Pathogen Peak “Averaging” in Potable Reuse Systems: Lessons Learned from Wastewater Surveillance of SARS-CoV-2

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ABSTRACT: This study describes wastewater concentrations of SARS-CoV-2 at seven different sampling locations in Southern Nevada (ranging from 4.2 to 8.7 log10 gc/L) and highlights several key variables affecting those concentrations, including COVID-19 incidence, sample type, and service area population. This information is important for implementing wastewater-based epidemiology, but it also provides insight relevant to the design and regulation of potable reuse systems. Specifically, smaller systems may be more prone to influent concentration spikes that can drive enteric pathogen risk during disease outbreaks. It may be possible to leverage reactor hydraulics to achieve peak “averaging” in these scenarios, although it then becomes important to consider how elevated risks at the lower percentiles potentially offset benefits at the upper percentiles. Informed by SARS-CoV-2 concentration dynamics, the current study simulated relative risk for a hypothetical enteric pathogen. Simulated reactor hydraulics (i.e., dispersion) increased pathogen concentrations by up to 2.6 logs at lower percentiles but also decreased concentrations by up to 1.1 logs at the upper percentiles that sometimes drive public health risk. Collectively, these data highlight the importance of considering outbreak conditions, pathogen spikes, and peak “averaging” in the design and operation of treatment systems and in the development of regulatory frameworks.

KEYWORDS: SARS-CoV-2, wastewater-based epidemiology, quantitative microbial risk assessment (QMRA), potable reuse, dispersion, primary clarifier

1.0. INTRODUCTION

Recent quantitative microbial risk assessments (QMRAs) show that public health risk in potable reuse systems is highly sensitive to two conditions: (1) rapid changes in treatment performance due to off-specification1 or failure conditions2 and (2) inclusion of pathogens, specifically norovirus, for which only molecular data are available.3 In fact, the draft direct potable reuse (DPR) regulations recently developed in California4 used a single molecular data point of 9.17 log10 gc/L5 to characterize raw sewage concentrations for norovirus. This yielded a virus log reduction value (LRV) target of 16, which was subsequently increased to 20 logs to account for the possibility of a treatment process failure. There are several layers of potential conservatism inherent in this approach that will drive the adoption of highly complex advanced treatment trains for DPR. However, there may be alternative approaches for assessing risk in these systems that still demonstrate adequate protection of public health but reduce reliance on high-end assumptions (i.e., worst-case scenarios).

The COVID-19 pandemic has renewed interest in wastewater-based epidemiology6 and will ultimately yield an abundance of molecular data sets describing SARS-CoV-2 and enteric virus concentrations in raw sewage. Regardless of the molecular target, the resulting data sets may provide critical information for conducting and interpreting QMRAs for potable reuse. For example, the discrepancy between molecular and cell culture data is particularly relevant for SARS-CoV-2. Its RNA is routinely detected in raw sewage, but infectious SARS-CoV-2 has not yet been isolated from wastewater7 and often cannot be cultured even when assaying urine or feces collected directly from infected individuals.8 Without accounting for ratios of genome copies to infectious viral units (GC/IU ratios), a QMRA based solely on molecular data would overestimate COVID-19 risk for exposure through water.9 Similar results have been observed for nonenveloped enteric viruses (e.g., enterovirus and adenovirus) in raw sewage, for which GC/IU ratios can reach ~100 000:1.10 Thus, when using molecular data to identify risk-based treatment targets, it is important to consider how GC/IU assumptions might affect the overall level of conservatism, particularly when there is a mismatch between the methods used to quantify pathogen
dose (e.g., molecular) and the methods used in developing the dose response model (e.g., cell culture). Some dose response models have been developed with molecular data, but the fecal GC/IU ratios inherent in the resulting dose response models may not be consistent with the infectivity ratio for influent wastewater.

