied the regions that now make up Kyrgyzstan and western China.

[4] Michael Dols, trans., “Ibn al-Wardī’s Risālah al-naba’ ‘an al-waba. A Translation of a Major Source for the History of the Black Death in the Middle East,” in *Near Eastern Numismatics. Iconography, Epigraphy, and History: Studies in Honor of George C. Miles*, ed. D. K. Kouymijian (American University of Beirut, 1974), 443–55, at 448.

[5] M. J. Müller, “Ibnulkhatibs Bericht über die Pest,” *Sitzungsberichte der königliche bayerischen Akademie der Wissenschaften zu München* 2 (1863): 1–34, 22. Translated by Monica H. Green.

in February 1349 at almost the exact same time as Ibn al-Wardi in Aleppo, framed the pandemic within an even tighter chronological window than al-Wardi's 15 years. He suggested it spread in just three years. This timing matches the reported outbreaks in 1346 in the Mongol realms of the Golden Horde and the collapsed Ilkhanate. Yet Ibn Khatima also provides our first evidence that observers identified *two* different sites of origin:

> There are disagreements about when and where this event began. I have been informed from a reliable source, narrating from the Christian merchants who came to us in Almería that it had started in the lands of Khita [western China/central Asia]. ... It [the plague] continued to spread from the lands of Khita and reached neighboring regions as far as western Iran (*'Iraq al-'Ajam*) and the territories of eastern Anatolia (*bar al-turkiyyah*). I have also been informed from other Christians arriving to us [in Almería] that they had been informed that it had started in Ethiopia (*arḍ al-ḥabashah*) and had spread from there to neighboring areas and territories as far as Egypt and Syria.[6]

This account, written by a keen observer who, so far as we know, never traveled outside of Iberia but clearly paid close attention to the stories he was told by travelers, suggests that the narratives we have been piecing together of alternate trajectories and chronologies—plague arising out of western lands of the collapsed Ilkhanate realm in Greater Armenia (covered in Lesson 1) and plague arising out of Egypt rather than being introduced into it (from Lesson 2)—were in fact perceived by contemporaries, too.

Why, then, have our modern narratives been so wedded to what scholars call the "Quick Transit Theory," the idea of a *single* introduction of plague into a hitherto unsuspecting world? Why do maps of the pandemic so confidently place arrows showing directions and times of spread into and out of the Black Sea?

I. Mapping inferences: Three misdirections, three new turning points

Maps, especially those using dates and arrows to indicate the timing and directionality of events or processes, are incredibly powerful in fixing the *reality* of events in our minds. What we forget is how flimsy the evidence to support them sometimes is.

Three elements of popular Black Death maps have been extraordinarily influential in shaping modern stories of the pandemic:

- A proposed western transit of plague across the Central Asian steppe from lake Issyk Kul (or the nearby village of Kara-Djigach) in Kyrgyzstan over to the Crimean Peninsula in the Black Sea and the city of Caffa, between 1338 and 1346
- A proposed southern transit of plague from the Black Sea to Alexandria (in Egypt) in 1347

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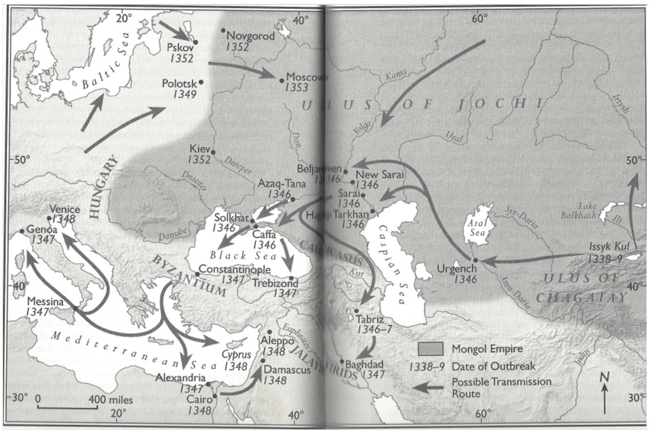
6. Ibn Khatima, *The Attainment of the Goal of the Seeker for Information Concerning the Epidemic*, trans. Mohamad Ballan; used with permission.

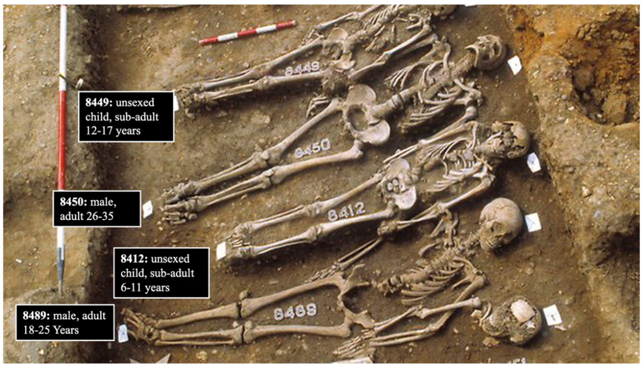
- And a proposed eastern transit of plague from western Europe to eastern Europe after 1348, completing plague's alleged post-Black Death clockwise transit through the Mediterranean and Europe

Maps created over the course of the 19th and 20th centuries were produced based on the same *written* sources that have been used to write the accounts found in textbooks. The pandemic dating they imply seems to support the "15-year window" that Ibn al-Wardi and Ibn al-Khatib had proposed. Ibn Khatima's "3-year window," meanwhile, fits with a narrative focusing just on plague's transmission out of the Golden Horde (where outbreaks in 1346, including at Caffa, are well documented) over to Iberia where Ibn Khatima was writing in 1349. Ibn al-Wardi's longer chronology was particularly influential because it became the foundation for Arabic-language plague scholarship, which was imported into European plague scholarship in the 18th century. Since the maps were constructed out of information in the texts, authors and illustrators simply filled in arrows to make sense of the geographies their written sources were conjuring up.

This is where the scientific study of genetic material that has been preserved in historical remains—a field called paleogenetics—comes in. The era of paleogenetics in plague history began in 2011, when three nearly complete genomes of *Yersinia pestis* were retrieved from the East Smithfield cemetery in London. However, when this first work was completed, the researchers did not fully engage with the existing plague scholarship. When originally presented, the genomes were simply assumed to support the narrative of the textbooks: Plague came with terrifying suddenness, introducing into Europe a single new, highly lethal strain of the disease in 1347/1348. And since the genetic characteristics of this allegedly single genotype suggested it had evolved from an earlier form found in Central Asia, this evidence was assumed to have simply provided further support to the standard narrative of the Quick Transit across Central Eurasia. In subsequent years, retrievals of *Yersinia pestis* genomes from other medieval and early modern sites seemed to show further development of this new lineage within Europe.



