Assessment of source water pathogen contamination

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ABSTRACT

During the last decade, the source to tap risk-based approach to pathogens in drinking water has been largely promoted. This paper addresses the issue of source water pathogen contamination, which is the first step of quantitative microbial risk assessment. It is focused on a selection of pathogens considered to be a major risk to human health. Source water quality is highly variable and understanding the reasons for this variability is important as it will influence the requirements for treatment, treatment efficiency and the resulting health risk associated with the finished water.

A framework for source water microbial quality assessment based on catchment surveys and monitoring programmes was set and tested on ten water sources. The monitoring programmes included faecal indicators and pathogens, during both baseline and hazardous event conditions. Concentrations varied greatly within and between systems. Faecal indicators were shown to be poor surrogates for pathogen presence and concentrations. There was no recurring evidence that the pathogens correlated together and links between microbial parameters appeared to be very site specific. Such variability between systems shows the importance of running local monitoring programs for use in risk assessment. Finally, pathogen detection methods are not yet optimal due to their sensitivity and to the lack of knowledge on viability and infectivity of pathogens. A great effort needs to be made in the future to ensure better quality data as this may have large implications in the statistical risk assessment calculations.

Key words | catchment to tap, *Cryptosporidium*, drinking water, enterovirus, *Giardia*, norovirus, risk assessment, source water, variability

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NOMENCLATURE

CTS	Catchment to Tap System
QMRA	Quantitative Microbiological Risk Assessment
SD	Standard Deviation
WWTP	Waste Water Treatment Plant

INTRODUCTION

Standards for drinking water microbial quality rely on faecal indicator bacteria (*E. coli*, Total Coliforms, Enterococci) in drinking water and assume that, if faecal indicator bacteria are not present, the water is microbiologically safe. This has been increasingly challenged over the years. Several authors have shown that outbreaks of waterborne disease have occurred despite the absence of faecal indicators in source water and/or treated water (Barrell *et al.* 2000). Furthermore, many publications report the limited correlation between the presence and concentration of faecal indicators and the presence and concentration of waterborne pathogens. They demonstrate in particular that faecal indicator bacteria are poor surrogates for protozoa and viral pathogens (Petrilli *et al.* 1974; Berg & Metcalfe 1978; Melnick & Gerba 1982; Payment *et al.* 1985; Rose *et al.* 1986; Barrell *et al.* 2000; Griffin *et al.* 2001; Nwachuku *et al.* 2002). Finally, assuming safety from testing a small volume of treated water is not satisfactory anymore.

doi: 10.2166/wh.2007.133

The use of a risk-based approach to pathogens in drinking water has been supported by many researchers and institutions to ensure safe drinking water during the last decade (WHO/IWA, to be published). WHO promotes the use of a comprehensive risk assessment and risk management approach that encompasses all steps in water supply from catchment to tap. In the recently revised WHO *Guidelines for Drinking Water Quality* (WHO 2004), such approaches are part of the Water Safety Plans.

This paper addresses the issue of source water pathogen contamination, which is the first step in quantitative microbial risk assessment from catchment to tap. Pathogens considered to be of high risk to human health and potentially present in source water used for drinking water supply were selected:

- Protozoa: *Cryptosporidium* and *Giardia*
- Bacteria: Campylobacter and *E. coli* 0157:H7
- Viruses: enterovirus and norovirus

Current QMRA techniques are reliant on the understanding of the overall tendencies and variations in microbial quality of the source water (Teunis & Havelaar 1999). Understanding the reasons for variations in source water quality is important, as it will influence the requirements for treatment, treatment efficiency and the resulting health risk associated with the finished water. Possible variations are due to the specificities of the catchment, seasons, peak events, etc. It is important to quantify baseline and peak contamination. Outbreaks of disease through drinking water have indeed occurred as a result of hazardous events, such as heavy rainfall, which lead to peak pathogen loads in source water (Stelzer & Jacob 1991; Atherholt *et al.* 1998; O'Connor 2002; Signor *et al.* 2005).

The objectives of this paper are to present a validated framework for the evaluation of microbiological source water quality. After a short presentation on pathogens in source water, the methodology is introduced along with some specific examples on peak events and monitoring strategies. It is based on a catchment survey, which purpose is to develop an overview of the catchment and to understand the contributing factors to water contamination, and pathogen monitoring in source water. Finally, full results and data analysis are discussed.

BACKGROUND ON PATHOGENS IN SOURCE WATER

A full review on pathogens in water sources is available from the MicroRisk website (Pond *et al.* 2004).

