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Review

A review on microbial contaminants in stormwater runoff and outfalls: Potential health risks and mitigation strategies

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HIGHLIGHTS

- Stormwater has been considered as an alternative water source.
- Microbial contamination hinders stormwater reuse.
- WSUD is effective in removing pathogens but requires more validation.
- QMRA analysis can facilitate decision making and risk management efforts.

GRAPHICAL ABSTRACT



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ABSTRACT

Demands on global water supplies are increasing in response to the need to provide more food, water, and energy for a rapidly growing population. These water stressors are exacerbated by climate change, as well as the growth and urbanisation of industry and commerce. Consequently, urban water authorities around the globe are exploring alternative water sources to meet ever-increasing demands. These alternative sources are primarily treated sewage, stormwater, and groundwater. Stormwater including roof-harvested rainwater has been considered as an alternative water source for both potable and non-potable uses. One of the most significant issues concerning alternative water reuse is the public health risk associated with chemical and microbial contaminants. Several studies to date have quantified fecal indicators and pathogens in stormwater. Microbial source tracking (MST) approaches have also been used to determine the sources of fecal contamination in stormwater and receiving waters. This review paper summarizes occurrence and concentrations of fecal indicators, pathogens, and MST marker genes in urban stormwater. A section of the review highlights the removal of fecal indicators and pathogens through water sensitive urban design (WSUD) or Best Management Practices (BMPs). We also discuss approaches for assessing and mitigating health risks associated with stormwater, including a summary of existing quantitative microbial risk assessment (QMRA) models for potable and non-potable reuse of stormwater. Finally, the most critical research gaps are identified for formulating risk management strategies.

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1. Introduction

Water authorities worldwide are exploring alternative water sources to meet ever-increasing demands for potable and non-potable water due to the adverse impacts of climate change on water supplies. Stormwater has been considered as an alternative water source for both potable (drinking) and non-potable uses (gardening, landscaping, and irrigation) (McArdle et al., 2011; Page et al., 2014c; Page et al., 2015). There are several advantages to using stormwater, including (i) reducing demands on the urban potable water supply (ii) diversification of water supplies (iii) reducing discharge of untreated urban stormwater to urban streams and marine outfalls. Despite these advantages, stormwater has not been widely adopted as an alternative water due to a perceived lack of information on the presence and risk from microbial and chemical contaminants.

The chemical quality of stormwater has been reviewed and indicated the presence of numerous contaminants including heavy metals, polychlorinated biphenyls, polycyclic aromatic hydrocarbons, halogenated aliphatics, halogenated ethers, monocyclic aromatics, phenols and cresols, phthalate esters, nitrosamines, pesticides, and other organics, especially in urban and/or industrialized areas (Makepeace et al., 1995; Eriksson et al., 2005; Baun et al., 2006; Huber et al., 2016). Risk assessments of chemical contaminants in stormwater have suggested that in some cases, contaminants may exceed concentrations in the environment that are relevant for ecological endpoints, but may be lesser contributors to human health risks (Eriksson et al., 2005; Baun et al., 2006; Eriksson et al., 2007). Non-carcinogenic risks due to ingestion of fish in stormwater-contaminated waterbodies have been identified as a potential concern (Bickford et al., 1999). Iron levels exceeding Australian guidelines and elevated (but below guideline) levels of Arsenic have also been identified as potential risks for managed aquifer recharge with stormwater, with overall chemical risks from various compounds posited to be low (Page et al., 2010a, 2010b). Heavy metals and pathogens are thought to be the drivers of human health risks for exposure to stormwater (Page et al., 2010a, 2010b, 2010c, 2010d; Chong et al., 2013; Ma et al., 2016). Indeed, public perception of microbial risks, in particular, remains a crucial barrier to the expansion of water recycling and reuse (Higgins et al., 2002). Therefore, the current review will focus on microbiological contaminants in stormwater and their associated risks.

Pathogenic bacteria, viruses and protozoa can be found in stormwater runoff and subsequently transported to environmental water bodies through sewer overflows, defective septic systems, agricultural runoff, defecation from wild animals and discharge of treated sewage (Ahmed et al., 2005; Noble et al., 2006; Rajal et al., 2007). The pathogens present in various animal fecal sources will differ from those in sewage (Schoen and Ashbolt, 2010; Soller et al., 2015; Federigi et al., 2019), and therefore stormwater is likely to contain a different pathogen profile than sewage. Studies have reported a high prevalence of fecal indicator bacteria (FIB) and enteric pathogens in stormwater (Noble et al., 2006; Rajal et al., 2007; AWQC, 2008; Sidhu

et al., 2012a; Cizek et al., 2008). The microbial quality of water is assessed by FIB such as *Escherichia coli* (*E. coli*) and *Enterococcus* spp. (USEPA, 2000). These indicators are abundant in the intestine of warm-blooded animals, and their presence in waters indicates fecal contamination and the likely presence of potential pathogens.

One major limitation of FIB is their poor correlation with the presence of pathogens, especially protozoans and enteric viruses (Hörman et al., 2004; Selvakumar and Borst, 2006; McQuaig et al., 2009). Another limitation of FIB is that they cannot provide information regarding the sources of fecal contamination (Field and Samadpour, 2007; Stoeckel and Harwood, 2007). Remediation strategies can be more effectively implemented if the potential sources of fecal contamination and pathogens are known in stormwater (Sidhu et al., 2012b). Since the monitoring of FIB in water does not provide information on origin, e.g., human or animal feces, researchers have developed a set of analytical tools collectively known as “microbial source tracking (MST) tools.” These tools can be used to obtain information on whether the fecal contamination in water came from human or animal wastewater or both (Harwood et al., 2014).

Epidemiological studies indicated that the risks of gastrointestinal illness (GI) among swimmers can be high when the water is contaminated with untreated sewage, as presumably indicated by the presence of elevated levels of FIB (Cabelli et al., 1982; Wade et al., 2006; Marion et al., 2010). However, mixed sources of fecal contamination (human and animal feces) are often expected to be found in stormwater. Epidemiological data are lacking regarding the human health impacts from mixed source of fecal contamination, which may pose different human health risks.

Several studies in the research literature have provided quantitative data on potential pathogens in roof-harvested rainwater stored in tanks (Ahmed et al., 2008a; Ahmed et al., 2014a; Dobrowsky et al., 2014). However, pathogen abundance data in stormwater runoff and outfalls are still scarce. Therefore, the objective of this review is to summarize the concentrations of traditional and alternative fecal indicators, MST marker genes and potential pathogens in stormwater runoff and outfalls. A section of this review has been dedicated to summarizing available quantitative microbial risk assessments (QMRA) for potable and non-potable uses of stormwater. The focus for reviewing available QMRA models is to summarize the types of assumptions used to model pathogen fate, transport, and exposure in order to identify data gaps and areas where further attention is warranted. Additionally, a review of fecal indicators and pathogen log removal values (LRVs) through Water Sensitive Urban Design (WSUD) or Best Management Practices (BMPs) of stormwater runoff has been compiled. Finally, risk mitigation approaches and the most critical research gaps are identified concerning the public health aspects of stormwater reuse.

Peer-reviewed journal articles, reports, conference proceedings, and guidelines published from 2005 to 2018 were taken into consideration. Electronic databases including PubMed, Google Scholar, and Web of Knowledge were used to obtain the information. The literature search

was performed using the keywords “(stormwater OR sensitive urban design OR WSUD OR green infrastructure OR low impact development OR Low impact urban design and development) AND (pathogen OR microb- OR bacter- OR protozoa OR source tracking OR MST OR fecal indicator OR fecal contamination OR health risk OR QMRA) and included studies that are reported in English.

2. Fecal indicators

Routine monitoring of stormwater quality focuses on quantification of *E. coli* and *Enterococcus* spp. High concentrations ($>4 \log_{10}$ CFU/100 mL) of FIB are generally found in stormwater runoff and receiving waters (Jiang et al., 2015). Most of the stormwater or outfall samples often exceed the sample threshold value of FIB for the designated recreational use of waters by one or more orders of magnitude. For example, if we consider the 95th percentile value for *Enterococcus* spp./100 mL water, many stormwater samples will exceed the threshold value classified as Class D (i.e., > 501 CFU/100 mL) by the National Health & Medical Research Council (NHMRC) Guidelines for Recreational Use of Water (NHMRC, 2008). The NHMRC used information from WHO (2003) and Kay et al. (2004) to estimate that in Class D there would be greater than a 10% chance of illness per single exposure.

Storm events have the potential to resuspend sediment-bound FIB and pathogens back into water column resulting in elevated contamination levels (An et al., 2002; Cizek et al., 2008; Krometis et al., 2010; Sidhu et al., 2012a). The elevated FIB concentrations generally occur at or just before the peak inflow of the storm hydrograph. Stumpf et al. (2010) determined the loading of FIB over dry and wet weather conditions in tidal creeks in North Carolina, USA. The authors reported 30 and 37 times greater loadings of *E. coli* and *Enterococcus* spp. in storm flow compared to base flow. *E. coli* and *Enterococcus* spp. were weakly correlated ($r^2 = 0.13$ to 0.32) with total suspended solids, while strong associations ($r^2 = 0.40$ to 0.78) were observed between FIB and streamflow rate and various stages (base, rising, peak and falling) of the hydrograph. The authors also noted a large intra-storm variability in FIB concentrations and recommended intensive sampling throughout a storm in order to accurately quantify FIB rather than collecting a single grab sample.

Rural or high density residential areas are reported to contribute 30–50 times greater *E. coli* levels in stormwater compared to light or sparsely populated residential area (McCarthy et al., 2006). Paule-Mercado et al. (2016) investigated the variability of FIB concentrations in agricultural, mixed land use and urban catchments with variable catchment area, land use, and land cover. The urban site had the greatest level (*E. coli* $7.39 \log_{10}$ MPN/100 mL; fecal streptococci $7.21 \log_{10}$ CFU/100 mL) of FIB concentrations compared to agricultural site (*E. coli* $2.51 \log_{10}$ MPN/100 mL; fecal streptococci $2.48 \log_{10}$ CFU/100 mL) because of runoff from commercial markets and impervious cover, sewer and septic overflows. The authors noted intra-event variability of FIB across the monitoring sites. FIB concentrations increased during the peak flow and then decreased as the storm progressed. Levels of FIB significantly ($p < 0.05$) varied between early and late summer seasons with higher FIB concentrations observed in early summer. Anthropogenic activities and impervious cover were found to influence positive correlations ($r > 0.6$) between FIB numbers and environmental parameters such as temperature, turbidity, and total suspended solids.

Although, FIB monitoring in stormwater is a common practice, there are uncertainties associated with stormwater flow and *E. coli* (McCarthy et al., 2008; Harmel et al., 2006). Uncertainties of discrete *E. coli* samples and flow measurements were >30 and 97%, respectively. *E. coli* event mean concentration uncertainties varied between 10 and 52% and that uncertainties relating to site mean concentrations ranged from 35 to 55% (McCarthy et al., 2008). Sample collection procedures (5–30%), laboratory analysis, preservation/storage, and flow also contributed substantial (14–28%) uncertainties (Harmel et al., 2006; Harmel et al., 2010, 2016).