Despite COVID-19 primarily being respiratory in nature, SARS-CoV-2 is known to cause secondary infections in the gastrointestinal tract,\(^1\) hence its frequent detection in wastewater. Interestingly, recent efforts to link COVID-19 incidence with observed wastewater SARS-CoV-2 concentrations\(^12\)–\(^14\) suggest that fecal shedding dynamics may be similar to those of norovirus, particularly with respect to peak load and duration.\(^3\),\(^15\)–\(^17\) Vo et al.\(^14\) estimated that fecal shedding of SARS-CoV-2 peaked at 9.2 log\(_{10}\) gc/g and decreased exponentially over 25 days. Fecal shedding of norovirus has been shown to peak at 9.2–12.2 log\(_{10}\) gc/g\(^15\) or 5–9 log\(_{10}\) gc/g,\(^17\) with durations of up to 60 days. These similarities suggest that concentration dynamics for SARS-CoV-2 may offer valuable insight into raw wastewater concentrations of some enteric pathogens, notably norovirus. Amoueyan et al.\(^7\) previously questioned whether building-scale norovirus concentrations\(^8\) or potentially nonrepresentative spikes\(^9\) should be incorporated into a community-scale QMRA. Subsequent dynamic modeling of norovirus transmission\(^10\) suggested that extreme norovirus concentrations might actually be reasonable even in large systems. SARS-CoV-2 may offer additional evidence to address these types of uncertainties.

Another important consideration in the development of risk-based regulations for pathogen control is the stage of treatment in which pathogen concentrations are enumerated or LRV accounting commences. For example, California uses raw wastewater as the starting point for LRV accounting, while Texas uses wastewater effluent.\(^21\) Although lower pathogen concentrations may challenge method sensitivity in the Texas approach, improved wastewater quality may lead to higher pathogen recoveries, reductions in matrix interference, and more reliable data overall. Another often overlooked aspect of this comparison is that downstream enumeration incorporates the effects of dispersion within the wastewater treatment plant, effectively attenuating intermittent spikes in pathogen load and potentially reducing their impact on risk calculations. Even when pathogens are enumerated in raw wastewater, the effects of downstream dispersion can still be characterized through modeling efforts.

The current study focuses on two specific themes relevant to the preceding discussion. First, SARS-CoV-2 concentrations observed in Southern Nevada wastewater are presented in the context of sample type (grab vs composite and raw influent vs primary effluent) and service area population, with the goal of demonstrating that composite sampling of wastewater influent may mask peak pathogen concentrations. Consequently, QMRAs relying on composite sample data sets may underestimate exposure risk in certain scenarios, particularly for small systems.\(^22\),\(^23\) Second, the implications of concentration spikes are described in terms of relative risk for a hypothetical virus, specifically one characterized by a SARS-CoV-2 concentration distribution and a norovirus dose response model. This relative risk assessment offers a conceptual analysis of how reactor hydraulics, including dispersion in primary clarifiers, can be leveraged in a potable reuse treatment train to achieve peak “averaging”—a concept that has already been considered in the development of DPR regulations for chemicals in California.\(^8\) On the basis of these themes, the study set out to answer two questions: (1) how does dispersion impact risk during transient conditions (e.g., a pathogen surge resulting from a local outbreak) and (2) does dispersion provide demonstrable benefits that obviate the need for regulatory targets based exclusively on deterministic worst-case scenarios (i.e., extreme concentrations)? More generally, the intent of this analysis was to better understand the importance of hydraulic considerations when performing a QMRA for potable reuse.

### 2.0. METHODOLOGY

#### 2.1. Wastewater Surveillance of SARS-CoV-2 in Southern Nevada

Concentrations of SARS-CoV-2 RNA were monitored at seven different wastewater treatment facilities in Southern Nevada, with sample types ranging from 24 h composite influent for Facilities 1–3, midmorning grab influent (~8:00 am) for Facilities 4–6, and late-morning grab primary effluent (~10:00 am) for Facility 7. The average daily flow at these facilities ranged from 0.8 million gallons per day (mgd) to 100 mgd, and the corresponding sewered populations ranged from 16 000 to 872 000. Weekly samples were collected on Mondays between 08/24/2020 and 03/01/2021 for six of the facilities, and Facility 4 was added on 12/14/2020. This monitoring period captured the largest COVID-19 case surge of the pandemic for Southern Nevada, with daily incidence starting at ~20 cases per 100 000 people in late August, rising to a peak of ~90 in early January, and then declining to ~10 in early March (Figure S1).\(^24\)