Source water is vulnerable to contamination from many origins. Humans and animals are all sources of faecal contamination. It has been shown that many rivers in Europe are significantly contaminated with microbes arising from municipal wastewater and/or livestock (EEA 2003). Furthermore, source water, and particularly surface water, is often used for purposes such as irrigation, recreation and transport, which may also affect water quality. Groundwater contamination may be induced by different practices in the management of domestic wastewater and livestock manure.

Wastewater treatment plants are an obvious high risk source of pathogens both in terms of number and strain of pathogens. During periods of high rainfall or plant failure, WWTP may release significant amounts of poorly treated effluent. Moreover, pathogens may be dispersed in the environment through the use of sewage sludge as fertilizer. Agricultural practices are an important source of contamination especially from *Cryptosporidium* oocysts, *Giardia* cysts, and Campylobacter (Lack 1999; Monis & Thompson 2003; Carey *et al.* 2004). As well as direct runoff into surface water, animal waste is often collected in impoundments from which effluent may infiltrate groundwater. Other sources of faecal contamination that may be a threat to water sources are stormwater discharges, combined sewer overflows (CSOs), accumulation of pathogens in sediment and wild animals.

The ability of pathogens to survive in surface water is variable. In general, survival is extended when water temperature is low. Other factors that influence survival include sunlight intensity and the presence of aquatic microorganisms that may use the pathogens as food source or cause pathogen disintegration. Adsorption to particles facilitates survival. A summary of the major influencing factors on pathogen survival is listed in Table 1. Table 2 outlines the disappearance rate and time for a 50% reduction in concentration of pathogens in surface water using examples of published data.

In groundwater, disappearance rates are lower. Pathogens may be removed during soil transfer by adsorption and inactivation. Inactivation is influenced by many factors such as soil temperature, moisture, pH, microflora and organic carbon content. International literature reveals that viruses

Table 1 | Major factors influencing pathogen inactivation in surface water (Pond *et al.* 2004)

	Solar radiation	Temperature	Salinity	Predation
Cryptosporidium	Medium	High	Medium	Low
Giardia	Medium	High	Medium	Low
Campylobacter	High	High	Medium	Low
E. coli 0157:H7	High	High (none)	Medium	Low
Enterovirus	High	High	Medium	Low
Norovirus	Likely High	Likely High	Unknown – likely Medium	Low

survive longer in groundwater than faecal bacteria. No data on the survival of protozoa are available yet, but it may be assumed that these pathogens survive longer than viruses (Medema *et al.* 2003).

Many studies have been undertaken to investigate the occurrence of Campylobacter, *Cryptosporidium* and *Giardia* in source water (see Table 3). Less work has concerned the levels of viruses and *E. coli* 0157:H7. In all cases presented hereafter, it should be kept in mind that the sampling and testing methods varied. This may affect pathogen counts and comparability of data.

METHODOLOGY: CATCHMENT SURVEY AND MONITORING PROGRAMME

Assessment of source water quality is based on a proper understanding of the catchment and on a relevant monitoring programme.

The purpose of the catchment survey is to develop an overview of the catchment and to understand the contributing factors to water contamination. It should include details on the catchment (size, water intake, water uses, etc.) and its hydrology, hydrogeology and climate, plus a description of the potential sources of faecal contamination. Raw water quality is influenced by both point sources (example: WWTP) and non-point sources (urban and agricultural runoff). The list should be as exhaustive as possible. A full outline for catchment survey is proposed in (WHO/IWA, to be published). Table 4 provides basic information on the 12 systems assessed in the MicroRisk project.

Table 2 | Disappearance of selected pathogens in surface water (Medema *et al.* 2003)

	Disappearance rate (per d)	Time for 50% reduction of concentration (d)
Cryptosporidium	5.7×10^{-3}–4.6×10^{-2}	15–150
Giardia	0.023–0.23	3–30
Enterovirus	0.01–0.2	3–70

Risk is generally higher during hazardous/peak events rather than in baseline conditions. It is therefore essential to consider these events in the risk assessment process. The following conditions may cause great variations in source water quality: precipitation, thaw/snowmelt, low water during dry periods, upstream incidents (failures, waste water discharges), cleaning of the river course, farming practices, presence of wildlife, etc. Other types of event may be identified locally. Heavy rainfall is the most common cause of peak contamination events. It is associated with high surface runoff and discharge of untreated wastewater, which may lead to high pathogen loads in source water.

