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Agriculture, capital, and infectious diseases

SARS-CoV-2, the coronavirus that has swept the world, represents only one of a series of novel pathogen strains that have suddenly emerged or re-emerged as human threats this century. These outbreaks – avian and swine influenza, Ebola Makona, Q fever, Zika, among many others – are more than matters of bad luck. Nearly all can be tied distally or directly to changes in production or land use associated with intensive agriculture, even as other modes of production have been implicated, logging and mining among them (Jones et al. 2013).

Monoculture production – crop and livestock alike – drives the deforestation and development that increases the rate and taxonomic scope of pathogen spillover from wildlife to food animals and the labor that tends them. Once these pathogens enter the food chain, such production can select for increases in pathogen deadliness, genetic recombination, and antigenic shifts out from underneath immune suppression. By the expansive trade that now characterizes such production, the newly evolved strains can be exported from one side of the world to the other.

SARS-CoV-2 and the other novel pathogens are not just matters of an infectious agent or clinical course. They cannot be fixed merely by the latest in vaccines and other prophylaxes, as important as these biomedical interventions may be. Farther out, the webs of ecosystemic relations that industry and state power have pinned back to their own advantage have had a foundational effect on the emergence and evolution of these new strains (RG Wallace et al. 2015). The wide variety of pathogens, representing different taxa, source hosts, modes of transmission, clinical courses, and epidemiological outcomes, mark different parts and pathways of something of the same regimens in land use and value accumulation spread across the world.

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We find this new context reproduced region by region. Despite differing in their particularities, local circuits of production operate within the same web of global expropriation and its environmental impacts. At one end of the production circuit, the complexity of primary forest typically bottles up “wild” pathogens. Logging, mining, and intensive plantation agriculture drastically streamline that natural complexity (R Wallace et al. 2018). While many pathogens on such “neoliberal frontiers” die off with their host species as a result, a subset of infections that once burned

out relatively quickly in the forest, if only by the irregular rate of encountering their typical host species, are now propagating much more widely across susceptible populations.

The vulnerability to infection that human populations suffer on the receiving end of the spillovers is routinely exacerbated by austerity programs impacting both environmental sanitation and public health. Even in the face of efficacious vaccines, the outbreaks that emerge out of their environmental margins are increasingly characterized by greater geographic extent, duration, and momentum. What were once local spillovers are now suddenly epidemics, some finding their way onto global networks of travel and trade.

Ebola offers a now archetypical example (RG Wallace and R Wallace 2016). Ebola Makona, the Zaire ebolavirus variant underlying the regional outbreak in West Africa 2013-2015, appeared conventional in its initial genetics, case fatality ratio, incubation period, and serial interval. Unlike previous outbreaks that wiped out a village or two, however, Makona infected 35,000 people, killing 11,000, leaving bodies in the streets of major capital cities.

How to account for the difference if not by the Ebola virus itself? It is instead the socioecological background through which the pathogen spread – from local environmental and social spaces out to global relational geographies – that shifted. Multilateral structural adjustment and a multinational land rush encroached upon regional forests and truncated medical infrastructure. New incursions of monoculture plantation – palm oil, sugar cane, cotton, and macadamia among other crops – were tied to new rounds in land enclosure, consolidation, and commodification of previous subsistence trading. These shifts increased the interface between Ebola-bearing species of bats attracted to such plantations and the now partially proletarianized laborers who cultivated them. The resulting increases in Ebola spillover likely accelerated the emergence of a human-to-human infection (Rulli et al. 2017, Olivero et al. 2017).

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Diseases of other taxa tag the other end of the circuit of production. Highly pathogenic and suddenly human-adapted avian and swine influenzas typically first emerge as newly identifiable infections in intensive operations located closer to major cities in both fully industrialized countries and those in the middle of undergoing economic transitions to more industrialized regimes. Of the thirty-nine documented transitions from low to high pathogenicity in avian influenzas from 1959 on, Dhingra et al (2018) identified all but two occurred in commercial poultry operations, typically of tens or hundreds of thousands of birds.

On the other hand, reassortment events, wherein different H5 and H7 influenza strains traded genomic segments, occurred largely in countries undergoing eco-

conomic transitions. These latter environments appear to be characterized by a greater mix of production systems, permitting different combinations of co-circulating strains. Indeed, such intensive poultry operations are so inundated with circulating strains that they serve as their own reservoir for new subtypes (Olson et al. 2014). Wild waterfowl are no longer the only source.

Other pathogens emerge in more complex origins across these circuits. SARS-1 and now SARS-2, our COVID-19 strain, appear to have emerged out of mixed niches spread across their associated regional circuits of production. Non-human SARS specimens have been isolated in greater Hubei, Wuhan's province, as far back as 2004, in both bats – Shortridge's horseshoe bat and the greater horseshoe bat – and farmed masked palm civets (Hu et al. 2005, Tang et al. 2006). The isolates appear part and parcel of a wide range of animal SARS distributed across China, including in adjacent provinces Anhui and Jiangxi, well within Wuhan's wild foods catchment, but also as far south as Guangdong, another source from which SARS-2 may first have arisen (Forster et al. 2020).