Sample collection, processing, and analysis followed a modification of Gerrity et al.\(^12\) Specifically, instead of combining tangential hollow fiber ultrafiltration (HFUF) with centrifugal ultrafiltration, 10 L samples from Facilities 1 and 7 were processed with HFUF alone (REXCEED-25S, 30 kDa, Asahi Kasei Medical Co., Tokyo, Japan) to maintain consistency with ongoing, long-term monitoring at those sites. For practical reasons, including sample throughput and sample volume limitations, 150 mL samples from all other facilities were processed with Centricon centrifugal ultrafilters (Centricon Plus-70, 100 kDa, Millipore Sigma, Burlington, MA). Concentrations were determined using duplicate RT-qPCR reactions targeting the N1, N2, E_Sarbeco, and orf1a genes of SARS-CoV-2. All concentrations were reported as averages across the four gene targets in gene copies per liter (gc/L), after adjusting for equivalent sample volume and sample-specific recovery of spiked bovine coronavirus (average recovery was 54 ± 24% for HFUF and 19 ± 17% for Centricon). Method details, including limits of detection (LoDs) and quantification (LoQs) and quality assurance and quality control (QA/QC) considerations, were provided by Gerrity et al.\(^12\) Lognormal distributions were fit to each facility’s data set using the lognfit function in MATLAB (Mathworks, Natick, MA), with Facility 4 used as the case study for the subsequent relative risk assessment.

#### 2.2. Reactor Hydraulics Modeling

The modeling effort focused on two concentration scenarios for Facility 4: (1) a base e log-normal distribution determined from the entire data set (μ = 14.2 and σ = 2.0) and (2) a modified base e log-normal distribution that excluded the maximum observed concentration of 8.7 log\(_{10}\) gc/L (μ = 13.7 and σ = 0.9). For scenario 2, a concentration spike was simulated by assuming approximately one concentrated slug of sewage arrived at the...
facility each day. This was accomplished by modeling the probability of a concentration spike as 1/96 (or one 15 min time interval per day), which ensured consistency with the QMRA tool described later. In effect, scenario 2 resulted in a flatter distribution of influent concentrations ~99% of the time, which might be expected in a larger system or with composite sampling, but it still captured the possibility of a daily spike in pathogen load (i.e., a potential outlier). The daily spike was defined as the maximum concentration observed after 10,000 simulations of the scenario 1 log-normal distribution (9.5 log$_{10}$ gc/L), which is actually consistent with the maximum norovirus concentration reported in Eftim et al.\textsuperscript{5} and the 95th percentile norovirus concentrations predicted in Amoueyan et al.\textsuperscript{20}

Reactor hydraulics were modeled as (a) a nonideal pipeline or tank with a hydraulic retention time of 15 min and a baffle factor of 0.7 (or Peclet number = 20)\textsuperscript{25} and (b) a nonsteady-state completely stirred tank reactor (CSTR) simulating a primary clarifier with a hydraulic retention time (HRT) of (i) 1 h or (ii) 3 h. Effluent concentrations for the nonideal tank were calculated using the dispersed flow model for an open reactor.\textsuperscript{26} The corresponding concentration profile for a hypothetical tracer pulse is illustrated in Figure 1. For scenario 1 (log-normal distribution), the effluent from the nonideal tank was essentially an aggregate of multiple slugs of influent wastewater (Figure 2); an example effluent concentration profile is shown in Figure 3A. For scenario 2, the effluent from the nonideal tank was assumed to be the sum of a random concentration from the modified log-normal distribution and an attenuated spike (when applicable, on the basis of the aforementioned probability of 1/96). The spike was assumed to be attenuated by 91.6% on the basis of the peak C/C$_0$ of 0.084 shown in Figure 1. An example concentration profile for scenario 2 is shown in Figure 3B.

