

Social Media and the New World of Scientific Communication During the COVID-19 Pandemic

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The human and social toll of the coronavirus disease 2019 (COVID-19) pandemic has already spurred several major public health “lessons learned,” and the theme of effective and responsible scientific communication is among them. We propose that Twitter has played a fundamental—but often precarious—role in permitting real-time global communication between scientists during the COVID-19 epidemic, on a scale not seen before. Here, we discuss 3 key facets to Twitter-enabled scientific exchange during public health emergencies, including some major drawbacks. This discussion also serves as a succinct primer on some of the pivotal epidemiological analyses (and their communication) during the early phases of the COVID-19 outbreak, as seen through the lens of a Twitter feed.

Keywords. COVID-19; social media; scientific communication; Twitter.

The coronavirus disease 2019 (COVID-19) pandemic, and our knowledge about the virus, has exponentially grown since media reports of a cluster of acute respiratory infections in Wuhan, Hubei Province, China, were first reported in December 2019 [1]. By 8 January 2020, the etiology of these cases was identified as a novel betacoronavirus, then named 2019-nCoV, and 41 cases had been reported [2]. Three months later, more than 1.3 million cases and 75 000 deaths had been reported across the world [3]. The human and social toll of this pandemic has already spurred several major public health “lessons learned,” and the theme of effective and responsible scientific communication is among them.

The expansion of the outbreak has demanded a rapid response from public health authorities; fundamental epidemiological and scientific evidence has been acquired at breakneck speed to support those decisions. The demanding pace and large volume of COVID-19 science generated in the last 3 months, however, has made timely scientific communication through the conventional route of published biomedical journals at best challenging, and at worst obsolete. Twitter has an estimated global user network of 330 million monthly users, including

an extensive network of scientists and epidemiologists who frequently use this media for scientific exchange [4, 5]. We propose that Twitter has played a fundamental—but often precarious—role in permitting real-time global communication between scientists during the COVID-19 epidemic, on a scale not seen before.

Here, we discuss 3 key facets to Twitter-enabled scientific exchange during public health emergencies, including some major drawbacks. This discussion also serves as a succinct primer on some of the pivotal epidemiological analyses (and their communication) during the early phases of the COVID-19 outbreak, as seen through the lens of a Twitter feed. We do not cover the other major roles of Twitter and other social media during this epidemic, including transmission of rapid situational awareness reports, advisories, and public education from formal public health agencies and normative bodies [6, 7]. Similarly, concerns of malignant misinformation about COVID-19 deliberately spread through this medium are beyond the scope of this commentary [8].

OUTBREAK GENOMICS IN THE AGE OF TWITTER

Twitter accelerated the rapid, global dissemination of the first whole genome sequence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from a consortium led by Fudan University, Shanghai, to the global science community approximately 10 days after the first alerts of the SARS-CoV-2 outbreak [9]. This sequence data permitted development of a polymerase chain reaction diagnostic assay, the protocol of which was disseminated mere days later through Twitter [10]. Between 11 and 18 January the first genomic analyses of viral genomes sequenced from Chinese cases, and then initial Thailand cases, were posted in real time to Twitter [11]. Aside

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from confirming that this novel zoonotic coronavirus was distinct from the previous 2003 SARS outbreak, these early results suggested the outbreak was seeded by a single or small number of zoonotic spillover events [12]. Subsequent genomic analyses—again circulated through Twitter—supplied further evidence of human-to-human transmission (rather than repeated zoonotic spillovers), have allowed estimates of the SARS-CoV-2 evolutionary rate, and provided the first evidence of weeks-long cryptic circulation in the United States (Washington State) [13, 14]. The latter, critical finding was principally communicated through Twitter with subsequent mainstream media coverage [15]. Aside from enabling dissemination and discussion of these important phylogenetic analyses across multiple scientific disciplines and other stakeholders, Twitter also amplified the sharing of bioinformatic freeware and protocols to optimize SARS-CoV-2 sequencing efficiency and quality [16–18].