Given the genetics of SARS-2 – a recombinant of bat and pangolin strains – the increasingly formalized wild food trade in all likelihood played a foundational role in the emergence of the COVID-19 outbreak (Challender et al 2019, Xiao et al. 2020, Li et al. 2020). The trade, including now pangolin farming, shares with industrial agriculture sources of capital and economic geographies encroaching on Central China's hinterlands. Whether the outbreak began at the infamous Wuhan live food market itself or at the other periurban terminus is beside the point. Instead, we need readjust our conceptual sights on the processes by which living organisms are turned into commodities and entire production chains – animal, producer, processor, and retailer – entrained as disease vectors.

References

- Challender, D.W.S., Sas-Rolfes, M., Ades, G.W.J., Chin, J.S.C., Ching-Min Sun, N. et al., 2019. Evaluating the feasibility of pangolin farming and its potential conservation impact. *Global Ecology and Conservation*, 20:e00714.
- Dhingra, M.S., Artois, J., Dellicour, S., Lemey, P., Dauphin, G. et al., 2018. Geographical and historical patterns in the emergences of novel Highly Pathogenic Avian Influenza (HPAI) H5 and H7 viruses in poultry. *Front. Vet. Sci.*, 05 <https://doi.org/10.3389/fvets.2018.00084>
- Forster, P., Forster, L., Renfrew, C. and Forester, M., 2020. Phylogenetic network analysis of SARS-CoV-2 genomes. *PNAS*, 117(17): 9241-9243.
- Hu, W., Bai, B., Hu, Z., Chen, Z., An, X., Tang, L., Yang, J., Wang, H. and Wang, H., 2005. Development and evaluation of a multitarget real-time Taqman reverse transcription-PCR assay for detection of the severe acute respiratory syndrome-associated coronavirus and surveillance for an apparently related coronavirus found in masked palm civets. *J. Clin. Microbiol.*, 43:2041-2046.
- Jones B.A., Grace, D., Kock, R., Alonso, S., Rushton, J., Said, M.Y., McKeever, D., Mutua, F., Young, J., McDermott, J. and Pfeiffer, D.U., 2013. Zoonosis emergence linked to agricultural intensification and environmental change. *PNAS* 110: 8399–8404.

- Li, X., Gao, Y., Wang, C., and Sun, B., 2020. Influencing factors of express delivery industry on safe consumption of wild dynamic foods. *Revista Científica*, 30(1):393-403.
- Olivero, J., Fa, J.E., Real, R., Márquez, A.L., Farfán, M.A., Vargas, J.M., Gaveau, D., Salim, M.A., Park, D., Suter, J., King, S., Leendertz, S.A., Sheil, D. and Nasi, R., 2017. Recent loss of closed forests is associated with Ebola virus disease outbreaks. *Nature Scientific Reports*, 7:14291.
- Olson, S.H., Parmley, J., Soos, C., Gilbert, M., Latorre-Margalef, N., Hall, J.S., Hansbro, P.M., Leighton, F., Munster, V. and Joly, D., 2014. Sampling strategies and biodiversity of influenza A subtypes in wild birds. *PLoS One*, 9(3):e90826.
- Rulli, M.C., Santini, M., Hayman, D.T.S. and D'Odorico, P., 2017. The nexus between forest fragmentation in Africa and Ebola virus disease outbreaks. *Nature Scientific Reports*, 7:41613.
- Tang, X.C., Zhang, J.X., Zhang, S.Y. et al., 2006. Prevalence and genetic diversity of coronaviruses in bats from China. *Journal of Virology*, 80(15):7481-7490.
- Wallace, R., Chaves, L.F., Bergmann, L.R., Ayres, C., Hogerwerf, L., Kock, R. and Wallace, R.G., 2018. *Clear-Cutting Disease Control: Capital-Led Deforestation, Public Health Austerity, and Vector-Borne Infection*. Springer, Cham.
- Wallace, R.G. et al., 2015. The dawn of Structural One Health: A new science tracking disease emergence along circuits of capital. *Social Science & Medicine*, 129:68-77.
- Wallace, R.G. and Wallace, R. (eds). 2016. *Neoliberal Ebola: Modeling Disease Emergence from Finance to Forest and Farm*. Springer, Cham.
- Xiao, K., Zhai, J., Feng, Y., Zhou, N., Zhang, X. et al. 2020. Isolation and characterization of 2019-nCoV-like coronavirus from Malayan pangolins. *bioRxiv*. <https://www.biorxiv.org/content/10.1101/2020.02.17.951335v1>.



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