Quantification of Source Loading Inputs for a Microbial Risk Assessment Tool

May 2020

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May 2020
Report No. 2020/EXT/1699
ISBN 978-1-99-000933-4

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Client Report CSC20010

Prepared with support from Envirolink Large Advice Grant HZLC158

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PREPARED FOR:	**Horizons Regional Council, Environment Canterbury and Hawkes Bay Regional Council**
CLIENT REPORT No:	**CSC20010**
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ACKNOWLEDGEMENTS

ESR wishes to thank Envirolink for funding this research under contract HZLC158 and Environment Canterbury, Horizons Regional Council and Hawkes Bay Regional Council for supporting the Envirolink funding application.

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1. INTRODUCTION

Transport of microbial pathogens is a potential risk from various land use activities, such as application of faecal waste to land, and domestic on-site wastewater treatment systems disposal fields. Risk to human health occurs when these wastes, containing pathogens, infiltrate into groundwater resources used for drinking water. In 2010, it was recognised that one particular land use, domestic septic tanks, posed a risk to the quality of groundwater. In response, the *Guidelines for Separation Distances Based on Virus Transport between On-site Domestic Wastewater Systems and Wells* was published (Moore et al., 2010). These guidelines considered appropriate setback distances from septic tanks in order to protect drinking water sourced from wells. The guidelines calculated separation distances for domestic on-site wastewater treatment systems based on virus transport and removal in the subsurface environment.

Since the release of the 2010 guidelines, increased awareness of other potential sources of microbial groundwater contamination, not just from on-site wastewater treatment systems, have become an issue worthy of consideration for many regional councils in New Zealand. Regional councils need to be able to assist consent planners and rural and peri-urban communities in making decisions about the management of a range of activities near drinking water supply wells. A microbial risk assessment tool is one such tool that could be used in this context, focusing on the risk to human health from drinking-water where microbial pathogens are discharged onto or into land near a drinking-water supply well. Some existing land use activities fall within designated drinking-water protection zones (often defined retrospectively after the activity commenced), which triggers the requirement for a resource consent. Councils need a defensible method to support any recommendations to grant or decline these consents based on quantitative risk modelling.

Environment Canterbury and other regional councils have applied for an EnviroLink Tools Grant to engage ESR and GNS to develop a microbial risk assessment tool. This tool proposes to determine the microbial risks associated with multiple land use practices such as:

- Multiple domestic on-site wastewater management systems (i.e. septic tanks)
- Community size on-site wastewater management systems
- Dairy farming

- Sheep and beef farming
- Wildfowl
- Stormwater systems
- Stockyards
- Animal effluent/manure application to land

The first step in developing this tool involves the collation and quantification of the source loading inputs for the modelling and ultimately the assessment tool. Environment Canterbury, Horizons Regional Council and Hawkes Bay Regional Council have applied for a Large EnviroLink Advice Grant to engage ESR to collate microbial loading rates and provide the concentrations of different pathogens in faecal matter from the above identified land use practices. The report provides truncated tables pertaining to the complete data collated on all the above sources.

2. METHODOLOGY

2.1 LITERATURE REVIEW

Four scientific bibliographic databases and search engines were searched, namely ‘Web of Science’, ‘Science Direct’, ‘Pub Med’, and ‘Google’. Peer-reviewed journal articles, reports, technical notes and book chapters, that met the requirements for inclusion were included in the collation. Target publications were scientific journal articles, reports, technical notes and book chapters published in the last thirty years (1990–2020). Key word searches used are shown in Table 1 below.

Table 1: Key word search for the various land uses.

Land use	Key words used in search
Multiple domestic On-site Wastewater Management Systems (OWMS)	- On*site wastewater management systems AND microbial loading OR microbial concentration - On*site wastewater disposal systems AND microbial loading OR microbial concentration - Septic tanks AND microbial loading OR microbial concentration - Small biological wastewater system AND microbial loading OR microbial concentration - Decentralised wastewater AND microbial concentrations
Community size On-site Wastewater Management Systems	As above plus: - AND Marae - AND school - AND camping ground - AND subdivision
Dairy farming	- Dairy cows AND Campylobacter - Dairy cows AND Cryptosporidium - Dairy cows AND Enterococci OR Enteroccus - Dairy cows AND Escherichia - Dairy cows AND pathogens - Dairy cows AND f*eces OR faeces - Dairy cows AND shedding - Dairy cows AND environmental loading OR f*ecal loading
Sheep and beef farming	- Sheep AND as above - Beef AND as above - Cattle AND as above
Wildfowl	- Canada geese AND as above - Ducks AND as above - Seagulls AND as above - Swans AND as above
Stormwater systems	- Stormwater AND microbial loading - ‘Storm water’ AND microbial loading - Stormwater AND ‘Escherichia coli’ OR Campylobacter OR Salmonella OR enterococci OR Cryptosporidium OR Giardia
Stockyards	- Animal AND stockyard AND microbial loading

	- Animal AND 'stockyard' OR 'holding pen' AND 'Escherichia coli' OR Campylobacter OR Salmonella OR enterococci OR Cryptosporidium OR Giardia
Animal effluent/manure application	- Farm dairy effluent AND microbial indicators OR faecal indicators OR *E. coli* OR pathogens - FDE[1] AND microbial indicators OR faecal indicators OR *E. coli* OR pathogens - Farm dairy effluent AND land application AND microbial loading

Well over 100 articles were identified and accepted for inclusion as meeting the following criteria:

- the article was written in English,
- the article was primarily concerned with the concentration of microbial or loading rates of indicators and/or pathogens sourced from one or more of the various land uses identified in Section 1, page 5,
- the article described microbial concentrations or loading rates from field studies.

These articles are listed in the bibliography at the end of this report.

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[1] FDE: Farming Dairy Effluent

3. RESULTS

The following sections provide truncated tables of the results of the literature searches for microbial loading rates from various land uses.

3.1 MULTIPLE DOMESTIC ON-SITE WASTEWATER TREATMENT SYSTEMS (OWMS)

As in 2010, there remains a dearth of information concerning quantitative measured enteric virus concentrations within domestic On-site Wastewater Management Systems (OWMS) (Blaschke et al., 2016; Farnleitner et al., 2010; Canter and Knox, 1985). There is more data available for large centralised wastewater systems with regards to enteric virus concentrations (Dahling et al., 1989; Greening et al., 2000; Lodder and Husman, 2005). The enteric virus concentration data that is available for domestic OWMSs is largely variable compared to the data that is available for homogenised effluent from centralised treatment systems. This is because the concentrations within individual domestic OWMSs depend on whether there are infected people in the individual dwelling. When occupants of a household are unwell, the peak concentrations of those enteric viruses being shed into the OWMS will be much higher than a centralised wastewater facility, which offers dilution with non-contaminated wastewater (Blaschke et al., 2016). The literature review also found that microbial concentrations were typically sourced from a single OWMS not multiple. The microbial loading rates for domestic OWMSs are given in Table 2 below.