For the primary clarifier, all effluent concentrations were based on a conservative tracer assuming no reaction or die-off in a nonsteady state CSTR according to eq 1:

$$C_{te,t+1} = C_t e^{-(t_{t+1}-t_{t+1})/\tau} + C_{in,t+1}(1 - e^{-(t_{t+1}-t_{t+1})/\tau})$$

(1)

where $C_t$ = clarifier effluent concentration at $t_{t+1}$ (gc/L); $C_{te,t+1}$ = clarifier effluent concentration at $t$ (gc/L); $C_{in,t+1}$ = clarifier influent concentration at $t_{t+1}$ (gc/L); $t_{t+1} = $ time step $n + 1$

(hours), $t_c = $ time step $n$ (hours), $\tau = $ theoretical hydraulic retention time (HRT) = 1 or 3 h.

Example concentration profiles for the CSTR scenarios are shown in Figure 4.

2.3. Quantitative Microbial Risk Assessment. A QMRA was performed to estimate the risk of infection due to exposure to a hypothetical enteric virus in a potable reuse application. The baseline concentration profile of the hypothetical enteric virus was assumed to follow the distribution of SARS-CoV-2 (Figure 2). Example effluent concentration profile for the nonideal pipeline or tank reactor for scenario 2’s modified log-normal distribution with periodic spikes. The large peak shows how a concentrated slug of influent wastewater (3.5x10$^9$ gc/L) is attenuated and dispersed in the nonideal pipeline/tank.

![Figure 1](https://example.com/figure1.png)

**Figure 1.** Concentration profile for a conservative tracer pulse in a nonideal pipeline or tank reactor with a 15 min hydraulic retention time and a baffle factor of 0.7 (Peclet number = 20). Due to dispersion in the nonideal reactor, the peak concentration is attenuated by 91.6% (i.e., maximum C/C$_0$ = 0.084).

![Figure 2](https://example.com/figure2.png)

**Figure 2.** Schematic of the scenario 1 modeling approach for the nonideal pipeline or tank reactor. Multiple slugs of influent wastewater comprise the pipeline/reactor effluent, each with a different relative contribution based on reactor hydraulics (i.e., exit age distribution). The pie chart illustrates the relative contribution of 24 slugs of influent wastewater, with each slug having a concentration assigned randomly from the log-normal distribution in scenario 1.

![Figure 3](https://example.com/figure3.png)

**Figure 3.** (A) Example effluent concentration profile for the nonideal pipeline or tank reactor in scenario 1. The effluent concentration was determined using the approach illustrated in Figure 2. (B) Example effluent concentration profile for the nonideal pipeline or tank reactor for scenario 2’s modified log-normal distribution with periodic spikes. The large peak shows how a concentrated slug of influent wastewater (3.5x10$^9$ gc/L) is attenuated and dispersed in the nonideal pipeline/tank.

![Figure 4](https://example.com/figure4.png)

**Figure 4.** Example concentration profiles for the CSTR scenarios are shown.
was on relative rather than absolute risk, a single GC/ IU ratio of 1:1 was assumed for all scenarios. The QMRA assumed a point estimate virus LRV of 12 for the potable reuse treatment train, consistent with California’s earlier groundwater reuse regulations.\textsuperscript{27} Infection risk was calculated using a hypergeometric dose response function for norovirus (\(\alpha = 0.04\) and \(\beta = 0.055\))\textsuperscript{3,28} and a total ingestion volume of 2 L per day divided across eight 250 mL ingestion events.\textsuperscript{1} Importantly, it was not the intent of this study to estimate absolute risk for SARS-CoV-2 or norovirus. Instead, SARS-CoV-2 concentrations and the norovirus dose response function were used to characterize relative risk for a hypothetical enteric pathogen and elucidate the role of dispersion in protecting public health.