Another limitation of FIB is that they do not often correlate well with the presence of pathogens in environmental waters. The appropriateness of using FIB to indicate the presence of pathogens especially viruses and protozoa in stormwater has been questioned (Jiang et al., 2001; Schroeder et al., 2002; Jiang, 2004; Robertson and Nicholson, 2005; Signor et al., 2005; AWQC, 2008). This is somewhat expected as FIB in stormwater are sourced from feces of both human and animals, while human pathogens especially enteric viruses in urban stormwater mainly derived from sewage. In addition, the decay rates of FIB may be significantly different than those of viruses (Ahmed et al., 2014b). Hence, monitoring of FIB and interpreting their concentrations in terms of human health risks may not yield any meaningful outcomes.

As a result of these limitations, FIB are generally not used directly for risk estimation. However, some *E. coli* strains such as enteropathogenic *E. coli* (EPEC), enterohemorrhagic *E. coli* (*E. coli* O157:H7 or other EHEC), enterotoxigenic *E. coli* (ETEC), and others are pathogenic to humans and can be used for risk estimation purposes. Although these subsets are not routinely measured, general FIB can be used as a preliminary screening tool prior to testing for other pathogens. Additionally, ratios of FIB to pathogens are used occasionally for risk assessment purposes (Pettersen et al., 2016).

3. MST marker genes in stormwater

Fecal contamination in stormwater can originate from point and non-point sources. Human health risk will be different depending on the sources. Untreated sewage poses the greatest risks to humans and the environment due to high concentrations of enteric viruses (EC, 2000; Fong et al., 2010; Soller et al., 2010). Sewage may be introduced into stormwater through illicit connections, cross connection between sewer pipes, storm drains and leakages into sewers through broken lines or poor pipe joints (Pitt, 2004). The presence of sewage in stormwater can be problematic due to the likely co-presence of pathogens. Identifying the presence of sewage in stormwater using is not straightforward due to dilution, infiltration, and lack of sensitive detection methods (Panasiuk et al., 2015). However, microbial source tracking (MST) marker genes are used to identify human feces and other sources of animal fecal contamination such as cattle, dogs, pigs, and birds in water (Harwood et al., 2014; Ahmed et al., 2016).

Human feces-associated marker genes such as *Bacteroides* HF183 (HF183), crAssphage CPQ_056 and CPQ_064, pepper mild mottle viruses (PMMoV), human polyomaviruses (HPyV), and Lachno3 are currently being used to determine the presence of human fecal contamination in environmental waters by research laboratories and water quality managers. These marker genes are sensitive and accurate analytical approaches of human fecal contamination due to high host-specificity and abundance in human and animal feces (Boehm et al., 2013). Several studies have reported the presence of human feces-associated marker genes in stormwater runoff and outfall samples (Table 1). Sidhu et al. (2012a) reported the presence of the *Bacteroides* HF183 (16 of 21 samples were positive for HF183 during both dry and wet weather samples) and *Enterococcus faecium* enterococci surface protein (*esp*) marker gene (8 of 23 samples were positive for *esp* during both dry and wet weather samples) in stormwater run-off samples and suggested the ubiquitous presence of sewage in the urban environment.

MST field studies have identified aging infrastructure as a contributor to sewage intrusion into stormwater system (Marsalek and Rochfort, 2004; Sauer et al., 2011; Guérineau et al., 2014). Several studies have reported the greater concentrations of the HF183 marker gene in stormwater samples (Sercu et al., 2011; Van De Werfhorst et al., 2014; Paar 3rd et al., 2015) (Table 1). Olds et al. (2018) observed high levels of human *Bacteroides* (HB) and Lachno2 in the Milwaukee estuary and at the lower reaches of the three major rivers forming the estuary in Milwaukee, WI, USA after storm events. Concentrations of these marker genes were one to three orders of magnitude higher (4.04 – $5.59 \log_{10}$ GC/L of HB and 4.04 – $6.27 \log_{10}$ GC/100 mL of Lachno2) in stormwater

samples during storm events compared to low flow periods (3.53 log₁₀ GC/100 mL of HB and 3.71 log₁₀ GC/100 mL of Lachno2). A further increase in the order of a magnitude of marker genes was observed during the combined sewer overflow (CSO) event compared to storm events. The marker gene contamination level was high enough to exceed acceptable GI risk benchmark of 32 to 36 per 1000 primary contact recreators in rivers or swimming at nearby beaches (USEPA, 2012a).

Staley et al. (2016) quantified *Bacteroides* HF183 in storm water outfalls and several sites along the Humber River in Toronto, Canada. HF183 was detected at all sites, with greater concentrations in outfall samples (mean outfall concentrations of 6.22 log₁₀ GC/L). Their results indicated ubiquitous sewage contamination at storm water outfalls and throughout the Humber River. Steele et al. (2018) used digital PCR to quantify

the HF183 marker gene in samples collected from multiple storm events from San Diego River ($n = 23$) and Tourmaline Creek ($n = 21$) that discharge to popular surf beaches in San Diego, CA, USA. The authors noted 6.45–6.95 log₁₀ GC HF183/L in stormwater discharges from Tourmaline Creek and 5.30–6.24 log₁₀ GC/100 mL in stormwater discharges from the San Diego River. The HF183 marker was consistently detected with human pathogen NoV (96% positive agreement in San Diego River and 72% positive agreement in Tourmaline Creek).

Ahmed et al., 2018c examined the extent of sewage contamination in an urban recreational lake located in Sydney, Australia that receives wet weather overflows using two human feces-associated crAssphage marker genes (CPQ_056 and CPQ_064). The concentrations of both markers were higher (CPQ_056 ranging from 3.40 to 7.62 log₁₀ GC/L

Table 1

Prevalence and concentrations (log₁₀ GC/L) of sewage and animal-associated marker genes in stormwater runoff and outfall samples.

Marker genes (host)	Country	Number of samples tested (% occurrence)	Mean/median ± SD (range) in positive samples* (log ₁₀ GC/L)	References
HF183 (human)	Qld, Australia	7 (57)	–	Ahmed et al., 2007
HF183 (human)	Qld, Australia	10 (40)	–	Ahmed et al., 2008b
HF183 (human)	Qld, Australia	11 (54.5)	–	Ahmed et al., 2012
HF183 (human)	Tampa, USA	12 (58.3)	3.79 ^a ± 0.33 (3.38–4.21)	Ahmed et al., 2018a
HF183 (human)	Virginia, USA	130 (100)	4.00 ^b –5.47 ^b	Liao et al., 2015
HF183 (human)	Philadelphia, USA	14 (100)	3.50 ^b (0.11–6.91)	McGinnis et al., 2018
HF183 (human)	North Carolina, USA	37 (13.5)	(4.05–> 4.69)	Parker et al., 2010
HF183 (human)	Boston, USA	18 (94.4)	6.23 ^a ± 1.01 (3.50–7.50)	Paar 3rd et al., 2015
HF183 (human)	California, USA	14 (43)	5.27 ^a ± 1.43 (3.59–7.17)	Sercu et al., 2011
HF183 (human)	Qld, Australia	12 (92)	–	Sidhu et al., 2012a, 2012b
HF183 (human)	Qld, NSW, Victoria, Australia	23 (96)	–	Sidhu et al., 2013
HF183 (human)	Ontario, Canada	NM	(2.73–4.17)	Staley et al., 2015
HF183 (human)	Toronto, Canada	59 (69.5)	4.22 ^a (2.55–8.65)	Staley et al., 2016
HF183 (human)	California, USA	44 (97.7)	3.49 ± 0.69 ^a (2.30–5.09)	Steele et al., 2018
HF183 (human)	California, USA	26 (27)	4.69 ± 1.69 ^a (2.61–7.17)	van De Werfhorst et al., 2014
HF134 (human)	Qld, Australia	7 (71)	–	Ahmed et al., 2007
HF134 (human)	Qld, Australia	10 (70)	–	Ahmed et al., 2008b
BacHum-UCD (human)	California, USA	14 (92.9)	5.47 ^a ± 5.83	Bambic et al., 2015
HF183, BacHum-UCD (human)	Milwaukee, USA	828 (57)	3.51 ^a –6.61 ^a	Sauer et al., 2011
HuBac (human)	North Carolina, USA	45 (100)	4.82 ^a – 6.89 ^a	Gentry-Shields et al., 2012
nifH (human)	Australia	11 (18.2)	–	Ahmed et al., 2012
nifH (human)	North Carolina, USA	45 (31.1)	1.23 ^a – 4.11 ^a	Gentry-Shields et al., 2012
nifH (human)	California, USA	14 (43)	–	Sercu et al., 2011
nifH (human)	Qld, NSW, Victoria, Australia	23 (43)	–	Sidhu et al., 2013
nifH (human)	California, USA	26 (19.2)	–	van De Werfhorst et al., 2014
Enterococcus surface protein (esp) (human)	Qld, Australia	7 (71)	–	Ahmed et al., 2007
Enterococcus surface protein (esp) (human)	Qld, Australia	11 (18)	–	Ahmed et al., 2012
Enterococcus surface protein (esp) (human)	Qld, Australia	12 (58)	–	Sidhu et al., 2012a, 2012b
Lachno2 (human)	Milwaukee, USA	NM	4.98 ^a ± 1.71 (4.27–6.43)	Olds et al., 2018
Lachno2 (human)	Milwaukee, USA	10 (70)	4.94 ^a ± 1.02 (3.50–6.73)	Feng et al., 2018
Lachno12 (human)	Milwaukee, USA	10 (90)	3.56 ^a ± 0.78 (3.12–5.60)	Feng et al., 2018
Lachno3 (human)	Milwaukee, USA	10 (70)	3.85 ^a ± 1.20 (2.65–6.23)	Feng et al., 2018
Human <i>Bacteroides</i> (human)	Milwaukee, USA	10 (60)	4.21 ^a ± 0.52 (3.35–4.93)	Feng et al., 2018
Human <i>Bacteroides</i> (human)	Milwaukee, USA	NM	4.78 ^a ± 0.45 (4.25–5.74)	Olds et al., 2018
HPyV (human)	Qld, Australia	11 (18.2)	–	Ahmed et al., 2012
HPyV (human)	Philadelphia, USA	14 (28.6)	(0.27–1.29)	McGinnis et al., 2018
HPyV (human)	Australia	12 (41.6)	–	Sidhu et al., 2012a, 2012b
HPyV (human)	Qld, NSW, Victoria, Australia	23 (52)	–	Sidhu et al., 2013
CrAssphage CPQ_056 (human)	Tampa, USA	12 (41.6)	4.19 ^a ± 0.52 (3.62–4.91)	Ahmed et al., 2018a
CrAssphage CPQ_064 (human)	NSW, Australia	20 (100)	4.55 ^a ± 0.89 (3.40–6.03)	Ahmed et al., 2018c
CrAssphage CPQ_064 (human)	NSW, Australia	20 (90)	4.15 ^a ± 0.77 (3.13–5.47)	Ahmed et al., 2018c
PMMoV (human)	Philadelphia, USA	14 (100)	2.99 ^b (1.34–4.62)	McGinnis et al., 2018
BacCow (cow)	California, USA	15 (86.7)	4.75 ^a ± 5.17	Bambic et al., 2015
BacCan (dog)	USA	15 (100)	4.67 ^a ± 4.74	Bambic et al., 2015
DG37 (dog)	Toronto, Canada	59 (16.9)	–	Staley et al., 2016
DG3 (dog)	California, USA	44 (70.4)	2.44 ^a ± 0.47 (1.53–3.57)	Steele et al., 2018
DogBact (dog)	Milwaukee, USA	10 (40)	4.43 ^a ± 0.79 (3.61–5.28)	Feng et al., 2018
Gull4 (seagull)	Toronto, Canada	59 (37.3)	(2.15–4.52)	Staley et al., 2016
LeeSeagull (seagull)	California, USA	44 (93.2)	3.42 ^a ± 0.62 (1.80–4.47)	Steele et al., 2018

–: Quantitative data were not provided; NM: Not mentioned; *: where available; ^a = mean (overall mean concentrations were calculated by authors from the available data); ^b = median.

and CPQ_064 ranging from 2.90 to 6.95 log₁₀ GC/L) in 20 of 20 (for CPQ_056) and 18 of 20 (for CPQ_064) samples collected after storm events compared to a dry weather event (10 of 10 samples were qPCR negative for the CPQ_056 and 8 of 10 were negative for the CPQ_064 marker genes) suggesting that sewage contamination was transported by urban stormwater runoff to the studied lake.

