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Assessing the Risk of Acute Gastrointestinal Illness Attributable to Three Enteric Pathogens from Contaminated Private Water Wells in Ontario

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Assessing the risk of acute gastrointestinal illness attributable to three enteric pathogens from contaminated private water wells in Ontario

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A B S T R A C T

The province of Ontario compromises the largest groundwater reliant population in Canada serving approximately 1.6 million individuals. Unlike municipal water systems, private well water is not required to meet water quality regulatory standards and thus source maintenance, treatment and testing remains the responsibility of the well owner. Infections associated with private drinking water systems are rarely documented given their typically sporadic nature, thus the human health effects (e.g., acute gastrointestinal illness (AGI)) on consumers remains relatively unknown, representing a significant gap in water safety management. The current study sought to quantify the risk of waterborne AGI attributed to *Giardia*, shiga-toxin producing *E. coli* (STEC) and norovirus from private drinking water sources in Ontario using Monte Carlo simulation-based quantitative microbial risk assessment (QMRA). Findings suggest that consumption of contaminated private well water in Ontario is responsible for approximately 4823 AGI cases annually, with 3464 (71.8%) and 1359 (28.1%) AGI cases predicted to occur in consolidated and unconsolidated aquifers, respectively. By pathogen, waterborne AGI was attributed to norovirus (62%; 2991/4823), *Giardia* (24.6%; 1186/4823) and STEC (13.4%; 646/4823). The developed QMRA framework was used to assess the potential health impacts of partial and total well water treatment system failure. In the unlikely event of total treatment failure, total mean annual illnesses are predicted to almost double (4217 to 7064 cases per year), highlighting the importance of effective water treatment and comprehensive testing programs in reducing infectious health risks attributable to private well water in Ontario. Study findings indicate significant underreporting of waterborne AGI rates at the provincial level likely biasing public health interventions and programs that are effective in monitoring and minimizing the health risk associated with private well water.

1. Introduction

Approximately 1.6 million Ontarians rely on a private well water supplies, with most residing in rural regions (Statistics Canada, 2019). Individuals using private wells as their primary drinking water source are at an elevated risk of acute gastrointestinal illness (AGI) (Uhlmann et al., 2009; Bradley et al., 2021). Private water wells are subject to contamination by enteric pathogens consequent to factors including improper land application/disposal of manure, septic system leakage, and contaminated run-off (overland flow) resulting from extreme weather events (e.g., flooding, high-intensity rainfall, snowmelt) (Murphy et al., 2017). Further, private water wells are not required to meet the regulatory standards of the Ontario Safe Drinking Water Act (2002) or the Ontario Clean Water Act (2006), and thus source maintenance, testing and other measures to ensure potability remain the responsibility of the well owner (Kreutzwiser et al., 2011). Navigating guidelines and recommendations can prove challenging for property owners, as can the cost of efficacious treatment systems, making access to clean water a critical health equity issue in Ontario. Quantifying the true extent of AGI attributable to consumption of contaminated private well water also remains a challenge as cases of laboratory-confirmed AGI reported in Ontario's integrated Public Health Information System (iPHIS) do not distinguish infections based on their likely source of transmission (e.g., drinking water, food, animal contact or person-to-person transmission) (Vrbova et al., 2012). Moreover, the estimated number of AGI cases associated with waterborne pathogens is severely under-reported and likely significantly under-represents the true burden of infection; private groundwater contamination events are often prolonged (i.e., ongoing), sporadic, and/or limited to a single household (i.e., groundwater source) and are therefore difficult to identify (Haagsma et al., 2013). Compounding this, individuals experiencing gastrointestinal infection frequently do not seek medical care as disease mild and self-limiting, resulting in a lack of laboratory confirmation and source identification (Hrudey and Hrudey, 2007; Haas et al., 2014; Graydon et al., 2020).

The susceptibility of private drinking water sources to microbial contamination and associated outbreaks has been reported throughout

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the literature (Hynds et al., 2014a; Murphy et al., 2017). A recent global review examining contamination of domestic groundwater systems by shiga-toxin producing *E. coli* (STEC) found that private (i.e., unregulated, serving a single household) groundwater samples (15/800; 1.9%) and supplies (15/631; 2.4%) were characterised by higher detection rates compared to equivalent municipal samples (0/92) and supplies (0/32) (Chique et al., 2021). Likewise, three recent Canadian studies have reported that the risk of sporadic infections caused by five enteric pathogens (*Campylobacter, Salmonella, STEC, Giardia* and *Cryptosporidium*) differ by drinking water source type, with highest rates encountered among private (ground)water consumers (Uhlmann et al., 2009; Galanis et al., 2014; Murphy et al., 2016). Further, Borchardt et al. (2021) sampled 131 wells for fecal contamination in Wisconsin, United States; approximately 40% (32/79) of *E. coli* positive wells had markers concurrently present for pathogens including enteric viruses and protozoa. Illness associated with private drinking water systems is rarely documented given the sporadic nature of infections, thus the human health effects (e.g., acute gastrointestinal illness, hospitalizations) remain relatively unknown, representing a recognized gap in water safety and quality management strategies.

Quantitative microbial risk assessment (QMRA) represents a valuable tool for estimating the burden of disease associated with waterborne illness and thus supports water safety planning and management (Petterson and Ashbolt, 2016; Owens et al., 2020). QMRA aims to employ best available information, using an iterative (simulation-based), probabilistic approach to account for variability and uncertainty (via sensitivity analysis) to understand the potential human health effects from microbial exposures and ultimately provide guidance for evidence-based policy development (Ramírez-Castillo et al., 2015). Several previous studies have utilized QMRA to estimate the human health risk posed by private drinking water sources (Hunter et al., 2011; Hynds et al., 2014a; Balderrama-Carmona et al., 2015; Murphy et al., 2016; Balderrama-Cormona et al., 2015). However, due to data scarcity these studies have resulted in very high levels of uncertainty and variability with the potential to either over or underestimate human health risk. For example, Murphy et al. (2016) utilized QMRA to estimate the human health risks associated with private wells and small water systems across Canada, concluding that private groundwater consumers had a higher risk of contracting enteric infections than those supplied by publicly managed systems. However, QMRAs are inherently generalised, and rarely account for site-specific conditions or temporal variations in real time (e.g., contaminant ingress mechanisms), thus may misrepresent the inherently complex and fluid nature of groundwater contamination (Smeets et al., 2010; Bichai and Smeets, 2013). Accordingly, the need for larger, increasingly adapted databases that account for contamination pathways (e.g., microbiological, physical, hydrogeological, temporal) are essential to minimize the limitations of previous QMRAs (Latchmore et al., 2020; White et al., 2021; Borchardt et al., 2021).

The objective of the current study was to quantify the risk of waterborne AGI attributed to *Giardia*, shiga-toxin producing *E. coli* and norovirus from private drinking water sources in Ontario as these represent the most frequently reported protozoan, bacterial and viral water-borne pathogens in Canada, and contribute to significant morbidity and mortality, both regionally and internationally (Hynds et al., 2014b; Wallender et al., 2014; Murphy et al., 2016; Health Canada 2019; Owens et al., 2020; Sorensen et al., 2021). The presented QMRA was hydrogeologically delineated and employed a large spatiotemporal groundwater quality dataset (>700,000 samples) (Latchmore et al., 2020), permitting spatio-temporally specific exposure distributions for several model inputs, including private well water consumption, annual contamination duration and contamination event overlap (i.e., re-occurrence) (Lavallee et al., 2021a; Latchmore et al., 2022). Study findings will identify the human health risk attributable to private drinking water systems in rural communities in Ontario. Finally, presented models will serve as an effective template for public health

agencies and provincial governments to safeguard private drinking water systems and diminish health risks.

2. Methods

2.1. Model framework

Previous research has found that *E. coli* detection rates in Ontario private well water differ significantly based on hydrogeological setting (i.e., consolidated vs. unconsolidated aquifers) (Latchmore et al., 2020; White et al., 2021). Latchmore et al. (2020) report significantly higher detection rates associated with consolidated aquifers, suggesting that human exposure to waterborne pathogens is likely mediated by hydrogeological setting. Further, given the importance of accounting for sensitive sub-populations due to differing dose-response relationships, and the need for age-adjusted incidence rates for public health planning, QMRA models have been separated based on age (</>10 years of age). Accordingly, the overarching risk estimation framework comprised 12 models (three pathogens x two hydrogeological settings [i.e., consolidated, and unconsolidated aquifers] x two age categories [i.e., adults and children <10]) for estimating the exposure and subsequent human health risks associated with private well water consumption in Ontario.