All risk calculations were performed in DPRisk, a publicly available QMRA tool developed using the R statistical language (Text S1).\textsuperscript{29} The inputs for DPRisk included a file containing 10 000 influent wastewater pathogen concentrations (separate input files for each modeling scenario) and the aforementioned assumptions. DPRisk then generated an underlying 10 000-parameter data set for ingestion-specific risks (based on 15 min time intervals) that was sampled repeatedly to generate daily risks (from eight discrete ingestion events per day) and annual risks (from 365 daily risks). For each modeling scenario, the tool generated a total of 36 500 daily risk estimates and 100 annual risk estimates. Relative risk was then determined by dividing the percentile-sorted risks for each tank/clarifier scenario by the percentile-sorted risks for the baseline scenarios.

### 3.0. RESULTS AND DISCUSSION

#### 3.1. Wastewater Surveillance of SARS-CoV-2 in Southern Nevada.

Median SARS-CoV-2 concentrations were similar for Facilities 2–6 (5.9–6.2 \(\log_{10}\) gc/L), despite those samples varying by type (i.e., composite vs grab influent) and sewershed size (i.e., between 16 000 and 757 000 people) (Figure 5). This is likely attributable to similar COVID-19 incidence and case trajectories throughout most of Southern Nevada (Figure S1). However, there are several notable distinctions between the data sets: (1) generally lower concentrations for Facilities 1 and 7 and (2) considerably larger concentration ranges for the grab influent samples from Facilities 4–6. For Facility 1, the downward shift in the distribution can likely be explained by the lower COVID-19 incidence within the sewershed, with a peak of 63 new daily cases per 100 000 people (Figure S1). In contrast, Facilities 2 and 3—the other locations with composite samples—reached peaks of 114 and 94 new daily cases per 100 000 people, respectively (Figure S1). The downward shift in concentration for Facility 7 was likely caused by a combination of physical removal via solids settling,\textsuperscript{30} dilution from commercial flows (i.e., the Las Vegas Strip), and diurnal variability, as the late-morning grab primary effluent actually reflected influent wastewater arriving between 5:00 and 6:00 am.\textsuperscript{12}

As highlighted by the high \(\sigma\) values for the log-normal distributions for Facilities 4–6, grab sampling of wastewater influent resulted in greater week-to-week variability in SARS-CoV-2 concentrations (Figure 5). In particular, concentrations...
at Facility 5 exceeded 7.0 log_{10} gc/L on three separate occasions, and Facility 4 reached a maximum concentration of 8.7 log_{10} gc/L in a single sample at the end of December. This exceptionally high concentration was likely caused by a combination of grab sampling aligning with a concentrated slug of sewage and the fact that Facility 4 is a relatively small system, which makes it more susceptible to the effects of concentrated slugs. Periodic spikes in concentration were not observed in the grab primary effluent samples from Facility 7, presumably due to dispersion in the large collection system and the primary clarifier specifically.

These data highlight three important concepts: (1) it may be possible to explain pathogen concentrations by infection incidence in the local community—a concept that is explored in greater detail in Vo et al.; (2) grab samples may be more appropriate than composite samples for determining peak pathogen concentrations, although the timing and frequency of sample collection are also critical; and (3) “averaging” of peak concentrations may be inherent to large sewersheds but can potentially be achieved through engineered unit processes (e.g., primary clarifiers) as well. Beyond SARS-CoV-2, each of these concepts has important implications for understanding and mitigating enteric pathogen risk in potable reuse systems.

3.2. Influent Concentrations for a Hypothetical Enteric Virus. Facility 4’s influent wastewater exhibited similar median concentrations (~6 log_{10} gc/L) in both modeling scenarios (1, log-normal distribution; 2, modified log-normal distribution with spikes), but they differed considerably at the extremes (Figure 6). The modified log-normal distribution was nearly 2 logs higher at the lower percentiles but 1.3 logs lower at the 99th percentile, immediately prior to the onset of the pathogen spikes. This was due to “flattening” of the raw wastewater concentration distribution by omitting the peak concentration.