A recent map of the Black Death, showing the alleged transits of plague from the region of Issyk Kul (Kyrgyzstan) via a northern route to Caffa on the Black Sea, and from the Black Sea to Alexandria in Egypt.



East Smithfield Black Death Cemetery, Mass Burial Trench 1 (east cemetery), London,excavated in 1986-1988. Two of the retrieved Yersinia pestis genomes in 2011 came from this trench.

By 2024, more than 100 *Yersinia pestis* genomes from late medieval and early modern Europe had been made available, and many inferences about the plague's history are stronger than they've ever been before. As researchers have continued to analyze this new evidence, it's clear that some of it does not confirm aspects of the earlier historical narrative. Indeed, by now, everything we have learned about the *limits* of perception in the Middle Ages—the inability to perceive the bacterial world—should lead us to expect that the older narratives drawn from the historical (written) record that we have inherited needed adjusting.

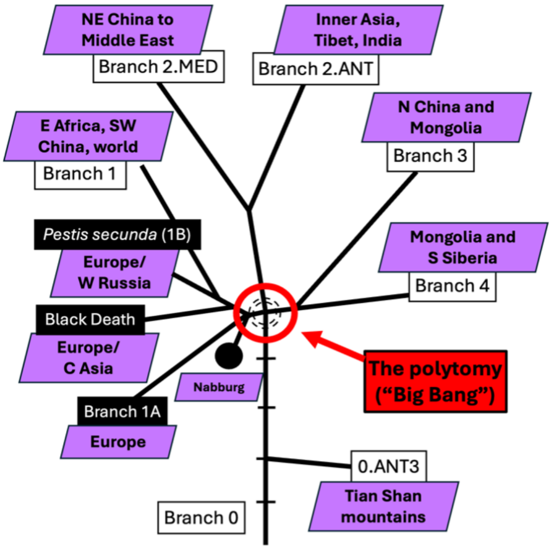
Sample MIN86 6330, the source of the tooth sampled for the 2011 Nature study on the Black Death genome, held at the Human Bioarchaeological Centre.

Surprisingly, it wasn't our textual sources that were preventing a more informed, biologically persuasive account of the Black Death from emerging from the new evolutionary biology. It was the mindset we were bringing to them that was the problem. The maps, surprisingly, have proved the biggest obstacle to adjusting our perspectives… because we assumed they were true! However, if instead of reading the genetics through these old maps, we instead look at the data through the lens of phylogeny—the method biologists themselves employ to study evolutionary relationships—distinct moments in *Yersinia pestis*'s late medieval history become clear that prove helpful to our investigation.

II. The narratives emerging from genetics: The Big Bang

The study of phylogeny allows researchers to identify key turning points, or divergences, in the spread of bacteria (and other organisms). These turning points are also called polytomies. For *Yersinia pestis*, one polytomy, the so-called Branch 1 Divergence, has implications for plague's history in Asia and East Africa. It is still (as of mid-2025) being researched and must await future assessment. Another polytomy, what is here called the Nabburg Polytomy, will be addressed in Lesson 4. A third polytomy, which we will explore here, is called the Big Bang (though it's completely unrelated to the other common usage of this term, describing the theoretical start of the universe's expansion). This Big Bang is actually the unique result of phylogenetic analysis from modern *Yersinia pestis* genomes and the earliest ancient DNA (henceforth abbreviated as aDNA) retrieved from the East Smithfield Cemetery in London.

Below is a simplified form of the *Yersinia pestis* phylogenetic tree, drawing on a 2023 study. What is a phylogenetic tree, and how does one "read" it?



A schematic diagram of the Big Bang, showing the relations of the new branches of the Yersinia pestis phylogenetic tree that evolved out of the older Branch 0. These include Branch 1 which has been found in all medieval and early modern European plague sites thus far tested.

A phylogenetic tree is nothing more than a family tree. Just as your family tree shows your relationship to your parents, grandparents, siblings, cousins, aunts, uncles, and the rest of your extended family, so a phylogenetic tree shows the relationships of any strain or species with others that are closely related. In this tree, the purple labels indicate the geography of the major *Yersinia pestis* lineages formed just before and just after the Big Bang. The branch labels in white represent strains documented from modern genomes, while those in black have been drawn from aDNA. Immediately upon publication of the first Black Death aDNA *Yersinia pestis* genomes in 2011, it was clear how these genomes from 14th-century London related to modern *Yersinia pestis* genomes throughout the world. Molecular genetics allowed us to see the global history of this pathogen in a single diagram.

Since 2011, *Yersinia pestis*'s unfolding evolutionary history has expanded both the chronology and the geography of plague's medieval history. The new evolutionary history of plague made possible by the recovery of the medieval genomes brought into view a historical event that had hitherto been completely unknown: the Big Bang. Simply put, the Big Bang refers to the massive proliferation of one specific strain of *Yersinia pestis* (coming from Branch 0) into four new geographic regions. Once transmitted to these new regions (and there may have been more than four initially), *Yersinia pestis* flourished. In fact, the reason we can reconstruct the Big Bang is because those four new lineages (Branches 1, 2, 3, and 4 on the diagram) still survive to the present day.

Where did the Big Bang happen? We can't say precisely, but we can guess. The Big Bang would have been a kind of spillover event. Because of where related strains are still found in the present day, we can infer that long-tailed or grey marmots (*Marmota caudata* and *Marmota baibacina*, respectively), two species found in the Tian Shan mountains that lie between Kyrgyzstan and China, harbored one type of *Yersinia pestis* that had likely been circulating at this border between desert and mountains for at least the previous millennium and a half. The new lineages that emerged from the Big Bang are found in other, non-adjacent marmot species in Asia. And they have been found in human remains throughout Europe, dating from the14th century to the 18th. Whatever caused the Big Bang, its effects spread throughout the continent.

The Big Bang is, therefore, the prelude to the Black Death of the 1340s, pushing plague's history back into an earlier era. But how far back? And why did it happen? Confirmation that Asia was part of the geography of the Second Plague Pandemic seemed to validate all the medieval accounts claiming it "came from the East." But since, genetically speaking, the Big Bang seemed to have happened so close to the time of the Black Death itself (only two positions—out of 4.6 million nucleotides—on the *Yersinia pestis* genome were initially found separating the two events), the immediate effect of the discovery of the Big Bang was to validate the short chronology (15 years, based on Ibn al-Wardi's account) for the pandemic narrative.