OPEN-SOURCE EPIDEMIOLOGY: EARLY COVID-19 LINE LISTING AND EPIDEMIC PARAMETER ESTIMATION THROUGH SOCIAL MEDIA

As with other outbreaks, early estimation of epidemic parameters during the first month of the COVID-19 epidemic has been critical to predict the epidemic trajectory and inform decision making. Twitter played a key role in soliciting volunteers to crowd-source line-list case data from media reports and other open data sources. These constantly updated line-lists were shared by multiple independent groups, thereby enabling cross-comparisons for completeness [19–21]. Indeed, such open-source line-list data remain more comprehensive than what is currently published by some other countries now experiencing major COVID-19 epidemics.

Early basic reproductive number (R_0) estimates were shared on Twitter (including links to independent websites and preprint repositories) by independent groups of epidemiologists [22, 23]. This permitted side-by-side comparisons of this indicator of viral transmissibility, as recently summarized by Majumder et al [23]. Rapid commentary on Twitter by scientists provided careful interpretation and caveats around these published R_0 estimates [24, 25, 26], and also emphasized the inherent limitations of extrapolating predictions of epidemic trajectories from R_0 estimates [24, 27]. As further noted by Majumder et al, the uncertainty intervals of these open-source R_0 estimates collectively overlapped with subsequently published formal R_0 estimates [28, 29].

Accurate approximation and interpretation of the COVID-19 case-fatality ratio (CFR) has been critical for resource planning and risk messaging. Real-time discussions on Twitter have highlighted requirements and considerations for severity assessments, such as the importance of case follow-up and early outbreak sampling bias in inflating early CFR estimates, as well as making distinctions between the infection fatality ratio and the CFR [30–32]. These discussion points were vital to frame

any early comparisons of COVID-19 morbidity and mortality with that of seasonal or pandemic influenza [33–35].

It is important to acknowledge, however, the continued importance of rigorously peer-reviewed journal publications of COVID-19 clinical and epidemiological characteristics, especially when accompanied by expert editorials, and particularly given the exponential rise of preprint publications, which may vary in quality [36]. This is particularly important to consider as there are recent data by Majumder et al that suggest public discourse of epidemiological phenomena have been driven more by preprints than formal subsequent peer-reviewed publications [23].

SNAKES AND LADDERS: THE OPPORTUNITIES AND CHALLENGES OF TWITTER IN SCIENTIFIC CONDUCT AND COMMUNICATION DURING PUBLIC HEALTH EMERGENCIES

As highlighted in an early 2020 *Nature Microbiology* editorial, global scientists openly reprimanded a group who published a genomic SARS-CoV-2 analysis through Twitter but failed to properly acknowledge the source of this molecular data [37]. Such open critique through this medium helps enable codes of conduct around epidemic sequence data sharing [38]. Real-time rebuttal, coupled with supporting preprint analyses, led to fast rejection of an invalid scientific conclusion that snakes were a probable animal reservoir for SARS-CoV-2, a claim that had led to widespread misinformation [39, 40]. Similarly, prompt corrections over journalist misinterpretations of supposed pangolin origins to the SARS-CoV-2 outbreak have been valuable.

In this way, Twitter has facilitated vital counternarratives from the scientific community during these and other instances of controversial scientific communication, be they claims of the zoonotic origins of SARS-CoV-2, alarmist interpretation of upper-end R_0 estimates, or confusion on whether particular public health policies were grounded on goals of “herd immunity.” Twitter has and continues to serve as a valuable medium to discuss the caveats and future directions in applying infectious disease models in COVID-19 decision making [41–44]. Still, Twitter remains the double-edged sword of rapid scientific communication during the ongoing COVID-19 pandemic. As advocated on Twitter itself, scientists will need to exercise great care in their communication using this and other social media to share their research as this outbreak unfolds throughout 2020 [45].

Notes

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