In the current study, several structural and algorithmic amendments have been made to the traditional four-tiered QMRA approach as model components/inputs and algorithms are bespoke depending on the specific objectives of the risk assessment. The major mathematical tasks of a QMRA are exposure assessment, hazard characterization and risk characterization (Haas et al., 2014). For the purpose of the current study, where appropriate, all terminology and descriptions have been adopted from Haas et al. (2014). The 3-step province-scale stochastic QMRA model was developed as follows (Fig. 1):

Step 1. Exposure Assessment

$$ED = C_{ecoli} \text{ x } 1/R \text{ x PI x } V_{DW} \quad (1)$$

where ED = daily exposure per person (cfu/day), C_{ecoli} = *E. coli* loading (cfu/mL), R = detection sensitivity (%), PI = pathogen contribution (%), Vdw = Daily water consumption (mL/day).

Step 2. Hazard Characterization

$$PDinf_{STEC} \text{ or } PDinf_{norovirus_{adults}} = [1 - (1 + ED \text{ / } \beta)]\alpha \quad (2a)$$

$$PDinf_{giardia} = 1 - \exp(-ED * r) \quad (2b)$$

$$PDinf_{norovirus_{children}} = P * (1 - \exp(-ED)) \quad (2c)$$

where: PDinf = daily probability of infection (%), ED = daily exposure per person (CFU/day), β = Beta Poisson parameter value, α = Beta Poisson parameter value, *r* = Exponential parameter value, *P* = Fractional Poisson parameter

$$PA \text{ } inf = [1 - (1 - PDinf)^{DUR}] \text{ x Fc} \quad (2d)$$

where PA*inf* = annual probability of infection (%), DUR = contamination duration (days/annum), Fc = contamination frequency (%)

Step 3. Risk Characterization

$$\text{Health burden per annum} = PAinf \text{ x Pop } (1 - NCon) \text{ x AR} \quad (3)$$

where PA*inf* = probability of infection per annum (%), Pop = affected population/population at risk (number with well water as primary drinking source), NCon = rate of non-consumption (%), AR = attack rate (%)   Statistical distributions were developed and tested using R (version 3.2.1) and RStudio (version 1.1.447) with the add-on packages ggplot2 (version 3.2.1), fitdistrplus (1.0–14) and mc2d (version 0.1–21). Anderson-Darling and Kolmogorov-Smirnov statistics were used to examine goodness-of-fit between fitted parametric distributions and
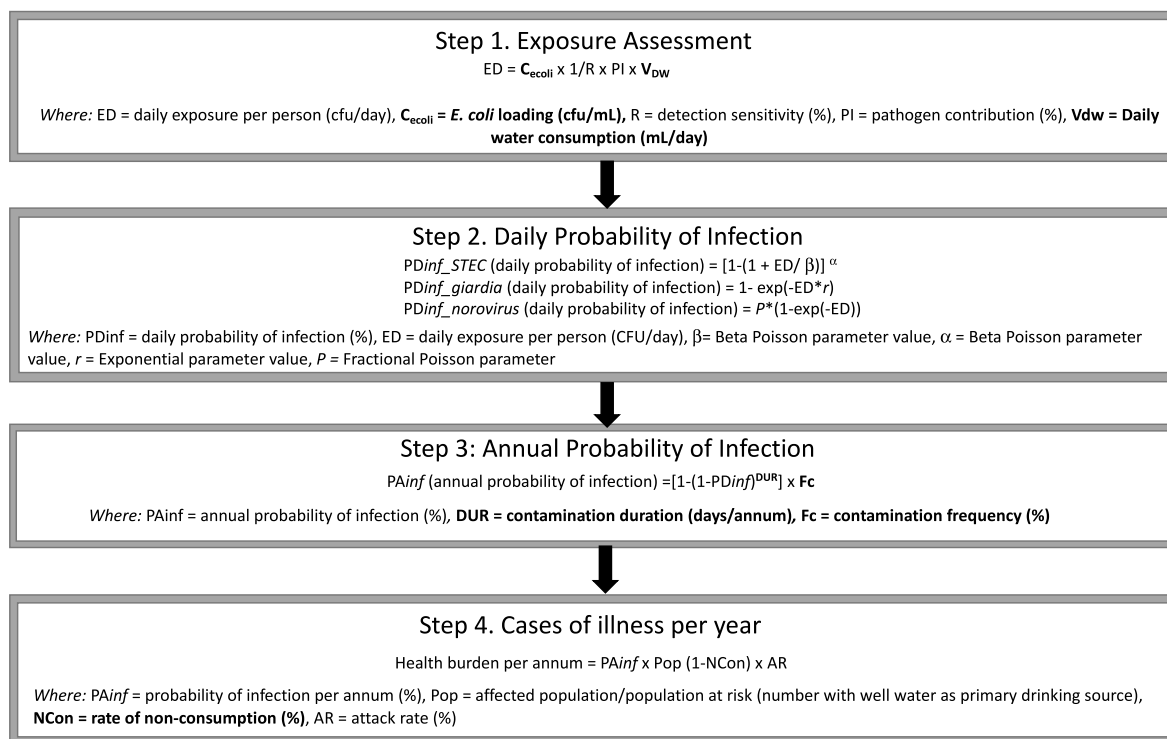
Fig. 1. Schematic diagram of QMRA model used to estimate the disease burden of STEC, Giardia and norovirus from consumption of contaminated private well water in Ontario (adapted from Haas et al., 2014; Murphy et al., 2016).

empirical data for all statistical distributions (Delignetter-Muller and Dutang, 2015). All simulations were run in R using 2-dimensional Monte Carlo (2DMC) simulations with the package mc2d (Pouillet and Delignetter-Muller, 2010). This approach was chosen based on previous risk estimates from private groundwater wells (Burch et al., 2021) as it permits individual and concurrent measurement of the effects of parameter variability and uncertainty on risk estimates and distributions. More specifically, variability in this case refers to irregularity in natural conditions and subsequent exposures (e.g., water consumption patterns, *E. coli* loading), while uncertainty refers to discrepancies associated with simulated model parameters (e.g., pooling of pathogen contribution literature) (Pouillet and Delignetter-Muller, 2010). Each 2DMC simulation was based on 10,000 iterations. A summary of model inputs is provided in Table 1. Sensitivity analysis was carried out using Spearman's rank order correlation coefficient to determine the significant input variables contributing to uncertainty in the risk calculations (Cummins et al., 2010; Hunter et al., 2011). Scenario analysis is a well-recognized tool in environmental change research and is the process of modeling potential future outcomes by considering the impact of alternative events on model inputs (Schweizer and Kurniawan, 2016). The developed QMRA simulations assessed the potential health impact of a private well water treatment system completely failing or partially failing (e.g., range of 0%–100% treatment efficacy). It is important to note that the majority of private wells in Ontario do not have microbiological treatment systems installed. Scenario analysis was undertaken using the multivariable nodes as a third dimension in the mc2d package (Delignetter-Muller and Dutang, 2015).

2.2. Model inputs

2.2.1. Private well data sources

The current study combined the Well Water Information System (WWIS) and the Well Water Testing Dataset (WWTD) from 2010 to 2017, inclusive. The WWIS is the dataset of well records maintained by the Ontario Ministry of the Environment, Conservation and Parks

(MECP). Well records include details pertaining to well construction, location, pump test results, source-specific geological profile, and general information regarding well water quality (MECP, 2019). The WWTD comprises all results of bacteriological testing performed at one of the eleven provincial laboratories. A full description of dataset development has previously been described in Latchmore et al. (2020); briefly, the WWTD-WWIS dataset was created by merging the WWTD with the WWIS via an interactive, nearest-neighbour, fuzzy logic-based (inexact string matching) custom algorithm. Private well water samples were specifically matched to sources using minimum haversine distance, with a "one well-one distance" approach used to ensure accuracy. A total of 156,033 wells (458,910 samples) were geographically associated with consolidated aquifers and 83,211 wells (243,951 samples) were associated with unconsolidated aquifers. According to the Ministry of the Environment, Conservation and Parks (2014), approximately 70% and 30% of private well users have wells constructed in consolidated and unconsolidated aquifers, respectively. All submitted well water samples were processed and analyzed for Total Coliforms (TC) and *Escherichia coli* via direct membrane filtration and culture, based on MECP Method #E3407 (membrane filtration method using DC Agar for the simultaneous detection and enumeration of TC and *E. coli* in Drinking Water (Ministry of the Environment, Conservation and Parks, 2010). Description and analyses of the WWTD-WWIS have been presented in Latchmore et al. (2020), and White et al. (2021) (Figs. S8–S9). Further, only *E. coli* results (excluding TC results) have been included in the current study as it represents a specific indicator of recent fecal ingress and, if present, suggests a potential threat to public health and is used in waterborne QMRA. The recommended acceptable limit of *E. coli* is 'none' (<1) detectable in a 100 mL sample (Health Canada, 2019).