Table 2: Domestic On-site Wastewater Management Systems (OWMS) microbial loading rates (ordered by microorganism)

Country of origin	Year of publication	Source	Microorganism	Concentration (min)	Concentration (max)	Concentration units	References
Ireland	2014	6 domestic OWMS's, Ireland	Bacteroidales bacteria (BacHum)	8.23×10^3	5.72×10^4	gene copy concentration / 50ml	Keegan et al., 2014
USA	2015	North Carolina (Site 1)	*Clostridium perfringens*	3.00×10^1	7.00×10^2	cfu/100 ml	Schneeberger et al., 2015
USA	2015	North Carolina (Site 2)	*Clostridium perfringens*	1.00×10^2	4.20×10^4	cfu/100 ml	Schneeberger et al., 2015
USA	1998	1 High School OWMS	Coliphage (male-specific)	6.74×10^5 *		Coliphage/L	DeBorde et al., 1998
USA	1998	1 High School OWMS	Coliphage (somatic)	4.66×10^5		Coliphage/L	DeBorde et al., 1998
NZ	2001	1 domestic OWMS, Rotorua	*E. coli*	1.20×10^6		cfu/100 ml	Pang et al., 2004
Scotland	2016	32 domestic OWMS's Scotland	*E. coli*	1.00×10^3	1.00×10^7	mpn/100 mL	Richards et al., 2016
USA	2015	North Carolina (Site 1)	*E. coli*	2.40×10^3	9.80×10^4	cfu/100 mL	Schneeberger et al., 2015
USA	2015	North Carolina (Site 2)	*E. coli*	1.40×10^4	6.10×10^5	cfu/100 mL	Schneeberger et al., 2015
Ireland	2014	6 domestic OWMS's	*E. coli*	1.00×10^5		mpn/100 mL	Keegan et al., 2014
NZ	2019	1 domestic OWMS, Lincoln	*E. coli*	9.03×10^1	2.87×10^2	cfu/mL	Humphries et al., 2019
NZ	2001	1 domestic OWMS, Rotorua	*E. coli*	1.2×10^6		cfu/100 mL	Pang et al., 2004
USA	2015	North Carolina (Site 1)	Enterococci	1.70×10^3	3.70×10^5	cfu/100 ml	Schneeberger et al., 2015
USA	2015	North Carolina (Site 2)	Enterococci	1.10×10^4	3.10×10^6	cfu/100 ml	Schneeberger et al., 2015
NZ	2019	1 domestic OWMS, Lincoln	Enterococci	1.90×10^1	6.37×10^2	cfu/ml	Humphries et al., 2019
USA	1998	1 High School OWMS	Enterovirus	0.26	4.4	virus/L	DeBorde et al., 1998
NZ	2004	1 domestic OWMS, Rotorua	Faecal coliforms	2.30×10^6		cfu/100 ml	Pang et al., 2004
NZ	2001	OWMS effluent, Rotorua	Faecal coliforms	4.00×10^5		cfu/100 ml	Pang et al., 1996
NZ	1986	OWMS effluent	Faecal coliforms	2.30×10^6	5.1×10^6	cfu/100 mL	Sinton 1986
USA	2010	3 domestic OWMS's, Florida	Fecal coliforms	1.20×10^5	7.80×10^6	cfu/100 ml	Katz et al., 2010
USA	2011	1 commercial OWMS (restaurant), Wisconsin	Norovirus GI	7.96×10^4		genome copies/L	Borchardt et al., 2011

Country of origin	**Year of publication**	**Source**	**Microorganism**	**Concentration (min)**	**Concentration (max)**	**Concentration units**	**References**
USA	2020	3 domestic OWMS's	Norovirus GII	1.58×10^5	7.94×10^7	genome copies/L	Jahan et al., 2020
NZ	2019	1 domestic OWMS, Lincoln	phage	1.67×10^1	1.32×10^2	pfu/ml	Humphries et al., 2019
NZ	2004	1 domestic OWMS, Rotorua	phage (MS2 F-RNA phage)	1.01×10^6		pfu/100ml	Pang et al., 2004
Australia	2005	38 domestic OWMS's Australia	Thermotolerant coliforms	1.00×10^6		cfu/100 ml	Charles et al., 2005
Scotland	2016	32 domestic OWMS's, Scotland	Total coliforms	1.00×10^3	1.00×10^8	mpn/100 ml	Richards et al., 2016
Ireland	2014	6 domestic OWMS's, Ireland	Total coliforms	1.00×10^6	1.00×10^6	mpn/100 ml	Keegan et al., 2014

* Averaged result.

3.2 COMMUNITY SIZE ON-SITE WASTEWATER MANAGEMENT SYSTEMS

As mentioned in Section 3.1 there is more data available for large centralised wastewater systems with regards to enteric virus concentrations than an individual OWMS (Dahling et al., 1989; Greening et al., 2000; Lodder and Husman, 2005). The same can be said for community size on-site wastewater management systems. For the purpose of this report, community size systems included schools, marae, camping grounds and small subdivisions. The review of the literature revealed no additional microbial loading rates other than what is presented in Table 2 above.

3.3 DAIRY FARMING

Results for dairy farming microbial counts and loading rates are generally presented as outputs per animal per day. The loading rates calculated in this report account for the prevalence observed in animals during each study. A truncated table of the data collated is presented in Table 3 below. Further tables showing the prevalence during each study is provided in Table 4 below. Where there was little information on concentrations of microbes in NZ faecal samples, international studies were used alongside NZ prevalence data to generate loading rates. In addition, prevalence data can help to inform priority research on pathogen concentrations in NZ animals with high prevalence.

Table 3: Dairy Cow farming microbial loading rates (ordered by microorganism)

Country of origin	Year of publication	Season/time of year	Region	Bovine Source	Animals/samples per study	Microorganism	Loading rates (min)	Mean loading rate	Loading rates (max)	Units for faecal concentration	References
NZ	2008	Spring	National data (All 4 provinces)	Adult	40	*Campylobacter*		$3. \times 10^8$		MPN/g	Moriarty et al. (2008)
		Summer			40			1.1×10^6			
		Autumn			40			3.6×10^6			
		Winter			35			2.4×10^5			
		All seasons			155			6.8×10^6			
		Spring	Waikato		10	*Campylobacter*		4.8×10^8		MPN/g	Moriarty et al. (2008)
		Summer			10			2.4×10^5			
		Autumn			10			6.8×10^6			
		Winter			10			8.4×10^5			
		All seasons			40			3.8×10^6			
		Spring	Manawatu		10	*Campylobacter*		7.6×10^7		MPN/g	Moriarty et al. (2008)
		Summer			10			1.5×10^6			
		Autumn			10			2.4×10^5			
		Winter			10			2.4×10^5			
		All seasons			40			4.4×10^5			
		Spring	Canterbury		10	*Campylobacter*		3.6×10^9		MPN/g	Moriarty et al. (2008)
		Summer			10			1.0×10^9			
		Autumn			10			3.8×10^7			
		Winter			5			2.4×10^5			
		All seasons			35			2.9×10^8			
		Spring	Southland		10	*Campylobacter*		1.0×10^8		MPN/g	Moriarty et al. (2008)
		Summer			10			2.4×10^5			
		Autumn			10			4.4×10^5			
		Winter			10			5.1×10^7			
		All seasons			40			7.4×10^6			