Hazardous events are site-specific and should be identified for each system. This can be done by performing an analysis of historical data, which gives information on event type, intensity, frequency, duration, seasonality, etc. This analysis is also helpful to define an appropriate peak event sampling strategy. Indeed, sampling peak events is difficult and should be well thought of before starting sampling programmes.

The monitoring programme needs to be designed specifically for each system, especially for peak event

Table 3 | International review on pathogen concentrations in water bodies

Pathogen	Water body	Concentrations	Country	Reference
Cryptosporidium	Surface water	0.006–2.5 oocysts/L	UK	Badenoch (1990)
	Surface water	0–252.7 oocysts/L	11 countries	Smith & Grimason (2003)
	River water	4.1–12 oocysts/L	The Netherlands	Medema *et al.* (1996)
	Spring fed lake	0.24 oocysts/L	Ireland	Garvey *et al.* (2002)
	Surface water	3.8–21 oocysts/L	Honduras	Solo-Gabriele *et al.* (1998)
	River	<5 oocysts/L	France	Rouquet *et al.* (2000)
Giardia	River	2.3 cysts/L	Canada	Ong *et al.* (1996)
	Surface water	5 cysts/L	8 countries	Smith & Grimason (2003)
	River	10–100/L	The Netherlands	Medema *et al.* (1996)
	Streams	0.1–5.2 cysts/L	USA	Ongerth *et al.* (1989)
	Surface water	0.02 cysts/L	Russian region	Egorov *et al.* (2002)
Campylobacter	Surface water	109,000 MPN/L	Germany	Feuerpfiel *et al.* (1997)
	River water	100–360/L	UK	Bolton *et al.* (1982)
	River	<100–2,400 CFU/L		Stelzer *et al.* (1989)
	River	<2–93 MPN/L	Australia	Ashbolt (2004)
	River	<1.2–110 MPN/L	Australia	Savill *et al.* (2001)
E. coli 0157	River and lake	>2000/L	Germany	Schindler (2001)
Enterovirus	Drinking WTT	0.0006 MPN/L	USA	Payment *et al.* (1985)
	River	0.3–4/L up to 13/L	The Netherlands	Theunissen *et al.* (1998)
	Dune filtrate	<0.003–13/L	The Netherlands	Theunissen *et al.* (1998)
	River	0.66–29/L	Worldwide	Gerba *et al.* (1996)
	Surface water	0.0033–0.46 PFU/L	Finland	Horman *et al.* (2004)

contamination assessment (see examples in the following section). MicroRisk recommendations are:

- Baseline contamination – full year of monthly samples
- Peak contamination – at least two full events

Monitoring included pathogens (*Cryptosporidium*, *Giardia*, Campylobacter, *E. coli* 0157:H7, enterovirus and norovirus), faecal indicators (*E. coli*, Clostridia, Total Coliforms, Enterococci) and physico-chemical characteristics (turbidity, conductivity, temperature, pH). When possible, water flow was also evaluated in order to distinguish baseline from rain event contamination.

Standard methods of sampling, sample processing and analysis were used to ensure comparable results. Even then,

Table 4 | MicroRisk catchment to tap systems

CTS	Country	Source water	Protection	Climate	Catchment km²
1	United Kingdom	River	No	Humid oceanic	12,917
2	The Netherlands	River	No	Humid oceanic	198,735
3	France	River	No	Humid oceanic	10,050
4	France	River	No	Mediterranean	522
5	Sweden	River with controlled input	No	Temperate maritime	50,180
6	Sweden	Reservoir	No		50,180
7	Germany	Groundwater & river bank filtration	No	Humid oceanic	145
8	Australia	Reservoir	No	Mediterranean	140
9	The Netherlands	Reservoir	No	Humid oceanic	198,735
10	France	Reservoir	No	Humid oceanic	30
11	Germany	Reservoir	Yes	Humid oceanic	300
12	France	Aquifer	Yes	Humid oceanic	100

there remain limitations and sources of uncertainty due to the sensitivity of the methods, particularly for viruses and protozoa, and to the lack of knowledge on the viability and infectivity of *Cryptosporidium* oocysts, *Giardia* cysts and viruses. Quality control data were only provided for *Cryptosporidium* and *Giardia*. The recovery rates turned out to be quite low (<50%). In addition, conditions of high turbidity seemed to interfere with the analysis, making it more difficult to assess peak concentrations.