In addition to human-feces associated bacterial markers, viruses such as HAdV species A-F and HPyV (urine indicator) have been used to detect human fecal contamination in stormwater runoff (Brownell et al., 2007; Ahmed et al., 2012; Sidhu et al., 2013). However, none of these studies provided the concentrations of these viruses in stormwater samples. Quantifying viral markers in stormwater samples can be difficult due to factors such as their low numbers in sewage, dilution and loss due to recovery and DNA extraction (Horswell et al., 2010; Wong et al., 2012).

Compared to human feces-associated markers, less information is available on the prevalence and concentrations of animal feces-associated marker genes. Staley et al. (2016) determined the concentrations of seagull-associated Gull4 marker gene in a river and stormwater outfall samples in Ontario, Canada. River sites were frequently (5 of 7 sites where gull fecal contamination was detected) impacted by gull fecal contamination. Two of five storm outfalls were also positive for gull feces. Bambic et al. (2015) reported the moderate occurrence of cattle and dog markers in stormwater samples ranging from 4.67 and 4.75 log₁₀ GC/L. Storm events led to an increase (4.67 and 4.75 log₁₀ GC/L) in cattle and dog feces-associated *Bacteroides* marker genes compared to dry events (3.23 and 3.20 log₁₀ GC/L).

Corsi et al. (2014) tested 63 samples over a 17-month period across the three sampling locations in Milwaukee River, WI, USA for human and bovine viruses. Twenty samples were collected during low-flow periods and 43 were collected during rainfall or snowmelt runoff periods. Three of the seven bovine viruses analyzed were detected during the study period. Bovine polyomavirus was present most often (32%) followed by bovine rotavirus group A (19%), and bovine viral diarrhea virus type 1 (5%). Bovine viruses were present in 46% of runoff samples resulting from precipitation and snowmelt and 14% of low-flow samples. Maximum concentrations for these three viruses ranged from 6.7 to 11 GC/L. Bovine viral diarrhea virus type 2, coronavirus, enterovirus, and adenovirus were not detected. The results suggested the presence of bovine fecal contamination in stormwater runoff. This is particularly important because a recent study reported the high risks of gastrointestinal illness from cattle feces contaminated water due to protozoan pathogens *Cryptosporidium* and *Giardia* spp. (Soller et al., 2010).

Fecal contamination in stormwater originate from point and non-point sources, and this is supported by the fact that a number of stormwater outfall samples had high FIB with low or no human *Bacteroides*, suggesting that FIB may have originated from non-human sources (Sauer et al., 2011). Therefore, markers targeting different animal species of zoonotic pathogen potential need to be employed to obtain more information on the magnitude of animal fecal contamination in addition to sewage contamination.

Most of the stormwater studies provided MST results in the presence/absence form. The presence/absence results of any given marker in a sample should be interpreted with care. Mere presence of a marker does not represent any risk as the marker concentrations are generally greater in sewage or animal feces compared to pathogens. In contrast, lack of detection of a marker does not necessarily indicate the sample is free from other contaminants and safe for human exposure. Multiple lines of evidence (i.e., a toolbox approach) are required before implementing remediation or assessing human health risk (Ahmed et al., 2012; Mauffret et al., 2012).

4. Pathogens in stormwater

Increased urbanisation will increase the dissemination of waterborne pathogens in the environments (Hofstra, 2011). Information on

the concentrations of pathogens in stormwater is needed for risk assessment and management for beneficial reuse. However, the data on the occurrence and levels of pathogens in stormwater runoff is limited. This is because collecting stormwater samples during storm events can be challenging. Grab samples are easy to collect, and the cost associated with sampling is low, but only represent a snapshot of the water quality at the time of collection (Harmel et al., 2010). Automated samples are more accurate and appropriate for stormwater sampling as they collect representative samples. However, it has to be installed at a specific location, requiring construction of infrastructure and regular maintenance. Other factors such as the presence of high concentrations of suspended solids, grease and PCR inhibitors make it difficult to detect pathogens with molecular based methods (USEPA, 1999; Stenstrom et al., 1984; Rajal et al., 2007).

Table 2 shows the occurrence and concentrations (where available) of bacterial, protozoa, and viral pathogens in stormwater. Sidhu et al. (2012a) investigated the presence of human pathogens in the urban stormwater runoff in Australia. HAdV was frequently detected from all sampling sites during wet weather conditions suggesting their widespread presence. *Campylobacter jejuni*, *Campylobacter coli*, and *Salmonella enterica* were also detected during wet weather conditions. Based on the results, the authors suggested that some degree of treatment of captured stormwater would be required if it were to be used for non-potable purposes. However, the authors did not mention LRVs that would be required for the safe use of stormwater.

Corsi et al. (2014) studied the prevalence, as well as hydrological and seasonal variations of enteric viruses in an urban watershed, a rural sub watershed and the Milwaukee River mouth, WI, USA. The authors processed large volumes of water samples (56–2800 L) over a 17 months duration to account for variability throughout changing hydrologic and extended (24-h) low-flow periods. Human and bovine viruses were detected in 49 and 41% of samples ($n = 63$), respectively. All human viruses analyzed were detected at least once including HAdV (40% of samples), norovirus (NoV) GI (10%), enterovirus (EV) (8%), rotavirus (RoV) (6%), NoV GII (1.6%) and hepatitis A virus (HAV) (1.6%). Human viruses were present in 63% of runoff samples resulting from precipitation and snowmelt, and 20% of low-flow samples. Maximum human virus concentrations were >2.47 log₁₀ GC/L.

Steele et al. (2018) used digital qPCR to quantify a number of bacterial and viral pathogens in stormwater samples from multiple storm events from two different watersheds that discharge to popular surf beaches in San Diego, CA, USA. This is the most comprehensive study reviewed that determined the concentrations of several human health significant pathogens in stormwater discharges in the USA. Among the enteric viruses tested, NoV were highly prevalent in both the San Diego River and Tourmaline Creek with concentration ranging from 1.39 to 2.69 log₁₀ GC/100 mL of water. The prevalence of HAdV were much lower than NoV; 9% of the samples in Tourmaline creek and 22% of the samples in San Diego River were positive for HAdV with concentration ranging from 1.14 to 1.61 log₁₀ HAdV GC/100 mL of water. Enterovirus was not detected in any of the water samples tested. Among the two bacterial pathogens (*Campylobacter* spp., and *Salmonella* spp.), *Campylobacter* spp. was the most commonly detected pathogens (100 and 45% samples were positive at San Diego River and Tourmaline Creek, respectively compared to 25 and 10% samples were positive for *Salmonella* spp. at San Diego River and Tourmaline Creek, respectively. *C. coli* (87%) and *C. lari* (78%) were the most frequently detected species in stormwater discharges from San Diego River, while *C. lari* (48%) and *C. jejuni* (29%) were the most commonly detected in Tourmaline Creek. The authors stated that such data is an important step forward for assessing risk associated with stormwater.

Data generated using qPCR need to be interpreted carefully because qPCR assays quantify both viable and dead pathogens and do not provide information on the infectivity status of the pathogen tested. Also, complex water matrix such as stormwater generally contain various organic substances, salts, acid and detergents which may inhibit PCR

Table 2
Prevalence and log₁₀ concentrations of potential pathogens in stormwater samples.

Potential pathogens	Country	Land use characteristics	Methods used	No. of samples tested (% of sample positive)	Mean/median ± SD (range) in positive samples [95% CI upper limit]*	References
Bacterial pathogens						
<i>Campylobacter</i> spp.	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (45)	1.96 ^a ± 0.90 (1.15–3.48) [3.48] GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (100)	2.54 ^a ± 0.35 (1.52–3.05) [3.05] GC/100 mL	
<i>Campylobacter</i> spp.	Brisbane, Australia	Urban residential, industrial, agricultural and rural	PCR	12 (100)	–	Sidhu et al., 2012a, 2012b
<i>Campylobacter</i> spp.	Sydney, Australia	Untreated sewerage urban	Culture-based	59 (3.38)	<0.30 ^b ± <0.30 (NM–1.17) [<0.30] MPN/L	AWQC, 2008
<i>C. coli</i>	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (10)	1.40 ^a (1.34–1.46) GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (87)	1.97 ^a ± 0.29 (1.50–2.61) [2.09] GC/100 mL	
<i>C. coli</i>	Brisbane, Australia	Urban residential, industrial, agricultural and rural	PCR	12 (67)	–	Sidhu et al., 2012a
<i>C. jejuni</i>	Brisbane, Australia	Urban residential, industrial, agricultural and rural	PCR	12 (67)	–	Sidhu et al., 2012a
<i>C. jejuni</i>	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (29)	1.69 ^a ± 0.16 (1.50–1.93) [1.93] GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (17)	1.66 ^a ± 0.15 (1.53–1.80) [1.80] GC/100 mL	
<i>C. lari</i>	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (48)	1.38 ^a ± 0.18 (1.20–1.71) [1.71] GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (78)	1.61 ^a ± 0.30 (1.20–2.15) [2.15] GC/100 mL	
<i>E. coli eaeA</i>	Tampa, USA	Urban, industrial and residential	MFQPCR	12 (41.6)	5.09 ^a ± 0.23 (4.72–5.29) [5.29] GC/L	Ahmed et al., 2018b
<i>L. pneumophila</i>	Tampa, USA	Urban, industrial and residential	MFQPCR	12 (25)	4.51 ^a ± 0.57 (4.13–5.17) [5.17] GC/L	Ahmed et al., 2018b
<i>Salmonella</i> spp.	Brisbane, Australia	Urban residential, industrial, agricultural and rural	PCR	12 (91.6)	–	Sidhu et al., 2012a
<i>Salmonella</i> spp.	Georgia, USA	48% forested, 45% agricultural and 7% urban	MPN combined with PCR	58 (51.7)	0.031 ^a –0.82 ^a MPN/100 mL ^c	Harris et al., 2018
<i>Salmonella</i> spp.	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (10)	1.39 ^a ± 0.51 (0.90–1.93) [1.93] GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (25)	0.92 ^a ± 0.12 (0.80–1.15) [1.15] GC/100 mL	
<i>Salmonella</i> spp.	Tampa, USA	Urban, industrial and residential	MFQPCR	12 (8.33)	5.10 GC/L ^d	Ahmed et al., 2018b McGinnis et al., 2018
<i>Salmonella</i> spp. (<i>invA</i> gene)	Philadelphia, USA	Residential and green space	qPCR	14 (7.14)	–	
<i>Salmonella</i> spp. (<i>ttr</i> gene)				14 (21.4)	(0.30–0.60) GC/L	
Protozoa pathogens						
<i>Cryptosporidium</i> spp.	New York, USA	Five sites representing various land use such as little anthropogenic impacts, suburban woodlots and high degree of impervious surfaces and developed areas	IMS and microscopy	–	0.63 ^a ± 0.28 (0.23–0.86) oocysts/L	Cizek et al., 2008
<i>Cryptosporidium</i> spp.				–	0.21 ^a ± 0.26 (–0.04–0.57) oocysts/L	
<i>Cryptosporidium</i> spp.	California, USA	High density dairy farms	IMS and microscopy	350 (21)	(1.04–3.30) oocysts/L	Miller et al., 2008
<i>Cryptosporidium</i> spp.	Sydney, Australia	Untreated sewerage urban	NM	59 (37.3)	1.43 ^b ± 1.53 (NM–2.13) [2.00] oocysts/10 L	AWQC, 2008
<i>Cryptosporidium</i> spp.	Atlanta, Louisville, USA	Highly impervious commercial and various land uses	IMS and microscopy	24 (12)	1.91 ^a ± 0.91 (1.77–2.00) [2.63] oocysts/100 L	Arnone and Walling, 2006