2.2.2. Population at risk

The total at-risk population was estimated from Census data (2019; Table 1) and comprised individuals whose primary drinking water source is an inadequately treated or untreated private well. Based on Census data, approximately 34% of individuals who treat their well

Table 1
Summary of QMRA input variables, descriptions, and distributions.

Input	Variable	Distribution	Source
E. coli loading	Cecoli	Consolidated – Negative Binomial ($r = 0.753$, $p = 6.81$) Unconsolidated – Negative Binomial ($r = 0.739$, $p = 7.29$)	Current Study
Contamination Frequency (day/year)	Fc	Consolidated – Beta ($\alpha = 0.0106$, $\beta = 0.322$) Unconsolidated – Beta ($\alpha = 0.00739$, $\beta = 0.323$)	Current Study (supplementary material)
Contamination Duration	DUR	Consolidated – Log-normal ($\mu = 0.0772$, $\sigma = 0.0546$) Unconsolidated – Weibull ($\mu = 1.4544$, $\sigma = 28.0393$)	Current Study
Pathogen Contribution *STEC* *Giardia* *Norovirus*	PI	Uniform (min = 0.014, max = 0.019)	Murphy et al. (2016) Allen et al. (2017) Borchardt et al. (2021) Pang et al. (2021)
Detection Sensitivity	R	Uniform (min = 0.93, max = 1)	Hynds et al., (2014a) Unpublished Data
Consumption Volume (mL/day)	VDW	Adult: Exponential (rate = 0.00088; 1132 mL/day; SD = 649 mL/day) Children (<10 years) Exponential (rate = 0.00111; 905 mL/day; SD = 519 mL/day)	Lavallee et al. (2021a) Lavallee et al. (2021a) Pintar et al. (2009)
Dose Response: *STEC* *Giardia* *Norovirus*	β:α	Beta-Poisson ($\alpha = 398.9$ $\beta = 3.96 \times 10^4$) Exponential (r = 0.0199) Beta-Poisson ($\alpha = 0.04$ $\beta = 0.05$) Fractional Poisson ($P = 0.72$)	Teunis et al. (2008a) Teunis and Havelaar (2002) Regli et al. (1991) Teunis et al. (2008b) Messner et al. (2014)
Attack Rate: *STEC* *Giardia* *Norovirus*	AR	See Table 4	Pooled-analyses (n = 50)
Affected Population	Pop	0.11 (11% of the Ontario population on private well water) 1,031,800 at-risk (after considering treatment)	Statistics Health Canada (2019)
Rate of non-consumption	NCon	0.185	Lavallee et al. (2021a)

water, use a treatment system effective against microbial contamination (e.g., reverse osmosis, membrane filtration, shock chlorination) (Statistics Canada, 2019); the total at-risk population was estimated to be approximately 1,031,800 (Table 2), presuming treatment systems are properly maintained and managed.

Vulnerable sub-populations, namely, immunocompromised individuals, the elderly, women during pregnancy, and children, are characterized by an increased risk in terms of severity (including hospitalisations, development of sequelae, and prolonged effects) and mortality when exposed to enteric pathogens (Gerba et al., 1996). Vulnerable sub-populations in the current QMRA comprised infants (<1 year), children (1–10 years) and elderly (>65 years), mirroring a previous study by Hynds et al. (2014b). Due to insufficient data regarding the distribution of immunocompromised individuals and pregnant women, these sub-populations have not been accounted for in the current study. According to Census data, and assuming these

Table 2
Total and vulnerable population served by private water wells in Ontario (as of 2019; adapted from Statistics Canada, 2019).

Age category	Total	Proportion of provincial population served by private well water (%)
Infants (<1)	13,775	1.1
Children (1–10)	147,421	8.5
Adults (11–64)	1,119,200	72
Elderly (>65)	293, 379	19.2
Total Vulnerable Population	454,575	28.8
Total population	1,573,775	
Total at-risk population (after water treatment)	1,031,800	

sub-populations are randomly distributed across the province, this population compromises approximately 28.8% (454,575 individuals) of the total population (Statistics Canada, 2019): Infants – 1.1%, Children – 8.5%, Elderly – 19.2% (Table 2).

2.2.3. Contamination frequency

Determination of contamination frequency in private well water in Ontario was undertaken using the WWTD-WWIS dataset from 2010 to 2017, inclusive, via analyses of the proportion of wells contaminated at least once per year (Table 3). Private wells had *E. coli* present on 4.0% and 2.9% of sampling occasions in consolidated and unconsolidated aquifers, respectively (Table 3). Correspondingly, contamination frequency was estimated using detection rates reported by Latchmore et al. (2020); an estimated 3 and 4 contamination events per 100 wells per year is expected to occur in consolidated and unconsolidated aquifers, respectively, thus the majority of contaminated private wells are characterized by one contamination event per year. Sampling results from both aquifer types were fit to determine the most appropriate distribution. Goodness of fit tests indicate the beta distribution provided the best fit for both consolidated ($\alpha = 0.0106$, $\beta = 0.322$) and unconsolidated aquifers ($\alpha = 0.00739$, $\beta = 0.323$) (Figs. S1 and S2).

2.2.4. Escherichia coli concentration

E. coli concentration (CFU/100 mL) in private well water was fit and distributed using the WWTD-WWIS dataset. To estimate *E. coli* loading, two probabilistic distributions (i.e., consolidated, and unconsolidated aquifers) were developed using data from all contaminated private wells (≥1 CFU/100 mL; Table 3). The negative binomial distribution provided

Table 3
E. coli occurrence in private well water in Ontario stratified by aquifer type and year.

Year	Consolidated (Annual detection rate)	Average *E. coli* concentration for positive samples (CFU/100 mL)	Unconsolidated (Annual detection rate)	Average *E. coli* concentration for positive samples (CFU/100 mL)
2010	3004/63,954 (4.7%)	7.41	1204/33,681 (3.6%)	7.32
2011	2934/62,577 (4.7%)	7.49	1121/33,881 (3.3%)	7.55
2012	2100/59,526 (3.5%)	6.94	929/32,776 (2.8%)	6.75
2013	2840/57,520 (4.9%)	6.85	1134/31,349 (3.6%)	8.37
2014	2482/56,002 (4.4%)	7.06	888/29,773 (3.0%)	7.54
2015	1999/52,866 (3.8%)	7.23	772/27,907 (2.8%)	7.80
2016	1322/52,486 (2.5%)	5.52	499/27,781 (1.8%)	5.65
2017	1821/53,979 (3.4%)	4.73	559/26,803 (2.1%)	5.87
	4.0%	**6.65**	**2.9%**	**7.10**

Table 4
Results of pooled-analyses (n = 50; Table S1) and distribution fitting for clinical variables. Based on previous literature the beta-general, PERT, lognormal, logistic, normal and pareto distributions were all tested for fit.

Variable	N	Range	Distribution	Parameters	Goodness of fit p
Attack rate	13[a]	Min – 6.7%	Logistic	μ = 0.224 s = 0.095	0.87
	22[b]	Max – 64%	Normal	μ = 0.243	0.85
	15[c]	Min – 3.1%	Normal	σ = 0.169	0.78
		Max – 92%		μ = 0.243	
		Min – 5%		σ = 0.169	
		Max – 63%			
HUS rate[a]	8	Min – 0.3%	Normal	μ = 0.077	0.948
		Max – 27.2%		σ = 0.027	
Hospitalization rate	5[a]	Min – 7.5%	Normal	0.013	0.999
	2[b]	Max – 35.7%		0.030	
	2[c]		Deterministic		
			Deterministic		
Mortality rate[a]	4[a]	Min – 0.3%	Logistic	μ = 0.023 s = 0.011	0.95
		Max – 6.3%			

[a] STEC data.
[b] Norovirus data.
[c] Giardia data.

an appropriate fit for *E. coli* loading among private wells located in both consolidated ($r = 0.753$, $p = 6.81$) and unconsolidated ($r = 0.739$, $p = 7.29$) aquifers, respectively (Figs. S3 and S4).