Country of origin	Year of publication	Season/time of year	Region	Bovine Source	Animals/samples per study	Microorganism	Loading rates (min)	Mean loading rate	Loading rates (max)	Units for faecal concentration	References
NZ	2014	Autumn	Waikato	Adult: partial herd home/pasture	45	*Campylobacter jejuni*	0.0×10^0	6.8×10^4	1.1×10^{10}	MPN/g	Rapp et al. (2014)
		Winter			45		0.0×10^0	3.4×10^6	3.4×10^{10}		
		Spring			45		0.0×10^0	2.7×10^6	3.4×10^9		
		Summer			45		0.0×10^0	1.4×10^5	3.4×10^{10}		
		Winter			105		5.42×10^5	4.3×10^7	6.8×10^9		
		Summer			105		2.71×10^4	2.7×10^6	3.4×10^9		
		Autumn		Adult:pasture	45		0.00×10^0	0.0×10^0	3.4×10^{10}		Rapp et al. (2014)
		Winter			45		0.00×10^0	5.4×10^5	1.3×10^{10}		
		Spring			45		0.00×10^0	8.5×10^5	3.4×10^9		
		Summer			45		0.00×10^0	1.7×10^6	6.8×10^{10}		
		Winter			105		8.51×10^6	6.8×10^7	3.4×10^8		
		Summer			105		1.75×10^4	5.4×10^6	1.3×10^8		
		Winter		Adult: stand-off_pads	105		1.90×10^6	3.0×10^7	1.2×10^{10}		Rapp et al. (2014)
		Summer			105		0.00×10^0	2.4×10^6	1.9×10^8		
USA	2008		Texas	Adult	4	*Campylobacter*		4.0×10^5		CFU/mL	Krueger et al. (2008)
				Adult steers	18	*Campylobacter jejuni*		5.1×10^7			
Denmark	2002	August to October	Southern Jutland	Calf ≤ 4 months	107	*Campylobacter* (thermophilic)		2.6×10^8		CFU/g	Neilsen (2002)
				Young cattle >4 months	105			3.9×10^6			
				Adult	120			2.9×10^5			

Country of origin	Year of publication	Season/time of year	Region	Bovine Source	Animals/samples per study	Microorganism	Loading rates (min)	Mean loading rate	Loading rates (max)	Units for faecal concentration	References
NZ	2008	All seasons	Four districts*	Adult	155	*Cryptosporidium*	1.29 x 10^{3}		3.2 x 10^{4}	Oocysts/g	Moriarty et al. (2008)
NZ	2005	Spring	Manawatu	Calf-new born	156	*Cryptosporidium parvum*	0.00 x 10^{0}		5.2 x 10^{9}	Oocysts/g	Grinberg et al. (2005)
Spain	2007		Galicia NorthWestSpain	Adult	379	*Cryptosporidium parvum*	3.2 x 10^{3}	1.2 x 10^{5}	7.46 x 10^{5}	Oocysts/g	Castro-Hermida et al. (2007)
USA	2001	Calving season	South Eastern New York	Calf - 4 to 21 days old	478	*Cryptosporidium parvum*		3.89 x 10^{0}¥		Oocysts/g	Nydam et al. (2001)
Japan	2000	June to March	Hyogo prefecture	Calf <30 days	30	*Cryptosporidium parvum*	3.72 x 10^{9}	6.00 x 10^{11}	1.1 x 10^{12}	Oocysts/g	Uga et al. (2000)
Canada	1999	Spring-Summer	Lethbridge, Alberta	Calf 1-120 days	20	*Cryptosporidium*	0.0 x 10^{0}		2.0 x 10^{9}	Oocysts/g	O' Handley et al. (1999)
NZ	2008	Winter	Hamilton	Adult	64	*E. coli*	2.32 x 10^{6}	4.8 x 10^{7}	1.7 x 10^{9}	MPN/g	Donnison et al. (2008)
		Winter			48		5.38 x 10^{4}	1.4 x 10^{7}	8.1 x 10^{8}		
		Winter			64			3.1 x 10^{8}			
		Winter			48			8.7 x 10^{7}			
		Summer		Adult	21	*E. coli*		1.7 x 10^{9}		MPN/g	Vanderholm (1984)
NZ	2008	spring	National data (All 4 provinces)	Adult	40	*E. coli*		1.9 x 10^{9}		MPN/g	Moriarty et al. (2008)
		summer			40			2.3 x 10^{9}			
		autumn			40			2.9 x 10^{9}			
		winter			35			2.7 x 10^{8}			
		all seasons			155			2.0 x 10^{9}			
		Spring	Waikato		10	*E. coli*		3.2 x 10^{10}		MPN/g	Moriarty et al. (2008)
		Summer			10			5.5 x 10^{9}			
		Autumn			10			6.8 x 10^{9}			
		Winter			10			2.7 x 10^{10}			
		All seasons	Waikato		40			1.3 x 10^{10}			
		Spring	Manawatu		10	*E. coli*		7.7 x 10^{9}		MPN/g	Moriarty et al. (2008)
		Summer			10			1.5 x 10^{9}			
		Autumn			10			7.5 x 10^{9}			
		Winter			10			9.2 x 10^{8}			
		All seasons			40			2.3 x 10^{9}			
		Spring	Canterbury		10	*E. coli*		3.2 x 10^{8}		MPN/g	Moriarty et al. (2008)

Country of origin	Year of publication	Season/time of year	Region	Bovine Source	Animals/samples per study	Microorganism	Loading rates (min)	Mean loading rate	Loading rates (max)	Units for faecal concentration	References
NZ	2008	Summer			10			1.7×10^9			
		Autumn			10			2.7×10^8			
		Winter			5			7.7×10^6			
		All seasons			35			4.2×10^8			
		Spring	Southland		10	*E. coli*		6.2×10^7		MPN/g	Moriarty et al. (2008)
		Summer			10			4.5×10^9			
		Autumn			10			1.1×10^9			
		Winter			10			1.2×10^8			
		All seasons			40			5.7×10^8			
Japan	2004	All seasons		Adults at slaughter	97	STEC** *E. coli* *(stx PCR positive)*	0.00×10^0		9.7×10^8	CFU/g	Fukushima and Seki (2004)
		All seasons			97	STEC *E. coli* Group 1 *(stx1&/or stx2;* and *eae;* and *hly* virulence genes*)*	0.00×10^0		1.5×10^8	CFU/g	
USA	1995	All seasons	11-14 states	Calves	965	*E. coli* O157:H7	7.97×10^5	2.1×10^7	8.0×10^7	CFU/g	Zhao et al. (1995)
NZ	2008	spring	National data (All 4 provinces)	Adult	40	Enterococci		2.2×10^6		MPN/g	Moriarty et al. (2008)
		summer			40			2.2×10^7			
		autumn			40			1.5×10^7			
		winter			35			1.9×10^7			
		all seasons			155			1.1×10^7			
		Spring	Waikato		10	Enterococci		2.6×10^6		MPN/g	Moriarty et al. (2008)
		Summer			10			6.4×10^7			
		Autumn			10			6.9×10^6			
		Winter			10			1.1×10^7			
		All seasons			40			1.2×10^7			
		Spring	Manawatu		10	Enterococci		1.1×10^6		MPN/g	Moriarty et al. (2008)
		Summer			10			5.7×10^7			
		Autumn	Manawatu		10			5.9×10^5			
		Winter			10			1.2×10^7			
		All seasons			40			5.7×10^6			
		Spring	Canterbury		10	Enterococci		4.0×10^6		MPN/g	Moriarty et al. (2008)
		Summer			10			6.9×10^6			