FOCUS ON DIFFERENT EXAMPLES

Surface water (CTS 3)

Historical river flow and turbidity data was investigated to identify local hydrological events and design an appropriate sampling programme. Peak rain events were described from the analysis of sorted river flow and turbidity data (Figure 1). From the shape of the turbidity curves, 25% of the rain events appeared significant. The following peak event definition was drawn: river flow $>150\,m^3/s$ and turbidity $>$ 12 NTU.

The peak event sampling programme was based on the turbidity threshold because river flow was not available in real time. However, validation as a peak event sample required respect of both thresholds.

The sampling phase (January 2004–May 2005) was very poor in peak events. Figure 2 shows two proper periods only (January and April 2004) and only one sample was collected on 22 January 2004. This sample was loaded in *Cryptosporidium* and *Giardia* but not in *E. coli* 0157:H7 (Table 5).

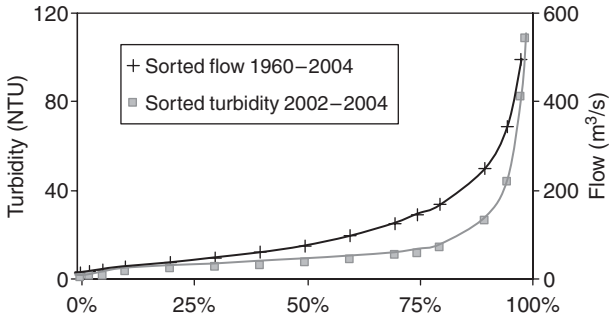

Figure 1 | Sorted river flow and turbidity data for CTS 3.

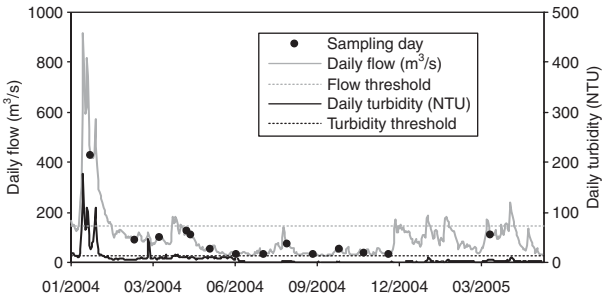

Figure 2 | River flow and turbidity conditions for the full sampling period in CTS 3.

River bank filtration (CTS 7)

Source water is river bank filtrate mixed with groundwater. Peak contamination events come from fast and high rising water levels in the connected river. These events cause faster groundwater flow in the direction of the abstraction wells, thus reducing bank filtration efficiency, and they reduce the thickness of the vadose zone, which may contribute to groundwater contamination.

Peak events were identified from the analysis of river water level variations within 5 d over 50 years (Figure 3). Increases of water level of at least 3 m within 5 d occurred with an average of 3.9 d per year (1.1%). This 3-m-within-5-d threshold was used to start peak contamination sampling.

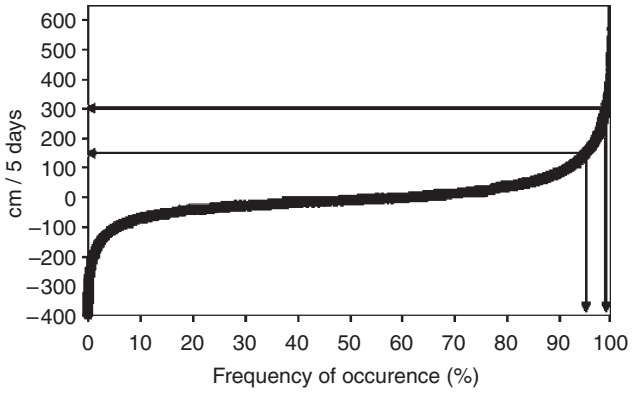

Figure 3 | Changes of river water level within 5 d in CTS 7 (1953–2003).

Contamination monitoring in CTS 7 showed that peak events yield peak contamination in *Cryptosporidium* and faecal indicators in the river. However, river bank filtrate samples only showed higher faecal indicator concentrations; pathogens remained undetected (see examples in Figure 4). Nevertheless, microbiological risk can be expected with fast and high rising water levels in the connected river.