(continued on next page)

Table 2 (continued)

Potential pathogens	Country	Land use characteristics	Methods used	No. of samples tested (% of sample positive)	Mean/median \pm SD (range) in positive samples [95% CI upper limit]*	References
<i>C. parvum</i> or <i>hominis</i>	Sydney, Australia	Untreated sewer urban	NM	59 (8.47)	0.77 ^b \pm 1.07 (NM-1.83) [1.25] oocysts/10 L	AWQC, 2008
<i>Giardia</i> spp. Raw samples	New York, USA	Five sites representing various land use such as little anthropogenic impacts, suburban woodlots and high degree of impervious surfaces and developed areas	IMS and microscopy	–	0.59 \pm 0.28 (0.00–0.86) cysts/100 mL	Cizek et al., 2008
<i>Giardia</i> spp. Centrifuged				–	0.01 \pm 0.16 (–0.09–0.17) cysts/100 mL	
<i>Giardia</i> spp.	Sydney, Australia	Untreated sewer urban		59 (18.6)	2.00 ^b \pm 2.53 (NM-3.40) [2.34] cysts/10 L	AWQC, 2008
<i>Giardia</i> spp.	Atlanta, Louisville, USA	Highly impervious commercial and various land uses	IMS and microscopy	24 (96)	3.55 ^a \pm 0.98 (2.30–4.47) [4.33] cysts/100 L	Arnone and Walling, 2006
Enteric viruses						
HAdV	California, USA	Highly urbanized	qPCR	8 (12.5)	3.98 ^d GC/L	Ahn et al., 2005
HAdV	Milwaukee, USA	Highly urbanized	qPCR	1 (100)	3.11 ^d GC/L	Sauer et al., 2011
HAdV	Sydney, Australia	Untreated sewer urban	PCR	59 (3.38)	–	AWQC, 2008
HAdV	California, USA		Nested-PCR	(7)	–	Surbeck et al., 2006
HAdV	Brisbane, Australia	Mainly residential and commercial	PCR	23 (91.3)	–	Sidhu et al., 2013
HAdV	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (9)	1.18 ^a \pm 0.03 (1.15–1.20) [1.20] GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (22)	1.30 ^a \pm 0.17 (1.20–1.61) [1.61] GC/100 mL	
HAdV	Brisbane, Australia	Highly urbanized	PCR	7 (71.4)	–	Ahmed et al., 2012
HAdV 40/41	California, USA	Urban, agricultural and natural	qPCR	21 (4.76)	1.36 ^d GC/100 mL	Rajal et al., 2007
HAdV A	Philadelphia, USA	Residential and green space	qPCR	14 (7.14)	<0.01 ^{c,d}	McGinnis et al., 2018
HAdV C, D, F	Philadelphia, USA	Residential and green space	qPCR	14 (14.28)	(0.1–1.41) GC/L	McGinnis et al., 2018
HAdV	California, USA	Agricultural (25%), Urban (25%) and open space (50%)	qPCR	15 (6.70)	–	Bambic et al., 2015
HAdV	Brisbane, Australia	Urban residential, industrial, agricultural and rural	PCR	12 (91.6)	–	Sidhu et al., 2012a
Enterovirus	California, USA	Highly urbanized	RT-PCR	8 (12.5)	–	Ahn et al., 2005
Enterovirus	Sydney, Australia	Untreated sewer urban	PCR	59 (22.0)	–	AWQC, 2008
Enterovirus	Milwaukee, USA	Highly urbanized	qPCR	1 (100)	4.28 ^d GC/L	Sauer et al., 2011
Norovirus GI + GII	South coast, England	Arable (42%), woodland (21%), grassland (18%), urban (6.4%)	qRT-PCR	5 (100)	(2.93–4.87) GC/L	Campos et al., 2015
NoV GI	Milwaukee, USA	Highly urbanized	qRT-PCR	1 (100)	3.18 ^d GC/L	Sauer et al., 2011
NoV GI	Philadelphia, USA	Residential and green space	qRT-PCR	1 (14)	1.86 ^d GC/L	McGinnis et al., 2018
NoV GII	San Diego, USA	Tourmaline Creek – Highly urban residential and commercial	Digital qPCR	21 (72)	2.04 ^a \pm 0.33 (1.39–2.72) [2.72] GC/100 mL	Steele et al., 2018
		San Diego River – Urban residential, commercial and industrial		23 (96)	2.07 ^a \pm 0.32 (1.58–2.69) [2.66] GC/100 mL	

NM: Not mentioned; –: Quantitative data not available; *: where available; ^a = mean (overall mean concentrations were calculated by authors from the available data); ^b = median; ^c: data not log transformed; ^d: single quantifiable sample.

reaction. PCR inhibitory substances may produce false negative results of pathogens in stormwater samples. For example, Corsi et al. (2014) reported a 63% inhibition rate across virus analysis, while Steele et al. (2018) reported 10–15% inhibition rate. This problem can be overcome by including a sample processing control (SPC) (Shanks et al., 2016).

Digital qPCR may also offer an advantage over qPCR when dealing with samples with inhibitory substances (Dingle et al., 2013; Cao et al., 2016). This is because in digital qPCR sample is partitioned into many wells are droplets unlike qPCR which measures the target as it occurs with comparison with a standard curve.

Cizek et al. (2008) characterized the partitioning behaviour of *Cryptosporidium* and *Giardia* with traditional and alternative fecal indicators (*E. coli*, *Enterococcus* spp., and *Clostridium perfringens*) and a viral surrogate (coliphage) in stormwater runoff. Both protozoa exhibited similar levels of particle association during dry weather (roughly 30%) with an increased level observed during wet weather events (*Giardia* 60% and *Cryptosporidium* 40%). During wet weather events, FIB, coliphage and protozoa concentrations increased (~1–2 orders of magnitude) in tributaries examined in the Kensico Reservoir. FIB did not exhibit a strong one-to-one relationship with *Cryptosporidium* or *Giardia* in terms of total concentration or the settleable fraction in the Kensico Reservoir. The authors also found *C. perfringens* spores (Spearman $r = 0.13$ and coliphage $r = 0.11$) were the best indicators for *Cryptosporidium*. This is because the inactivation rates of *C. perfringens* and *C. parvum* were reported to be in the same order of magnitude (Hijnen et al., 2000).

In general, concentrations of pathogens in stormwater are poorly reported and some data may not be useful to infer risk or for quantitative microbial risk assessment (QMRA). For example, several studies have failed to detect or provided the percentage of samples positive for pathogens without giving quantitative numbers (Surbeck et al., 2006; Rajal et al., 2007; Sidhu et al., 2012a; Bambic et al., 2015). Most of the stormwater studies determined the concentrations of genus *Cryptosporidium* and *Giardia*. However, in urban stormwater there is evidence that most samples do not contain human infectious genotypes that are capable of causing illnesses in humans rather contain genotypes that infect animals. For instance, data from Jiang (2004) studying three United States sewered urban stormwater catchments found that only about 5% of around 100 *Cryptosporidium* oocyst types characterized were potentially human-infective.

Recent studies reported high risks due to *Campylobacter* spp. through reuse of stormwater in the Netherlands (Sales-Ortells and Medema, 2015) and Australia (Murphy et al., 2017). These studies, however, only measured members of the genus *Campylobacter* to estimate risk. Genus *Campylobacter* is comprised of 25 species, two provisional species and eight sub-species, with only a few species of human health significance (Man, 2011). Further research should focus on determining the levels of *C. jejuni*, *C. coli* or other pathogenic species such as *C. lari* and *C. upsaliensis* in stormwater for more accurate risk assessment.

Finally, the persistence of pathogens in stormwater compared to wastewater or other matrices has not been well characterized but can provide useful information for QMRA. A systematic review by Boehm et al. (2018) of pathogen persistence in surface waters indicated few decay constants available for protozoan and viral pathogens or viral surrogates, with viruses having the greatest degree of persistence. A comparison of the HF183 MST marker with NoV indicated that the first order decay coefficient k was higher for HF183 than NoV. To the author's knowledge, a similar meta-analysis has not been performed for pathogens in stormwater. Sidhu et al. (2015) estimated a T_{90} value of <3 days for bacterial pathogens, and <120 days and >200 days for *Cryptosporidium* spp. oocysts and enteric viruses, respectively in recycled stormwater used for managed aquifer recharge. Due to the persistence of viral pathogens, these microorganisms are likely to drive concerns for human health risk.

5. Health risk assessment approaches

Various approaches for assessing the health risks of microbial contaminants have been applied in the stormwater context including epidemiological approaches and quantitative microbial risk assessment (QMRA) models. Epidemiological studies observe patterns of disease in conjunction with environmental exposure and provide inferences rooted in observed health outcomes, and for this reason are highly valuable for assessing health risks. The findings of several epidemiological studies have supported a relationship between stormwater exposure

and waterborne illness for stormwater-impacted waterbodies (Haile et al., 1999; Colford Jr et al., 2007; Soller et al., 2017). However, due to the study sizes and expense required to achieve predictive power in epidemiological studies and difficulty attributing risks to a particular exposure source and/or pathway, often QMRA approaches are used to assess risks where effect sizes are projected to be small due to low environmental concentrations. QMRA uses a process of hazard identification, exposure assessment, dose response analysis, and risk characterization to predict the risk of an infection or disease-related outcome based on an exposure to environmental media (Haas et al., 2014). To the author's knowledge, there has not been an epidemiological study for potable or non-potable uses of stormwater resources. However, studies by Ashbolt and Bruno (2003) and Soller et al. (2017) have demonstrated the utility of combining both epidemiological and QMRA information where feasible for stormwater-affected waterbodies.

