Pest og klima: Skal vi forstå pest blant mennesker, må vi forstå hvordan pest utspiller seg i naturen

Nils Chr. Stenseth

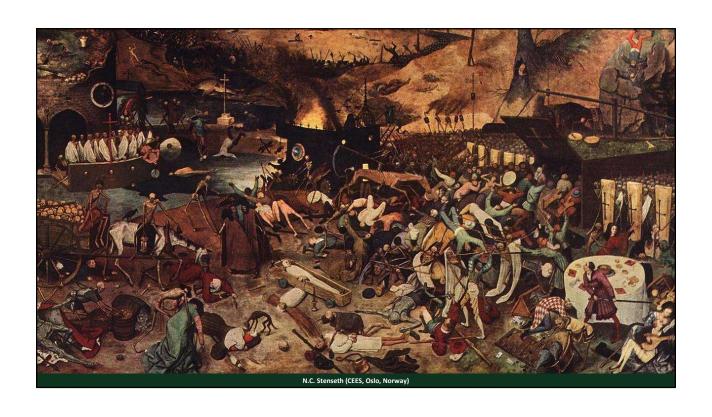
Professor of Ecology and Evolution at The Centre for Ecological and Evolutionary Synthesis (CEES), University of Oslo, Norway (www.mn.uio.no/cees/Stenset)
Founding and Past Chair of CEES - Centre for Ecological and Evolutionary Synthesis (CEES; www.cees.uio.no) at the Faculty of Mathematics and Natural Scienes,
University of Oslo, Norway

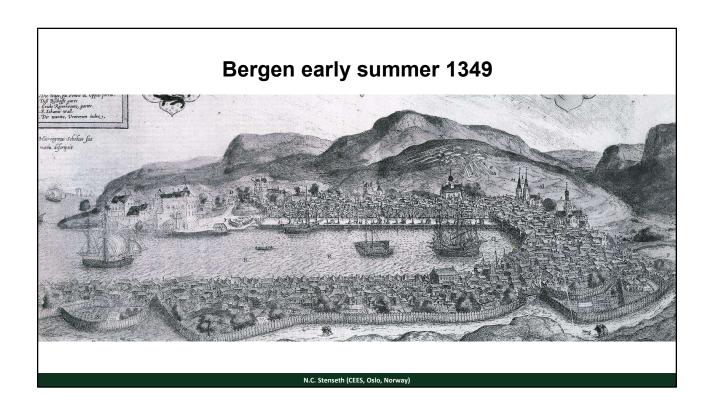
Deputy Chair of The Centre for Pandemics and One Health Research at the Faculty of Medicine, University of Oslo, Norway