Table 5 | Summary of faecal indicators and pathogen concentrations in surface water

	Baseline contamination	Rain event contamination
Faecal indicators		
E. coli	10^2–10^4 MPN/L	10^3–10^4 MPN/L and up to 50,000 MPN/L
Clostridia	≈3,000 n/L and up to 17,500 n/L	5,000–6,000 n/L
Enterococci	10^2–10^3 n/L	$>10^3$ n/L
Total Coliforms	10^3–10^5 MPN/L	30,000–130,000 MPN/L
Pathogens		
Cryptosporidium	0.05–0.5 n/L and up to 4.6 n/L	Concentrations not clearly higher
Giardia	0.01–1 n/L and over 40 n/L in one case	Concentrations not clearly higher
Campylobacter	0–100 MPN/L but up to 15,000 in one case	Concentrations not clearly higher
E. coli 0157:H7	10–100 CFU/L and up to >1,000 CFU/L	Concentrations not clearly higher
Enterovirus	Rarely detected	≈300 n/L in one CTS
Norovirus	Not detected (one CTS tested)	≈150 n/L in one CTS

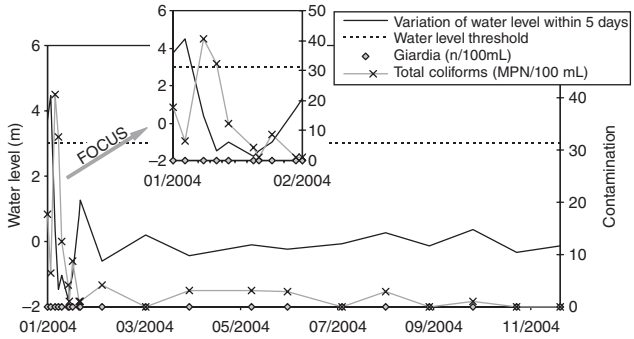

Figure 4 | Peak event and chronic contamination monitoring in CTS 7 (bank filtrate).

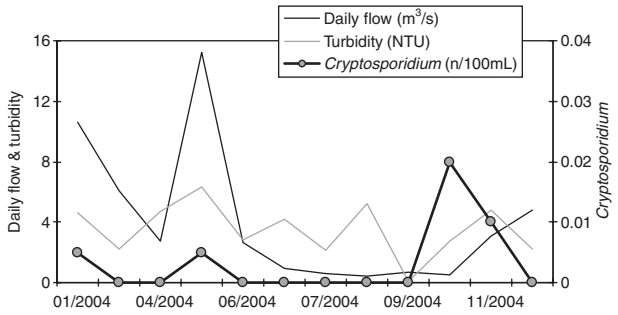

Figure 5 | Contamination in *Cryptosporidium* in CTS 4.

Mediterranean context (CTS 4)

CTS 4 has a Mediterranean climate. In summer, the combination of low river water and high volumes of WWTP effluents due to the tourist season does not favour dilution of contamination, which may yield peak events.

The river microbiological quality was monitored monthly for a full year but summer months did not show higher contamination. See example for Cryptosporidium in Figure 5. This shows that the contamination risk is not necessarily higher during summer months in this context.

RESULTS AND DISCUSSION

Summaries of faecal indicators and pathogen concentrations are given in Table 5 for surface water, pathogens not being present in groundwater. Pathogen concentration mean and standard deviation were determined for each CTS as a first approach of pathogen variability, as well as minimum and maximum values (Table 6). These statistics were calculated from the positive samples only. Quality control data are not consistent for all systems and pathogens and analytical recovery is not considered. Raw data are presented directly and pathogen contamination may be underestimated.

Pathogen concentrations varied greatly within and between systems. Pathogens were not detected in the groundwater sources. In surface water, *Cryptosporidium* and *Giardia* were often present but in low concentrations (*Cryptosporidium*: 0.01–0.5 n/L and up to 4.6 n/L; *Giardia*: 0.01–1 n/L and over 40 n/L in one case). Concentrations were not clearly higher during rain events. Campylobacter was found in 4 out of 9 tested systems. Rain event concentrations were not really higher either. An extreme Campylobacter value was detected (15,000 MPN/L in CTS 2) but not linked to any event. *E. coli* 0157:H7 was more commonly encountered but usually at low concentrations, even though CTS 3, CTS 4 and CTS 10 showed high concentrations, particularly during rain events. Enteroviruses concentrations were either very low or undetectable except for CTS 5 in rainy conditions (up to 370 n/L). Noroviruses were investigated in CTS 5 only and detected in rainy conditions (up to 167 n/L). CTS 9 and CTS 10 appeared as the most contaminated systems. Both of them are highly vulnerable because of onsite sanitation, cattle and sheep farming and manure spreading.