Undertaking QMRA for various exposures to stormwater can nevertheless be challenging due to difficulties in discerning the sources and concentrations of pathogen contamination in stormwater, and assumptions regarding pathogen sources, fate, and transport are needed depending on the availability of site-specific information. Several ($n = 16$) QMRA studies have relied upon concentrations of pathogens observed in stormwater-impacted coastal, recreational waters, or drinking source waters for assessment of health risks (Donovan et al., 2008; Soller et al., 2010; ten Veldhuis et al., 2010; Fewtrell et al., 2011; Tseng and Jiang, 2012; Andersen et al., 2013; McBride et al., 2013; de Man et al., 2014; Sales-Ortells and Medema, 2014; Schoen et al., 2014; Soller et al., 2014; Adell et al., 2016; Krkosek et al., 2016; Lim et al., 2017; Soller et al., 2015; Soller et al., 2017), and two have used other modelling approaches for microbial health risks such as Bayesian network modelling (Goulding et al., 2012) or disease transmission models (Soller et al., 2006). These recreational water QMRAs are reviewed in detail by Federigi et al. (2019). However, few studies have conducted a QMRA for potable and non-potable reuse exposures to stormwater (Table 3). The focus on potable and non-potable uses here is due to the difficulty of comparing recreational exposures with multiple non-point as well as point sources of contamination with stormwater-only exposures. Stormwater-impacted recreational waterbody exposures using FIB as well as pathogens as index pathogens were very high in some cases, up to 1.0 for a homeless population ingesting *Giardia*, for example (Donovan et al., 2008). The risks from potable and non-potable uses of stormwater in Table 3 varied substantially depending on the target pathogen and exposure scenario. Risks were considered highest for viral pathogens, in most cases exceeding risk benchmarks for potable and non-potable use with the exception of toilet flushing in some cases (Lim et al., 2015; Murphy et al., 2017). The studies summarized in Table 3 indicate that potable and non-potable exposures to stormwater are likely to exceed water quality targets [e.g. up to a geometric 240 CFU/mL for recycled water (USEPA, 2012b)] and risk benchmarks (10^{-4} probability of infection or 10^{-6} disability adjusted life years per person per year (pppy) in the absence of additional treatment and/or BMPs depending on the area, end use, and source water. Microbial risks from harvested rainwater are considered as captured stormwater but have been reviewed elsewhere (Hamilton et al., 2019).

Factors such as temporal, regional, and compositional complexity of stormwater can make the quantification of pathogens more difficult than for some other matrices. Once concentration values are obtained, values can be corrected for recovery efficiency in a QMRA, however, low or variable recovery efficiencies can also complicate QMRA analysis. Furthermore, concentrations observed at the point of exposure may not be indicative of realistic exposure scenarios over time as they typically are not observed after a rainfall event during presumably peak pathogen concentrations, or dilution occurs at the point of exposure that in some cases will render concentrations of pathogens below the analytical detection limit (McBride et al., 2013). These factors must be taken into account when constructing QMRA models. Previous studies of pathogens in stormwater discharges have relied upon small samples sizes (Sidhu

Table 3
Quantitative microbial risk assessments (QMRA) for potable and non-potable reuse of stormwater resources

Pathogen	Applications	Exposure routes	Exposure frequency and duration	Risk Mean/Median (95 th percentile or upper bound) or calculated LRV	References
<i>Campylobacter</i> <i>Cryptosporidium</i> Rotavirus	Stormwater treated in wetland used for managed aquifer recharge	Ingestion	Ingestion 2 L/day	<i>C. parvum</i> - 1.5×10^{-3} DALY <i>Campylobacter</i> 4.6×10^{-3} DALY	Page et al., 2008
<i>Campylobacter</i> <i>Cryptosporidium</i> Rotavirus	Irrigation, toilet flushing, laundry, irrigation, firefighting	Ingestion	Municipal irrigation and nonpotable construction activities (50 mL/year); dual reticulation for indoor and outdoor use (toilet, laundry, irrigating food crops, ornamental garden irrigation) (670 mL/person/year); firefighting (1 L/person/year); commercial food crops (490 mL/person/year); non-food crops (50 mL/person/year)	Rotavirus 8.4×10^{-3} DALY Log removals to achieve target concentrations associated with a 10^{-6} DALYs/person/year calculated (0.8 log [<i>Cryptosporidium</i> spp.]- 2.6 log [rotavirus])	NRMCC-EPHC-NHMRC, 2009
<i>Campylobacter</i> <i>Cryptosporidium</i> Rotavirus	Managed aquifer recharge with captured urban stormwater	Aerosol ingestion, routine ingestion, and accidental ingestion	Ingestion of irrigation sprays 0.1 mL, 90/person/year; routine ingestion of irrigation sprays 1 mL, 90/person/year; accidental ingestion during irrigation 100 mL 1/person/year.	<i>Campylobacter</i> spray ingestion $4.6 \times 10^{-7}/<1.0 \times 10^{-10}$ (95 th $<1.0 \times 10^{-10}$) DALY; routine ingestion $1.5 \times 10^{-6}/<1.0 \times 10^{-10}$ (95 th $<1.0 \times 10^{-10}$) DALY; accidental ingestion $1.2 \times 10^{-7}/<1.0 \times 10^{-10}$ (95 th $<1.0 \times 10^{-10}$) DALY <i>Cryptosporidium</i> spray ingestion $6.2 \times 10^{-8}/1.6 \times 10^{-8}$ (95 th 2.5×10^{-7}) DALY; routine ingestion $6.2 \times 10^{-7}/1.6 \times 10^{-7}$ (95 th 2.5×10^{-6}) DALY; accidental ingestion $6.8 \times 10^{-7}/1.8 \times 10^{-7}$ (95 th 2.8×10^{-6}) Rotavirus spray ingestion $4.3 \times 10^{-6}/4.9 \times 10^{-7}$ (95 th 7.0×10^{-4}); routine ingestion $2.8 \times 10^{-5}/4.0 \times 10^{-6}$ (95 th 1.4×10^{-4}); accidental ingestion $4.2 \times 10^{-5}/3.9 \times 10^{-6}$ (95 th 1.6×10^{-4})	Toze et al., 2010
<i>Campylobacter</i> <i>Cryptosporidium</i> Rotavirus	Stormwater treated in wetland used for managed aquifer recharge	Ingestion	Ingestion 2 L/day	<i>C. parvum</i> : $2.8 \times 10^{-8}/<1 \times 10^{-10}$ DALY (95 th 1.1×10^{-8} , max 1.7×10^{-4}) <i>Campylobacter</i> : $<1 \times 10^{-10}$ DALY Rotavirus: $3.0 \times 10^{-7}/<1.0 \times 10^{-10}$ DALY (95 th 6.6×10^{-8} , 8.4×10^{-4})	Page et al., 2009; Page et al., 2010a; Page et al., 2010c; Page et al., 2010d
<i>Campylobacter</i> <i>Cryptosporidium</i> Rotavirus	Stormwater treated in wetland used for managed aquifer recharge	Ingestion	Not specified	<i>C. parvum</i> : $<1 \times 10^{-10}$ - $1.5 \times 10^{-3}/<1 \times 10^{-10}$ - 1.5×10^{-3} DALY (95 th $<1 \times 10^{-10}$ - 1.5×10^{-3}). <i>Campylobacter</i> : $<1 \times 10^{-10}$ DALY all parameters. Rotavirus $<1.0 \times 10^{-10}$ - $8.4 \times 10^{-4}/<1.0 \times 10^{-10}$ - 8.4×10^{-4} (95 th $<1.0 \times 10^{-10}$ - 8.4×10^{-4}).	Page et al., 2010b
<i>Campylobacter</i> <i>Cryptosporidium</i> Rotavirus	Stormwater treated in wetland used for managed aquifer recharge	Ingestion	Ingestion 2 L/day	<i>C. parvum</i> : Log reduction credits for 10^{-6} DALY risk open space irrigation 0.8-4.8, drinking 4.9- >6.0 (Page et al. 2012) <i>Campylobacter</i> : Log reduction credits for 10^{-6} DALY risk open space irrigation 1.3- >6.0, drinking 5.5->6.0 (Page et al. 2012)	Page et al., 2012

Table 3 (continued)

