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Editorial

Advances in Wastewater-Based Epidemiology in the *ES&T* Family of Journals

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The *Environmental Science & Technology* (*ES&T*) family of journals has served as a venue for many novel and urgent reports on the use of wastewater for tracking the occurrence of diseases in communities. This is known as wastewater-based epidemiology or wastewater monitoring for disease surveillance (hereafter, WBE). The journals have seen a surge in publications in this area since the start of the coronavirus disease 2019 (COVID-19) pandemic. WBE papers were focused on severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at that time; however, research quickly pivoted, and authors published papers focused on a diverse set of pathogens ranging from *Candida auris* to dengue virus. The rapid scientific advancements in this area, and the way those advancements are being quickly translated globally to fully functioning wastewater surveillance systems to inform public health decision making, are unprecedented. The science selected for publication in the *ES&T* family of journals is foundational to this advancement, and the journals are proud to have published this rapid application of skills and knowledge by the scientific community to this critically important topic.

To recognize this innovation and fast pace of change, a new special virtual collection entitled "Advances in Wastewater-Based Epidemiology" has been curated choosing 30 papers published in *ES&T*, *ES&T Letters*, and *ACS ES&T Water* since 2018 that represent important contributions to WBE science and translation. Below we describe some of the papers featured in the special virtual collection, and we provide suggestions for future work in this area, within the scope of the *ES&T* family of journals.

The field of WBE was of interest to the *ES&T* community even before the COVID-19 pandemic, highlighted for example by the work of Yan et al. in 2018,[1] included in this collection. Yan and colleagues demonstrated the use of municipal wastewater to effectively track salmonellosis disease in Honolulu, Hawai'i. In addition, the study showed *Salmonella* spp. strains in wastewater coincided with clinically circulating strains.

The COVID-19 pandemic launched the emerging WBE field into the international spotlight, with the *ES&T* family of journals playing a leading role. Medema et al.[2] published an early report affirming that what Yan et al. observed years earlier for an enteric bacterial pathogen was also true for the respiratory virus SARS-CoV-2: concentrations in wastewater track with reported clinical infections. Within a month, an influential Viewpoint by Bivins et al.[3] mobilized scientists globally to work toward advancing WBE through open sharing of methodologies and data. This virtual collection includes multiple contributions on innovations sparked by the community's response to the pandemic.

As the urgency of the COVID-19 pandemic subsided, authors pivoted to publishing papers that demonstrate the power of WBE for other diseases. Also included in the special virtual collection are some of the first reports of WBE being established for other respiratory pathogens such as influenza A virus by Wolfe et al.,[4] respiratory syncytial virus by Hughes et al.,[5] and human metapneumovirus by Boehm et al.;[6] antimicrobial resistance by Wang et al.[7] and Riquelme et al.;[8] fungal infections, specifically *C. auris*, by Barber et al.;[9] and emerging pathogens such as dengue virus by Wolfe et al.[10] and mpox virus by Wurtzer et al.[11]

This virtual collection showcases a diverse set of novel contributions to the field of WBE that can be classified within four topical areas: (1) new measurement methods, (2) modeling approaches, (3) fate processes, and (4) WBE validation. Methods papers describe the development and testing of new approaches for the detection and quantification of pathogens in wastewater, such as passive sampling (Schang et al.[12]), integration of loop-mediated isothermal nucleic acid amplification with paper devices (Cao et al.[13]), nucleic acid amplicon sequencing (Kang et al.[14]); direct detection of viral proteins using mass spectrometry (Lara-Jacobo et al.[15]); and targeted metagenomic nucleic acid sequencing (McCall et al.[16]). The Perspective by Kantor et al.[17] describes the complexity of estimating the recovery of biological targets from wastewater, a key component of biomarker metrology. Modeling papers offer approaches for interpreting WBE data by linking measurements to predictions of disease incidence in populations (Wolfe et al.[18]) and estimating how disease targets might be affected by decay and dilution within the sewage pipe network (Wiesner-Friedman et al.[19]). Fate papers investigate factors that influence pathogen occurrence in wastewater streams, such as adsorption to wastewater solids (Roldan-Hernandez and Boehm[20]) and persistence in wastewater (Muirhead et al.,[21] Bivins et al.,[22] and Harrison et al.[23]).