Country of origin	Year of publication	Season/time of year	Region	Bovine Source	Animals/samples per study	Microorganism	Loading rates (min)	Mean loading rate	Loading rates (max)	Units for faecal concentration	References
		Autumn			10			6.4 x 10^{7}			
		Winter			5			3.7 x 10^{7}			
		All seasons			35			8.1 x 10^{6}			
		Spring	Southland		10	Enterococci		3.3 x 10^{6}		MPN/g	Moriarty et al. (2008)
		Summer			10			6.7 x 10^{6}			
		Autumn			10			6.9 x 10^{7}			
		Winter			10			3.0 x 10^{7}			
		All seasons			40			2.6 x 10^{7}			
NZ	2008	All seasons	Four provinces*	Adult	155	*Giardia*	1.12 x 10^{3}		1.9 x 10^{4}	Cysts/g	Moriarty et al. (2008)
Spain	2007		Galicia NorthWestSpain	Adult	379	*Giardia*	6.0 x 10^{3}	6.9 x 10^{4}	1.21 x 10^{6}	Cysts/g	Castro-Hermida et al. (2007)
Australia	2000	Summer	Western Australia	Calf- 14 days to 70 days	36	*Giardia duodenalis*		9.7 x 10^{5}‡			O'Handley et al. (2000)
Canada	2000	Autumn	Lethbridge, Alberta	Calf- 14 days to 70 days	28	*Giardia duodenalis*		4.0 x 10^{6}‡			O'Handley et al. (2000)
Canada	1999	Spring-Summer	Lethbridge, Alberta	Calf 1-120 days	20	*Giardia duodenalis*	0.0 x 10^{0}	1.3 x 10^{6}‡	2.0 x 10^{9}		O'Handley et al. (1999)
NZ	2008	all seasons	National data	adult	155	*Salmonella*€		0.0 x 10^{0}		CFU/g	Moriarty et al. (2008)
		all seasons	Waikato					0.0 x 10^{0}			
		all seasons	Manawatu					0.0 x 10^{0}			
		all seasons	Canterbury					0.0 x 10^{0}			
		all seasons	Southland					0.0 x 10^{0}			
NZ	2005	Spring	Manawatu	Calves-new born	156	*Salmonella*		0.00 x 10^{0}		CFU/g	Grinberg et al. (2005)

* Manawatu and Waikato positive for *Cryptosporidium* and not detected in Canterbury and Southland

¥Loading rate between days 6 and 12 inclusive (taken directly from scientific article)

**STEC Shiga-toxin producing *Escherichia coli*

[‡] reported as cysts/calf/over the period day 14 to day 70. O'Handley et al. (2000) noted that single faecal sample of a calf at a specific time underestimates rates of *Giardia* and *Cryptosporidium* as 100 % of calves tested from birth to 4 months carried *Cryptosporidium* and /or *Giardia* at some point in the longitudinal study. The loading rates from O'Handley et al. (1999) for *Giardia* make an assumption of 100% prevalence because all calves tested positive for *Giardia* cyst shedding at some time point within the 120-day period of the study. This study makes some useful observations about shedding rates.

[€] Note the NZ studies by Al Mawley et al. (2015a &b) which identify *Salmonella* in dairy calves (Table 3b).

Table 4: Prevalence data for NZ dairy cattle

Year of paper	Region	Dairy cow Source	Age of animal	Microorganism	Animal Prevalence	Farm prevalence	Number of animals/samples	Reference
2015	North island (5 regions) and South Island (2 regions)	Calf	1-5 day old	Bovine Rotavirus	20.0%		429	Al Mawley et al. (2015a&b)
			9-21 day old		19.8%		797	
2015	North island (5 regions) and South Island (2 regions)	Calf	1-5 day old	Bovine Coronavirus	5.3%		429	Al Mawley et al. (2015a&b)
			9-21 day old		6.1%		797	
2012	Canterbury	Calf	<3 months old	*Cryptosporidium parvum*	3%		80	Abeywardena et al. (2012)
			3-15 months old	*Cryptosporidium parvum*	1%		100	
			<3 months old	*Cryptosporidium hominis*	10%		80	
			3-15 months old	*Cryptosporidium hominis*	4%		100	
2015	North island (5 regions) and South Island (2 regions)	Calf	1-5 day old	*Cryptosporidium parvum*	5.8%		429	Al Mawley et al. (2015a&b)
			9-21 day old		15.8%		797	
2003	Waikato	Adult		*Cryptosporidium parvum*	0.6%		354	Learmonth et al. (2003)
		Calf			10.9%		304	

Year of paper	Region	Dairy cow Source	Age of animal	Microorganism	Animal Prevalence	Farm prevalence	Number of animals/samples	Reference
2012		Bobby calf		*E. coli* O157	18%	24%	309	Irshad et al. (2012)
2015	North island (5 regions) and South Island (2 regions)	Calf	1-5 day old	*Enterotoxigenic E. coli* (K99)	3.2%		429	Al Mawley et al. (2015a&b)
			9-21 day old		Not tested		-	
2018	Northland,Waikato,Taranaki,Manawatu-Wellington,Canterbury,Southland	Calf	2-21 days	STEC* E. coli- Any"'Top 7" STEC	20.3%	75%	1508	Browne et al. (2018)
				STEC O157	1.9%	15%	1508	
				STEC O26	7.2%	23%	1508	
				STEC O45	2.9%	18%	1508	
				STEC O103	5.0%	35%	1508	
				STEC O145	9.8%	43%	1508	
				STEC O121	0.0%	0%	1508	
				STEC O111	0.2%	0.6%	1508	
2018	Northland	Calf	2-21 days	STEC E. coli- Any"'Top 7" STEC	44%	100%	15	Browne et al. (2018)
	Northland			STEC O157	1%	10%	15	
	Northland			STEC O26	0%	0%	15	
	Northland			STEC O45	18%	60%	15	
	Northland			STEC O103	8%	50%	15	
	Northland			STEC O145	35%	80%	15	
	Northland			STEC O121	0%	0%	15	

Year of paper	**Region**	**Dairy cow Source**	**Age of animal**	**Microorganism**	**Animal Prevalence**	**Farm prevalence**	**Number of animals/samples**	**Reference**
2018	Waikato	Calf	2-21 days	STEC E. coli- Any"'Top 7" STEC	15%	66%	15	Browne et al. (2018)
	Waikato			STEC O157	2%	17%	15	
	Waikato			STEC O26	6%	11%	15	
	Waikato			STEC O45	1%	9%	15	
	Waikato			STEC O103	6%	40%	15	
	Waikato			STEC O145	6%	37%	15	
	Waikato			STEC O121	0%	0%	15	
2018	Taranaki	Calf	2-21 days	STEC E. coli- Any"'Top 7" STEC	15%	58%	15	Browne et al. (2018)
	Taranaki			STEC O157	0%	0%	15	
	Taranaki			STEC O26	9%	32%	15	
	Taranaki			STEC O45	0%	0%	15	
	Taranaki			STEC O103	2%	16%	15	
	Taranaki			STEC O145	8%	32%	15	
	Taranaki			STEC O121	0%	0%	15	
2018	Manawatu-Wellington	Calf	2-21 days	STEC E. coli- Any"'Top 7" STEC	21%	83%	15	Browne et al. (2018)
	Manawatu-Wellington			STEC O157	9%	50%	15	
	Manawatu-Wellington			STEC O26	3%	8%	15	
	Manawatu-Wellington			STEC O45	2%	33%	15	
	Manawatu-Wellington			STEC O103	7%	42%	15	