Simulated dispersion also had an “averaging” effect on the reactor effluent concentrations, causing a considerable increase in concentration at the lower percentiles and a less dramatic attenuation at the upper percentiles for the Scenario 1 log-normal distribution (Figure 6A). At the lower percentiles, the reactors effectively increased the concentration of the hypothetical virus by up to 2.6, 2.5, and 2.0 logs for the pipeline/tank, 1-h primary clarifier, and 3-h primary clarifier, respectively. Reactor effluent concentrations were actually higher than the wastewater influent until the 80–90th percentiles. This indicates that, by ignoring the effects of mixing and dispersion, the typical QMRA approach relying on statistical distributions of raw influent concentrations may underestimate risk for the vast majority of ingestion events. However, the benefits of dispersion were realized beyond the 90th percentile, yielding net reductions in concentration by up to 0.7 logs for the 1-h primary clarifier and 1.1 logs for the 3-h primary clarifier and pipeline/tank.

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**Table 1. Sewershed attributes and parameters defining the base log-normal distribution fitted to each data set.**

| Facility | Population | Flow (mgd) | Lognormal μ | Lognormal σ |
|----------|------------|------------|-------------|-------------|
| 1        | 86k        | 42         | 12.2        | 1.0         |
| 2        | 255k       | 16k        | 13.7        | 0.8         |
| 3        | 757k       | 115k       | 13.7        | 1.4         |
| 4        | 68k        | 0.8        | 14.2        | 2.0         |
| 5        | 16k        | 6          | 14.2        | 1.4         |
| 6        | 134k       | 15         | 13.6        | 1.2         |
| 7        | 872k       | 100        | 11.9        | 1.0         |

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**Figure 5.** (Top) Summary of recovery-adjusted SARS-CoV-2 concentrations observed in weekly wastewater samples from seven different sewersheds in Southern Nevada. The data encompass seven months of sampling from 08/24/2020 to 03/01/2021; monitoring at Facility 4 commenced on 12/14/2020. The box-and-whisker plots indicate the minimum, 25th percentile, median, 75th percentile, and maximum concentrations observed for each facility. (Bottom) Sewershed attributes and parameters defining the base log-normal distribution fitted to each data set.

**Figure 6.** Wastewater influent and reactor effluent concentration profiles for the (A) scenario 1 log-normal distribution and the (B) scenario 2 modified log-normal distribution with spikes.
Similar effects on concentration were observed in scenario 2, although the difference between influent and reactor effluent concentrations at the lower percentiles was smaller, or negligible for the pipeline/tank, because of the modified log-normal distribution (Figure 6B). The 1-h and 3-h primary clarifiers were up to 1.1 and 1.2 logs higher in concentration, respectively, up to the 50th percentile. Beyond the 50th percentile, the intermittent spikes in influent virus concentration caused dramatic spikes in the primary effluent concentrations, with the 3-h clarifier spiking at the ∼50th percentile ($\Delta_{\text{max}} = 1.7$ logs) and the 1-h clarifier spiking at the ∼75th percentile ($\Delta_{\text{max}} = 1.9$ logs). Again, the benefits of dispersion were realized beyond the 99th percentile, due to attenuation of the influent wastewater spikes. At the upper extreme, the net reductions in concentration were the same as Scenario 1: a 0.7-log reduction for the 1-h primary clarifier and a 1.1-log reduction for the 3-h primary clarifier and pipeline/tank.

### 3.3. Relative Risk for a Hypothetical Enteric Virus.

Figure 7 illustrates the impacts of the pipeline/tank or primary clarifier on risk, relative to the wastewater influent in scenarios 1 and 2. Because this QMRA targets a hypothetical virus characterized by SARS-CoV-2 concentrations and a norovirus dose response function, absolute risks have no real-world significance, hence there is no comparison with common public health benchmarks (e.g., $10^{-4}$ annual risk of infection). Instead, relative risks greater than 1 indicate increased risks due to the "averaging" effect of the reactors.