Reservoir water quality (CTS 8, 9, 10 and 11) looks often better than river water quality (CTS 1, 2, 3, 4 and 5). Reservoir concentrations were in the low range of Table 5 concentrations. *Giardia* is an exception, with the highest concentrations encountered in a reservoir during baseline conditions (CTS 9). In rain event conditions, reservoir and river water microbial quality were generally in the same range of values.

Rain events induced higher faecal indicator concentrations but results are not as clear for pathogens. This may be due to a number of reasons. Firstly, hydrological events were scarce during the sampling period. Fewer rain event samples were collected than baseline samples and the rain event population may not be fully representative. Secondly, turbidity is usually higher during rain events. This may affect the performance of analytical methods and concentrations may have been underestimated. Another possible reason is the dilution effect of rain events on concentrations.

Correlations between faecal indicators, pathogens and turbidity were investigated. They are illustrated by the

Table 6 | Baseline and rainfall pathogen contamination

Parameter	Event	Unit	Samples	Positives	Mean	SD	Min	Max
CTS 1	UK		River				Catchment = 12,917 km^2	
Cryptosporidium	Baseline	n/L	11	2	0.35	0.05	0.3	0.4
Cryptosporidium	Rain	n/L	1	1	0.4	–	–	–
Giardia	Baseline	n/L	11	0	–	–	–	–
Giardia	Rain	n/L	1	0	–	–	–	–
Campylobacter	Baseline	CFU/L	11	0	–	–	–	–
Campylobacter	Rain	CFU/L	1	0	–	–	–	–
E. coli O157:H7	Baseline	CFU/L	11	0	–	–	–	–
E. coli O157:H7	Rain	CFU/L	1	0	–	–	–	–
Enterovirus	Baseline	PFU/L	11	4	1.55	1.25	0.4	3.4
Enterovirus	Rain	PFU/L	1	0	–	–	–	–
CTS 2	The Netherlands		River				Catchment = 198,735 km^2	
Cryptosporidium	Baseline	n/L	11	3	0.005	0.005	0.001	0.012
Giardia	Baseline	n/L	11	3	0.02	0.009	0.003	0.023
Campylobacter	Baseline	MPN/L	69	57	1,703	2,701	0.4	15,000
Enterovirus	Baseline	PFU/L	3	2	0.015	0.009	0.005	0.024
CTS 3	France		River				Catchment = 10,050 km^2	
Cryptosporidium	Baseline	n/L	11	5	0.09	0.06	0.05	0.2
Cryptosporidium	Rain	n/L	1	1	0.5	–	–	–
Giardia	Baseline	n/L	11	10	1.16	1.33	0.05	4.7
Giardia	Rain	n/L	1	1	4.5	–	–	–
Campylobacter	Baseline	n/L	11	0	–	–	–	–
E. coli O157:H7	Baseline	CFU/L	11	10	10–100 (9)	–	>1,000 (1)	–
E. coli O157:H7	Rain	CFU/L	1	1	>1,000	–	–	–
Enterovirus	Baseline	PFU/L	11	0	–	–	–	–
Enterovirus	Rain	PFU/L	1	0	–	–	–	–
CTS 4	France		River				Catchment = 522 km^2	
Cryptosporidium	Baseline	n/L	12	3	0.12	0.06	0.05	0.2
Giardia	Baseline	n/L	12	11	0.36	0.22	0.05	0.75
Campylobacter	Baseline	n/L	11	0	–	–	–	–
E. coli O157:H7	Baseline	CFU/L	12	8	10–100 (3)	–	100–1,000 (2)	>1,000 (3)
Enterovirus	Baseline	FPU/L	12	0	–	–	–	–
CTS 5	Sweden		River with controlled input				Catchment = 50,180 km^2	
Cryptosporidium	Baseline	n/L	13	3	0.09	0.008	0.08	0.1
Cryptosporidium	Rain	n/L	10	5	0.16	0.05	0.1	0.2
Giardia	Baseline	n/L	12	2	0.09	0.07	0.016	0.16
Giardia	Rain	n/L	10	4	0.18	0.08	0.1	0.3

Table 6 | (*continued*)