Pathogen	Applications	Exposure routes	Exposure frequency and duration	Risk Mean/Median (95 th percentile or upper bound) or calculated LRV	References
HAdV	Irrigation*	Aerosol ingestion, accidental ingestion	Boating 1 mL 52 times/year; irrigation aerosols 1 mL 90 times/year; irrigation accidental ingestion 100 mL 1 time/year.	Rotavirus: Log reduction credits for 10 ⁻⁶ DALY risk open space irrigation 1.3–3.4, drinking 5.5–6.0 (Paget al. 2012) Log removal credits calculated to achieve 10 ⁻⁶ DALY for adenovirus for irrigation (aerosol) 2.3–3.2/1.4–2.5 (95 th 2.9–3.8), irrigation (accidental ingestion) 2.4–3.2/1.5–2.5 (95 th 2.9–3.8)	Sidhu et al., 2012b
<i>E. coli</i> O157:H7	Riverbank filtration managed aquifer recharge	Ingestion	3.12 ± 1.17 L/day (Normal distribution)	0.115 (no treatment) - 0.00165 DALYs/person/year (with treatment)	Bartak et al., 2015
HAdV NoV	Toilet flushing, showering, and consumption of irrigated lettuce	Aerosol inhalation, aerosol ingestion, lettuce consumption	Four flushes/day, one 20 min shower/day; Lettuce consumed 90, 180, or 270 times/year. Toilet and shower inhalation volumes calculated based on aerosols produced by fixtures and aerosol volumes.	Adenovirus: Toilet flushing annual infection risk 1.1 × 10 ⁻⁷ –8.9 × 10 ⁻⁷ (95 th 2.7 × 10 ⁻⁷ –1.2 × 10 ⁻⁶); DALY risk 3.0 × 10 ⁻⁹ –2.4 × 10 ⁻⁸ (95 th 7.2 × 10 ⁻⁸ –3.1 × 10 ⁻⁸). Showering annual infection risk 3.6 × 10 ⁻⁷ –5.3 × 10 ⁻⁵ (95 th 1.3 × 10 ⁻⁶ –3.5 × 10 ⁻⁴); DALY risk 1.1 × 10 ⁻⁸ –1.6 × 10 ⁻⁶ (95 th 3.5 × 10 ⁻⁸ –9.3 × 10 ⁻⁶). Norovirus: Toilet flushing annual infection risk 5.3 × 10 ⁻⁷ –1.3 × 10 ⁻⁴ (95 th 1.6 × 10 ⁻⁶ –1.34 × 10 ⁻⁴); DALY risk 1.0 × 10 ⁻²⁰ –1.5 × 10 ⁻¹⁶ (95 th 5.3 × 10 ⁻¹⁹ –3.2 × 10 ⁻¹⁵). Showering annual infection risk 3.4 × 10 ⁻⁴ –4.3 × 10 ⁻² (95 th 1.6 × 10 ⁻³ –1.9 × 10 ⁻¹); DALY risk 1.1 × 10 ⁻¹⁴ –6.3 × 10 ⁻¹¹ (95 th 1.4 × 10 ⁻¹⁰ –1.0 × 10 ⁻⁷). Food crop annual infection risk 8.0 × 10 ⁻⁴ –9.8 × 10 ⁻¹ (95 th 2.6 × 10 ⁻²); DALY risk 8.0 × 10 ⁻¹⁴ –1.1 × 10 ⁻⁶ (95 th 3.3 × 10 ⁻¹⁰ –1.8 × 10 ⁻⁵)	Lim et al., 2015
<i>Campylobacter</i> <i>Cryptosporidium</i> RoV	Managed aquifer recharge with stormwater	Ingestion	Open space irrigation 1 mL, 50/year; toilet flushing 0.01 mL, 1,100/year; drinking 2 L/day	Log removals calculated to meet health targets for viruses (1.0–8.6), protozoa (0–>10.8), and bacteria (0.5–>16.0)	Page et al., 2015
<i>Campylobacter</i> spp. (human) <i>Campylobacter</i> spp. (zoonotic) <i>L. pneumophila</i>	Recreational exposure to urban stormwater plaza receiving street and roof runoff	Ingestion, inhalation	Ingestion: exposure volume triangular (0, 0.051, 5) mL/event; Inhalation: aerosolization ratio Normal (mean, SD 10 ^{-8.07} , 10 ^{0.3}), inhalation rate normal (mean log (22.7), SD 0.06 L/min), exposure duration 21 ± 5 min, exposure frequency mean 2.7 events/year for high rainfall, mean 6.5 events/year for low rainfall	<i>Campylobacter</i> spp. (human): 4.5 × 10 ⁻² (95 th 1.2 × 10 ⁻¹)/person/event <i>Campylobacter</i> spp. (zoonotic): 2.5 × 10 ⁻³ (95 th 9.2 × 10 ⁻³)/person/event <i>L. pneumophila</i> : 1.2 × 10 ⁻⁹ (95% 5.2 × 10 ⁻⁹)/person/event	Sales-Ortells and Medema, 2014, Sales-Ortells and Medema, 2015
<i>Campylobacter</i> ^a <i>Salmonella</i> spp. RoV HAdV <i>Cryptosporidium</i> ^a	Stormwater harvesting system in residential development, car park, or large urban catchment with ageing infrastructure; avian- or human sewage- driven contamination	Aerosol ingestion by community residents, Hand-to-mouth exposure by participants in sporting activities, Hand-to-mouth exposure of council workers watering trees, Accidental drinking incident	Aerosol ingestion 0.1 mL, weekly; hand-to-mouth exposure during sporting activities 1 mL, weekly; hand-to-mouth exposure of tree watering council workers 1 mL, daily; accidental drinking 100 mL, single exposure. Various sources of <i>E. coli</i> assumed.	<i>Campylobacter</i> aerosols 2.7 × 10 ⁻⁹ –0.1 (95 th 1.5 × 10 ⁻⁷ –7.0 × 10 ⁻²); hand-to-mouth 2.7 × 10 ⁻⁸ –0.15 (95 th 1.5 × 10 ⁻⁶ –0.12); accidental ingestion 2.7 × 10 ⁻⁶ –0.24 (95 th 1.5 × 10 ⁻⁴ –0.21) <i>Salmonella</i> spp. aerosols 1.3 × 10 ⁻¹² –5.0 × 10 ⁻⁵ (95 th 4.1 × 10 ⁻¹⁰ –7.0 × 10 ⁻²); hand-to-mouth 1.3 × 10 ⁻¹¹ –0.15 (95 th 4.1 × 10 ⁻⁹ –0.12)	Petterson et al., 2016

(continued on next page)

Table 3 (continued)

Pathogen	Applications	Exposure routes	Exposure frequency and duration	Risk Mean/Median (95 th percentile or upper bound) or calculated LRV	References
				Rotavirus aerosols 1.4×10^{-3} (95 th 4.3×10^{-1}); hand-to-mouth 1.3×10^{-2} (95 th 0.21); accidental ingestion 0.31 (95 th 1.0)	
				Adenovirus aerosols 1.3×10^{-3} (95 th $4.3e-1$); hand-to-mouth 1.3×10^{-2} (95 th 0.35); accidental ingestion 0.72 (95 th 1.0)	
				<i>Cryptosporidium</i> ^a aerosols 2.9×10^{-8} (95 th 7.7×10^{-7}); hand-to-mouth 2.9×10^{-7} (95 th 7.7×10^{-6}); accidental ingestion 2.9×10^{-5} (95 th 7.6×10^{-4})	
<i>Campylobacter</i>	Toilet flushing, irrigation, and swimming in stormwater wetland using different stormwater treatments (wetlands, biofilters, and traditional treatment trains)	Aerosol ingestion, routine ingestion (hand-to-mouth)*	Garden irrigation aerosol ingestion 0.1 mL/event, 90 events/person/year; garden irrigation (routine hand-to-mouth exposure) 1 mL/event, 90 events/person/year; Municipal irrigation 100 mL/event, 1 event/person/year; toilet flushing 0.01 mL/event, 1100 events/person/year. Multiple treatment options and dose response models evaluated.	Garden irrigation aerosol ingestion: per infection 1.1×10^{-9} - 3.1×10^{-3} , annual risk 1.0×10^{-7} - 1.4×10^{-1} (95 th 1.4×10^{-7} - 7.0×10^{-1}), DALY risk 1.3×10^{-10} - 2.2×10^{-1} (95 th 2.2×10^{-10} - 1.1×10^{-3}) Garden irrigation routine ingestion hand-to-mouth: per infection 1.1×10^{-6} - 2.4×10^{-1} , annual risk 1.0×10^{-6} - 2.4×10^{-1} (95 th 1.6×10^{-6} - 4.9×10^{-1}), DALY risk 1.4×10^{-9} - 3.9×10^{-4} (95 th 2.5×10^{-9} - 9.5×10^{-4}) Garden irrigation accidental ingestion: per infection 1.1×10^{-10} - 3.7×10^{-4} , annual risk 1.2×10^{-7} - 1.7×10^{-1} (95 th 1.7×10^{-7} - 7.8×10^{-1}), DALY risk 1.6×10^{-10} - 2.7×10^{-4} (95 th 2.7×10^{-10} - 1.2×10^{-3}) Municipal irrigation: per infection 1.1×10^{-8} - 2.6×10^{-3} , annual risk 1.0×10^{-6} - 1.4×10^{-1} (95 th 1.4×10^{-6} - 6.1×10^{-1}), DALY risk 1.3×10^{-9} - 2.3×10^{-4} (95 th 2.2×10^{-9} - 2.3×10^{-4}) Toilet flushing: per infection 1.1×10^{-8} - 2.4×10^{-1} , annual risk 5.6×10^{-7} - 2.4×10^{-1} (95 th 7.9×10^{-7} - 4.7×10^{-1}), DALY risk 7.2×10^{-10} - 3.9×10^{-4} (95 th 1.2×10^{-9} - 9.3×10^{-4})	Murphy et al., 2017
<i>Mastadenovirus</i> (adenovirus) Norovirus <i>Campylobacter</i> spp. <i>Salmonella</i> spp. <i>Giardia</i> spp. <i>Cryptosporidium</i> spp.	Indoor use (toilet flushing and clothes washing), accidental ingestion of treated non-potable water (cross-connection with potable water), unrestricted outdoor irrigation, drinking	Ingestion	Toilet flushing (3×10^{-5} L/day, 365 d/y), clothes washing (1×10^{-5} L/day, 365 d/y), irrigation and dust suppression (1×10^{-3} L/day, 50 d/y), Cross-connection of treated water with potable water (2 L/day, 1 day/year, 10% of population exposed), potable consumption (2 L/day, 365 days). Multiple dose response models used.	Log removals to achieve target concentrations associated with a 10^{-4} annual infection risk calculated: Norovirus: toilet flushing 2.5-7.3, unrestricted irrigation 3.2-8.0, indoor use 5.0-7.9, drinking 9.3-12.4. Mastadenovirus: toilet flushing 2.1-4.1, unrestricted irrigation 2.8-4.8, indoor use 3.9-5.9, drinking 6.9-8.9 <i>Cryptosporidium</i> spp.: toilet flushing 0.8-3.8, unrestricted	Schoen et al., 2017

Table 3 (continued)

Pathogen	Applications	Exposure routes	Exposure frequency and duration	Risk Mean/Median (95 th percentile or upper bound) or calculated LRV	References
				irrigation 1.6–4.5, indoor use 2.8–5.7, drinking 5.7–8.6	
				<i>Giardia</i> spp.: toilet flushing 0.5–2.5, unrestricted irrigation 1.3–3.3, indoor use 2.5–4.5, drinking 5.4–7.4	
				<i>Campylobacter</i> spp.: toilet flushing 1.4–3.4, unrestricted irrigation 2.1–4.1, indoor use 3.1–5.1, drinking 6.2–8.2	
				<i>Campylobacter</i> spp.: toilet flushing 0–1.8, unrestricted irrigation 0.6–2.6, indoor use 1.8–3.8, drinking 4.6–6.6	

^a Species not specified and based on surrogate data; dose response models for *C. jejuni*, *S. enterica*, *Cryptosporidium* spp. were used; *only potable and non-potable exposure scenarios included

et al., 2012a, 2012b; McBride et al., 2013; Sales-Ortells and Medema, 2015), limiting the ability to capture the large variability in stormwater pathogen concentrations due to potentially diverse fecal contamination sources (human and multiple animal fecal wastes, affecting the types of index pathogens chosen for the QMRA), rainfall patterns, decay rates, and other factors.

Monitoring efforts conducted to inform QMRAs by Petterson et al. (2016) and McBride et al. (2013) confirmed that variability in pathogen concentration is indeed high between rainfall and baseline events. There is therefore a need to look at a scenario-conditional risk estimate (sometimes referred to as “conditional risk”), rather than averaging or annualizing over time without regard to rainfall events. Pathogens can survive on urban surfaces and building materials, for example, and could furthermore be introduced into stormwater during subsequent rain events without the presence of an ongoing fecal source. This further supports the need for comparison of stormwater wet-weather risks with dry event (baseline) risks (Taylor et al., 2013).

Some of the principal challenge in conducting a QMRA for stormwater is determining the concentration of pathogens in stormwater discharges or harvesting systems, and addressing the complexities of their transport and inactivation prior to arrival at a human receptor. In lieu of a detailed hydrodynamic or fate and transport models for pathogens, simplified assumptions of decay and dilution between a pathogen source and human receptor are often made. Dilution factors are sometimes applied to estimate pathogen loads between stormwater and receiving recreational bodies; for example, McBride et al. (2013) used a 30-fold dilution factor applied to the concentrations of pathogens observed in stormwater discharges. Other studies have applied an estimated microbial decay factor for particular pathogens or indicators as surrogates for pathogens in stormwater, sometimes also coupled with a dilution factor (Petterson et al., 2016; Lim et al., 2015). The use of hydrodynamic mixing and inactivation models such as those applied by Andersen et al. (2013) could be used to obtain more accurate site-specific dilution information, or a distribution of dilution factors could be incorporated into a Monte Carlo approach in QMRA models as performed in Soller et al., 2017.