2.2.5. Contamination duration

An understanding of microbial survival in private groundwater sources and the subsurface environment is critical for the development of increasingly accurate waterborne infection risk assessments. Using the WWTD-WWIS dataset, the authors examined the die-off rate (CFU/100 mL per day decline) and subsequent duration of *E. coli* contamination in private well water in Ontario, and the methodology is explained in depth by: Latchmore et al. (2022). Further, the probability of contamination event overlap, defined as one or more contamination events occurring sequentially resulting in an event characterized by increased duration and a point increase in concentration, in Ontario private well water was calculated. A new *E. coli* loading variable was created if contamination event overlap were to occur (Latchmore et al., 2022). Briefly, private well water samples from the WWTD-WWIS dataset were analyzed relative to extracted "contamination sequences", defined as two or more *E. coli* positive samples in series within one calendar year, and delineated by aquifer type (consolidated/unconsolidated). Thus, all contamination sequences are source-specific, with each sequence pertaining to one well and one calendar year and compiled independently for both aquifer types. Extracted contamination sequences were used to assess contamination duration, defined as number of days (per annum) with *E. coli* > 0 CFU/100 mL, for individual private wells.

The *E. coli* die-off rate (per day decline of *E. coli* concentration [CFU/100 mL]), defined as the average *E. coli* concentration divided by the number of days from mean contamination concentration to zero CFU/100 mL (negative test result), was separately calculated for wells associated with consolidated and unconsolidated aquifers. Study findings indicate a median *E. coli* die-off rate of 0.38 CFU/100 mL per day and 0.64 CFU/100 mL per day, for private wells located in unconsolidated and consolidated aquifers, respectively (Latchmore et al., 2022). equating to first-order die-off rates of 0.0054 h^{-1} to 0.0089 h^{-1}. Contamination events associated with unconsolidated aquifers were significantly longer (days/annum) compared to consolidated aquifers (t = 82.10; p < 0.0001). Contamination frequency (section 2.2.3), employed in concurrence with calculated mean concentration and mean time to zero (Table 2) predict mean durations of 21 (CI: 1.92–80.7; min 0 max 347) and 16 (CI: 3.31–53; min 0 max 208) "annual contamination days" among wells located in consolidated and unconsolidated aquifers, respectively, based on one contamination event. Thus, while contamination events are shorter in consolidated aquifers, they experience more

contamination days per year. The Anderson-Darling and Kolmogorov-Smirnov statistics indicate the two parameter Weibull distribution provides a statistically appropriate fit for contamination duration in unconsolidated aquifers, while the log-normal distribution provides a statistically appropriate fit in consolidated aquifers (Figs. S6 and S7).

2.2.6. Private well water consumption

A province-wide online survey was employed between May and August 2018 to investigate levels of awareness, attitudes, risk perceptions and beliefs among private well users in Ontario (Lavallee et al., 2021b) (n = 1162). As part of this work, 81.5% of respondents (n = 947) reported their daily well water consumption (i.e., tap water). Results indicated a mean daily well water consumption rate of 1132 mL/day (SD = 649 mL/day). To develop a discrete mean value (and continuous distribution for use in QMRA), deterministic midpoint values were assigned to each consumption range based on an assumption of within-range normality and subsequently distributed as previously described by Hynds et al. (2012). Goodness of fit tests (e.g., Anderson-Darling and Kolmogorov- Smirnov) indicate the log-normal (p < 0.001), exponential (p < 0.001) and normal distributions all provide a similar fit for total daily well water consumption (Figure A.5). However, the log-normal and normal distributions significantly overestimate water consumption within the upper quartile and therefore the exponential distribution was employed (Lavallee et al., 2021a).

Consumption estimates for vulnerable sub-populations (i.e., children <10 years old) were more difficult to ascertain given the age distribution of the province-wide survey was predominantly individuals over the age of 25 years old (1161/1169; 99.5%). Therefore, a distribution was developed using previously published estimates from Pintar et al. (2009) in concurrence with the province-wide survey data. More specifically, Pintar et al. (2009) reported that children (<10 years of age) consume approximately 20% less well water than adults. Therefore, using the private well water consumption estimates for adults reported by Lavallee et al. (2021a) [1132 mL/day], daily private well water consumption for children was estimated by applying a 20% decrease to the adult consumption distribution. Thus, the consumption estimate for children was characterised by a mean daily well water consumption rate of 905.6 mL/day (SD 519 mL/day). Goodness of fit indicate an exponential distribution (p < 0.001) provides an appropriate fit for daily well water consumption for children (rate = 0.00111).

2.2.7. Pathogen contribution

Previous studies have identified positive correlations between *E. coli* in private groundwater systems and the presence and concentration of

bacterial pathogens ($r = 0.636$, p = 0.02; Hynds et al., 2014a) and viruses (r = 0.33, p < 0.001; Fout et al., 2017). Further, it is difficult to monitor drinking water for all fecal pathogens due to limitations in currently available technologies and the large sample volumes required for detection (e.g., up to 100 L) (Cabral, 2010; Felleiter et al., 2020). Therefore, the presence and concentration of enteric pathogens were extrapolated from total *E. coli* CFU per 100 mL. In the context of the current risk assessment, pathogen contribution is defined as the likely ratio of laboratory confirmed *E. coli* to enteric pathogens in private well water in Ontario. The current study employed a uniform distribution of the most recent point estimates of pathogen occurrence (0.014–0.019; Table 1) utilized in QMRA of waterborne infection and pathogen occurrence studies to account for variability and uncertainty throughout the studies (Murphy et al., 2016; Allen et al., 2017; Burch et al., 2021). More specifically, Murphy et al. (2016) utilized a point estimate of 1.9% (7/371) derived from a pooled analysis of previously published data on pathogen occurrence. Similarly, Burch et al. (2021) utilized a point estimate of 1.4% (2/138) obtained from a study which examined enteric pathogen presence in private well water in northeastern Wisconsin (Borchardt et al., 2021). Lastly, Allen et al., 2017 identified an estimate of 1.7% (2/118) obtained from an Ontario, Canada based study assessing the presence of enteric viruses in private and municipal well water.

2.2.8. Dose-response parameters

The overall purpose of the dose-response assessment is to establish a relationship between the level of pathogen exposure and the probability of an adverse human health reaction (Haas et al., 2014). The human response after exposure to a waterborne pathogen is highly variable based on multiple underlying factors including pathogen (strain) virulence, immune status of the individual and magnitude of exposure (Buchanan et al., 2000).

2.2.8.1. Shiga toxin producing E. coli (STEC).
The Beta-Poisson (BP) model is a frequently used, single-hit dose-response model and has previously been applied to shiga-toxin producing *E. coli* (Haas et al., 2000; Hynds et al., 2014; Murphy et al., 2016). Utilizing data from previous human outbreaks, Teunis et al. (2008) developed a hierarchical BP dose-response model on which current estimates are based. More specifically, in the current study, the 95th percentile predictive parameters ($\alpha = 398.9$, $\beta = 3.96 \times 10^4$) were employed, where ED is the dose and α and β are parameters of the BP distribution (Equation (2a)).

2.2.8.2. Giardia.
The exponential dose response model (Equation (2b)) is the most frequently used for depicting *Giardia* exposure in waterborne QMRA (Balderrama-Carmona et al., 2017). The exponential dose-response curve was used with $r = 0.0199$ (Rose and Slifko, 1999; Teunis and Havelaar, 2002; Balderrama-Carmona et al., 2014).

2.2.8.3. Norovirus.
For individuals >10 years, the modified BP model (Equation (2a)) has been identified as the most appropriate fit for norovirus and has been utilized in previous waterborne QMRA, allowing for comparability of QMRA estimates across studies (Teunis et al., 2008b; Murphy et al., 2016). More specifically, Teunis et al., 2008b, estimated that approximately half (50%) of all norovirus genome copies are infectious, with each infectious virus capable of causing an infection. The BP model was used with the parameters ($\alpha = 0.04$, $\beta = 0.05$; Equation (2a)).