Marmota caudata (long-tailed marmot), the species of marmot that now hosts strains of Yersinia pestis that share a common ancestor with the Black Death strains.

Here is where those maps played a role. Why was Issyk Kul, the lake in Kazakhstan near Kara-Djigach, on the map at all? We can confidently conclude that Kara-Djigach was a plague site because 10 of the gravestones from the particularly lethal year 1338-1339 had the word *mawtana* (epidemic) written on them. That was enough for the World Health Organization plague specialist, Robert Pollitzer, to imply that the 1346 plague outbreak in Caffa was a direct result of a plague outbreak eight years earlier in Kyrgyzstan. For although *mawtana* just means "epidemic" generically, Pollitzer knew that recent field studies in Kyrgyzstan had demonstrated the continuing presence of *Yersinia pestis* in local marmot populations. Pollitzer did not include a map indicating the direction of spread, but such maps fixing Issyk Kul on the medieval plague map became a fixture of plague histories from the 1970s on. And these maps almost always included an arrow, pointing from the Central Asian lake westward to the Crimea and thus making a historical argument that the plague unidirectionally spread from east to west. Hence, it is not surprising that in 2022, when geneticists recovered *Yersinia pestis* genomes from the graves in Kara-Djigach that had dated headstones, they concluded triumphantly that they had established the origin of the Black Death. After all, the genomes they had retrieved, they claimed, fell at an evolutionary state just *before* the Big Bang and the formation of Branch 1, the lineage that was carried to western Eurasia.

Sampling of headstones from the Kara-Djigach archeological site.

III. The narratives emerging from history: grain, armies, and Mongol expansion

By the time the geneticists published this work in 2022, however, historians had already been busy re-reading documentary accounts from the 13th century, where they noted clinical descriptions that sounded a lot like plague. The first credible evidence for plague outbreaks in human populations in the 13th century comes from northern China. After moving out of Mongolia in 1206, the Mongols progressed to northern China. In a series of sieges, the Mongols took one major city after another. After several of these sieges, there were reports of epidemics—always at the point of the siege being lifted. Our most detailed description comes from a Chinese physician, Li Gao (1180-1251) who wrote a description of the Mongol siege of the city of Kaifeng (then the largest city in northern China) in 1232-1233. The outbreak at Kaifeng occurred not in the heat of battle, but when there was a lull: The enemy had withdrawn for the moment, the siege was lifted, no combat had taken place for half a month. Li later interviewed his patients and an extensive network of contacts to gather information about epidemics associated with other sieges. He ended up creating a new system of medicine to address this new disease he and others had witnessed, which caused what he called Internal Damage. To be clear: We are not certain that the plague spread first among the Mongols, but sources we have from Li suggest that it was circulating much earlier than many scholars once thought.

Map showing the location of various sites in northern China where epidemics were reported following Mongol sieges.

After the appearance of this plague-like disease at sieges in China, we next catch a glimpse of it on the campaign across Iran led by Hulegu (ca. 1217-1265), one of Chinggis Khan's grandsons. The Mongol armies had first moved westward in the 1220s, but their hold on many of these western territories was precarious, and in the mid-1250s Hulegu undertook another huge campaign to permanently bring the western lands under Mongol control. One of the preparations for the campaign (which took several years of planning and stocking of provisions) was the collection of food supplies. As one chronicler, Quṭb al-Shirazi (d. 1311), a Persian astronomer and physician, described it:

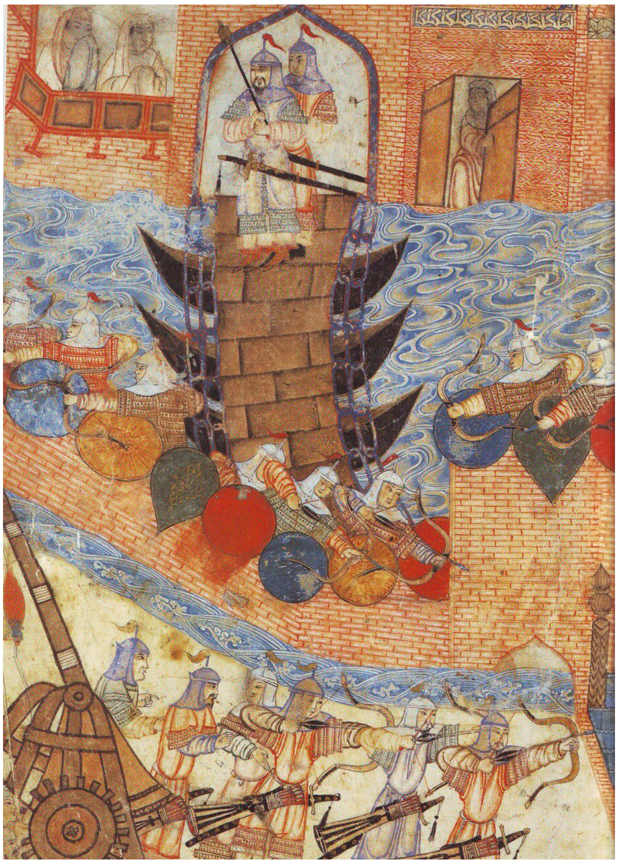
> From all the provinces, Hulegu's commanders arranged the distribution of provisions and supplies without limit and beyond compare transported by donkey, camel, cow, asses and such like. Such was the organization that noodles, cooked porridge, and pounded millet [*gavrus-i kufteh*] had been

> brought from the provinces of Northern China and Uyghuristan to [the sites of several sieges]; and every half *farsang*[7] they had stacked so much flour, rice and necessities in bags of fine linen [that] everywhere great hills appeared.[8]

This text is particularly important for clarifying the origin of the grains being imported: the provinces of Northern China and Uyghuristan—exactly the rich agricultural areas at the eastern base of the Tian Shan mountains from which plague emerged in the Big Bang.

In October 1257, Hulegu's forces set out for Baghdad from his nearby base camp in present-day northern Iran, reaching it early in the New Year. According to several sources, "pestilence" broke out after a very short siege. Later in this account, it was made clear that Hulegu's own armies were also afflicted. In the next year and a half, similar epidemics broke out in other regions the Mongols attacked in Syria. A later account from North Africa reported that a "stench" arising from the Mongols' attack on Baghdad arrived as far west as Tunisia, sickening the sultan, and engulfing the region in disease.