Year of paper	Region	Dairy cow Source	Age of animal	Microorganism	Animal Prevalence	Farm prevalence	Number of animals/samples	Reference
	Manawatu-Wellington			STEC O145	7%	42%	15	
	Manawatu-Wellington			STEC O121	0%	0%	15	
2018	Canterbury	Calf	2-21 days	STEC E. coli- Any"'Top 7" STEC	18%	79%	15	Browne et al. (2018)
	Canterbury			STEC O157	1%	7%	15	
	Canterbury			STEC O26	11%	43%	15	
	Canterbury			STEC O45	2%	14%	15	
	Canterbury			STEC O103	3%	29%	15	
	Canterbury			STEC O145	7%	43%	15	
	Canterbury			STEC O121	0%	0%	15	
2018	Southland	Calf	2-21 days	STEC E. coli- Any"'Top 7" STEC	26%	92%	15	Browne et al. (2018)
	Southland			STEC O157	8%	1%	15	
	Southland			STEC O26	14%	50%	15	
	Southland			STEC O45	2%	25%	15	
	Southland			STEC O103	7%	42%	15	
	Southland			STEC O145	9%	50%	15	
	Southland			STEC O121	0%	0%	15	
2006		Adult		STEC *E. coli*-stx1 gene	4%		72	Cookson et al. (2006)
				STEC *E. coli*-stx2 gene	6%		72	
				STEC *E. coli*-stx1 + stx2 genes	0.0%		72	

Year of paper	**Region**	**Dairy cow Source**	**Age of animal**	**Microorganism**	**Animal Prevalence**	**Farm prevalence**	**Number of animals/samples**	**Reference**
				STEC *E. coli*-stx1 +eae gene	1.4%		72	
				STEC *E. coli*-stx2 + eae genes	0.0%		72	
				STEC *E. coli*-stx1 gene				
				STEC *E. coli*-stx2 gene				
				STEC *E. coli*-stx1 + stx2 genes				
2012	Canterbury	Calf	<3 months old	*Giardia duodenalis* Assemblage:** E (78%), A (22%)	11%		80	Abeywardena et al. (2012)
			3-15 months old	*Giardia duodenalis* Assemblage: E (100%)	2%		100	
2008		Calf - 3-4months old		*Giardia* Assemblage: A (88%), B (12%)	31%		1170	Winkworth et al. (2008)
2003	Waikato	Adult		*Giardia intestinalis*	4.5%		354	Learmonth et al. (2003)
		Calf			10.5%		304	
2000		Calf - ≤8weeks old		*Giardia* Assemblage: A (73%), B (27%)	41%		700	Hunt et al. (2000)
2015	North island (5 regions) and South Island (2 regions)	Calf	1-5 day old	*Salmonella*	6.0%		429	Al Mawley et al. (2015a&b)
			9-21 day old		0.5%		797	

*STEC Shiga-toxin producing *Escherichia coli*

** *Giardia* Genotype Assemblages A & B occur in human infections and are potentially zoonotic, whereas Assemblage E is non-zoonotic.

3.4 SHEEP AND BEEF FARMING

Where there was little information on concentrations of microbes in NZ faecal samples, international studies were used alongside NZ prevalence data to generate loading rates. In addition, prevalence data helps to inform priority research on pathogen concentrations in NZ animals with high prevalence.

Table 5: Sheep (ovine) farming microbial loading rates (ordered by microorganism). Loading rates are calculated per animal/day*

Country of origin	Year of publication	Ovine Source	Microorganism	Loading rates (min)	Median/Mean loading rate	Loading rates (max)	Units	References
Scotland	2009	adult	*Campylobacter*		7.5×10^{7}			Ogden et al., 2009
NZ	2011	lambs	*Campylobacter*		4.0×10^{8}		CFU/g	Moriarty et al., 2011
NZ	2011	≥1 year	*Campylobacter*		9.5×10^{5}		MPN/g	Moriarty et al., 2011
Australia	2017	pre-slaughter at saleyards	*Campylobacter*	1.0×10^{7}	1.3×10^{8}	5.64×10^{10}	organisms/g	Yang et al., 2017
Belgium	2008	lambs	*Cryptosporidium*	0.0×10^{0}	1.3×10^{6}	5.91×10^{7}	oocysts/g	Geurden et al., 2008
Spain	2007	adult	*Cryptosporidium parvum*	6.4×10^{2}	4.2×10^{3}	4.09×10^{4}	oocysts/g	Castro-Hermida et al., 2007
NZ	2011	lambs	*Cryptosporidium*		3.8×10^{6}		oocysts/g	Moriarty et al., 2011
NZ	2011	lambs	*E. coli*		9.1×10^{11}		MPN/g	Moriarty et al., 2011
NZ	2011	≥1 year	*E. coli*		2.4×10^{10}		MPN/g	Moriarty et al., 2011
Scotland	2005	adult	*E. coli* O157	0.0×10^{0}	1.1×10^{7}	1.46×10^{8}	CFU/g	Ogden et al., 2005
Australia	2017	pre-slaughter at saleyards	*E. coli* O157/O145	1.1×10^{6}	2.1×10^{7}	1.64×10^{8}	organisms/g	Yang et al., 2017
NZ	1997	adult	Enterococci		1.8×10^{7}		CFU/g	Anderson et al., 1997
NZ	2011	lambs	Enterococci		2.2×10^{11}		MPN/g	Moriarty et al., 2011
NZ	2011	≥1 year	Enterococci		1.0×10^{9}		MPN/g	Moriarty et al., 2011

Country of origin	Year of publication	Ovine Source	Microorganism	Loading rates (min)	Median/Mean loading rate	Loading rates (max)	Units	References
Belgium	2008	lambs	*Giardia*	0.0×10^{0}	1.8×10^{6}	4.71×10^{7}	cysts/g	Geurden et al., 2008
NZ	2011	lambs	*Giardia*		1.6×10^{4}		cysts/g	Moriarty et al., 2011
Australia	2014	pre-weaning (12weeks)	*Giardia*	1.5×10^{4}	4.1×10^{6}	3.10×10^{11}	cysts/g	Yang et al., 2014
Australia	2014	post-weaning (19weeks)	*Giardia*	2.0×10^{4}	3.1×10^{6}	3.55×10^{11}	cysts/g	Yang et al., 2014
Australia	2014	pre-slaughter (29weeks)	*Giardia*	2.2×10^{4}	2.8×10^{7}	1.65×10^{12}	cysts/g	Yang et al., 2014
Spain	2007	adult	*Giardia duodenalis*	4.6×10^{3}	9.3×10^{4}	8.67×10^{5}	cysts/g	Castro-Hermida et al., 2007
Australia	2017	pre-slaughter at saleyards	*Salmonella enterica*	2.8×10^{6}	4.3×10^{7}	2.08×10^{9}	organisms/g	Yang et al., 2017

* the numbers of samples/animals in each study are available from ESR.