Given that young children are particularly susceptible to this disease, requiring medical attention more frequently than any other age group, a fractional Poisson model was identified as being most appropriate for children (<10 years of age) (Messner et al., 2014). The fractional Poisson model is recommended when the pathogen(s) of interest are more virulent and/or for pathogen(s) that likely provoke an acute immune response in exposed individuals, such as norovirus (Messner et al., 2014). Further, given the likelihood of low doses, and the susceptibility

of children, the fractional Poisson was the preferred method where P is the fractional Poisson parameter ($P = 0.72$; Equation (2c)).

2.2.9. Pooled - analyses

To accurately calculate risk estimates several pathogen-specific clinical variables are necessary including attack rate, secondary infection rate and hospitalization rate. Thus, fifty published academic peer-reviewed articles relating to waterborne *STEC*, *Giardia* and norovirus outbreaks and events were reviewed and analyzed with specific variables extracted (Table 4; Table S1). Kolmogorov-Smirnov tests were employed to assess goodness-of-fit between parametric distributions and empirical metadata for development of statistical (input) distributions (Delignetter-Muller and Dutang, 2015) (Table 5) (see Table 6 and Table 7).

3. Results

3.1. Exposure assessment

QMRA simulations predict that 97.5% of adult private well water users who drink from *E. coli* contaminated sources consume 0–10 *E. coli* CFU/day. This translates into a predicted mean daily consumption, during a contamination event, of 6 CFU/day and 4 CFU/day for those served by private wells located in consolidated and unconsolidated aquifers, respectively. The maximum likely rate of ingestion found at very high *E. coli* concentrations (e.g., >70 CFU/day) in concurrence with maximum daily well water consumption (>3500 mL/day) was 80 CFU/day and 50 CFU/day in consolidated and unconsolidated aquifers, respectively. Moreover, QMRA simulations predict that 97.5% of children (<10 years of age) consume 0–8 CFU/day with a predicted mean daily consumption of 3 CFU/day and 2 CFU/day for those served by private wells located in consolidated and unconsolidated aquifers, respectively. The maximum likely rate of ingestion found at very high *E. coli* concentrations (e.g., >70 CFU/day) in concurrence with maximum daily well water consumption (>3500 mL/day) was 58 CFU/day and 39 CFU/day in consolidated and unconsolidated aquifers, respectively.

3.2. Hazard characterization

During a contamination event, both daily and annual probabilities of

Table 5
Daily and annual probability of infection of STEC, *Giardia* and norovirus attributable to private well water in Ontario.

	Daily Probability of Infection (PD*inf*)		Annual Probability of Infection (PA*inf*)	
	Adults	Children	Adults	Children
STEC	4.1×10^{-3} (SD 3.8 × 10^{-2})[a] 3.8×10^{-3} (SD 3.7 × 10^{-2})[b]	5.2×10^{-3} (SD 4.1×10^{-2})[a] 4.4×10^{-3} (SD 3.7×10^{-2})[b]	1.30×10^{-2} (SD 2.5 × 10^{-2})[a] 1.36×10^{-2} (SD 2.4 × 10^{-2})[b]	1.4×10^{-2} (1.9×10^{-2})[a] 1.5×10^{-2} (2.1×10^{-2})[b]
Norovirus	1.5×10^{-2} (SD 9.1 × 10^{-2})[a] 1.1×10^{-2} (SD 8.2 × 10^{-2})[b]	2.3×10^{-2} (SD 1.2×10^{-1})[a] 1.6×10^{-2} (SD 1.0×10^{-1})[b]	7.9×10^{-2} (SD 5.6 × 10^{-2})[a] 8.1×10^{-2} (SD 5.6 × 10^{-2})[b]	3.6×10^{-1} (2.5×10^{-1})[a] 3.7×10^{-1} (2.6×10^{-1})[b]
Giardia	6.2×10^{-3}[a] (SD 5.2 × 10^{-2})[a] 4.9×10^{-3} (SD 4.6 × 10^{-2})[b]	8.0×10^{-3} (SD 5.7×10^{-2})[a] 6.7×10^{-3} (SD 5.3×10^{-2})[b]	2.2×10^{-2} (SD 4.6 × 10^{-2})[a] 2.6×10^{-2} (SD 4.0 × 10^{-2})[b]	2.7×10^{-2} (3.6×10^{-2})[a] 2.9×10^{-2} (4.0×10^{-2})[b]

[a] consolidated.
[b] unconsolidated.

Table 6
Predicted illnesses per annum attributable to STEC, *Giardia* and norovirus from untreated private well water in Ontario for adults and children (95% confidence interval).

	Annual Illnesses		Crude Incidence Rates	
	Adults	Children	Adults	Children
STEC	417 (341–493)[a] 160 (148–290)[b]	49 (35–55)[a] 20 (17–23)[b]	63.4/ 100,000[a] 56.8/ 100,000[b]	75.3/ 100,000[a] 71.8/ 100,000[b]
Giardia	731 (614–858)[a] 311 (270–350)[b]	99 (85–111)[a] 45 (39–50)[b]	111.2/ 100,000[a] 110.4/ 100,000[b]	152.3/ 100,000[a] 134.4/ 100,000[b]
Norovirus	1870 (1717–2020)[a] 728 (684–769)[b]	298 (289–306)[a] 95 (90–122)[b]	284.5/ 100,000[a] 258.4/ 100,000[b]	458.4/ 100,000[a] 341.1/ 100,000[b]
Total Illness	4217	607	449.1/ 100,000	653.6/ 100,000

STEC Public Health Ontario 2020: *132* cases, 0.9 rate per 100,000, 49 hospitalizations, 3 deaths.
Giardia Public Health Ontario 2020: *834* cases, 5.7 rate per 100,000, 4 hospitalizations, 0 deaths.
[a] consolidated.
[b] unconsolidated.

infection, from pathogen contaminated private well water for adults and children were calculated from Equation (2)*a-d* (Table 1). Overall, the highest daily and annual probabilities of infection within both hydrogeological settings and sub-populations (i.e., adults and children under the age of 10) were attributed to norovirus followed by *Giardia* and STEC. Among adults, the predicted mean daily likelihood of symptomatic infection due to a contamination event in contaminated private wells located in consolidated aquifers were 1.5×10^{-2} (0.015; SD = 9.1×10^{-2}), 6.2×10^{-3} (SD = 5.2×10^{-2}) and 4.1×10^{-3} (SD = 3.8×10^{-2}), for norovirus, *Giardia* and STEC, respectively. The mean annual probability of infection ranged from 1.3×10^{-2} (0.013; SD = 2.5×10^{-2}) for STEC to 7.9×10^{-2} (0.079; SD = 5.6×10^{-2}) for norovirus. Among children, the daily mean probabilities of infection were higher with daily risks of 2.3×10^{-2} (0.023; SD = 1.2×10^{-1}), 8.0×10^{-3} (SD = 5.7×10^{-2}) and 5.2×10^{-3} (SD = 4.1×10^{-2}) attributed to norovirus, *Giardia*, and STEC, respectively. Among the <10-year sub-population, mean simulated annual probabilities of infection ranged from 1.4×10^{-2} (0.014; SD = 1.9×10^{-2}) to 3.6×10^{-1} (0.36; SD = 2.5×10^{-1}) for STEC and norovirus, respectively. Likewise, in unconsolidated aquifers, the highest mean daily and annual probability of infection was associated with norovirus, followed by *Giardia* and STEC (Table 1). More specifically, daily probability of infection ranged from 3.8×10^{-3} (SD = 3.7×10^{-2}) to 1.1×10^{-2} (0.011; SD = 8.2×10^{-2}) for adults and from

4.4×10^{-3} (SD = 3.7×10^{-2}) to 1.6×10^{-2} (0.016; SD = 1.0×10^{-1}) for children. Annual probability of infection ranged from 1.36×10^{-2} (0.0136; SD = 2.4×10^{-2}) to 8.1×10^{-2} (0.081; SD = 5.6×10^{-2}) for adults and from 1.5×10^{-2} (0.015; SD = 2.1×10^{-2}) to 3.7×10^{-1} (0.37; SD = 2.6×10^{-1}) among children (Table 2).