Parameter	Event	Unit	Samples	Positives	Mean	SD	Min	Max
Campylobacter	Baseline	n/L	13	1	10	–	–	–
Campylobacter	Rain	n/L	10	0	–	–	–	–
E. coli O157:H7	Baseline	n/L	13	0	–	–	–	–
E. coli O157:H7	Rain	n/L	10	0	–	–	–	–
Enterovirus	Baseline	n/L	12	0	–	–	–	–
Enterovirus	Rain	n/L	7	3	330	57	250	370
Norovirus	Baseline	n/L	12	0	–	–	–	–
Norovirus	Rain	n/L	7	3	148	26	111	167
CTS 7	Germany	Groundwater and river bank filtration					Catchment = 145 km^2	
Cryptosporidium	Baseline	n/L	11	0	–	–	–	–
Cryptosporidium	Rain	n/L	10	0	–	–	–	–
Giardia	Baseline	n/L	11	0	–	–	–	–
Giardia	Rain	n/L	10	0	–	–	–	–
CTS 8	Australia		Reservoir				Catchment = 140 km^2	
Cryptosporidium	Baseline	n/L	51	2	0.1	0	0.1	0.1
Giardia	Baseline	n/L	51	1	0.1	–	–	–
CTS 9	The Netherlands		Aquifer				Catchment = 198,735 km^2	
Cryptosporidium	Baseline	n/L	25	25	0.33	0.92	0.01	4.56
Giardia	Baseline	n/L	25	25	1.34*	2.91*	0.01	41.3
Campylobacter	Baseline	n/L	37	32	72.3	117	0.4	500
Enterovirus	Baseline	PFU/L	12	0	–	–	–	–
CTS 10	France		Reservoir				Catchment = 30 km^2	
Cryptosporidium	Baseline	n/L	9	5	0.54	0.40	0.1	1
Cryptosporidium	Rain	n/L	4	1	1.9	–	–	–
Giardia	Baseline	n/L	9	6	0.73	1.03	0.1	3
Giardia	Rain	n/L	4	3	0.37	0.17	0.2	0.6
Campylobacter	Baseline	MPN/L	9	2	10–100 (2)	–	–	–
Campylobacter	Rain	MPN/L	4	1	10–100	–	–	–
E. coli O157:H7	Baseline	MPN/L	9	3	10–100 (3)	–	–	–
E. coli O157:H7	Rain	MPN/L	4	4	10–100 (2)	–	>1,000 (2)	–
Enterovirus	Baseline	PFU/L	9	0	–	–	–	–
Enterovirus	Rain	PFU/L	2	0	–	–	–	–
CTS 11	Germany		Reservoir				Catchment = 300 km^2	
Cryptosporidium	Baseline	n/L	11	11	0.039	0.014	0.019	0.06
Cryptosporidium	Rain	n/L	10	10	0.053	0.030	0.031	0.132
Giardia	Baseline	n/L	11	1	0.004	–	–	–

Table 6 | (*continued*)

Parameter	Event	Unit	Samples	Positives	Mean	SD	Min	Max
Giardia	Rain	n/L	10	2	0.006	0.002	0.004	0.008
Campylobacter	Baseline	CFU/L	9	0	–	–	–	–
CTS 12	France		Aquifer			Catchment = 100 km^2		
Cryptosporidium	Baseline	n/L	10	0	–	–	–	–
Giardia	Baseline	n/L	10	0	–	–	–	–
Campylobacter	Baseline	MPN/L	10	0	–	–	–	–
E. coli O157:H7	Baseline	MPN/L	10	0	–	–	–	–
Enterovirus	Baseline	PFU/L	10	0	–	–	–	–

*The maximum value of 41.3 is not used in the calculation of the mean and the standard deviation.

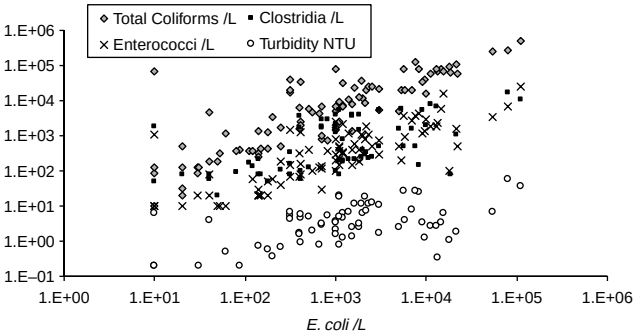

Figure 6 | Faecal indicators concentrations and turbidity versus *E. coli* for all.

following scatter plots. Figure 6 represents Total Coliforms, Clostridia, Enterococci concentrations and turbidity as a function of *E. coli* concentrations for the complete dataset. It shows that faecal indicators are generally well correlated together and, to a lesser extent, with turbidity.