It is unclear (and may never be known) whether it was the Mongols themselves who first encountered these plague-bearing marmots in the Tian Shan Mountains, or some other groups the Mongols allied with in the region. Occasional hunters may have been infected by encounters with these marmots, just as happens today. But those are isolated instances. To start a *pandemic* chain of transmission, *Yersinia pestis* had to move out of marmot populations (which do not normally inhabit human spaces) into other rodent populations more accustomed to being around people. And whatever that second environment was—among rodents who do live next to humans—the spread must have repeated, allowing the bacteria to move surreptitiously with the human population as the Mongol Empire expanded. The current theory to explain plague's long-distance transmission after the Big Bang is that it moved through grain supplies intended to sustain the Mongol armies. The grain supplies would have attracted rodents, along with their fleas.



Depiction of the Siege of Baghdad in 1258, from the Diez Codex.

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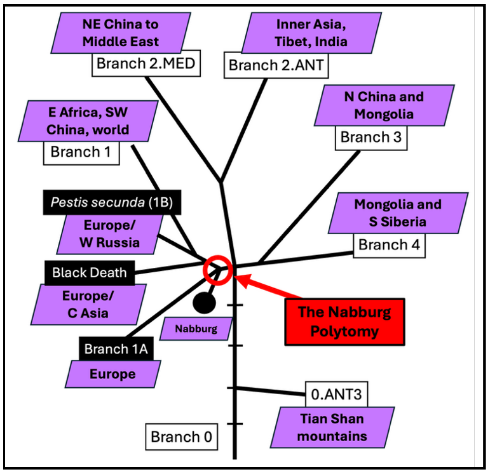
[7] A *farsang* is unit of measure: how far a person can walk in a day.

[8] Quṭb al-Dīn al-Shīrāzī, *The Mongols in Iran: Quṭb al-Dīn al-Shīrāzī's Akhbār-i Moghūlān*, trans. and ed. G. Lane (Routledge, 2018), 50.

IV. The complex biology of the Second Plague Pandemic

Bringing the biology of plague into our historical thinking means more than focusing on the symptoms of plague in its human victims (as we did with Guy de Chauliac in Lesson 1) or reckoning with its possible routes and mortality levels (as we did with Ibn Battuta in Lesson 2). It also means thinking through the complexity of plague as a disease involving the bacterium, insect vectors, and animal hosts. That biological complexity must have taken time to establish itself in each region where plague created new long-term reservoirs.

All the aDNA that has gone into making up the phylogenetic tree depicted on this page comes from human bodies. But humans are nothing more than accidental missteps in *Yersinia pestis'* long-term evolution, playing a role mostly in the long-distance transmission of the organism. Evolutionarily, humans are a dead end for *Yersinia pestis.* It was the fleas and rodent hosts that allowed plague to proliferate in the new reservoirs, where they were largely invisible to us.



A schematic diagram of the late medieval genetic divergences of Yersinia pestis, with the Nabburg Polytomy highlighted.

Evolutionary biologists have a mantra: Everything alive today had ancestors. "Well, duh!," you might be saying. But think about it. It means that everything alive today carries parts of its ancestors into the present. By studying the genetic makeup of both living things *and* the fragments of organisms from the past (aDNA), we can trace whole family histories. With a phylogenetic tree, however, instead of looking at family lore or birth certificates to establish degrees of relation, we look at the genome itself. Patterns of common changes allow us to say that certain strains are closely related to each other. A phylogenetic tree is what allows us to connect past and present together.

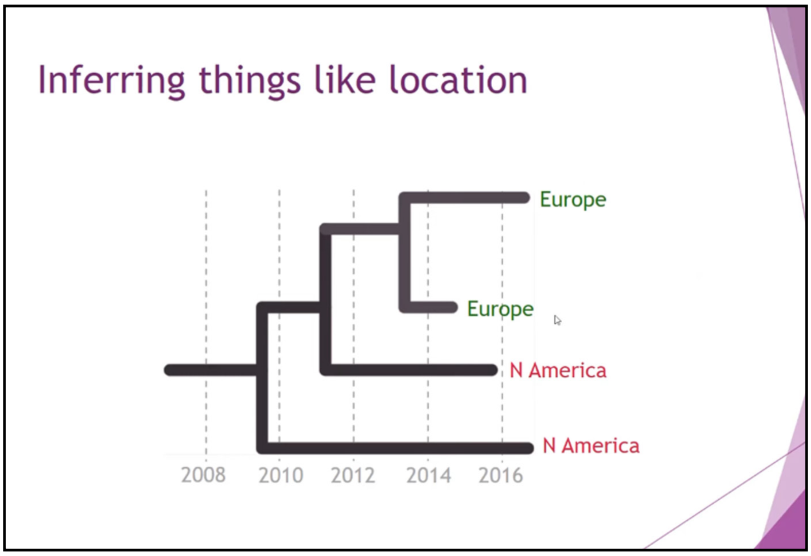
An illuminated initial 'C' opening the chapter on "Cemeteries" in an encyclopedia made in London after the Black Death.

Scientists are already tracking disease outbreaks with molecular genetics. For example, from the moment the first genome sequence of SARS-CoV-2 was shared in January 2020, the world was able to watch, in almost real time, the evolution of the viral pathogen that caused the COVID-19 pandemic. Similarly, in 2024, molecular genetics was used to track the transmission of the avian flu virus, H5N1, between humans and dairy cows in the United States. Although only about 100 genomes of *Yersinia pestis* have yet been retrieved from late medieval and early modern Eurasia, geneticists have been making claims for the past decade about the directionality of the spread of different strains of the pathogen.

Wait, you may be asking, why do we have to learn so much science in a history class? The answer is that it's evolutionary genetics that discovered the Big Bang, and it is genetics that allows us to connect the Big Bang to the East Smithfield Black Death Cemetery in London, and to connect those medieval genomes to strains of plague that still persist in the modern world. Genetics also connected this story to the marmots. And genetics reveals the Nabburg Polytomy (whose significance we'll learn more about in Lesson 4). Genetics is therefore the thread that ties the whole story together and allows us to see so much that Ibn Battuta couldn't see.

However, genetics cannot date anything. Although geneticists have been talking for years about "molecular clocks"—the idea that changes in the genome occur at a regular (and therefore, predictable) rate—the idea is sometimes misleading. A phylogenetic tree can show that one "event" happened before another: The polytomy we call the Big Bang happened before the pandemic we call the Black Death. But beyond that, historical dating is beyond the capacity of this field.