Table 6: Prevalence data for NZ sheep

Year of paper	Sheep Source	Microorganism	Prevalence	Number of sheep	Reference
2011	lambs	*Salmonella*	1.9%	105	Moriarty et al. (2011)
	lambs	STEC *E. coli*	3.8%	105	
	≥1 year	*Salmonella*	0.0%	220	
	≥1 year	STEC *E. coli*	0.9%	220	
	≥1 year	*Cryptosporidium*	3.6%	220	
2006	lambs(3-4months_old)	STEC *E. coli*-stx1 gene	48%	46	Cookson et al. (2006)
	lambs(3-4months_old)	STEC *E. coli*-stx2 gene	9%	46	
	lambs(3-4months_old)	*STEC E. coli*-stx1 + stx2 genes	17%	46	
	lambs(3-4months_old)	STEC *E. coli*-stx1 +eae gene	0%	46	
	lambs(3-4months_old)	*STEC E. coli*-stx2 + eae genes	0%	46	
	ewes	STEC *E. coli*-stx1 gene	**56%**	**50**	
	ewes	STEC *E. coli*-stx2 gene	**18%**	**50**	
	ewes	*STEC E. coli*-stx1 + stx2 genes	28%	**50**	
	ewes	STEC *E. coli*-stx1 +eae gene	4%	**50**	
	ewes	*STEC E. coli*-stx2 + eae genes	0%	**50**	

Table 7: Beef cattle farming microbial loading rates (ordered by microorganism). Loading rates are outputs per animal/day.

Country of origin	Year of paper	Bovine Source	Animals per study	Microorganism	Loading rates (min)	Median/Mean loading rate	Loading rates (max)	Units	References
UK	1998	beef cattle	360	*Campylobacter* (thermophilic)		1.4×10^7		MPN/g	Stanley et al., 1998
USA	2008	beef cattle	4	*Campylobacter*		4.0×10^5		CFU/mL	Krueger et al., 2008
Scotland	2009	beef cattle	474	*Campylobacter*		1.6×10^8		CFU/g	Ogden et al., 2009
USA	2008	beef cattle	18	*Campylobacter jejuni*		3.5×10^8		CFU/mL	Krueger et al., 2008
USA	2012	beef cattle	201	*Cryptosporidium* (subset = *C. andersonii*)		3.00×10^7		oocysts/g	Oates et al., 2012
USA	2003	beef cattle	240	*Cryptosporidium parvum*		3,900 to 9,200		oocysts/g	Atwill et al., 2003
Japan	2004	beef cattle plus dairy	479	*E. coli* O157:H7	4.1×10^7		4.1×10^{10}	CFU/g	Fukushima and Seki 2004
Japan	2004	beef cattle plus dairy	605	STEC *E. coli*	0.0×10^0		3.9E+11	CFU/g	
Japan	2004	beef cattle	479	STEC *E. coli* (*stx* PCR positive)	0.0×10^0		9.2E+11	CFU/g	
Japan	2004	beef cattle	479	STEC *E. coli Group 1 (stx1&/or stx2; and eae; and hly virulence genes*	0.0×10^0		1.3E+11	CFU/g	
USA	2012	beef cattle	201	*Giardia*		7.70×10^6		cysts/g	Oates et al., 2012
USA	2009	feedlot cattle in pens	226	*Giardia duodenalis*	0.0×10^0		7.4E+07	cysts/g	Hoar et al., 2009
USA	2009	feedlot cattle in pens	242	*Giardia duodenalis*	0.0×10^0		4.7E+06	cysts/g	

USA	2009	feedlot cattle in pens	236	*Giardia duodenalis*	0.0×10^{0}		4.2E+07	cysts/g	
USA	2009	feedlot cattle in pens	240	*Giardia duodenalis*	7.3×10^{5}		6.7E+06	cysts/g	
USA	2009	feedlot cattle in pens	240	*Giardia duodenalis*	5.5×10^{6}		1.1E+09	cysts/g	
USA	2009	feedlot cattle in pens	238	*Giardia duodenalis*	0.0×10^{0}		1.2E+08	cysts/g	
USA	2009	feedlot cattle in pens	240	*Giardia duodenalis*	1.0×10^{6}		8.9E+08	cysts/g	
USA	2009	feedlot cattle in pens	240	*Giardia duodenalis*	1.5×10^{7}		2.2E+09	cysts/g	

Table 8: Prevalence data for NZ beef cattle

Year of paper	Sheep Source	Microorganism	Prevalence	Number of cattle	Reference
2014	<7 day old bobby calves at slaughter	STEC *E. coli (stx1, stx2, eae, ehxA genes)*	2.7%	299	Irshad et al. (2014)
		enteropathogenic *(EPEC) E. coli* *(eae, bfpA* gene but *stx* negative)	12.4%	299	
		All *E. coli* (stx1_&/_stx2_&/_eae_&/_ehxA genes)	17.7%	299	
2006	weaned calves (3-4months_old)	STEC *E. coli*-stx1 gene	2%	91	Cookson et al. (2006)
		STEC *E. coli*-stx2 gene	19%	91	
		STEC E. coli-stx1 + stx2 genes	0	91	
		STEC *E. coli*-stx1 +eae gene	14%	91	
		STEC E. coli-stx2 + eae genes	1%	91	
2006	Heifers (<12months_old)	STEC *E. coli*-stx1 gene	0%	24	Cookson et al. (2006)
		STEC *E. coli*-stx2 gene	38%	24	
		STEC E. coli-stx1 + stx2 genes	0%	24	
		STEC *E. coli*-stx1 +eae gene	13%	24	
		STEC E. coli-stx2 + eae genes	0%	24	

3.5 WILDFOWL

Where there was little information on concentrations of microbes in NZ faecal samples for particular wildfowl species, international studies were used alongside NZ prevalence data to generate loading rates. Prevalence data helps to inform priority research on pathogen concentrations in NZ wildfowl with high prevalence.

Table 9: Wildfowl microbial loading rates (ordered by wildfowl type).

Country of origin	Year of publication	Bovine Source	Animals per study	Microorganism	Loading rates (min)	Median/Mean loading rate	Loading rates (max)	Units	References
NZ	2011	Black swans	80	*Campylobacter* spp.		8.53×10^{4}		MPN/g	Moriarty et al. (2011)
			80	*E. coli*		7.98×10^{8}		MPN/g	
			80	Enterococci		4.59×10^{8}		MPN/g	
			80	*Salmonella* sp.		0.00×10^{0}		MPN/g	
NZ	2011	Canada geese	80	*Campylobacter* spp.		1.21×10^{6}		MPN/g	Moriarty et al. (2011)
			80	*E. coli*		9.03×10^{6}		MPN/g	
			80	Enterococci		6.25×10^{6}		MPN/g	
			80	*Salmonella* sp.		0.00×10^{0}		MPN/g	
Scotland	2009	Ducks	46	*Campylobacter*		1.8×10^{7}		CFU/g	Ogden et al. (2009)
NZ	2011	Ducks	80	*Campylobacter* spp.		1.99×10^{4}		MPN/g	Moriarty et al. (2011)
		Ducks	80	*E. coli*		3.18×10^{10}		MPN/g	
USA	2003	Ducks	16	*E. coli*	1.60×10^{8}		3.40×10^{8}	CFU/g	Haack et al. (2003)
NZ	2011	Ducks	80	Enterococci		3.39×10^{10}		MPN/g	Moriarty et al. (2011)
NZ	2007	Ducks	2	Enterococci		1.14×10^{8}		CFU/g	Anderson et al. (1997)
USA	2003	Ducks	13	Enterococci	5.60×10^{8}		1.30×10^{9}	CFU/g	Haack et al. (2003)

