

Reply to Alfani: Reconstructing past plague ecology to understand human history

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Alfani (1) provides important reflections on our recent work, which argues against long-term wildlife-based plague reservoirs in historical Europe (2). Without natural reservoirs in Europe during the past 2,000 y, the plague bacterium (Yersinia pestis) must have repeatedly spilled over from local medium-term reservoirs (3) or was introduced repeatedly from outside Europe by rodents (e.g., rats) and their ectoparasites (e.g., fleas) by infected people or contaminated goods (Fig. 1). While recognized for the Third Pandemic in Europe (4), the hypothesis of several reintroductions of Y. pestis into Europe remains under debate for late-antique and medieval outbreaks. Two hypotheses of plague continuity in Europe have been proposed (5): local persistence in reservoirs and external reimportation.

Questioning the importance of rodents and their ectoparasites during past Pandemics in Europe, our study (2) thus contrasts the main factors and processes of plague transmission known from the Third Pandemic in other continents, where wildlife plague reservoirs have been and continue to be essential. Our study also points to the possible importance of human ectoparasites in the interhuman transmission of bacteria (6).

Asking whether long-term wildlife-based plague reservoirs have ever existed in Europe is an important question in the ongoing debate on the processes underlying the spatiotemporal dynamics of human plague over at least the past 2,000 y. To make progress here, a truly interdisciplinary approach is required. In line with Alfani (1), we prioritize two research questions: i) Why plague disappeared from Europe between and after three pandemics, and ii) what role did European rodent and human ectoparasites play in generating the observed patterns of human plague outbreaks across Europe over the past two millennia.

- The end of the Third Pandemic in Europe could theoretically be attributed to a lack of long-term (4, 7) and burnout of medium-term plague reservoirs around 300 y earlier (8). However, it could also have resulted from a combination of natural and societal factors, including improved hygiene standards, together with effective control measures (4, 7). Recently, virulence attenuation of the plague bacterium (5) and the selection of a more robust innate immunity against Y. pestis (9) have been suggested as factors contributing to the end of the First and Second Pandemics in Europe (7).
- The evidence is accumulating for the importance of human-to-human transmission mediated by ectoparasites during plague outbreaks in Europe (6). Though the human flea (Pulex irritans) seems not suitable (10), there are other ectoparasites, such as lice, which may have played a critical role. In addition to the examples

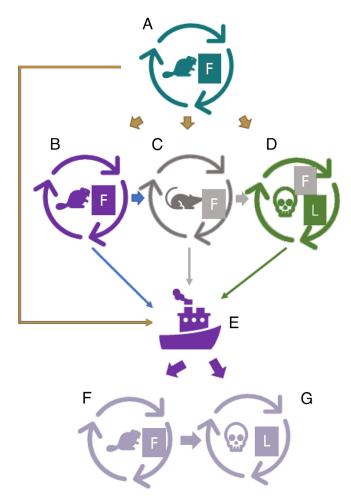


Fig. 1. Simplified schema of plague introduction in new places without longterm reservoirs (F and G in the figure). Y. pestis can cycle between enzootic rodents (A), epizootic wild rodents (B), epizootic peri-domestic rodents (C), or humans and their associated ectoparasites (D) [e.g., fleas (F) or lice (L)]. At any of these stages, Y. pestis can be transported to another place (without longterm reservoir) by means of contaminated goods, rodents, people, and/or ectoparasites (E). If no reservoir is settled in the new place, plague may circulate among medium-term reservoir (F) and/or humans and their ectoparasites (G).

raised by Alfani, the 1900 plague outbreak in Glasgow was likely caused by human-to-human transmission (11). However, much research still needs to be carried out on the role of ectoparasites and human plague, for which case studies should be prioritized.

The authors declare no competing interest.

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Further reconstructions of the ecology of plague and life cycle of Y. pestis in wild and domestic mammals and human populations are needed to understand the course of human history in time and space. The expected insights will also help us be prepared for future pandemics.

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