When it comes to faecal indicator and pathogen correlations, results are not as clear. In CTS 11 (Figure 7), *E. coli* and Total Coliforms concentrations vary together but *Cryptosporidium* concentrations remain in a small range of values independent of faecal indicator increase. The same is observed for rain event samples. They all induce higher *E. coli* concentrations (>10 MPNL/100 mL) and Total Coliforms concentrations (>35 MPNL/100 mL) but *Cryptosporidium* concentrations seem to be independent of such conditions.

Figure 8 shows another example of *Cryptosporidium* versus *E. coli* concentrations (CTS 5). Although these do not appear to be correlated in most cases, the greater rain event yielded higher concentrations of both *E. coli* and *Cryptosporidium*.

Pathogen correlation is different in each case and generalization is impossible. There is no recurring evidence

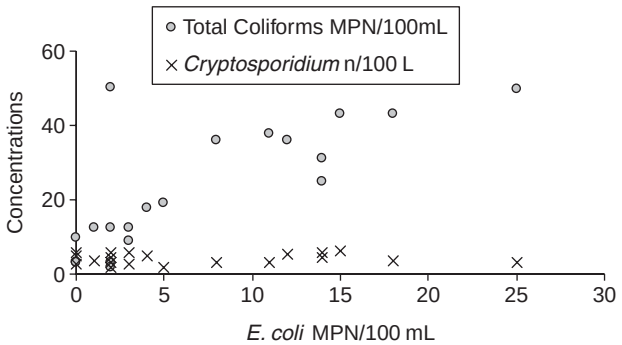

Figure 7 | Total Coliforms and *Cryptosporidium* versus *E. coli* concentrations in CTS 11.

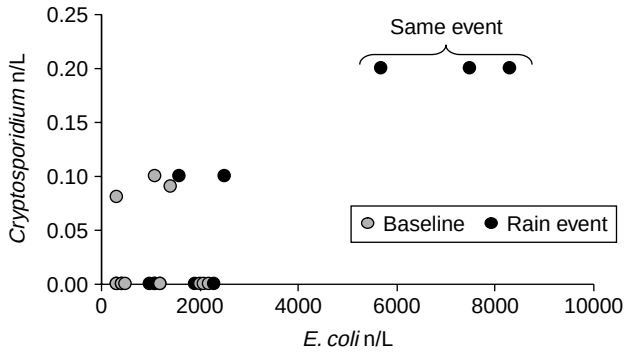

Figure 8 | *Cryptosporidium* versus *E. coli* concentrations in CTS 5.

of pathogens correlated together, correlated with faecal indicators and/or correlated with turbidity in this dataset. Faecal indicators and turbidity appear to be poor surrogates for pathogen presence and concentrations, as reported in the international literature. Each system has its own behaviour, thus showing that source water quality and links between microbial parameters are site specific.

CONCLUSION

A framework based on a catchment survey and monitoring programmes in baseline and peak conditions was set to assess source water microbial quality. This methodology was applied to ten water sources. As a first approach to pathogen variability, pathogen concentration mean and standard deviation were determined for each system in baseline and rainy conditions. Concentrations varied greatly within and between systems. Groundwater concentrations were either very low and/or below detection limits and surface reservoir water quality was often better than river water quality. Hydrological peak events induced higher faecal indicators concentrations in surface water while groundwater seemed unaffected. Results were not as clear for pathogens. Three reasons are suggested: non-representative rain event sampling, performance of analytical methods hindered by high turbidity and the effect of dilution on concentrations.

In most cases, faecal indicators are well correlated among them and with turbidity. However, there is no recurring evidence of pathogen correlated together, correlated with faecal indicators and/or turbidity. Faecal indicators and turbidity appear to be poor surrogates for pathogen presence and concentrations, as reported in the international literature. Such variability between systems shows the importance of running local monitoring programmes for use in risk assessment.

At present, pathogen detection methods are not optimal. There are limitations and sources of uncertainty due to the sensitivity of analytical techniques and to the lack of knowledge about the viability and infectivity of cysts and viruses. A great effort needs to be made to ensure better quality data as this may have big implications in risk assessment.

ACKNOWLEDGEMENTS

This study has been performed as part of the MicroRisk project that is co-funded by the European Commission under the Fifth Framework Programme, Theme 4: "Energy, environment and sustainable development" (contract EVK1-CT-2002-00123). Its objective was to define and evaluate a scientific basis for managing drinking water safety from source to tap. We would like to thank all our partners who performed this source water quality assessment step and provided their data. See http://www.microrisk.com/ for further information.

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