3.3. Risk characterization

Province-wide, QMRA simulations predict a total of 4823 (crude incidence rates (CIR) among private well users = 467.8/100,000) cases of illness annually across all three pathogens due to consumption of contaminated private well water. The majority of cases are associated with norovirus for both adults and children, accounting for approximately 62% (2991/4823) of total cases, with 2598 and 393 cases of illness due to primary infections among adults and children, respectively (Table 2). *Giardia* infection accounted for 24.6% (1186/4823) of cases annually, with 1042 and 144 cases of illness among adults and children, respectively. Lastly, STEC infection accounted for 13.4% (646/4823) of total predicted illness with 577 and 69 cases among adults and children. These estimates equate to pooled age-specific crude incidence rates of 449.1/100,000 and 653.6/100,000 for adults and children for all three infections (Table 2).

Contaminated private wells located in consolidated aquifers were associated with more illness per year for all three pathogens in both age groups (i.e., adults and children) compared to contaminated private wells located in unconsolidated aquifers (Table 2). More specifically, for contaminated private wells located in consolidated aquifers QMRA simulations predict 3018 illness per year while unconsolidated aquifers were associated with 1199 illnesses per year in the adult population. In the pediatric simulations (<10 years of age), approximately 447 and 160 illness per year are predicted to occur as the result of contaminated private wells located in consolidated and unconsolidated aquifers, respectively.

Based on meta-analyses of previously reported hospitalization rates, the QMRA simulations predicts a total of 132 hospitalizations (CI: 22–163) per year due to primary infections attributable to contaminated private well water consumption in Ontario. By pathogen, STEC infection accounted for 64.4% (87/135) of all hospitalizations with 59 and 28 visits per year for adults and children, followed by norovirus (25.9%; 35/135) and *Giardia* (9.6%; 13/135) (Table 3). Based on previously reported hemolytic uremic syndrome (HUS) rates, the QMRA simulation predicts a total of 17 cases of HUS per year, with 11 and 6 among adults and children, respectively. Subsequently, approximately two to three HUS-related deaths per year due to exposure to contaminated private well water are predicted to occur in Ontario (Table 3).

3.4. Sensitivity and scenario analysis

Sensitivity analysis was undertaken for all twelve models (three

Table 7
Predicted HUS rates, hospitalization rates and mortality per annum attributable to STEC, *Giardia* and norovirus from untreated private well water in Ontario for adults and children (95% confidence interval).

	HUS cases*		Hospitalization		Mortality	
	Adults	Children	Adults	Children	Adults	Children
STEC	8 (6–11)[a] 3 (2–5)[b]	4 (<1–5)[a] 2 (<1–3)[b]	40 (80–111)[a] 19 (24–61)[b]	20 (2–15)[a] 8 (4–10)[b]	1.87 (0.99–2.6)[a] 0.892 (0.49–1.012)[b]	1 (0.09–0.65)[a] 0 (<1–1)[b]
Giardia	NA	NA	7 (4–12)[a] 3 (<1–6)	2 (<1–3)[a] 1 (0–1)	N/A	N/A
Norovirus	NA	NA	15 (26–60)[a] 5 (9–20)[b]	10 (7–15)[a] 5 (2–5)[b]	N/A	
Total	11	6	89	46	3	1

STEC Public Health Ontario 2020: *132* cases, 0.9 rate per 100,000, 49 hospitalizations, 3 deaths.
Giardia Public Health Ontario 2020: *834* cases, 5.7 rate per 100,000, 4 hospitalizations, 0 deaths.
[a] consolidated.
[b] unconsolidated.

pathogens x two hydrogeological settings [i.e., consolidated, and unconsolidated aquifers] x two age categories [i.e., adults and children <10]) using Spearman's rank order correlation with respect to predicted annual illness on all parameters in the models (Table S2). Findings indicate frequency of contamination (Fc) as the model parameter with the greatest overall impact on all twelve model predictions (correlation coefficient ranging from 0.655 to 0.659), followed by *E. coli* loading

(C_{ecoli}) and pathogen contribution (P1) (Table S2). Consumption volume had the lowest level of model output sensitivity in all models.

The current QMRA model assumes 100% treatment efficacy for individuals who treat their well water with a system that is theoretically effective against microbial contamination. However, given the high levels of uncertainty and variability associated with treatment efficacy (Hynds et al., 2014; Owens et al., 2020) scenario analysis was
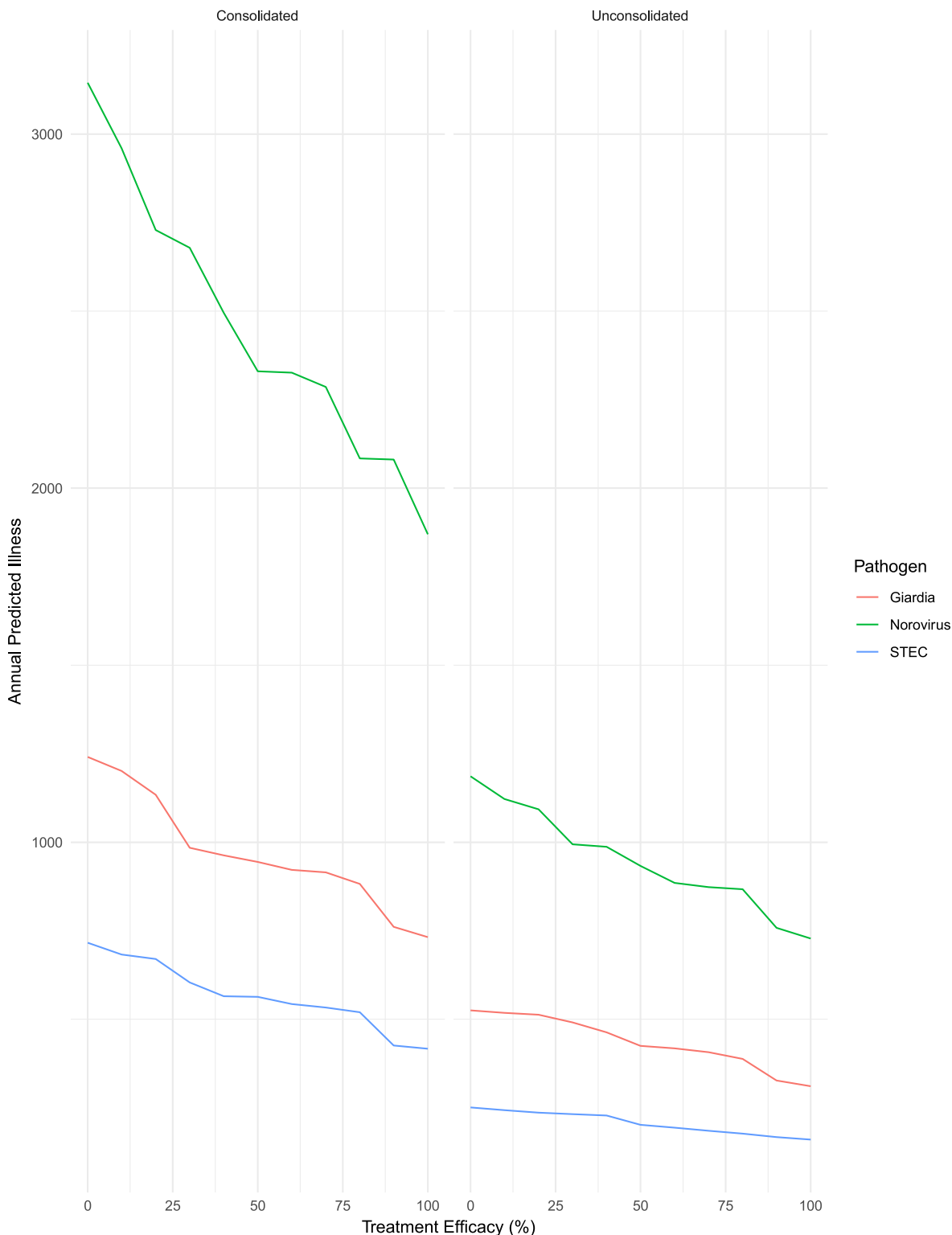

Fig. 2. Results of the scenario analysis of treatment efficacy (%) on number of predicted illnesses per year attributable to norovirus, *Giardia* and Shiga-toxin producing *E. coli* in the non-pediatric QMRA model in consolidated and unconsolidated aquifers.

undertaken to assess the potential of a private well water treatment system completely or partially failing (e.g., range of 0%–100% treatment efficacy), and the corresponding effect on predicted annual illness in all twelve models (Figs. 2 and 3). In the non-pediatric model, results indicate that total annual illness may increase from 4217 to 7064 cases per year for all three pathogens in the case of total treatment failure (Fig. 2). In the pediatric model total annual illness increased from 607 to

926 cases per year for total treatment failure (Fig. 3). Alternatively, with 50% treatment efficacy, total annual illness would increase to 5397 and 738 in the non-pediatric and pediatric models, respectively.