Improved characterization of different removal values for bacteria, protozoans and viruses in stormwater treatment processes can also improve QMRA estimates, as previous estimates have been based on FIB rather than pathogens themselves due to limited data (Davies et al., 2008; Page et al., 2010a, 2010b, 2010c, 2010d; Petterson et al., 2016). Limited information is available for pathogen removal by stormwater treatment barriers and would be informative for conducting risk

analyses. Additionally, these values can be compared with theoretical LRVs necessary to meet health risk targets (NRMCC-EPHC-AHMC, 2009; Page et al., 2015; Schoen and Garland, 2015; Schoen et al., 2017).

As stormwater concentrations of pathogens cannot always be directly measured, impacts to stormwater can also be estimated; Petterson et al. (2016) modelled avian contamination of stored stormwater resources with birds colonized by *Campylobacter* and *Salmonella* as well as pathogen inputs from human sewage using an epidemiologic approach, making use of information about disease incidence, pathogen excretion and known sewage flow rates to approximate loading rates in a typical sewage. Several recent studies used QMRA analysis to determine HF183 concentrations that represent human health risks to swimmers based on the recreational water quality criteria (RWQC) risk benchmark of 36/1000 primary contact recreators (USEPA, 2012a; Boehm et al., 2015; Ahmed et al., 2018d). Such approaches can also be undertaken to determine the health risks associated with different stormwater end use where the pathogen data is lacking or not available.

QMRA can be a useful tool for examining the potential human health risks related to rainfall events and can inform risk management practices (Bichai and Ashbolt, 2017). These assessments show that there are non-trivial risks associated with the use of stormwater resources to supplement water portfolios and in some cases guidelines are not sufficient to mitigate risks (Murphy et al., 2017). This is needed as stormwater harvesting areas can create new opportunities for co-mingling of potential animal habitats or reservoirs for animal fecal material and human recreational environments, where transmission of fecal pathogens can occur (Sales-Ortells and Medema, 2015; Petterson et al., 2016). While acknowledging the utility of QMRA, caution must be exercised when comparing risk estimates from QMRAs employing different methodologies. For example, a direct comparison of annual infection risks and annual disability adjusted life years (DALYs) (pppy) should be interpreted carefully as these methodologies can lead to different risk conclusions when compared to guideline values (Lim et al., 2015). Furthermore, it has been suggested that drinking water benchmarks could be too stringent for comparison with alternative water uses in some cases and warrants consideration of the development of more applicable guideline values (Mara, 2011; Schoen and Garland, 2015).

6. Reduction of microbial contaminants through WSUD/BMPs

Elevated levels of microbial contaminants in stormwater is of great concern for water safety. As a result, there is regulatory pressure to

remove contaminants so that risk benchmarks can be met. A variety of microbial contaminant mitigation measures can be used including the implementation of various types of stormwater infrastructure (Thurston et al., 2001; Struck et al., 2008). Fletcher et al. (2015) undertook a review of terminology associated with urban stormwater management in different countries. The terms reviewed included: WSUD, BMPs, Integrated Urban Water Management (IUWM), Low Impact Urban Design and Development (LIUDD), Low Impact Development (LID), Green Infrastructure, and Sustainable Urban Drainage Systems (SUDS). Their review identified that whilst the concepts are all underpinned by the principles of reducing disturbance to natural hydrology and mitigating the water quality impacts of urbanisation, there are subtle differences in the scope and focus of terms (Fletcher et al., 2015). However, for the purposes of this review the terms can be considered broadly analogous and are hereafter referred to as “WSUD”.

WSUD takes an integrated approach to managing stormwater that protects public health, while also mitigating the environmental impacts of urban development and provides for improved community amenity. WSUD has the objective of reducing the impact of urbanisation on the natural water cycle, and its principles can be applied at a range of scales (Lloyd et al., 2002). Davies (1996) proposed that, fundamentally, WSUD strives to maintain the water balance and water quality of an urbanized environment in much the same state as prior to urbanisation.

The approaches taken to implement WSUD will depend upon the development context and drivers for the adoption of WSUD. WSUD approaches often use a ‘treatment train’ where a series of treatment approaches are used to meet stormwater objectives. The approaches applied will depend upon the catchment characteristics, climate conditions and discharge requirements. Often the initial stages of a WSUD treatment train will focus on the removal of coarse sediments, which can help improve the treatment effectiveness of subsequent stages that use filtration and/or biological processes. In addition to the WSUD treatment approaches summarized below, non-structural catchment-scale approaches can be used to improve quality of runoff discharged to receiving waters (Wong, 2006). This can include buffers around waterways that limit potentially polluting land uses, and the revegetation of riparian zones. For example, Bryan et al. (2009) described the use of an adaptive management framework to reduce *Cryptosporidium* risk in an agricultural catchment in South Australia.

Although information regarding the degree of pathogen removal from various WSUDs can help for water quality managers and urban planners to design and maintain systems that adequately protect public health, data available on specific LRVs of pathogens through WSUD is limited (NRMMC-EPHC-NHMRC, 2009). Most studies have employed FIB to derive the LRVs of microbial removal in specific WSUD treatment processes and as such, and there is much less information on the removal of specific pathogens such as viruses and protozoa which have very different physico-chemical characteristics. A range of factors have an impact on the treatment capability of WSUD systems. The removal of pathogens varies from system to system and therefore, it may be useful to assess individual systems *in-situ* to account for local variability resulting from factors such as sedimentation, sunlight exposure, water temperature, and adsorption/desorption with biofilms (Jiang et al., 2015). Peng et al., 2016 highlighted that most microbe focused studies of stormwater biofilters focus on FIB, which are measured by culture-based methods, and less frequently by molecular based methods. These studies may be difficult to extrapolate to pathogens. There are few studies on the removal of pathogens, particularly viruses, in stormwater by biofiltration. Peng et al. (2016) also noted the need for more studies that use field-based measurements, rather than laboratory settings, as it captures the more variable and complex features of the urban environment that influences how effective WSUD approaches are likely to be in reducing pathogen loads.

One key resource for LRV in WSUD is the International Stormwater BMP Database. The database contains approximately 600 pairs of

influent and effluent data for fecal coliforms and *E. coli*. Among the 600 pairs, 100 pairs belong to *E. coli* from 12 sites in Portland, Oregon and the remaining 500 pairs are fecal coliform collected from 61 sites in California, Florida, Virginia, Ontario, New York, Texas, Georgia, North Carolina, and Oregon. Clary et al. (2008) analyzed the fecal coliform and *E. coli* datasets in the International Stormwater BMP database and provided results on how BMPs can effectively reduce fecal indicator concentrations in order to assist in meeting total maximum daily load (TMDL) goals. Swales and detention basins did not appear to effectively reduce FIB in effluent samples. Datasets for wetlands and manufactured devices were not of adequate size to draw meaningful conclusions. The authors concluded that the ability of BMPs to reduce FIB varies widely within BMP categories. No single BMP appears to be able to consistently reduce FIB in effluent to levels below instream primary contact recreation standard. Among the BMPs, retention pond and media filters appeared to have potential for bacteria removal in effluent.

Chandrasena et al. (2016) studied the removal of *E. coli* and *Campylobacter* spp. from urban stormwater by field-scale biofilters. *E. coli* LRVs (average 1.23–1.39 LRVs) were greater than that of *Campylobacter* spp. (average 0.88–0.99 LRVs) in both biofilters. The authors did not find any correlation between *E. coli* and *Campylobacter* spp. log removal performance suggesting that single organisms should not be employed to understand pathogen removal in urban stormwater treatment systems.

Such variations may affect performance evaluation as well as the impact of other factors including the selection of plants, use of a submerged zone in biofilters, and operation under wet vs. dry conditions (Jiang et al., 2015; Chandrasena et al., 2016). Generally, a one \log_{10} removal of FIB and pathogens can be expected if biofilters are properly designed accordingly to local guidance (Bichai and Ashbolt, 2017). However, the performance of such systems can be site specific, and therefore, undertaking *in situ* validation of specific devices has been recommended (Payne et al., 2015). While individual WSUD technologies performances are available, there is an expectation that there would be an improved or increased performance for the removal of contaminants when water is passed through a series of WSUD technologies prior to (re)use (Vogel et al., 2015).

This not only can increase the amount of contaminants removed, but can also enable a level of redundancy to be built in so that if treatment of an individual WSUD technologies declines, the resulting reduction in treatment capacity is covered by the rest of the WSUD treatment system. In addition, residence time is important for the removal of microorganisms, so the longer water is held within a WSUD treatment system, the greater the pathogen removal rates.

Table 4 provides information on the studied removal capacity of a range of WSUD treatment systems. While there is variability in the removal capacity of the different reported WSUD systems, in general all of these systems achieved 0.5 to 1 LRV for FIB and the bacterial pathogen *Campylobacter*. The results also show that bacterial removal is faster (or higher) than viral and protozoan pathogens, which tend to be more resistant to treatment processes, and therefore more able to survive through the different WSUD treatments. This is due to the differences in size surface characteristics, mode of reproduction and life cycle of viruses and protozoa which are different than those of bacteria (Hoff and Akin, 1986). In general, sequential treatment systems with a series of ponds, wetlands or combinations tend to improve pathogen removal from source water. For example, Reinoso et al. (2008) evaluated the removal of a variety of traditional and alternative fecal indicators such as coliphages, total coliform, *E. coli*, fecal streptococci and *C. perfringens* and pathogens such as *Cryptosporidium* spp. and *Giardia* spp. from domestic sewage in a treatment train including pond storage followed by surface and subsurface wetlands, with the overall *Cryptosporidium* and *Giardia* removal efficiency found to be as high as two \log_{10} . A new potential WSUD treatment component currently being studied is the addition of heavy metal (e.g., copper) labelled zeolite to filtration bed media. Laboratory research has demonstrated that copper coated zeolite can have LRV capability for bacteria such as *E. coli* greater than three \log_{10} (Li

et al., 2012). Stormwater can also be contaminated with viral and protozoan pathogens, both of which have higher treatment requirements than bacteria. However, the information on the effect of zeolites coated with heavy metals on these enteric non-bacterial pathogens is very limited. Silver/copper coated zeolites could reduce coronavirus by 2–3 LRVs (Bright et al., 2009) and silver-impregnated filtration pots reduced *Giardia* and *Cryptosporidium* by at least 96% (~1.5 LRV) (Adeyemo et al., 2015). More research would be needed to assess the treatment potential of copper-coated zeolite on a range of enteric viruses and protozoa under in-field conditions before its use could be justified as beneficial for the cost, particularly for the removal of pathogens.