Still, understanding how genetics can establish the order of events can be revealing, even if it's also challenging. The diagram below gives us an example of how *geographic* information can be combined with *chronological* information to draw inferences about the origin and course of epidemics. Each "split" in the diagram represents a divergence in the organism, and we can see where the samples were found, too. Should we infer that this "outbreak" started in North America and then moved to Europe? Perhaps, but new information could easily upend that inference and reveal that we were wrong. This is just an example used for practice, which you will be able to discuss in class, but it is a helpful reminder to be cautious about the inferences we can easily make as we begin to dig into the details of *Yersinia pestis* phylogenetic trees.


Inferring things like location

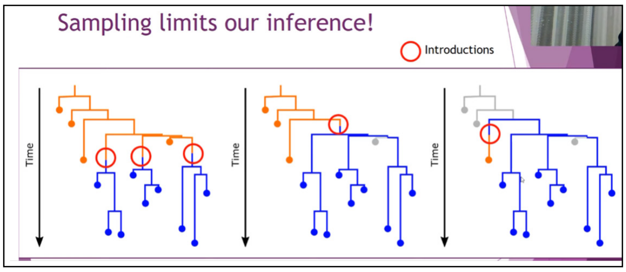
Example phylogenetic tree, illustrating how inferences about origin and course of epidemics might be made.

In sum, paleogenomics is built on a premise that a) genetic material from the past can be retrieved, and b) that these "ancestors" can be compared to their descendants (living strains) to determine how organisms have changed over time. In the case of *Yersinia pestis*, we are especially concerned to find out *where* those ancestors traveled in the past.

Step 1: Reading Phylogenetic Trees

Above, we took an initial look at the phylogenetic tree of the Big Bang. To study the Black Death, we need to look closely at just Branch 1, the only one of the four Big Bang offspring to have been studied paleogenetically and the only one (so far as we know) to have been carried westward in the Middle Ages across central Eurasia, reaching Europe and Africa.

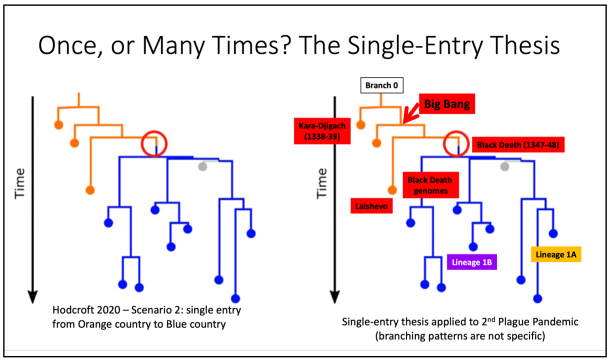
As mentioned above, our inferences about the directionality of the spread of a disease can change once we get evidence from a new genome. Let's consider another hypothetical example. Looking at the diagram below, we might infer that a pathogen passed from a hypothetical orange country to a blue country multiple times (scenario 1). Or maybe it passed into the blue country only once (scenario 2). Or maybe it was in the blue country all along and only passed once into the orange country (scenario 3). When we only have a few samples, it's hard to figure out which interpretation is correct.



Sampling limits our inference!

Different scenarios of pathogen introduction from one country to another, based on phylogenetic data. Each scenario tells a different story, even though the overall structure of the tree hasn't changed.

The process is made harder because most paleogenomes that are retrieved are not well-dated. The technique of radiocarbon-dating produces century-wide estimates. Such wide ranges, plus the limited number of samples means that with paleogenetics alone, there is a lot of room for interpretation.   So, let's go back to the hypothetical scenarios of regional introduction mentioned above. Here are the first two scenarios—both showing introductions from the "orange" country into the "blue" one, but now marked-up to show the actual debates occurring now in plague studies. Was there just *one* introduction, when the 1347-1348 Black Death brought plague into Europe, as depicted in the "The Single-Entry Thesis" below?



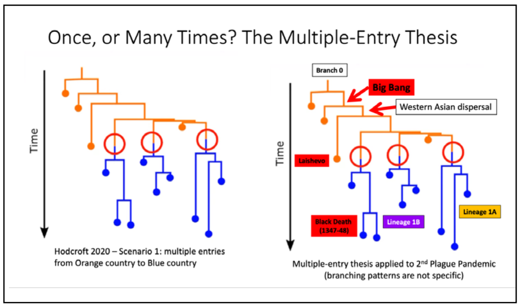
Once, or Many Times? The Single-Entry Thesis

Hodcroft 2020 – Scenario 2: single entry from Orange country to Blue country

Single-entry thesis applied to 2nd Plague Pandemic (branching patterns are not specific)

The Single-Entry Thesis, labeled screen capture from Emma Hodcroft

Or were there three introductions, as in the "Multiple-Entry Thesis" below, with the Black Death now being only one of the three?



Once, or Many Times? The Multiple-Entry Thesis

Hodcroft 2020 – Scenario 1: multiple entries from Orange country to Blue country

Multiple-entry thesis applied to 2nd Plague Pandemic (branching patterns are not specific)

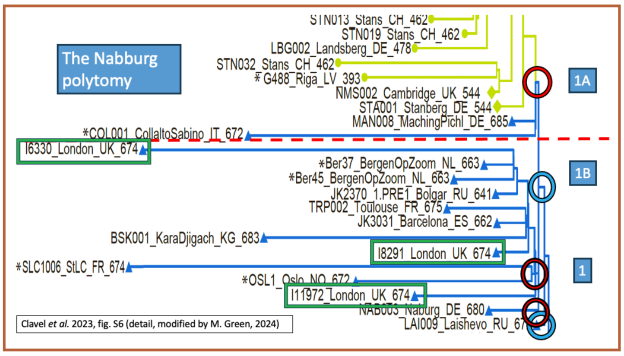
The Multiple-Entry Thesis, labeled screen capture from Emma Hodcroft

The difference between the two scenarios is huge in terms of their historical implications. The first implies that *Yersinia pestis* entered Europe (blue) from some area (in orange) *once* and only then began to diversify. Since the samples from that first introduction are assumed to be precisely dated to the traditional Black Death dates (1346-1353), that assigns a fixed beginning date to the existence of the new lineages. There's a clear before and after sequence: Before the Black Death, there was no genetic diversity of *Yersinia pestis* within Europe. The historical implication is also clear: There should be no *effects* of plague in Europe before the pandemic we call the Black Death (1347/1348), for the simple reason that the pathogen was not present.