Digitalt frokost-møte i regi av CIENS. 22.03.23 – 08:30-10:00

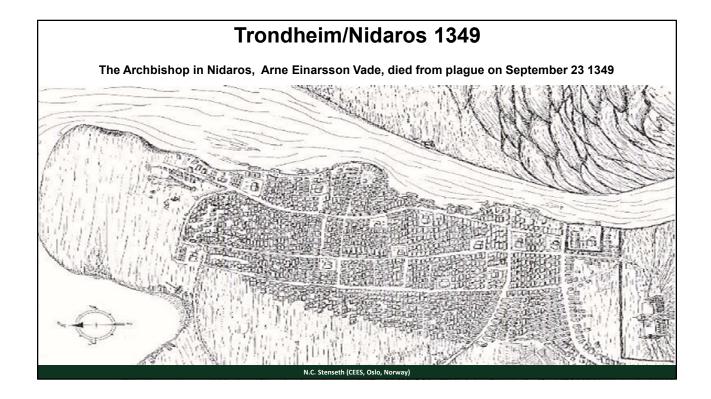


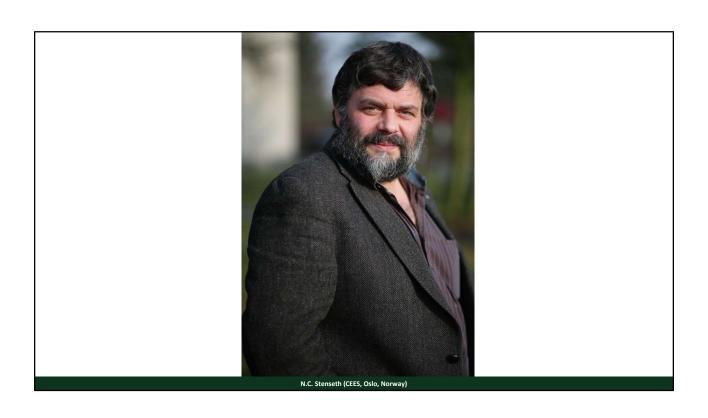




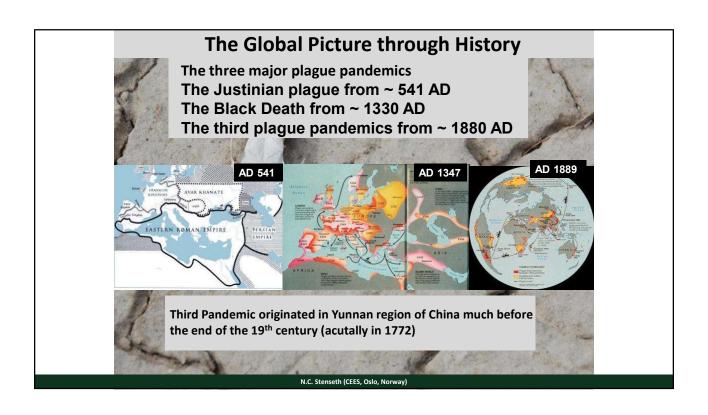
... with a rat carrying fleas infected with plague ...

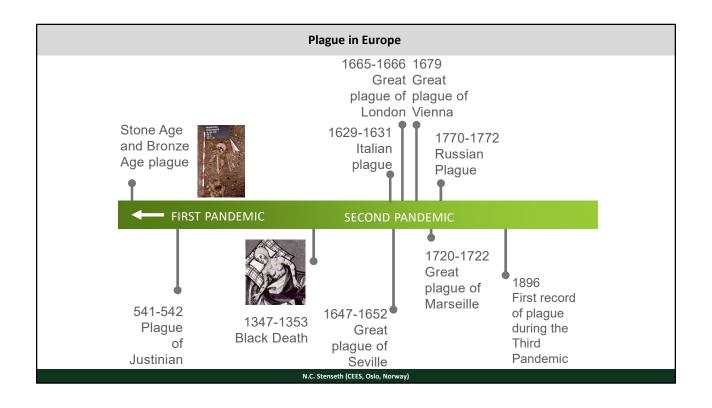
... after which it might have spared through the country with people and body lice and body fleas ...











Yersinia pestis is first and foremost found in wildlife – particularly wildlife rodents
Plague does occasionally spill over to the human population where it caused severe illness

N.C. Stenseth (CEES, Oslo, Norway

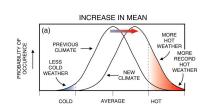
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Today - not in Europe

