LETTER TO THE EDITOR



Pandemic Legion History More Complex than Previously Thought

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read with much interest the Perspective article by Morens et al. entitled "Pandemic COVID-19 Joins History's Pandemic Legion" (1).

Morens and colleagues describe in the "early pandemic history" section the story of pathogens emerging around 12,000 years ago at the time of Neolithic agricultural revolution. As such, diseases such as "measles, smallpox, tuberculosis (TB), [and] gastric cancer (caused by *Helicobacter pylori*)" are cited as consequences of "conditions of intense human-animal proximity and environmental alterations." This assertion of the dating of the origin of these aforementioned pathogens is partially misleading. Both viruses (i.e., those causing measles and smallpox) emerged probably much later, while *Mycobacterium tuberculosis* and *Helicobacter pylori* started their association with humans before the agricultural revolution.

Historical records of viruses are scarce, and the reconstruction of their evolutionary history might be difficult (2–4). However, a recent phylogenetic study of a 1912 strain has placed measles virus (MV) divergence from rinderpest virus during the sixth century before the Common Era (BCE), possibly coinciding with the rise of large cities allowing measles epidemic sustainability (5).

For smallpox, the exact date of divergence of variola virus (VARV) from a zoonotic strain is more disputed, as molecular data gave an estimation of emergence for the most recent common ancestor between the 16th and the 17th century, while skin lesions seen in the mummy of Ramses V, who died in 1157 BCE, suggested earlier interactions (6). Camelpox virus and taterapox virus infecting gerbils very likely shared a common ancestor with VARV that might have evolved from a common rodent orthopoxvirus (7, 8). A recent study of ancient VARV samples from Viking remains discovered a sister clade and predated VARV emergence as early as 603 CE, confirming written accounts of likely smallpox infections in Europe from the late 6th century (6).

In contrast, the interactions of *M. tuberculosis* and *H. pylori* with humans represent much more sophisticated and longer stories. A thorough phylogeographic analysis of modern *H. pylori* diversity has shown that the *Homo sapiens* became its specific host before he started his migration out of Africa 60,000 years ago and no later than 100,000 years ago (14). For TB, recent studies have clearly demonstrated that in opposition to a frequently reported idea, human TB is not a zoonosis derived from bovine TB arisen as a consequence of cattle domestication (9). *M. tuberculosis* and *Mycobacterium bovis* share more than 99.95% nucleotide identity, and while they probably do have a common ancestor, *M. bovis* is definitely not the parent of *M. tuberculosis* (10, 11). Concerning *M. tuberculosis* emergence dating, several studies are conflicting (11), but at least one study estimated that the most recent common ancestor of *M. tuberculosis* existed 70,000 years ago (12).

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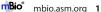
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Moreover, on *Yersinia pestis*, the agent of plague, Morens and colleagues mentioned the "plague of Athens" (430 to 425 BCE) as "perhaps the first recorded pandemic," although there is a wealth of data proving a much earlier presence of *Y. pestis* starting at least 4,900 years ago (4, 13).

Eventually, the conception of the agricultural revolution affecting health through direct emerging infections from domesticated livestock needs to become more balanced. The MV example has shown that emergence by accident is not the rule and that a pathogen needs more conditions than a close contact with human for sustainable success.