Now look at the second scenario. The Black Death genomes are still dated the same. And they can still be associated with the Black Death mortality as it is commonly understood because they come from more or less well-dated gravesites associated with that event. But because the other lineages, 1A and 1B, diverged from the Black Death lineages *before* any of them entered Europe (their branching points are all still in the "orange" region), the Black Death events no longer tell us anything about the within-Europe histories of the other lineages. They may have entered Europe via different routes than the Black Death lineages. They may have even entered Europe *before* the Black Death.

Step 2: Turning phylogenies into history

The research team that claimed to have proven that the Big Bang didn't happen until the early 14th century, perhaps even after 1338-1339 when the epidemic occurred at Kara-Djigach, based their analysis on only a handful of changes they found in the DNA, out of millions possible. A different technique for deriving phylogenetic trees is to look at the *whole* genome. The details are fun, but challenging, so we'll summarize them here. This phylogenetic tree is a detail from a 2023 study, which looked at the branching pattern of most of the early Branch 1 aDNA genomes.



Clavel *et al.* 2023, fig. S6 (detail, modified by M. Green, 2024)

Detail of the early Branch 1 lineages in the Yersinia pestis phylogeny. A genome from Russia (Laishevo) is, evolutionarily, the earliest post-Big Bang strain. After that, a dispersal of plague produced the strain found at Nabburg (Germany) and two other lineages, 1A and 1/1B (the red circles). The site at Nabburg is discussed in Lesson 4.

This is a crowded diagram, but your instructor will have more detailed views to show in class, allowing you to see this information in layers. The genomes shown on this phylogenetic tree include all the *Yersinia pestis* genomes retrieved from the 14th century as of the beginning of 2023. The entire diagram as a whole represents Branch 1, the lineage of plague that moved into western Eurasia, and that you might remember from the phylogenetic tree we looked at above.

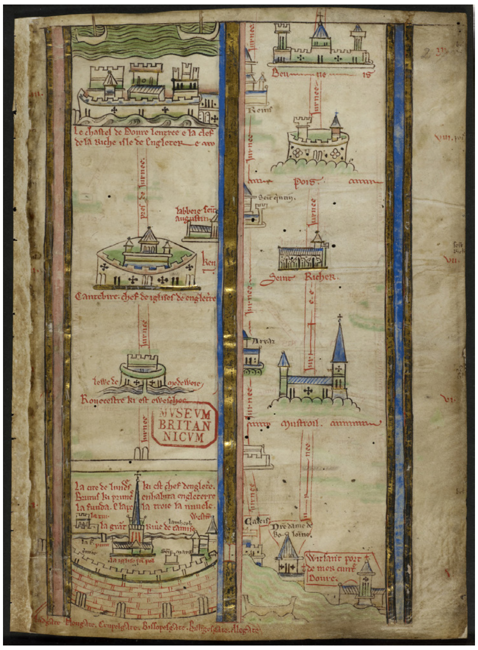
First, look at the two blue circles. These are the first sub-branching of Branch 1. One (the bottom blue circle) was found in Laishevo, Russia, in the Volga River basin, north of the Caspian Sea. It is the earliest example of Branch 1 so far identified after the Big Bang, and as far as we know, it seems to have died out.

The other branch (the top blue circle) represents the ancestor of all other strains that developed in Branch 1. That common ancestor then split three ways in an event that we can call the Nabburg Polytomy ("polytomy" just means a splitting into several new lineages at once. The Big Bang was a polytomy too—just very big one). The three red circles represent those three new branches. Lineage 1A (marked by the top red circle, leading to blue and green lines) are strains that entered Europe from a different route and lived on until at least the 18th century, spreading throughout Europe and causing every known outbreak there after the 14th century.

The bottom branch (the bottom red circle), is a strain of the genome found in the Central German town of Nabburg in the 1310s. As far as we know this strain also died out (just like the Laishevo genome). We'll be learning more about the town of Nabburg and this genome in Lesson 4, but we should note it now because it helps us define how early this split occurred. Because we suspect that the Nabburg genome dates to the 1310s, that tells us that this three-way split happened sometime before then. For now, it's the center branch of this Nabburg Polytomy, three-way split that is of immediate interest. That section, which begins with the middle red circle, is yet more complex, but it includes four strains associated with Black Death sites: in particular, two samples found at the London East Smithfield Cemetery dated to the Black Death (numbered 8291 and 11972), the genomes from Kara-Djigach, and genomes from Barcelona and Toulouse.

Step 3: Excavating plague's history in London

So, how can *history* be extracted from these branching patterns? Since we have *geographic* data for each of those genomes, we have a sense of how broadly these closely-related strains were circulating. Most obviously, we note that the genome from Kara-Djigach, dated 1338-1339, seems to share a direct common ancestor with the genomes found at Barcelona and Toulouse, as well as one of the London genomes. If this genetic relationship proves sound, it is powerful testimony to the ability of this cluster of strains to move great distances.



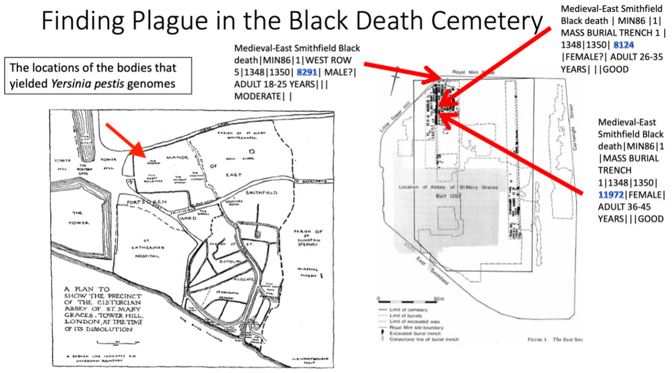
View of medieval London, ca. 1250.

We can also see when different strains show up in the same place. There are three genomes all found in London. But each is in its own separately branching lineage. Why is that significant? Because it tells us that plague's history in London is more complicated than researchers studying the Black Death once suspected.

First, since 2016 the strain numbered 6330 has been recognized to be part of a separate group from the other two. This is the 1B lineage, also known as the *pestis secunda* “the second pestilence.” We have documentary sources that allow us to date this strain to the second wave of plague that struck England in the early 1360s. Therefore, it’s not critical for our study of the Black Death itself.

More surprising is the apparent genetic (and therefore, historical) difference between strains numbered 8291 and 11972. Although these have been treated in prior publications as if they belong to the same genotype, their separate branches cause us to ask whether there is anything else different between them. In fact, there is.

Museum of London, Human Bioarchaeological Centre, sample MIN86 6330: Source of tooth sampled for the 2011 Nature study on the Black Death genome. Tooth extracted from the upper left maxilla, 2nd molar.