7. Stormwater treatment and risk mitigation

Stormwater harvesting systems generally require some level of treatment to minimise operational risks. Additional treatment may also be required for higher exposure uses to manage human health and environmental risks. The operational risks relating to stormwater quality are usually managed by the use of BMPs/WSUDs. For example gross pollutant traps and vegetated swales to remove sediment and leaves entering the stormwater harvesting scheme and potentially blocking pipes, irrigation nozzles or drip irrigation systems, or damaging pumps. Use of wetlands and bio retentive systems can also assist in reducing high loads of organic matter (e.g. leaf fall) as well as removing nitrogen and phosphorus through phytoremediation. Additional levels of treatment are often required to manage human health risks, where stormwater from a sewered residential catchment is used for public, open-space irrigation (e.g. in schools and sporting ovals). Here, human health risks can be managed by the use of on-site access controls to minimise exposure to irrigation water. For example, the use of withholding periods on public recreation ovals has been recommended to reduce the risks from pathogens (Page et al., 2014b).

Additional treatments may be required for higher exposure uses, for example the Australian Guidelines for Stormwater Harvesting and Reuse (NRMHC-EPHC-NHMRC, 2009) describes the derivation of these criteria in terms of LRVs and also lists default LRV values for a range of engineered treatments. These accepted default LRV tables can be then used along with catchment specific knowledge where possible exposure controls are used to determine the required level of treatment for pathogens. For example, Page et al. (2012) reported that risks from viruses have the highest required LRV targets and if they are met then protozoan and bacterial LRV targets will also be met. It was reported that for open space irrigation requires <2.0 LRV is sufficient for stormwater recycled via an aquifer and this can potentially be managed using chlorination and exposure controls. However, if in the same system where stormwater is recycled via an aquifer were to be used for drinking water, a LRV of 5.5 would be required to manage human health risks from viruses (Page et al., 2014c). Generally these default LRVs apply where there has been no stormwater catchment-specific assessment of the health risks posed by the quality of the stormwater. Where such a site specific risk assessment has been performed, alternative treatment could be adopted (e.g., lower LRV targets may be adopted where microbial source tracking has found negligible sewage contamination in a catchment).

8. Research gaps and conclusions

- Monitoring of FIB in stormwater may not be useful unless synergistically used with MST marker genes such as HF183, crAssphage or Lachno3 which are able to differentiate between sources of fecal contamination. This will provide additional information on the human health risks associated with stormwater from point and non-point sources of fecal contamination. Identifying and quantifying sources of human sewage in stormwater is most important followed by cattle due to the presence of a wide array of enteric viruses and zoonotic pathogens in these sources.

- The concentration of pathogens in stormwater, outfalls and receiving environmental waters can be high, especially in urban areas. Monitoring of traditional FIB takes 24–48 h and does not provide real-time information on the quality of recreational water. This is important from a human health perspective. Swimming area closure causes economic losses. Therefore, it is recommended that a rapid pathogen monitoring toolbox and standardized methods need to be developed that are able to quantify a number of reference pathogens in waterbodies with increased accuracy, reliability, and less technical training under various conditions. The toolbox can be used either in the laboratory or in the field to provide a rapid assessment whether the stormwater from a particular storm event presents a hazard to public health.
- Most of the stormwater quality monitoring studies focused on determining the concentrations of pathogens in urban stormwater. However, more data is required on the concentration of pathogens in stormwater sourced from a range of land uses. While sewage discharges are relatively well characterized, there remain gaps in our understanding of runoff from nonpoint sources. More studies are required to determine the concentrations of zoonotic pathogens in stormwater.
- Fecal contamination in stormwater is largely dependent on the land uses and mostly include sewage, septage and various animal feces. Therefore it is imperative to determine the sources of contamination. This will in turn provide a basis for cost-effective remediation and information on the immediate human health risks in stormwater impacted waters. Currently used FIB monitoring approaches are inadequate due to their presence in both human and animal feces. An MST toolbox comprised of various human and animal feces-associated marker genes needs to be employed which will allow managers to quickly identify the relative contribution of point and non-point sources of fecal contamination.
- The quality of stormwater in terms of microbial contaminants is poorly understood. Microbial risk will be the dominant acute health risks on stormwater reuse due to the risk of waterborne pathogens (Hrudey and Hrudey, 2014). However, in some cases, chemical risks may be the driving health concern and relationships between multi-contaminant exposures should be explored. Few QMRA studies addressing potable and non-potable exposures to stormwater were available. Most of the QMRA studies are based on conservative assumptions. More data are required on the concentrations of pathogens and recovery from water samples across sites and stormwater hydrographs. In addition, improved understanding of the influence of catchment characteristics and baseline levels of pathogens, meteorological factors, and decay of pathogens is required for accurate QMRA estimates.
- Different types of WSUD and BMPs are able to reduce microbial contamination, however, reliable information is still lacking on the performance of these treatment barriers. Standardized natural treatment validation protocol needs to be developed. Most studies determined the efficacy of WSUD or BMPs on the removal of microorganisms using FIB, while one or two studies investigated the LRVs of protozoa pathogens such as *Cryptosporidium* spp. or *Giardia* spp. Given the differences in size and characteristics of different groups of pathogens, it is unlikely that FIB LRVs will be representative for pathogens especially enteric viruses. Therefore, studies should focus on determining the removal of enteric viruses and other pathogens (i.e., bacterial and protozoans) of interest to determine the removal rates through different types of WSUD and BMPs, simultaneously. These data will be important for evaluating the effectiveness of WSUD/BMPs for reducing microbial contaminants in the receiving environments and can support improved QMRA models. The evaluation will focus not only on the performance of individual component of WSUD/BMPs but also on a series of different types of BMPs.
- Little is known regarding the decay of pathogens in stormwater or outfalls, and the relative differences in persistence between FIB, pathogens, and host-associated markers. As stormwater becomes aged,

Table 4
Percentage of log reduction values (LRVs) of FIB and pathogens through WSUD.

WSUD approach	Study description	Location (climate)	Development setting	FIB and pathogens (influent concentrations)	% or Log Reduction Value(LRVs)	Notes and Reference
Retention ponds	Experimental testing of retention pond to investigate environmental mechanisms that influence microbial removal efficiency	Edison, N.J., USA (humid continental)	Experimental design with prepared bacterially loaded stormwater	<i>E. coli</i> (approx. 5.30 log ₁₀ CFU/100 mL)	1	Highlights importance of detention time, where concentration decreases exponentially with time (up to 50 h residence) Struck et al., 2008
	A wet pond monitored as part of a WSUD (BMPs) pilot evaluation (waterfowl freq. observed)	North Carolina, USA (humid subtropical)	Residential catchment of 48.6 ha	<i>E. coli</i> (3.95 log ₁₀ CFU/100 mL) Fecal coliform (3.32 log ₁₀ CFU/100 mL)	0.26 0.52	Log reduction value from geometric mean of influent and effluent samples Hathaway et al., 2009
Constructed wetland	Constructed wetland monitored as part of a WSUD (BMPs) pilot evaluation	North Carolina, USA (humid subtropical)	Residential catchment of 6.4 ha	<i>E. coli</i> (3.98 log ₁₀ CFU/100 mL) Fecal coliform (3.38 log ₁₀ CFU/100 mL)	0.18 0.35	Log reduction value from geometric mean of influent and effluent samples Hathaway et al., 2009
	Secondary treated sewage flows into duckweed pond followed (6 days HRT) followed by subsurface flow wetland (3.8 days HRT)	Arizona (very hot summers and mild winters)	Secondary treated sewage flows into duckweed pond followed by subsurface flow wetland	<i>Giardia</i> (1.14 log ₁₀ cysts/100 L) Coliphage (2.39 log ₁₀ PFU/mL) Fecal coliforms (3.86 log ₁₀ CFU/100 mL)	87% 95% 98%	subsurface flow wetland cells have a maximum depth of 1.4 m and are 61 m long and 8.2 m wide, planted with <i>Typha domingensis</i> , <i>Scirpus olneyi</i> , and <i>Populus fremontii</i> , total HRT of 10 days Thurston et al., 2001
	Trickling filter process treated sewage flows into surface flow wetland	Arizona (very hot summers and mild winters)	Urban sewage	Adenovirus (2.79–5.17 log ₁₀ GC/L)	<1	The wetlands ~0.03 km ² in size, consisting of planted bulrush and cattails, 7 days HRT, removal calculated from inflow and outflow virus data Rachmadi et al., 2016
	Surface flow wetland, where outflow is harvested, where it undergoes comprehensive treatment train, then used for non-potable uses. This study reports on pathogen reductions from wetland inflow to outflow	Melbourne, Australia (temperate)	Mixed-use catchment of 1020 ha mostly residential (23% impervious)	<i>Campylobacter</i> spp. (2.23–2.99 log ₁₀ MPN/L) <i>E. coli</i> (2.60–4.00 log ₁₀ MPN/L)	0.05 (–0.9–1.25) 0.96 (0.19–1.79)	<i>E. coli</i> found to poor indicator for <i>Campylobacter</i> as a reference pathogen Direct fecal deposition by waterfowl feces was a microbial source to stormwater wetlands, and explained variable results. Meng et al., 2018
	Stormwater harvesting scheme that supplements irrigation water to suburban golf club	Melbourne, Australia (temperate)	SW collected from 17 ha residential catchment (70% impervious)	<i>Campylobacter</i> spp. (1.00 log ₁₀ CFU/L) <i>E. coli</i> (4.79 log ₁₀ CFU/L)	0.78 (0.35–1.57) 1.38 (0.4–1.84)	Median values with min and max in parentheses Chandrasena et al., 2016
Biofilter	Field-scale testing system	Melbourne, Australia (temperate)	Treating runoff from 0.5 ha university car park (100% impervious)	<i>Campylobacter</i> spp. (1.47 log ₁₀ CFU/L) <i>E. coli</i> (5.30 log ₁₀ CFU/L)	0.90 (–0.28–2.05) 1.18 (0.82–1.80)	Median values with min and max in parentheses Chandrasena et al., 2016
	Laboratory experimental set-up	Melbourne, Australia (temperate)	Water taken from nearby wetland, then dosed with pathogen seed cultures	<i>Clostridium perfringens</i> (3.79 log ₁₀ CFU/100 mL) <i>E. coli</i> (4.95 log ₁₀ CFU/100 mL)	3.20 1.30	Mean values for all sampling runs. Performance was significantly reduced for samples taken following dry period compared to wet periods. Li et al., 2012

pathogens will start to decay and as result, the human health risks will also decrease. Studies should focus on determining the decay of pathogens in stormwater and outfalls or recreational water contaminated with stormwater. *In-situ* decay studies are preferable over laboratory microcosm studies where it is difficult to mimic real world scenarios.

9. Conclusions

Stormwater reuse can contribute to water conservation and water quality improvement and be a great water source to meet the ever-increasing demand on water supplies. However, human and environmental health risks associated with stormwater need to be assessed carefully. This is due to the presence of fecal pollution and associated pathogen in stormwater that are capable of causing illnesses in humans.

The research gaps discussed in this paper and other uncertainties associated with the performance of stormwater treatment systems needs to be investigated. Health risks can be assessed using a QMRA analysis, thus facilitating decision-making and risk management efforts. This may, in turn, increase the confidence of regulators and public health managers for adopting stormwater practice widely.

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