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All for one and one for all: the true potential of whole-genome sequencing

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Global genomic databases of foodborne pathogens are important to create, maintain, and expand because we live in an integrated world in which international travel and trade of globally sourced products are extensive. The effects of contaminated products from international trade require responsible food safety bodies to take efforts to reduce these risks for public health. Monitoring and linking foodborne contamination events over time and space is crucial, and must be communicated rapidly to reduce the effects on public health. The speed at which regulators can interrupt the epidemiological curve through interventions, preventive controls, recalls, and notices is facilitated by the strong and predictive whole-genome sequencing (WGS) signals provided by globally shared genomes of the pathogens found in foods, the environment, and patients.[1]

In *The Lancet Infectious Diseases*, Roan Pijnacker and colleagues[2] report on a multi-country European outbreak of *Salmonella enterica* serotype Enteritidis linked to eggs from Poland. The evidence presented in this investigation showcased the usefulness and efficiency of coordinated WGS data collection during a regional outbreak in 2015–18. The rapid exchange of information between public health authorities and the traceability of information shared by food safety authorities can be essential in finding the vehicles of infection and coordinating risk management actions. The US Food and Drug Administration (FDA) has previously documented similar successes using WGS in the USA for understanding contamination events of S Enteritidis in shell eggs[3] and in many other commodities.[4] The improvements brought by WGS for outbreak response are particularly important for the most genetically homogeneous of foodborne pathogens, which is why S Enteritidis was a crucial case study for the FDA in adopting WGS for routine molecular epidemiology and as a regulatory tool in 2013.[1] To date, WGS has supported the FDA in more than 370 outbreak investigation and compliance cases.

For the **National Center for Biotechnology Information's Pathogen Detection web tools** see https://www.ncbi.nlm.nih.gov/pathogens/

The authors report that a crucial step for the success of their outbreak investigation was the strong triggering signal from the WGS data that enabled prioritisation of epidemiological follow-up of signals. The FDA has also observed this power of prediction using WGS,[5] which prompted the building of the GenomeTrakr network. Pathogen Detection web tools provide genomic linkages and phylogenetic trees daily for all 325 000 publicly released foodborne pathogen genomes. Additionally, PulseNet (managed by the US Centers for Disease Control and Prevention [CDC]) uploads to these projects at the National Center for Biotechnology Information (NCBI),[6] as does the US Department of Agriculture's Food Safety and Inspection Service. Together, the genomes in these projects are combined analytically to discover novel linkages among foodborne pathogens with roughly 4000 clusters monitored daily. These genomic data are globally available with free access to anyone who wishes to upload and compare bacterial genomes and corresponding descriptive metadata in real time. Importantly, in addition to the public NCBI database, each of the participating US agencies retains confidential information such as private patient attributes, commercial company details, and metadata surrounding precise collection points. Such an arrangement could easily conform to a real-time, data-sharing model for Europe as well.

One of our main concerns is that, although Pijnacker and colleagues[2] reported in the appendix to their study that FASTQ reads from all sequences in their study were deposited in NCBI (BioProject PRJNA248792), these data were not released during the outbreak investigation to allow direct comparisons to other publicly available data. We have observed closely related WGS clusters (ten or fewer SNPs) linked to illnesses, including isolates from contaminated food or the environment, from 72 countries including Australia,[7] Austria, Brazil, Canada,[8] Chile, China, Dominican Republic, Ecuador, Egypt, Ethiopia, India, Indonesia, Italy, Kenya, Mexico, Peru, the Philippines, Switzerland, Thailand, Turkey, Uganda, Vietnam, and the UK, but not Poland. When the release of data is delayed, determining epidemiological linkages becomes more difficult. We also disagree that technical barriers preclude the uploading of WGS data. It is our opinion that the benefit of publicly sharing WGS data in real time is vital for global public health. However, we do agree with the need to harmonise data interpretation and analyses, as is evident between the numerous US agencies that are engaged in GenomeTrakr and NCBI Pathogen Detection.[9,10] Indeed, there is an acute need to increase international harmonisation of WGS methods for maximising the benefit of global data sharing and use.[11,12]

Finally, Pijnacker and colleagues[2] note that it is likely that 12 non-EU countries were affected by the outbreak but were not detected because molecular typing is not routinely done in many countries. We would add that many countries with the infrastructure for WGS do not share their data globally in real time. The regional privatisation and emphasis on internal WGS databases, although useful locally, will only hinder more widespread epidemiological investigations to the detriment of global food safety and public health.[13]

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Measles resurgence in the USA: how international travel compounds vaccine resistance

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Hotez and colleagues[1] recent article highlights the increasing frequency of vaccine-preventable disease cases in Europe and the USA caused by very visible anti-vaccine movements.[2] The most troubling aspect of this development is the global increase in measles cases. From Jan 1, 2019, to April 26, 2019, the USA reported 704 confirmed measles cases spanning 22 states, compared with 372 reported cases in 2018, 120 in 2017,