4. Discussion

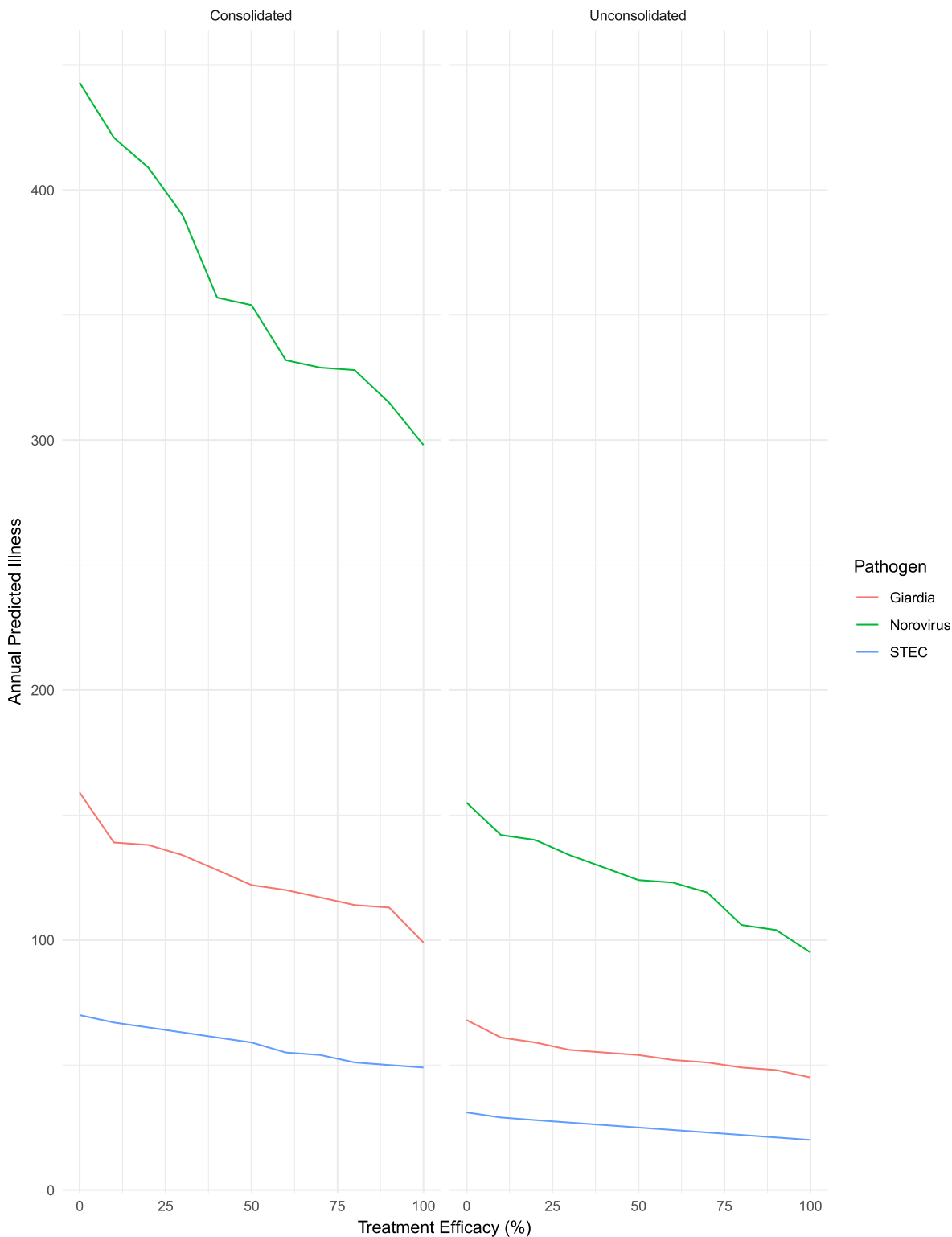An understanding of the spatio-temporal patterns of human health

Fig. 3. Results of the scenario analysis of treatment efficacy (%) on number of predicted illnesses per year attributable to norovirus, *Giardia* and Shiga-toxin producing *E. coli* in the pediatric QMRA model in consolidated and unconsolidated aquifers.

risk associated with private water wells is critical for improving water quality and public health surveillance. Most failures in private drinking water management are identified only after an outbreak has occurred, causing severe illness, and costing both private (e.g., households) and public systems (e.g., local public health authorities, hospitals) millions of dollars (Vicente and Christoffersen, 2006; Chyzheuskaya et al., 2017; Gilpin et al., 2020; Collier et al., 2021). For example, an outbreak of *E. coli* O157:H7 and *Campylobacter jejuni* in the small rural community of Walkerton, Ontario resulted in 2300 people symptomatically ill, seven deaths, and a directly measurable cost estimated at more than CAN$155 million (Majowicz et al., 2005; Meinhardt, 2006). It is important to note that the Walkerton outbreak was in a municipal well water system where cost information was available. Costing data for private well water systems is not available, further highlighting the gaps in knowledge regarding private wells, including in public health management and subsequent interventions. Moreover, the Walkerton outbreak was fundamental in bringing the gaps in rural and remote water quality management to the forefront of public health policies and services, as there is no justification for permitting lower public health standards (e.g., water quality and quantity) for rural and remote residents of Ontario than those residing in Urban areas (Majowicz et al., 2005). Due to the unregulated nature of private water wells and the lack of public health surveillance, QMRA likely represents the most robust planning tool for public health officials in terms of mitigating waterborne illness. The current study employed a hydrogeologically delineated QMRA using a large spatio-temporal groundwater quality dataset (>700,000 samples) and multiple spatially-specific variables (e.g., hydrogeological setting, consumption volumes) to provide an increasingly accurate estimation of the human health burden associated with private water wells.

4.1. Waterborne AGI rates

Developed simulations predict provincial incidence rates of 62.6, 114.9 and 1162 cases/100,000 private well users per year for STEC, *Giardia* and norovirus, respectively. In Ontario in 2019, the incidence rates for STEC and *Giardia* (attributable to all sources*)* were 1.6 and 8.9 cases/100,000 people across the entire population, based on laboratory-confirmed cases notified through the iPHIS monitored by Public Health Ontario (Ontario Agency for Health Protection and Promotion, 2020). Norovirus is not a reportable disease and, therefore, cases are not documented provincially. Extrapolating these estimates to the entire Ontario population, the current simulated waterborne incidence rates would be 569 (62.6/11% [private well water population]) and 1044 (114.9/11% [private well water population]) cases/100,000 per people per year for STEC and *Giardia*, respectively. Consequently, the extrapolations from the current study for STEC and *Giardia* exceed those reported provincially for all transmission sources by more than an order of magnitude; therefore, the health risk attributable to private drinking water is undoubtedly significantly underestimated based on provincial estimates (OAHPP, 2020). Previous studies have attempted to quantify AGI underreporting rates in Ontario and estimated that for each reported case of enteric illness, the number in the community is approximately 313 (Majowicz et al., 2005). Based on these estimates, the provincially reported STEC and *Giardia* rates (attributable to all sources) would be approximately 281.7 and 1784.1 cases per 100, 000 per person per year, thus the current study estimates, and extrapolations are conceivable.

Provincial AGI rates are likely lower than current study estimates for several reasons. Cases of waterborne infection are frequently mild or self-limiting, with cases tending to be sporadic in nature (i.e., one-off infection and/or limited to a single household) due to the inherent nature of the transmission source. Consequently, individuals do not typically seek medical care nor receive a laboratory-confirmed diagnosis which is required to be provincially documented, if indeed the disease is reportable (Hrudey and Hrudey, 2007; Haagsma et al., 2013; Haas et al., 2014). A recent province-wide survey of private well users across

Ontario indicated that 15% (168/1120) of respondents reported that at least one household member had presented with gastrointestinal symptoms in the 12-month period prior to surveying, of which just 13.7% had a clinically confirmed diagnosis (Lavallee et al., 2021a; Lavallee et al., 2022), suggesting an underreporting rate of approximately 86% (145/168). Applying this level of underreporting to the estimated AGI cases found in the current study (89/646 STEC; 162/1297 *Giardia*), simulated waterborne incidence rates that would be identified by the province attributable to private well water would be approximately 0.61 and 1.12 cases/100,000 per people per year for STEC and *Giardia*, respectively. Thus, given these theoretical estimates and comparing with actual reported provincial incidence rates for all sources in 2019 (1.6 and 8.9 cases/100,000 people per year), the hypothesis that the public health risk attributable to private wells is significantly underestimated and undocumented is further supported. Accessing a physician may be difficult for rural residents given the distance to hospital/clinic, wait times for general practitioners and the self-limiting nature of the infection (Shah et al., 2020).