Maps of the London East Smithfield Black Death Cemetery:

The London East Smithfield Black Death Cemetery was excavated by professional archaeologists in the 1980s. Detailed records were kept of where each body was found; these are distributed in different sections of the cemetery, mostly laid out in rows. The bodies that yielded genomes 8291 and 11972 were, in fact, buried in different parts of the cemetery: 8291 in the West Row, and 11972 in the long Mass Burial Trench at the center of the site. In terms of its position on the phylogenetic tree, strain 11972 seems more closely related to the genome from Kyrgyzstan (nearly 4,000 miles away) than it does to strain 8291, buried in the same cemetery two rows away.

It should be obvious now that the most important thing we want is historical dating. Are strains 8291 and 11972 really from the same outbreak? If so, how can we explain the presence of two distinct strains in the same burial ground? In the case of the London cemetery, no radiocarbon dating was done because the date of the burials was assumed based on the presence of coins. These could be confirmed to date to about 1348-1349 (from Row 6 in the cemetery), which established the date for the whole burial ground. Thus, it seems as though two strains of plague may have both been circulating in London during the period that we know as the Black Death. One had been circulating for a relatively short time; the other appears to have been circulating far longer.

To sum up: Although genomes don't have calendars, phylogenetic trees do reveal change-over-time narratives. The very concept of the Big Bang implied that something big happened before the Black Death. Hints of historical events between the Big Bang and the traditional dates of the Black Death have indeed been found, both in documentary sources and in the paleogenomes. More research will likely clarify the mysteries surrounding the spread of the medieval plague. But from what we can work out now, there appear to have been multiple lineages moving about Afro-Eurasia over a longer period of time, and earlier, than previous scholarship once thought.

Overall, the amount of new knowledge we have now of the Second Plague Pandemic is astounding compared to what was known in 2010. And we have not yet touched on the information the field of archaeology is making available, now that those researchers, too, can be confident that the sites they are excavating were in fact burial places of plague victims. We will see more of what archaeology can add in Lesson 4. However, we should not lose sight of the fact that while *we* can now know so much about the inherent virulence of plague and can broadly reconstruct the routes of its transmission, the people afflicted by plague in the Middle Ages, or witnessing its effects like Ibn Battuta, had no knowledge of any of the biological mechanisms of this horrible disease. Whereas Muslims could draw on ethical principles and religious understandings about plague that had been in development in the Islamic world since the time of the Prophet Mohammed (Lesson 2), Christians in Europe (as we will see) leaned toward an understanding of plague that blamed its appearance on human malice. The resulting violence was as deadly and horrible as the disease.

Some of the coins retrieved from the burial site of body 6120, "a female aged 26-35 years," in the London East Smithfield Black Death Cemetery, Row 6.

Further Reading

Barker, Hannah. “Laying the Corpses to Rest: Grain, Embargoes, and *Yersinia pestis* in the Black Sea, 1346-1348.” *Speculum* 96, no. 1 (January 2021): 97–126.

Carmichael, Ann G. “Universal and Particular: The Language of Plague, 1348–1500.” In *Pestilential Complexities: Understanding Medieval Plague*, edited by Vivian Nutton, 17–52. The Wellcome Centre Trust for the History of Medicine, 2008.

Clavel, Pierre, *et al.* “Improving the Extraction of Ancient *Yersinia pestis* Genomes from the Dental Pulp.” *iScience* 26, no. 5 (May 19, 2023): 106787.

Dols, Michael, trans. “Ibn al-Wardī’s *Risālah al-naba’ ‘an al-waba*. A Translation of a Major Source for the History of the Black Death in the Middle East,” in *Near Eastern Numismatics. Iconography, Epigraphy, and History: Studies in Honor of George C. Miles*, ed. D. K. Kouymijian, 443–55. American University of Beirut, 1974.

Favereau, Marie. *The Horde: How the Mongols Changed the World*. Harvard University Press, 2021.

Grainger, Ian, Duncan Hawkins, Lynne Cowal, and Richard Mikulski. *The Black Death Cemetery, East Smithfield, London*, MoLAS Monography Series 43. Museum of London Archaeology, 2008.

Green, Monica H. “The Four Black Deaths.” *American Historical Review* 125, no. 5 (2020): 1600–1631, including the online supplement, “Marmots and Their Plague Strains,” https://doi.org/10.17613/7020-8j08.

Green, Monica H. “A New Definition of the Black Death: Genetic Findings and Historical Interpretations.” *De Medio Aevo* 11, no. 2 (2022): 139–55.

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Further Reading

Green, Monica H. "The Pandemic Arc: Rethinking Narratives in the History of Medicine." *Journal of the History of Medicine and Allied Science* 79, no. 4 (October 2024): 345–62, https://doi.org/10.1093/jhmas/jrae008.

Green, Monica H. "Putting Asia on the Black Death Map." *The Medieval Globe* 8, no. 1 (2022): 59–87.

Green, Monica H. and Nahyan Fancy. "Plague History, Mongol History, and the Processes of Focalisation Leading up to the Black Death: A Response to Brack *et al.*," *Medical History* 68, no. 4 (Fall 2024): 411–35, https://doi.org/10.1017/mdh.2024.29.

Hawkins, Duncan. "The Black Death and the New London Cemeteries of 1348." *Antiquity* 64 (1990): 637–42.

Hodcroft, Emma. "Seeing the Epidemic Through the Trees – Why is Sequencing Important for COVID-19?" *Reatch Nano-talks*, recorded March 2020, https://www.youtube.com/watch?v=Dd1RSMETXfI. 23 mins.

Honeybourne, Marjorie B. "The Abbey of St Mary Graces, Tower Hill," *Transactions of the London and Middlesex Archaeological Society* 11 pt I (1952): 16–26.

Horák, Jan, Estella Weiss-Krejci, Jan Frolík, Filip Velímský, and Ladislav Šmejda. "The Cemetery and Ossuary at Sedlec near Kutná Hora: Reflections on the Agency of the Dead." In *Interdisciplinary Explorations of Postmortem Interaction: Dead Bodies, Funerary Objects, and Burial Spaces Through Texts and Time*, edited by Estella Weiss-Krejci, Sebastian Becker, and Philip Schwyzer, 269–95. Springer, 2022.

Hymes, Robert. "A Tale of Two Sieges: Liu Qi, Li Gao, and Epidemics in the Jin-Yuan Transition." *Journal of Song-Yuan Studies* 50 (2021): 295–363.