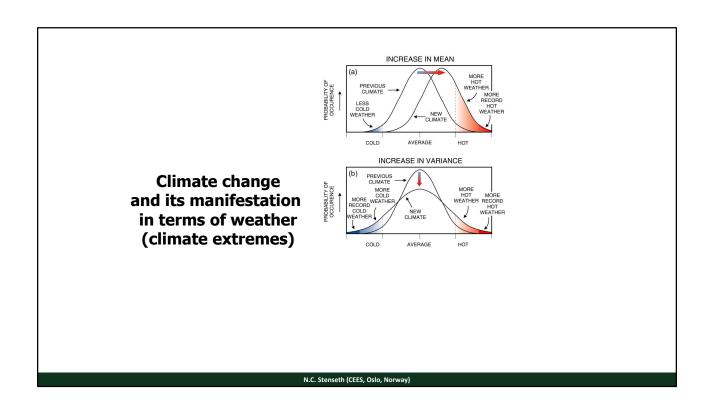


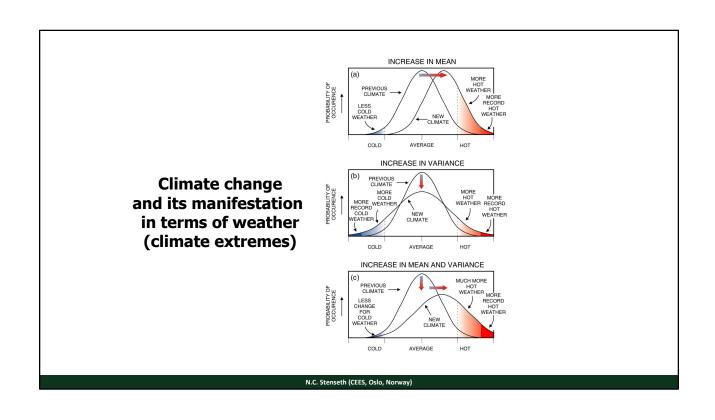
Outbreak of plague after a couple of years with warm (but not too hot) and humid (but not too wet) over a large area of steppes Spillover to the human population (directly or indirectly) following droughts over large areas of steppes

N.C. Stenseth (CEES, Oslo, Norway)



Climate change and its manifestation in terms of weather (climate extremes)





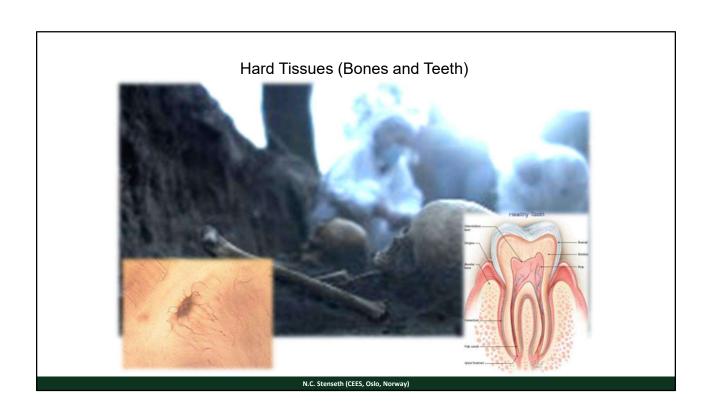
A common claim					
N.C. Stenseth (CEES, Oslo, Norway)					

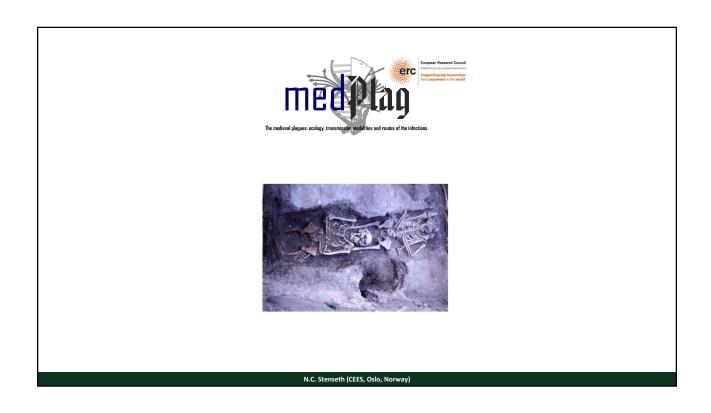
A common claim:

"There must have been a wildlife-based plague reservoir in Europe (during the medieval period)"

BUT: Boris V. Schmid *et al.* (in *PNAS* 2015) questioned that claim "Climate-driven introduction of the Black Death and successive plague reintroductions into Europe"

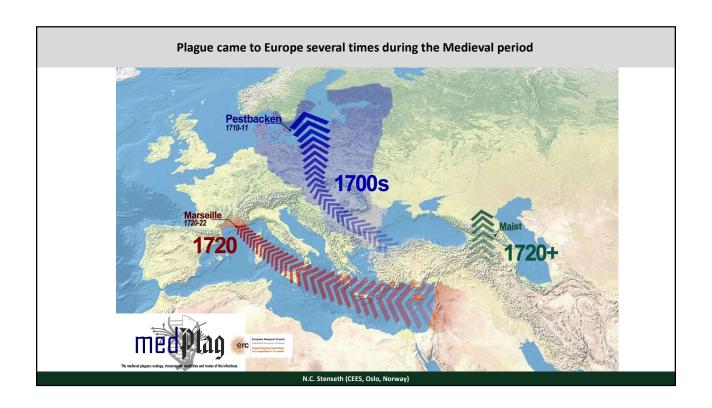
This has later been supported by aDNA studies by the Barbara Bramanti team in Oslo