Overall, 135 hospitalizations (87 STEC; 13 *Giardia*), 17 cases of hemolytic uremic syndrome (HUS) and three HUS related deaths per year due to infections attributed to contaminated private well water are predicted based on presented QMRA simulations. Provincially, during 2019, 62 and 14 hospitalizations were reported for STEC and *Giardia*, respectively, with zero STEC related deaths (OAHPP, 2020). Accordingly, current findings again highlight likely significant levels of underreporting and/or misdiagnosis occurring provincially. Previous studies have identified that waterborne illnesses are commonly misdiagnosed by the medical community unless a larger outbreak is happening (Meinhardt 2006; Haagsma et al., 2013). Additionally, there are several clinical and administrative procedures that must occur for an individual infection to be documented, with an etiologic agent and potential source identified, to the local Public Health Authority (Fig. S7). Consequently, given the sporadic nature of waterborne illnesses as they relate to private drinking water wells, and the process of confirming an individual infection, it is likely that some hospitalizations and deaths occurring in the province may be attributed to other etiological agents, co-infections and/or sources (e.g., foodborne, person to person contact). Low levels of provincially reported AGI, hospitalizations, and mortality rates attributable to private water wells may create a false sense of security with respect to waterborne transmission of disease, resulting in decreased household/domestic monitoring and public health measures, leaving private well water users increasingly exposed (Hooks et al., 2019).

Study findings indicate a cumulative annual risk estimate of 4.6×10^{-3} (i.e., illnesses per person per year) from all twelve models. Comparatively, on a per pathogen basis, Murphy et al., (2016), reported the daily probability infection to norovirus, *Giardia* and STEC was 43.9%, 0.053% and 0.0082%, for all of Canada, compared to 1.5% (norovirus), 0.62% (Giardia) and 0.38% (STEC) examined in the current study for Ontario. Conversely, Burch et al., 2021 did not identify norovirus, *Giardia* or STEC in their waterborne QMRA, highlighting the importance of regionally specific risk estimates as contamination source and occurrence differ based on region. The estimates provided in the current study are based on one of the largest available spatiotemporal groundwater quality datasets (702, 861 samples from 239,244 wells) over a seven-year period and contains spatially tailored model inputs (e.g., consumption volume, contamination duration). For example, contamination duration distributions utilized in the current QMRA remove the presumption of there being an equal probability of contamination 365 days per year, which has been employed in previous QMRAs (e.g., Murphy et al., 2016). Thus, the current overall risk assessment represents a more realistic estimate of overall illness associated with private water wells given the large sample used to create model inputs distributions. Finally, the uncertainty associated with all model inputs makes comparisons difficult and results must be interpreted with caution (Haas et al., 2014; Burch et al., 2021). Nonetheless,

the United States Environmental Protection Agency acceptable target (for public water systems) is 1×10^{-4} infections per person per year (Mara et al., 2007), which the overall (4.6×10^{-3}), consolidated aquifer (4.9×10^{-3}) and unconsolidated aquifer (4.4×10^{-3}) risk estimates all exceed by over an order of magnitude.

4.2. Scenario analysis: treatment efficacy

Findings indicate that approximately 34% of individuals who treat their well water, use a treatment system effective against microbial contamination. Scenario analyses indicate that in the (unlikely) event of total treatment failure among this population, total mean annual illness nearly doubled (4217 to 7064 cases per year for all twelve models), highlighting the importance of effective water treatment in reducing infectious health risks attributable to private well water in Ontario. Despite the recognized risk associated with untreated well water, many private well users do not employ a treatment system effective against microbial contaminants, or improperly maintain the systems, rendering them ineffective. (Kreutzwiser et al., 2011; Flanagan et al., 2015; Malecki et al., 2017; Seliga et al., 2022). It is important to note that utilizing a water treatment system is entirely voluntary and can be costly to the well owner, however, a doubling of illness due to failing treatment systems would lead to a significant increase in direct and indirect costs across healthcare systems and households. To reduce the risk associated with private well water to the acceptable target threshold, it is recommended that private well owners are provided with a comprehensive testing program that is reflective of their local groundwater environment and regularly engage in well water stewardship behaviours (e.g., routine testing, well maintenance and efficacious treatment). However, private well owners experiencing frequent and on-going contamination may require a treatment system that is effective against microbial contamination.

4.3. Study limitations

In the current study, and the majority of groundwater related QMRAs, the pathogen contribution input distribution represents a notable limitation, as the authors were unable to directly analyze the *E. coli* to pathogen ratio across the study area and were thus compelled to rely on previously published estimates which may misrepresent the overall human health risk. This is true of most published QMRAs. If possible, future waterborne QMRAs should be accompanied by a study of pathogen ratio sourced from specific or representative study locations to provide an increasingly accurate depiction of pathogen occurrence in private drinking water wells. Further, to model contamination duration, the current study employed distributions based solely on *E. coli* as an indicator of fecal contamination (Latchmore et al., 2022). However, there is variability and uncertainty in these estimates given varying survival times of viruses and protozoa in untreated groundwater due to differences in microbial characteristics, mechanisms, and resistance to treatment; therefore, waterborne AGI estimates produced in this study and similar QMRAs should be interpreted with caution. Finally, given the age demographic of the province-wide survey and limited Census data, it was not possible to separately examine the human health impact private water wells have on the elderly (>65-year-old), immunocompromised and pregnant women. It is speculated that the reported hospitalizations, HUS rates, and mortality rates from the current study are likely acquired by those of vulnerable sub-populations, but without age-specific data it is difficult to draw definitive conclusions. Future QMRAs should seek to acquire age-specific data on vulnerable sub-populations within the study location.

4.4. Recommendations

Sensitivity analysis of input variables found that all twelve models display similar patterns. The input variables of most importance were contamination frequency (r = 0.655 to 0.659) and *E. coli* loading (r = 0.357 to 0.420). Hynds et al. (2014b) previously identified the same variables to be most significant for a QMRA model of private well water in Ireland. Therefore, the recommendation put forth by Hynds et al., (2014) of improved groundwater protection is echoed here; while the frequency and concentration of private well water contamination varies across the globe, the primary mechanisms driving contamination are relatively analogous. Public health interventions should focus on improving well water stewardship behaviours (e.g., well maintenance and construction, treatment and testing) to mitigate the human health risk associated with localized contamination pathways. A previous study of private well owners in Ontario has identified three statistically distinct sub-groups (i.e., clusters) of private well owners based on well water stewardship, and exposure via well water consumption (Lavallee et al., 2022). Future work is ongoing to introduce these "socio-cognitive clusters" to create distinct "well user type" risk profiles to better understand how and to what extent human behaviour impacts well water susceptibility and human infection.

5. Conclusion

QMRA is a powerful mathematical tool for estimating the risk of exposure to, and subsequent infection from, waterborne pathogens in contaminated private well water supplies. Based on QMRA simulations, consumption of contaminated private well water in Ontario is responsible for approximately 4823 AGI cases annually. By pathogen, waterborne AGI is attributable to norovirus (62%; 2991/4823), *Giardia* (24.6%; 1186/4823) and STEC (13.4%; 646/4823). Further, while public health professionals can potentially quantify the health risk associated with private well water, the responsibility of mitigating the risk rests with well owners, even in the presence of evidence-based public health guidance. Thus, private well owners must be provided with the appropriate knowledge of their systems, the risk they pose and the tools to strengthen their own behaviours and stewardship actions. However, a one-size-fits all approach will not suffice, due to varying levels of knowledge, attitudes, and risk perception among private well owners. Therefore, the authors consider that levels of risk should be identified for subsets of private well owners themselves, as the potential health threat cannot be mitigated unless private well user socio-cognitive profile is identified and modified. Further, study findings highlight the likely significant underreporting of waterborne AGI rates at the provincial level which may skew public health interventions and programs that are effective in monitoring and minimizing the human health risk associated with private well water.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijheh.2022.114077.

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