The "per ingestion" relative risks essentially mirrored the relative concentrations presented in the previous section, with risk benefits being realized beyond the 90th and 99th percentiles for scenarios 1 and 2, respectively. Extending the ingestion-specific risks to daily and annual risk estimates resulted in another "averaging" effect. For scenario 1 (log-normal distribution), the reduction in daily risk at the upper percentiles reached maxima of 0.6 logs for the 1-h primary clarifier and 1.0 logs for the 3-h primary clarifier and pipeline/tank, while the reduction in annual risk was much lower at 0.09, 0.11, and 0.24 logs, respectively. Similar to the concentrations, the relative risk profiles were considerably different for scenario 2, but the net effect on relative daily risk was similar at the upper percentiles. The major difference was the relative annual risk for the pipeline/tank in scenario 2, which had a consistent reduction of ∼1.0 log because of how attenuation of the virus spike was modeled in this scenario. Recall that the intermittent spikes were attenuated by 91.6%
(Figure 1), which is consistent with the 1.0-log reduction in risk.

Therefore, the public health significance of dispersion/attenuation varies depending on the metric(s) under evaluation, specifically whether risk is assessed on a “per ingestion” vs daily vs annual risk basis. Historically, regulatory frameworks have emphasized annual risk, but there has been recent momentum in the potable reuse industry to consider daily risk in the development of regulations (SWRCB, 2021a; 2021b). In general, this analysis demonstrates that dispersion may increase public health risk for a majority of ingestion events but can reduce risk at the upper percentiles. Thus, the net outcome can be ambiguous. The more apparent benefit is realized in systems with “flatter” influent wastewater distributions and intermittent pathogen spikes (i.e., outliers), perhaps from short-term, localized outbreaks. Attenuation of these spikes can lead to reductions in “per ingestion”, daily, and annual risk, particularly when considering dispersion in nonideal tanks rather than complete mixing.

3.4. Implications for Potable Reuse Design and Regulatory Development. The SARS-CoV-2 wastewater surveillance data highlighted (1) the potential connection between infection incidence in the local community and influent wastewater concentrations, (2) the greater variability in influent wastewater concentrations in small systems, and (3) the effects of peak “averaging” due to sewershed size and/or sampling location within the wastewater treatment train. Each of these observations has important implications for the design, operation, and regulation of potable reuse systems and should be explored in greater detail. In particular, it would be advantageous to develop robust surveillance programs—coupling clinical data, wastewater data, and even consumer data—to better predict pathogen loads and even estimate public health risk in near-real-time for potable reuse systems.

With respect to hydraulics, many wastewater systems achieve dispersion in primary or secondary clarifiers, aeration basins, or even upstream of treatment in the collection system, but the corresponding effects on pathogen concentrations are rarely considered or quantified, thereby missing an opportunity to more accurately characterize the effects of peak “averaging” on pathogen concentrations. This concept has recently been integrated into draft DPR regulations in California to mitigate risks associated with chemical excursions, but this has not yet been extended to pathogens. This study demonstrates that certain hydraulic conditions inherent to wastewater treatment may reduce risk, or at least risk estimates, at the upper percentiles by either achieving pathogen reduction or by flattening concentration distributions to reduce the significance of extreme concentrations. In other words, systems leveraging dispersion may reduce the likelihood and/or significance of rare pathogen spikes. This could potentially shift regulatory focus to higher frequency conditions, reduce costs associated with potable reuse, and still provide equivalent levels of public health protection. That being said, when peak concentrations are not truly “outliers” and are simply high-end estimates of log-normal distributions, dispersion has a disproportionately adverse effect on “per ingestion” and daily risk. This may actually support the use of deterministic worst-case scenarios, as employed in the development of potable reuse regulations in California.

In general, this study demonstrates that the effects of dispersion are complex, as increased concentrations and risks at the lower percentiles may offset any benefits at the upper percentiles. In scenarios in which risk is driven almost entirely by the upper percentiles (e.g., during a catastrophic treatment process failure or a rare pathogen spike), dispersion may offer demonstrable benefits. This complexity demonstrates that the effects of dispersion likely need to be considered with targeted QMRAs for specific pathogens, scenarios, and systems in order to fully characterize the net outcome for public health. This study demonstrates the potential significance and benefits of dispersion and provides a framework for pursuing that assessment in future decision-making efforts.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acsestwater.1c00378.

Discussions of access to the DPRisk QMRA tool and figure of Southern Nevada’s sewershed-specific daily COVID-19 incidence from April 2020 through April 2021 (PDF)

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Notes

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