



Editorial

Li Wenliang, a face to the frontline healthcare worker. The first doctor to notify the emergence of the SARS-CoV-2, (COVID-19), outbreak



Dr Li Wenliang, who lost his life to the novel coronavirus, SARS-CoV-2, became the face of the threat of SARS-CoV-2 to frontline workers, the clinicians taking care of patients. Li, 34, was an ophthalmologist at Wuhan Central Hospital. On 30th December, 2019, when the Wuhan municipal health service sent out an alert, he reportedly warned a closed group of ex-medical school classmates on the WeChat social media site of “Seven cases of severe acute respiratory syndrome (SARS) like illness with links with the Huanan Seafood Wholesale Market” at his hospital. He was among eight people reprimanded by security officers for “spreading rumours”. In a tragic turn of events, he subsequently contracted SARS-CoV-2 and, after a period in intensive care, died on the morning of Friday 7th February, 2020 ([South China Morning Post, 2020](#)).

This case is a stark reminder of the risks of emerging disease outbreaks for healthcare workers (HCWs). Dr Li Wenliang's name is added to the long list of HCW that were at the forefront of outbreaks of SARS, Ebola, MERS and now SARS-CoV-2. It is important to recognise that it was the clinicians in Wuhan who sounded the alarm about the emergence of SARS-CoV-2 which was rapidly identified after these clinicians sent samples to a reference laboratory for next generation sequencing (NGS) ([Zhou et al., 2020](#)).

Global public health security is of primary importance to prevent outbreaks of diseases with epidemic potential and every effort to detect, report, and institute infection prevention and control measures should be made. Astute clinicians, access to laboratories with state of the art tools, and openness, transparency and quick reporting are crucial components of this response ([Kavanagh, 2020](#)). This requires an open flow of information and collaboration between laboratory experts and clinicians on the frontline who may be the first to observe unusual clustering of cases or uncommon clinical presentations, both of which should be reported immediately.

Healthcare workers are also one of the groups most at risk from outbreaks due to reemerging and novel pathogens. This has been seen in the current SARS-CoV-2 outbreak in China where as many as 1716 health workers have been reported to be infected by the virus with 6 deaths as on 14th February, 2020 ([WHO, 2020a](#)). In a single center case series of SARS-CoV-2 from Wuhan published recently, almost 29% of all patients were healthcare workers

presumed to have been infected in the hospital ([Wang et al., 2020b](#)).

The preliminary sequence data on the case cluster were obtained by NGS of specimens collected on 26th December 2019 through 7 January 2020 ([Lu et al., 2020](#)). The Chinese authorities ruled out SARS-CoV and MERS-CoV, and confirmed a novel coronavirus as the probable cause on 9th January, 2020 ([Hui et al., 2020](#); [Wang et al., 2020a](#)). The first genome sequence was released on virological.org the 12th January 2020, seventeen days after obtaining the first specimen and several additional genomic sequences were then shared on GISAID ([Wang et al., 2020c](#)). This is an impressive rapid progression from initial outbreak notification to identification of a novel pathogen.

The rapid identification of the SARS-CoV-2 virus by NGS illustrates the advances in molecular identification since the SARS-CoV (2003) and MERS-CoV (2012) outbreaks, where both viruses were initially identified by in vitro cell culture. Thus, clinician of the possibility of a new infectious disease coupled with NGS can serve to quickly identify novel pathogens and allow for the rapid initiation of control measures to reduce further spread and potentially prevent large-scale outbreaks.

The SARS-CoV outbreak originating from China in 2003 was first reported to the global health community by ProMED ([ProMED, 2003](#); [Carrion and Madoff, 2017](#); [Hamer et al., 2017](#)). It took six weeks for the authorities to acknowledge the outbreak had spread significantly from Guangdong throughout China after cases were reported from Hong Kong, Hanoi, Singapore, and Toronto.