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Two contrasting hypotheses:

Either the plague bacterium survived several hundred years in Europe (Hypothesis #1) or the plague bacterium was repeatedly re-introduced (Hypothesis #2)

Barbara Bramanti *et al.* (in *PNAS* 2021) reviewed available evidnce and found Hypothesis #1 the least likely one



RESEARCH ARTICLE ECOLOGY





No evidence for persistent natural plague reservoirs in historical and modern Europe

Nils Chr. Stenseth^{a,b,1,2}, Yuxin Tao^{c,1}, Chutian Zhang^{d,e,1}, Barbara Bramanti^{a,1}, Ulf Büntgen^{g,t,1}, Xianbin Cong^e, Yujun Cui¹, Hu Zhou^m, Lorna A. Dawsonⁿ, Sacha J. Mooney⁹, Dong Li^c, Henry G. Fell⁹, Samuel Cohn^e, Florent Sebbane^e, Philip Slavin^e, Wannian Liang^{d,e}, Howell Tong^{c,t}, Ruifu Yang^{1,2}, and Lei Xu^{d,e,2}

Contributed by Nils Stenseth; received June 8, 2022; accepted October 7, 2022; reviewed by Barbel Finkenstadt, Paul Slack, and David M. Wagner

Caused by Yersinia pestis, plague ravaged the world through three known pandemics: the First or the Justinianic (6th–8th century); the Second (beginning with the Black Death during c.1338–1353 and lasting until the 19th century); and the Third (which became global in 1894). It is debatable whether Y. pestis persisted in European wildlife reservoirs or was repeatedly introduced from outside Europe (as covered by European Union and the British Isles). Here, we analyze environmental data (soil characteristics and climate) from active Chinese plague reservoirs to assess whether such environmental conditions in Europe had ever supported "natural plague reservoirs". We have used new statistical methods which are validated through predicting the presence of modern plague reservoirs in the western United States. We find no support for persistent natural plague reservoirs in either historical or modern Europe. Two factors make Europe unfavorable for long-term plague reservoirs: 1) Soil texture and biochemistry and 2) low rodent diversity. By

Significance

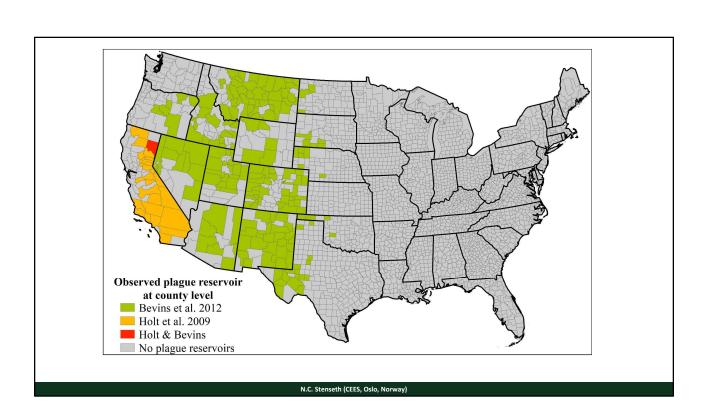
Plague killed millions of people during the three pandemics in the past two millennia. Despite much research, it remains unclear whether persistent natural plague reservoirs existed in Europe. To examine this question, we have developed a statistical model based on high-resolution and

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The basic idea of this PNAS paper