The fourth category, WBE validation papers, represents the bulk of WBE contributions to the *ES&T* journals. These

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papers establish the validity of WBE by relating pathogen biomarker concentrations to traditional measures of disease occurrence, including hospitalization rates, clinical positivity rates, or syndromic data, for example. A number of studies laid the foundation of WBE for COVID-19 disease surveillance. These studies demonstrated, across diverse geographic regions, that trends in SARS-CoV-2 concentrations in liquid wastewater and wastewater solids align with clinical cases (Medema et al.,[2] Duvallet et al.,[24] Graham et al.,[25] and Pillay et al.[26]). Thereafter, Lee et al.[27] showed that specific SARS-CoV-2 variants could also be detected in wastewater and their concentrations provide meaningful information about their prevalence in the population. Because SARS-CoV-2 is the most surveilled pathogen in history, WBE data in these reports could be benchmarked against the highest-quality clinical evidence possible. The resulting confidence in WBE enabled an expansion to other pathogens with less reliable clinical data, including various respiratory viruses and dengue virus (Wolfe et al.,[4,10] Boehm et al.,[6] Schoen et al.,[28] and Hughes et al.[5]), as well as the emerging pathogens mpox virus (Wurtzer et al.[11]) and *C. auris* (Barber et al.[9]). Although a major focus of WBE has been on surveillance through centralized wastewater treatment plants, Capone et al.[29] highlighted the potential for public health surveillance in regions with decentralized sanitation, and Wang et al.[7] described WBE for antimicrobial resistance genes in hospital wastewater.

This virtual collection also includes a commentary on WBE ethics by Hrudey et al.,[30] which falls outside of the aforementioned topical areas. The work, published at a time when WBE efforts were extensive globally, highlighted the need for ethical guidelines in the use of wastewater for public health surveillance and remains as relevant today as WBE programs continue to expand.

With WBE now firmly established and being scaled globally for disease surveillance, the *ES&T* family of journals invites authors to submit their high-quality WBE manuscripts to support the emerging field. But what do editors and reviewers expect from new submissions? Given our experience handling and reviewing WBE papers in the roles of editor and reviewers for the journals, we offer some guidance. First, papers should be technically rigorous and describe significant scientific advantages or novel WBE technologies. WBE submissions that describe novel, disruptive methods with the potential to influence ongoing surveillance programs or spark further innovation in research, deploy innovative modeling (i.e., mechanistic and statistical) approaches that provide novel insights into pathogen surveillance or transmission, elucidate novel mechanisms driving pathogen fate and transport processes in the relevant environments, or otherwise offer opportunities to dramatically influence the use or impact of WBE for surveillance are encouraged. Submissions that provide measurements should follow the Environmental Microbiology Minimal Information (EMMI) guidelines[31] and provide the EMMI checklist as Supporting Information.

Many scientists are working in the WBE research space, which comes with many benefits but also with challenges. One challenge is that scientists often pursue similar research objectives. To publish in *ES&T* journals, we have found that reviewers chiefly look for technical rigor, novelty, and innovation in WBE submissions, so it is essential that authors clearly describe the novelty of their work and how it stands above other work on similar topics. We have also found that papers that provide location-specific insights for disease targets already established through other publications tend to not fare well in peer review. Such papers are likely more appropriate for more discipline-specific journals, including journals focused on public health.

Finally, this virtual collection of recent research in the field offers insight into where new WBE research effort is needed. First, WBE can be used to track a growing number of viral diseases (respiratory, enteric, arboviruses, and sexually transmitted), but there have been limited studies on the application of WBE for diseases caused by bacteria and eukaryotes such as fungi. Potentially important bacterial candidates include *Treponema pallidum* (etiology of syphilis), *Mycobacteria* spp., *Bordetella pertussis* (etiology of whooping cough), and *Streptococcus* spp. (etiology of a wide range of diseases); an important fungal candidate is *Coccidioidomycosis* spp. (etiology of Valley fever). Expansion of WBE to other classes of pathogens may require, for example, innovation in detection and quantification methods. Second, pathogen agnostic approaches are the panacea of WBE and are needed to find and track a novel, emerging pathogen in the future (so-called "pathogen X"), and work in this area is needed. Third, creative approaches are needed to establish and validate WBE for community surveillance of diseases with poor or nonexistent clinical tracking; for example, even common respiratory diseases like those caused by seasonal coronaviruses are poorly tracked in communities. Fourth, work to better understand the sources, fate, and transport of pathogen biomarkers in the wastestream is needed, including research on the persistence of biomarkers, their adsorption to solids and interactions with sewer biofilms, or even their potential for growth (in the case of bacterial or fungal targets), as well as strength of sources from human excretions and potential inputs from non-human sources, including industrial and domesticated animal inputs. Finally, the metrology of biological targets in the environment remains a challenge and is far behind the metrology of physical characteristics of the environment (like temperature). Advances to improve the precision, accuracy, and repeatability of biological measurements in the environment are highly encouraged, as are advances in measurement methods that are simple and applicable in areas with limited resources.

The articles included in this virtual collection highlight the rapidity with which the community of authors contributing to the *ES&T* family of journals was able to build WBE into a powerful tool for infectious disease surveillance. We hope this collection, as well as other WBE articles published in the journals, spurs continued enthusiasm and innovation in the topic, and we look forward to seeing your contributions.

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Environ. Sci. Technol. 2024, 58, 11865−11868

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