In reporting the existence of a new respiratory disease to the WHO on December 31 st, the Chinese authorities formally acknowledged the outbreak much sooner this time, perhaps in part because of the ongoing spread of information on informal social media networks. ProMED posted the initial report of the unknown pneumonia outbreak in Wuhan on 30 December 2019 ([ProMED, 2019](#)). Since then, transmission of information has been relatively transparent, with the prompt sharing of the sequence of the virus and actual numbers of cases reported on a daily basis. The case figures have demonstrated the upward trajectory of the rapid spread of SARS-CoV-2 from Wuhan and Hubei Province to all of China.

On 13th February 2020 the Chinese authorities changed the case definition and the number of newly reported cases over the

prior 24 h jumped to 14,886 from a previous high of 4370 on 6th February 2020. This was not a real increase, but reflected the addition of the cumulative number of clinically diagnosed cases (without laboratory confirmation) to the reported number of laboratory confirmed cases and demonstrates how easily a case definition can influence numbers. On 19 February 2020, the Chinese authorities changed the case definition to include laboratory confirmed cases only and designating clinically diagnosed cases as suspected cases. This resulted in a rapid drop of daily newly confirmed cases, again demonstrating the impact of case definition on reported case numbers. As of 23 February 2020, WHO has reported a total of 78,007 cases with 2,462 deaths globally with reports of cases from 29 countries (WHO, 2020a,b).

A key question remains “what is the real number of people infected since many cases may be mild or asymptomatic?” A recent modelling estimated the population attack rate to be between 0.75 per 100,000 to 15.8 per 100,000 analysing rates down to prefecture level in China (Yang et al., 2020). Any determination of incidence will likely be an underestimate since it will not include mild and asymptomatic cases. Accuracy of such estimates will depend on the development of sensitive and specific serologic tests.

Recognizing disease in travelers is a particularly important aspect of surveillance for the importation of emerging infections. Multi-site collaborations such as the GeoSentinel Surveillance Network (Wilder-Smith and Boggild, 2018) can act as sentinel systems to recognize new patterns of disease in travelers from specific areas. Previous GeoSentinel data showed that despite receiving care at specialized post-travel medicine sites, up to 40% of returning ill travellers with febrile illness do not have a confirmed etiology; frequently no specific diagnostic testing is available to identify a cause (Freedman et al., 2006; Wilson et al., 2007; Leder et al., 2013). The current large-scale outbreak of a novel pathogen, SARS-CoV-2, highlights the critical importance of prioritizing the identification of disease etiology through clinician awareness and modern laboratory techniques such as NGS.

There has been widespread mourning of the sad demise of Dr Li from COVID-2019. Dr Li Wenliang's example as an astute clinician should inspire all of us to be vigilant, bold and courageous in reporting unusual clinical presentations. The SARS-CoV-2 outbreak underscores the responsibilities and the vulnerabilities of frontline health care workers in tackling novel and highly transmissible pathogens. We must use our knowledge and skills, with the backup of laboratory support, to rapidly detect and report any suspicion of emerging infections. Rapid, transparent communication is paramount when infectious diseases emerge. This is the only way to prevent major outbreaks and will save many lives.

Conflict of interests

The authors declare that they have no conflict of interests.