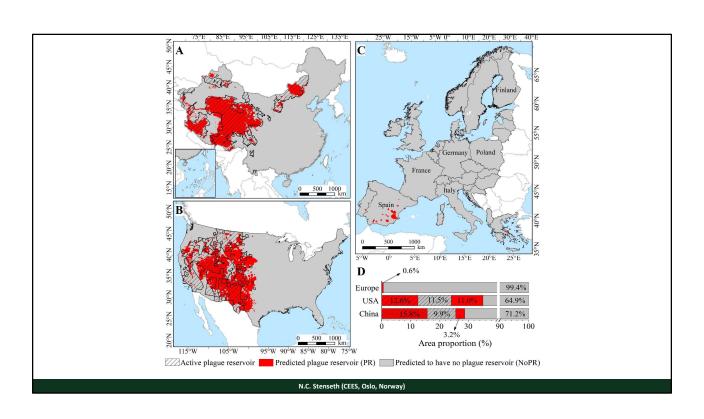
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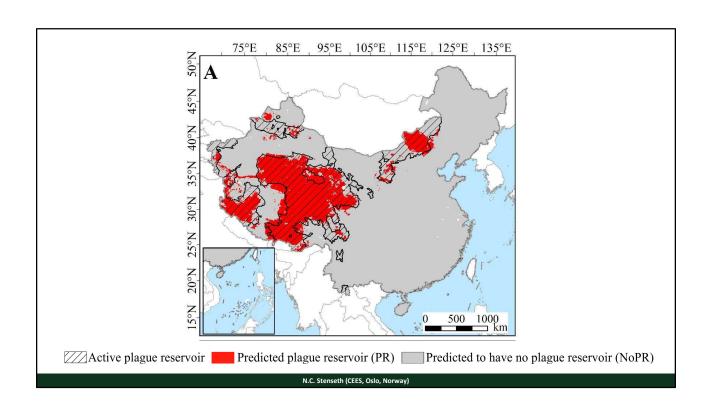
- 1. Develop a statistical model describing the environmental conditions for the existence of persistent rodent-based plague reservoirs using active plague reservoirs in China
- 2. The soil chemicals were in focus
- 3. Tested (or validated) this Chinese-based model against US data

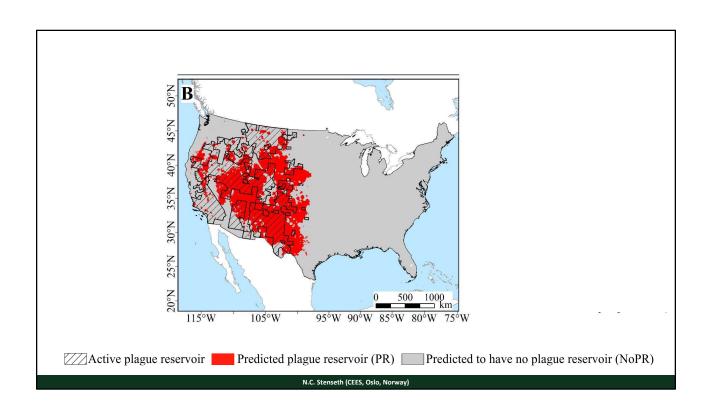


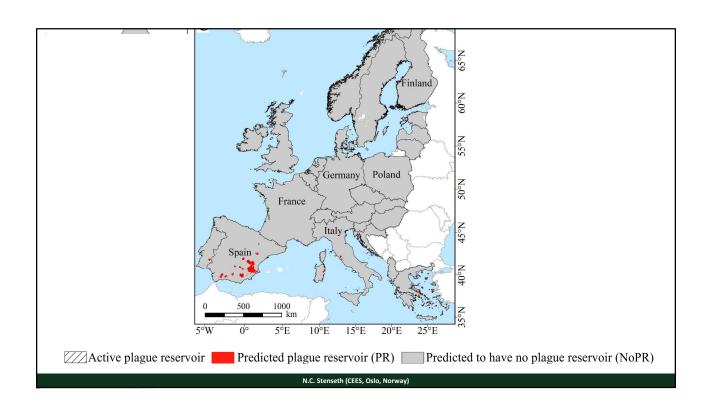
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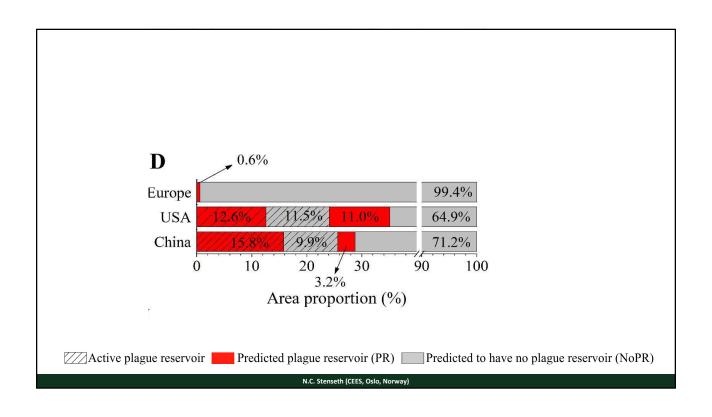
- 1. Develop a statistical model describing the environmental conditions for the existence of persistent rodent-based plague reservoirs using active plague reservoirs in China
- 2. The soil chemicals were in focus
- 3. Tested (or validated) this Chinese-based model against US data
- 4. Used this model to ask whether there ever has been persistent rodent-based plague reservoirs in Europe