England	1978	Ducks	unk	faecal coliforms		1.11×10^{10}		CFU/g	Gould et al. (1978)
		Ducks	unk	faecal streptococci		1.81×10^{10}		CFU/g	
NZ	2011	Ducks	80	*Salmonella* sp.		0.00×10^{0}		MPN/g	Moriarty et al. (2011)
England	1978	Ducks		Salmonella sp.		0.00×10^{0}			Gould et al. (1978)
USA	2003	Geese	16	*E. coli*		1.0×10^{6}		CFU/g	Haack et al. (2003)
		Geese	13	Enterococci		1.2×10^{5}		CFU/g	
Scotland	2009	Geese	68	*Campylobacter*		1.3×10^{7}		CFU/g	Ogden et al. (2009)
Scotland	2009	Gulls	216	*Campylobacter*		1.1×10^{5}		CFU/g	Ogden et al. (2009)
NZ	2011	Gulls	80	*Campylobacter* spp.		3.83×10^{4}		MPN/g	Moriarty et al. (2011)
		Gulls	80	*E. coli*		9.35×10^{8}		MPN/g	
USA	2003	Gulls	16	*E. coli*	1.60×10^{8}		3.40×10^{8}	CFU/g	Haack et al. (2003)
NZ	2011	Gulls	80	Enterococci		4.45×10^{8}		MPN/g	Moriarty et al. (2011)
NZ	2007	Gulls	2	Enterococci		2.08×10^{5}		CFU/g	Anderson et al. (1997)
USA	2003	Gulls	13	Enterococci	5.60×10^{8}		1.30×10^{9}	CFU/g	Haack et al. (2003)
NZ	2011	Gulls	80	*Salmonella* sp.		0.00×10^{0}		MPN/g	Moriarty et al. (2011)
USA	2012	Gulls	145	*Cryptosporidium*		0.00×10^{0}		oocysts/g	Oates et al. (2012)
		Gulls	145	*Giardia*		2.37×10^{1}		cysts/g	
Scotland	2009	Pigeon	255	*Campylobacter*		6.2×10^{5}		CFU/g	Ogden et al. (2009)
USA	2003	Pigeon	16	*E. coli*		1.4×10^{11}		CFU/g	Haack et al. (2003)
USA	2003	Pigeon	13	Enterococci		1.5×10^{11}		CFU/g	Haack et al. (2003)
Scotland	2009	unknown avian species	114	*Campylobacter*		3.7×10^{4}		CFU/g	Ogden et al. (2009)

Table 10: *Cryptosporidium* prevalence in NZ Wildfowl (concentration data not available)

Year of paper	Bovine Source	Animals per study	Microorganism	Prevalence	References
2011	Black swans	80	*Cryptosporidium* sp.	2.5%	Moriarty et al. (2011)
	Canada geese	80		5.0%	
	Ducks	80		1.3%	
	Gulls	80		0.0%	

3.6 STORMWATER SYSTEMS

Pathogens can be found in stormwater runoff and subsequently transported to environmental water bodies through sewer overflows, and urban and agricultural runoff. Faecal contamination in stormwater is largely dependent on the land use in the catchment and mostly includes sewage, septage and animal faeces. Storm events have the potential to re-suspend sediment-bound faecal indicator bacteria (FIB) and pathogens back into the water column, resulting in elevated levels of contamination. Depending on the catchment, runoff can be expected to occur year-round with stormwater runoff occurring primarily in winter and spring, and dry-weather runoff from irrigation of residential landscapes and car washing occurring when precipitation is low (Huang et al. 2018).

Routine monitoring of stormwater quality focuses on quantification of *E. coli* and enterococcus. Rainfall-induced microbial contamination of surface waters due to stormwater runoff, combined sewer overflows (CSO) and sanitary sewer overflows (SSO) has been well documented. High concentrations (>4 $\log_{10}$ cfu/100 ml) of FIB are generally found in stormwater runoff and receiving waters, and a number of studies report the presence of enteric pathogens or faeces-associated genetic markers in stormwater (Jiang et al. 2015, Noble et al. 2006, Rajal et al. 2007, AWQC 2008, Sidhu et al. 2012, Cizek et al. 2008, Steele et al. 2018). Nonetheless, data on pathogen abundance in stormwater runoff and outfalls remain scarce, and the overall quality of stormwater in terms of microbial contaminants is poorly understood (Ahmed et al. 2019).

In general, concentrations of pathogens in stormwater are poorly reported and some data may not be useful to infer risk or for QMRA (Ahmed et al. 2019). For example, several studies have provided the percentage for positive samples for pathogens without giving quantitative numbers (Surbeck et al. 2006, Rajal et al. 2007, Sidhu et al, 2012, Bambic et al., 2015).

Rural or high density residential areas are reported to contribute 30-50 times greater *E. coli* levels in stormwater compared with sparsely populated residential areas (McCarthy et al. 2006). Reports of high intra-event and inter-event variability, variation with season.

Care with qPCR data - complex matrices such as stormwater may contain various organic substances, salts, acids, detergents etc that may inhibit qPCR and produce false negative or low results (Ahmed et al. 2019)

Persistence of pathogens in stormwater compared with other matrices has not been well characterised. A systematic review by Bohem et al. 2018 indicated that few decay constants were available for protozoan and viral pathogens, with viruses having the greatest persistence.

Table 11: Stormwater systems microbial loading rates (grouped by study).

Country of origin	Year of publication	Source	Catchment land use	Microorganism	Arithmetic mean	Geometric mean	Loading rates (min)	Loading rates (max)	Units	References
Australia	2019	Stormwater drain	Unknown	*E. coli*			1.0×10^4	1.0×10^7	MPN/100 ml	Shen et al. 2019
Australia	2016	Stormwater drain	Urban – residential	*E. coli*		6.3×10^4	1.0×10^3	1.6×10^6	MPN/100 ml	Chandrasena et al. 2016
Australia	2016	Stormwater drain	Urban – residential	*Campylobacter*		1.0×10^1	2.1×10^0	1.8×10^2	MPN/100 ml	Chandrasena et al. 2016
South Korea	2016	Stormwater drain	Agriculture 56%, forest 18%, grassland 13%	*E. coli*			3.2×10^2	3.2×10^5	MPN/100 ml	Paule-Mercado et al. 2016
South Korea	2016	Stormwater drain	Mixed - bare land/construction 30%, forest 35%, grassland 9%, urban 20%	*E. coli*			1.0×10^3	1.0×10^6	MPN/100 ml	Paule-Mercado et al. 2016
South Korea	2016	Stormwater drain	Urban - urban 100%	*E. coli*			1.0×10^3	1.0×10^7	MPN/100 ml	Paule-Mercado et al. 2016
United States	2006	Combined sewer overflow	Urban - impervious commercial	*Total coliforms*			3.1E+05	3.1E+06	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - impervious commercial	*Faecal coliforms*			3.4E+04	3.7E+04	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - impervious commercial	*E. coli*			2.3E+04	2.9E+04	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - impervious commercial	*Enterococcus*			1.9E+04	2.6E+04	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - impervious commercial	*Cryptosporidium*			8.4E+01	1.0E+02	(oo)cysts/100 L	Arnone and Walling 2006