References

- Carrion M, Madoff LC. ProMED-mail: 22 years of digital surveillance of emerging infectious diseases. *Int Health* 2017;9:177–83.
- Freedman DO, Weld LH, Kozarsky PE, Fisk T, Robins R, von Sonnenburg F, et al. Spectrum of disease and relation to place of exposure among ill returned travelers. *N Engl J Med* 2006;354:119–30.
- Hamer DH, Khan K, German M, Madoff LC. Non-traditional infectious diseases surveillance systems. In: Peterson E, Chen LH, Schlagenhauf P, editors. *Infectious diseases: a geographic guide*. 2nd ed. Wiley Blackwell; 2017.
- Hui DS, Azhar EI, Madani TA, Ntoumi F, Kock R, Dar O, et al. The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health — the latest 2019 novel coronavirus outbreak in Wuhan, China. *Int J Infect Dis* 2020;91:264–6 [Published online 14 January 2020. [https://www.ijidonline.com/article/S1201-9712\(20\)30011-4/fulltext](https://www.ijidonline.com/article/S1201-9712(20)30011-4/fulltext)].
- Kavanagh MM. Authoritarianism, outbreaks, and information politics. *Lancet* 2020;395;. doi:[http://dx.doi.org/10.1016/S2468-2667\(20\)30030-X](http://dx.doi.org/10.1016/S2468-2667(20)30030-X) [Published 13 February 2020; online ahead of print].
- Leder K, Torresi J, Libman MD, Cramer JP, Castelli F, Schlagenhauf P, et al. GeoSentinel surveillance of illness in returned travelers, 2007–2011. *Ann Intern Med* 2013;158:456–68.
- Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020;395;. doi:[http://dx.doi.org/10.1016/S0140-6736\(20\)30251-8](http://dx.doi.org/10.1016/S0140-6736(20)30251-8) [Published online 29 January].
- ProMED. Pneumonia — China (Guangdong): request for information. 2003. . 10 February. [Accessed 23 February 2020] <https://promedmail.org/promed-post/?id=20030210.0357>.
- ProMED. Undiagnosed pneumonia — China (Hubei): request for information. 2019. . 30 December. [Accessed 23 February 2020] <https://promedmail.org/promed-post/?id=20191230.6864153>.
- South China Morning Post. Li Wenliang: an ‘ordinary hero’ at the centre of the coronavirus storm. 15 February. [Accessed 23 February 2020]. 2020. <https://www.scmp.com/news/china/society/article/3050733/li-wenliang-ordinary-hero-centre-coronavirus-storm>.
- Wang C, Horby PW, Hayden FG, Gao GF. A novel coronavirus outbreak of global health concern. *Lancet* 2020a;395;. doi:[http://dx.doi.org/10.1016/S0140-6736\(20\)30185-9](http://dx.doi.org/10.1016/S0140-6736(20)30185-9) [Published online 24 January].
- Wang D, Hu B, Hu C, Zhu F, Liu X, Zhang J, et al. Clinical characteristics of 138 hospitalized patients with 2019 novel coronavirus-infected pneumonia in Wuhan, China. *JAMA* 2020b;. doi:<http://dx.doi.org/10.1001/jama.2020.1585> [Published online 7 February].
- Wang L-F, Anderson DE, Mackenzie JS, Merson MH. From Hendra to Wuhan: what has been learned in responding to emerging zoonotic viruses. *Lancet* 2020c; (February). doi:[http://dx.doi.org/10.1016/S0140-6736\(20\)30350-0](http://dx.doi.org/10.1016/S0140-6736(20)30350-0).
- WHO. WHO Director-General's remarks at the media briefing on COVID-2019 outbreak on 14 February 2020. 2020. . [Accessed 24 February 2020] <https://www.who.int/dg/speeches/detail/who-director-general-s-remarks-at-the-media-briefing-on-covid-2019-outbreak-on-14-february-2020>.
- WHO. Coronavirus disease 2019 (COVID-19) situation report — 23. Geneva: WHO; 2020 12 February. [Accessed 23 February 2020].
- Wilder-Smith A, Boggild A. Sentinel surveillance in travel medicine: 20 years of GeoSentinel publications (1999–2018). *J Travel Med* 2018;25:1–7.
- Wilson ME, Weld LH, Boggild A, Keystone JS, Kain KC, von Sonnenburg F, et al. Fever in returned travelers: results from the GeoSentinel Surveillance Network. *Clin Infect Dis* 2007;44:1560–8.
- Yang Y, Lu Q-B, Liu M-J, Wang Y-X, Zhang AR, Jalali N, et al. Epidemiological and clinical features of the 2019 novel coronavirus outbreak in China. *medRxiv preprint* 2020;. doi:<http://dx.doi.org/10.1101/2020.02.10.20021675> [Accessed 23 February 2020].
- Zhou P, Yang X-L, Wang X-G, Hu B, Zhang L, Zhang W, et al. Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin. *bioRxiv* 2020;(January). . [Accessed 24 February 2020] <https://www.biorxiv.org/content/10.1101/2020.01.22.914952v2>.

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