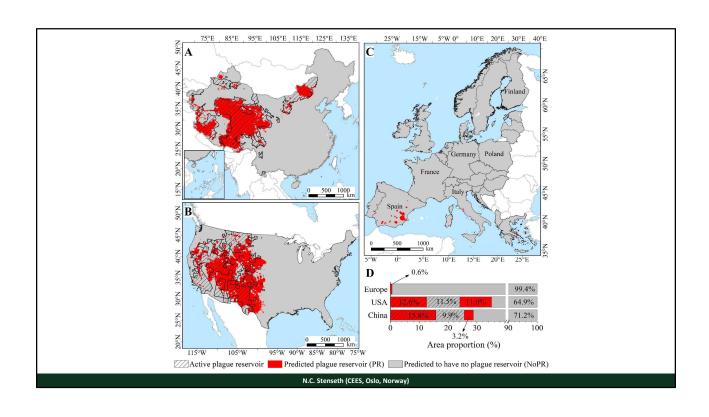




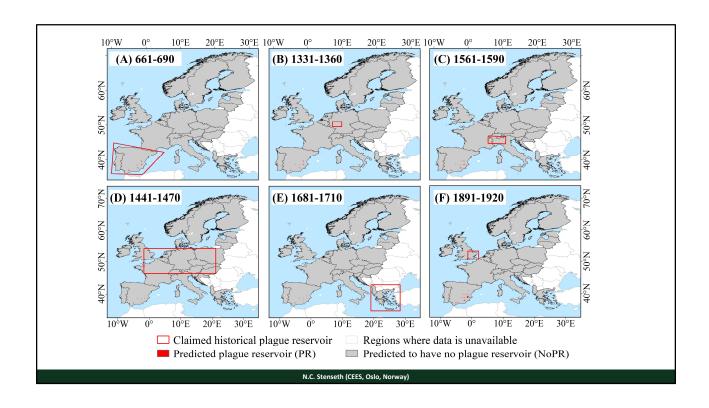








Pandemic	Period	Place	Sources
First	660-749	Iberian Peninsula	(18)
Second	1349-c.1400	South-Central Germany	(13, 14)
Second	c.1460-1640	Central Europe	(13)
Second	1348 - 16th century	Southern Alps* & Pyrenees	(15)
Second	16 th -19 th centuries	The Balkans	(19)
Second	1348-c.1500	Temperate climate zone of Europe, including East Anglia (UK)	(16)
Third	1906-1918	East Suffolk (UK)**	(16, 20)



	Hypothesis 1	Hypothesis 2
Main differences		
Origin of the outbreaks	Plague established in Western European reservoirs (for example, marmots in the Alps) (3, 4, 8)	Plague was repeatedly imported from Eastern European or Asian reservoirs (6, 7, 9, 11, 13)
Transmission	Mediated by rats infected by wild rodents, as in China during the Third Pandemic (3)	Imported by rats, humans, and goods and subsequently spread by chains of human transmission, as in Europe during the Third Pandemic (17, 22)
Vector	Xenopsylla cheopis and other rodent fleas	Any ectoparasite, including <i>Pulex irritans</i> , and body lice (14, 30)

Table 1. Main differences between the two competing hypotheses proposed to explain the phylogeny of Y. pestis of the second plague pandemic; genomic and evolutionary, historical and archaeological, and ecological arguments are considered