REFERENCES

- Morens DM, Daszak P, Markel H, Taubenberger JK. 2020. Pandemic COVID-19 joins history's pandemic legion. mBio 11:e00812-20. https:// doi.org/10.1128/mBio.00812-20.
- Pybus OG, Rambaut A. 2009. Evolutionary analysis of the dynamics of viral infectious disease. Nat Rev Genet 10:540–550. https://doi.org/10 .1038/nrg2583.
- Ho SYW, Duchene S. 2020. Dating the emergence of human pathogens. Science 368:1310–1311. https://doi.org/10.1126/science.abc5746.
- Spyrou MA, Bos KI, Herbig A, Krause J. 2019. Ancient pathogen genomics as an emerging tool for infectious disease research. Nat Rev Genet 20:323–340. https://doi.org/10.1038/s41576-019-0119-1.
- Dux A, Lequime S, Patrono LV, Vrancken B, Boral S, Gogarten JF, Hilbig A, Horst D, Merkel K, Prepoint B, Santibanez S, Schlotterbeck J, Suchard MA, Ulrich M, Widulin N, Mankertz A, Leendertz FH, Harper K, Schnalke T, Lemey P, Calvignac-Spencer S. 2020. Measles virus and rinderpest virus divergence dated to the sixth century BCE. Science 368:1367–1370. https://doi.org/10.1126/science.aba9411.
- 6. Muhlemann B, Vinner L, Margaryan A, Wilhelmson H, de la Fuente Castro C, Allentoft ME, de Barros Damgaard P, Hansen AJ, Nielsen SH, Strand LM, Bill J, Buzhilova A, Pushkina T, Falys C, Khartanovich V, Moiseyev V, Jorkov MLS, Ostergaard Sorensen P, Magnusson Y, Gustin I, Schroeder H, Sutter G, Smith GL, Drosten C, Fouchier RAM, Smith DJ, Willerslev E, Jones TC, Sikora M. 2020. Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. Science 369: eaaw8977. https://doi.org/10.1126/science.aaw8977.
- Haller SL, Peng C, McFadden G, Rothenburg S. 2014. Poxviruses and the evolution of host range and virulence. Infect Genet Evol 21:15–40. https://doi.org/10.1016/j.meegid.2013.10.014.
- 8. Esposito JJ, Sammons SA, Frace AM, Osborne JD, Olsen-Rasmussen M,

Zhang M, Govil D, Damon IK, Kline R, Laker M, Li Y, Smith GL, Meyer H, Leduc JW, Wohlhueter RM. 2006. Genome sequence diversity and clues to the evolution of variola (smallpox) virus. Science 313:807–812. https://doi.org/10.1126/science.1125134.

- Smith NH, Hewinson RG, Kremer K, Brosch R, Gordon SV. 2009. Myths and misconceptions: the origin and evolution of Mycobacterium tuberculosis. Nat Rev Microbiol 7:537–544. https://doi.org/10.1038/nrmicro2165.
- Garnier T, Eiglmeier K, Camus JC, Medina N, Mansoor H, Pryor M, Duthoy S, Grondin S, Lacroix C, Monsempe C, Simon S, Harris B, Atkin R, Doggett J, Mayes R, Keating L, Wheeler PR, Parkhill J, Barrell BG, Cole ST, Gordon SV, Hewinson RG. 2003. The complete genome sequence of Mycobacterium bovis. Proc Natl Acad Sci U S A 100:7877–7882. https://doi.org/ 10.1073/pnas.1130426100.
- Gagneux S. 2018. Ecology and evolution of Mycobacterium tuberculosis. Nat Rev Microbiol 16:202–213. https://doi.org/10.1038/nrmicro.2018.8.
- Comas I, Coscolla M, Luo T, Borrell S, Holt KE, Kato-Maeda M, Parkhill J, Malla B, Berg S, Thwaites G, Yeboah-Manu D, Bothamley G, Mei J, Wei L, Bentley S, Harris SR, Niemann S, Diel R, Aseffa A, Gao Q, Young D, Gagneux S. 2013. Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. Nat Genet 45: 1176–1182. https://doi.org/10.1038/ng.2744.
- Rascovan N, Sjogren KG, Kristiansen K, Nielsen R, Willerslev E, Desnues C, Rasmussen S. 2019. Emergence and spread of basal lineages of Yersinia pestis during the Neolithic Decline. Cell 176:295–305.e10. https://doi .org/10.1016/j.cell.2018.11.005.
- Megraud F, Lehours P, Vale FF. 2016. The history of *Helicobacter pylori*: from phylogeography to paleomicrobiology. Clin Microbiol Infect 22: 922–927. https://doi.org/10.1016/j.cmi.2016.07.013.