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Further Reading

Hymes, Robert. “Buboes in Thirteenth-Century China: Evidence from Chinese Medical Writings.” *The Medieval Globe* 8, no. 1 (2022): 1–57.

Jackson, Peter. *From Genghis Khan to Tamerlane: The Reawakening of Mongol Asia*. Yale University Press, 2023.

Jones, Elizabeth D. *Ancient DNA: The Making of a Celebrity Science*. Yale University Press, 2022.

Kacki, Sacha, Lila Rahalison, Minoarisoa Rajerison, Ezio Ferroglio, Rafaella Bianucci. “Black Death in the Rural Cemetery of Saint-Laurent-de-la-Cabrerisse Aude-Languedoc, Southern France, 14th century.” *Journal of Archaeological Science* 38, no. 3 (2011): 581–87.

Spyrou, Maria A., et al. “The Source of the Black Death in Fourteenth-Century Central Eurasia.” *Nature* 606 (June 23, 2022): 718–24.

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Image Citations

Page 1:
Scanning electron microphotograph depicting a mass of *Yersinia pestis* bacteria (the cause of bubonic plague) in the foregut of the flea vector , Rocky Mountain Laboratories, NIAID, NIH, Public Domain, https://commons.wikimedia.org/wiki/File:Yersinia_pestis.jpg

Page 2:
Travels of Ibn Battuta, 1325-1354, ORIAS, University of California Berkeley, Fair Use, https://orias.berkeley.edu/resources-teachers/travels-ibn-battuta

Page 3:
Ibn al-Wardi's *maqama* on plague, from Ibn Abi Ḥajala's *Daf' al-Niqma*, MS Laleli 1361, Suleymaniye Library, Istanbul, fol. 73b.

Page 5:
Highlighted map of the Black Death, in Marie Favereau, *The Horde: How the Mongols Changed the World* (Cambridge, MA: Harvard University Press, 2021), map, pp. 254-55, highlighting by Monica H. Green.
East Smithfield Black Death Cemetery, Mass Burial Trench 1, London, Museum of London Archaeology.

Page 6:
Museum of London, Human Bioarchaeological Centre, sample MIN86 6330: Source of tooth sampled for the 2011 *Nature* study on the Black Death genome. Tooth extracted from the upper left maxilla, 2nd molar. Photograph by Monica H. Green, 2016.

Page 7:
Schematic diagram of the Big Bang, Monica H. Green, based in part on Pierre Clavel, et al. "Improving the Extraction of Ancient *Yersinia pestis* Genomes from the Dental Pulp," *iScience* 26, no. 5 (May 19, 2023), fig. S6.

Page 8:
Marmota caudata, Khushboo & Rahul Sharma, via Flikr, https://www.flickr.com/photos/27566485@N02/34664185744
Extended Data Fig. 1: Available tombstone pictures from Kara-Djigach, Spyrou, M.A., Musralina, L., Gnecchi Ruscone, G.A. et al, "The source of the Black Death in fourteenth-century central Eurasia," *Nature* 606, 718–724 (2022). https://doi.org/10.1038/s41586-022-04800-3

Page 9:
Labelled map of Li Gao's reports of epidemic, in Robert Hymes, "A Hypothesis on the East Asian Beginnings of the *Yersinia pestis* Polytomy," *The Medieval Globe* 1 (Fall 2014), 285-308; repr. in: *Pandemic Disease in the Medieval World: Rethinking the Black Death*, ed. Monica H. Green (Amsterdam and Kalamazoo, MI: Arc-Medieval Press, 2015), pp. 285-308.

Page 10:
Persian painting of Hülegü's army besieging a city, Public Domain, https://commons.wikimedia.org/wiki/File:Persian_painting_of_H%C3%BCleg%C3%BC%E2%80%99s_army_attacking_city_with_siege_engine.jpg

Page 11:
Schematic diagram of the Big Bang highlighting the Nabburg Polytomy, Monica H. Green, based in part on Fig. S6, Clavel, Pierre, et al. "Improving the Extraction of Ancient *Yersinia pestis* Genomes from the Dental Pulp." *iScience* 26, no. 5 (May 19, 2023): 106787.
Initial 'C', a scene representing cemetery, miniature in Omne Bonum, London, England, 1360-1375, British Library, MS Royal 6 E VI, vol. 1, f. 267vb.

Page 12:
"Inferring things like location," screen capture from Emma Hodcroft, "Seeing the Epidemic Through the Trees – Why is Sequencing Important for COVID-19?" Reatch Nano-talks, recorded March 2020, https://www.youtube.com/watch?v=Dd1RSMETXfI, 23 mins.

Page 13:
"Sampling limits our inference!," screen capture from Emma Hodcroft, "Seeing the Epidemic Through the Trees – Why is Sequencing Important for COVID-19?" Reatch Nano-talks, recorded March 2020, https://www.youtube.com/watch?v=Dd1RSMETXfI, at 12 mins.
"Seeing the Epidemic Through the Trees – Why is Sequencing Important for COVID-19?" Reatch Nano-talks, recorded March 2020, https://www.youtube.com/watch?v=Dd1RSMETXfI, 23 mins.

Page 14:
Detail of the early Branch 1 lineages, Fig. S6, Pierre Clavel, et al. "Improving the Extraction of Ancient *Yersinia pestis* Genomes from the Dental Pulp," *iScience* 26, no. 5 (May 19, 2023): 106787, with labelling by Monica H. Green.

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Image Citations

Page 15:
Detail of itinerary by Matthew Paris from London to Jerusalem, between 1250 and 1259, London, British Library, Royal MS 14 C VII, f.2r, https://commons.wikimedia.org/wiki/File:Itinerary_by_Matthew_Paris_-_Historia_Anglorum_(1250-1259),_f.2_-_BL_Royal_MS_14_C_VII.jpg

Page 16:
Museum of London, Human Bioarchaeological Centre, sample MIN86 6330: Source of tooth sampled for the 2011 *Nature* study on the Black Death genome. Tooth extracted from the upper left maxilla, 2nd molar. Photograph by Monica H. Green, 2016
Map of the larger neighborhood of east London, in Marjorie B. Honeybourne, "The Abbey of St Mary Graces, Tower Hill," *Transactions of the London and Middlesex Archaeological Society* 11 pt I (1952): 16–26, at p. 21.

Page 17:
Coins from London East Smithfield Black Death Cemetery burial site of body 6120, in Ian Grainger, Duncan Hawkins, Lynne Cowal, and Richard Mikulski, *The Black Death Cemetery, East Smithfield, London*, MoLAS Monography Series 43, (Museum of London Archaeology, 2008), 17.