	Hypothesis 1	Hypothesis 2	
Main differences			
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Supporting information			
Population genomics	Western European strains (the Alpine clade) are basal in the subbranch (although of different eras). A model proposes Western European strains as ancestral sources for the transmissions (SI Appendix, Fig. S1)	The oldest (LA/009) and the most recent strains, in addition to Bolgar, are all from Eastern Europe (Russia) as well as all the strains of the 18th century; the majority of the Western European strains in the phylogeny come from ports	
History and archaeology	A hypothesis (16) suggests that the plagues from the 16th century in the Alps were not imported by major trade centers	Multiple historical records assert that plague was imported for outbreaks associated with the Black Death strains (partially reviewed in refs. 6, 7, 11, 13) for BRA (4), SPN (in the Alps), PEB10 (7), and OBS (5). Multiple records of importation are historically attested (18), particularly in harbors	
Climate	No climatic signal in support, although four datasets of climatic proxies were from the Alps (13)	Strong signals of climate-driven introductions of plague from Asia (13)	
Evolution	Y. pestis developed in Western European reservoir strains pla+lpla— and Delta49kb, possibly as a form of adaptation to the local host (rodents)	Y. pestis developed pla+/pla— and Delta49kb strains possibly as a form of adaptation to the new host (humans) and/or new vectors (fleas or body lice)	

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RESEARCH ARTICLE ECOLOGY





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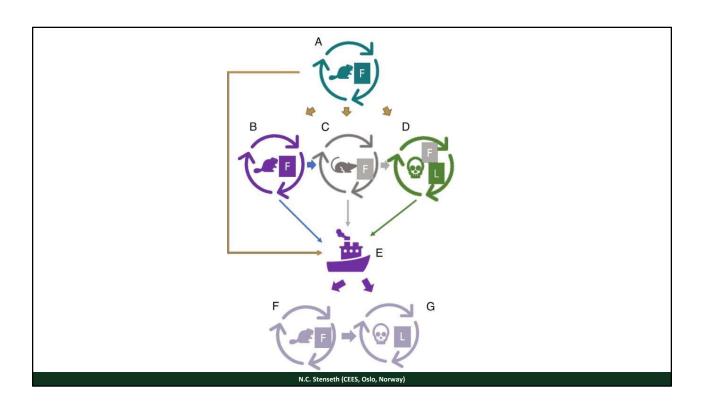
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Caused by Yersinia pestis, plague ravaged the world through three known pandemics: the First or the Justinianic (6th–8th century); the Second (beginning with the Black Death during c. 1338–1353 and lasting until the 19th century); and the Third (which became global in 1894). It is debatable whether Y. pestis persisted in European wildlife reservoirs or was repeatedly introduced from outside Europe (as covered by European Union and the British Isles). Here, we analyze environmental data (soil characteristics and climate) from active Chinese plague reservoirs to assess whether such environmental conditions in Europe had ever supported "natural plague reservoirs". We have used new statistical methods which are validated through predicting the presence of modern plague reservoirs in the western United States. We find no support for persistent natural plague reservoirs in either historical or modern Europe. Two factors make Europe unfavorable for long-term plague reservoirs: 1) Soil texture and biochemistry and 2) low rodent diversity. By

Significance

Plague killed millions of people during the three pandemics in the past two millennia. Despite much research, it remains unclear whether persistent natural plague reservoirs existed in Europe. To examine this question, we have developed a statistical model based on high-resolution and

Indeed there is no evidence for persistent natural plague reservoirs in neither historical nor modern Europe



There is no evidence for persistent natural plague reservoirs in neither historical nor modern Europe

This remains a hypothesis

Hopefully to be tested within and ERC Synergy project

Reconstructing the environmental, biological, and societal drivers of plague outbreaks in Eurasia between 1300 and 1900 $\rm CE$

cPI: Prof. Nils Chr. Stenseth

cHI: University of Oslo, Norway - epidemiology and plague ecology

PI: Prof. Philip Slavin; HI: University of Stirling, UK – environmental history and geo-archaeology

PI: Prof. Ulf Büntgen; HI: University of Cambridge, UK – paleoclimatology and -ecology

PI: Dr. Florent Sebbane; HI: INSERM, Lille, France - experimental biology and infectious epidemiology