United States	2006	Combined sewer overflow	Urban - impervious commercial	*Giardia*		4.2E+03	1.4E+04	(oo)cysts/100 L	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - commercial/office	*Total coliforms*		2.3E+06	5.7E+06	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - commercial/office	*Faecal coliforms*		3.3E+05	4.3E+05	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - commercial/office	*E. coli*		9.0E+02	5.3E+04	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - commercial/office	*Enterococcus*		3.8E+04	3.0E+05	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - commercial/office	*Cryptosporidium*		1.0E+02	1.0E+02	(oo)cysts/100 L	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - commercial/office	*Giardia*		1.5E+04	3.0E+04	(oo)cysts/100 L	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - parks, residential	*Total coliforms*		3.7E+05	4.2E+05	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - parks, residential	*Faecal coliforms*		8.8E+04	1.6E+05	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - parks, residential	*E. coli*		4.4E+04	7.0E+04	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - parks, residential	*Enterococcus*		1.1E+04	3.7E+04	cfu/100 ml	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - parks, residential	*Cryptosporidium*		5.9E+01	7.5E+01	(oo)cysts/100 L	Arnone and Walling 2006
United States	2006	Combined sewer overflow	Urban - parks, residential	*Giardia*		2.0E+02	5.0E+02	(oo)cysts/100 L	Arnone and Walling 2006

United States	1997	Combined sewer overflow		*Giardia*		2.9E+04	3.8E+04	1.1E+05	(oo)cysts/100 L	States et al. 1997
United States	1997	Combined sewer overflow		*Cryptosporidium*		2.0E+03	0.0E+00	3.0E+03	(oo)cysts/100 L	States et al. 1997
United States	1998	Combined sewer overflow		*Giardia*	6.1E+04	3.5E+04			(oo)cysts/100 L	Gibson et al. 1998
United States	1998	Combined sewer overflow		*Cryptosporidium*	1.3E+04	6.0E+03			(oo)cysts/100 L	Gibson et al. 1998
United States	1998	Combined sewer overflow		*Faecal coliforms*	3.8E+04	2.7E+04			cfu/100ml	Gibson et al. 1998
United States	2007	Stormwater runoff	Mixed urban, highway, natural, some agricultural	*Total coliforms*	5.0E+03		1.6E+01	1.3E+06	MPN/100 ml	Rajal et al. 2007
United States	2007	Stormwater runoff	Mixed urban, highway, natural, some agricultural	*E. coli*	316.2278		1.6E+00	1.6E+05	MPN/100 ml	Rajal et al. 2007
United States	2007	Stormwater runoff	Mixed urban, highway, natural, some agricultural	*Adenovirus (prevalence 0.02%)*						Rajal et al. 2007
United States	2007	Stormwater runoff	Mixed urban, highway, natural, some agricultural	*Enterovirus (prevalence 0%)*						Rajal et al. 2007
USA	2009	Stormwater drain	Office park (buildings, parking, landscaping)	*E. coli*		9.2×10^2			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Office park (buildings, parking, landscaping)	*E. coli*		6.6×10^2			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Residential	*E. coli*		2.1×10^3			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Residential	*E. coli*		2.4×10^3			MPN/100 ml	Hathaway et al. 2009

USA	2009	Stormwater drain	Residential, incl school	*E. coli*		1.3×10^3			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Municipal parking lot	*E. coli*		2.4×10^2			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Bus parking and overhead shelter	*E. coli*		3.6×10^1			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Bus parking and overhead shelter	*E. coli*		4.0×10^0			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Bus parking and overhead shelter	*E. coli*		1.8×10^2			MPN/100 ml	Hathaway et al. 2009
USA	2009	Stormwater drain	Rural	*E. coli*	1.5×10^3		2.2×10^1	>2419	MPN/100 ml	Kleinheinz et al. 2009
USA	2009	Stormwater drain	Semi-rural; small village (250-1000 people)	*E. coli*	7.9×10^2		6.0×10^1	1.8×10^3	MPN/100 ml	Kleinheinz et al. 2009
USA	2009	Stormwater drain	Semi-rural; small village (250-1000 people)	*E. coli*	1.9×10^3		6.6×10^2	>2419	MPN/100 ml	Kleinheinz et al. 2009
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Enterococcus*	10806.67	3760.247			cfu/100 ml	Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Norovirus (GI and/or GII)*		33.9			gene copies/100 ml	Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Enterovirus*						Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Adenovirus*						Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Campylobacter spp.*						Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%,	*Campylobacter jejuni*		5			gene copies/100 ml	Steele et al. 2018

			roads 19%, open space 13%					
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Campylobacter coli*		3.7	gene copies/100 ml	Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Campylobacter lari*		4.7	gene copies/100 ml	Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Salmonella*				Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Human MST*		525.5	gene copies/100 ml	Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Avian MST*	10806.67	3760.247	cfu/100 ml	Steele et al. 2018
USA	2018	Stormwater drain	Urban - residential 62%, roads 19%, open space 13%	*Canine MST*		33.9	gene copies/100 ml	Steele et al. 2018
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Faecal coliforms*	131		cfu/100 ml	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Faecal coliforms*	3548		cfu/100 ml	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is	*Faecal coliforms*	5248		cfu/100 ml	Brownell et al. 2007

			located on a barrier island off Florida's west coast				
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Enterococcus*	10000	cfu/100 ml	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Enterococcus*	16982	cfu/100 ml	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Enterococcus*	52481	cfu/100 ml	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Human marker enterococcal surface protein (esp) of Ent. faecium*	ND		Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Human marker enterococcal surface protein (esp) of Ent. faecium*	ND		Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Human marker enterococcal surface protein (esp) of Ent. faecium*	ND		Brownell et al. 2007

USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Human polyomavirus*	ND	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Human polyomavirus*	ND	Brownell et al. 2007
USA	2007	Stormwater drain	Urban - residential. Site is located on a barrier island off Florida's west coast	*Human polyomavirus*	ND	Brownell et al. 2007

Table 12: Indirect sampling of stormwater microbial loading rates (grouped by study).

Country of origin	Year of publication	Source	Catchment land use	Microorganism (prevalence %)	Arithmetic mean	Geometric mean	Loading rates (min)	Loading rates (max)	Units	References
Australia	2012	Creek receiving surface runoff	medium density urban (residential and industrial)	*E. coli*	2.3E+03		2.1E+02	4.3E+03	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	low intensity urban, some agriculture	*E. coli*	1.3E+04		8.4E+03	1.8E+04	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	medium density urban (residential and industrial)	*E. coli*	1.0E+04		8.9E+03	1.1E+04	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	medium density urban, some agriculture	*E. coli*	3.2E+03		4.6E+02	6.0E+03	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	rural (cattle, horses, sheep)	*E. coli*	2.5E+03		1.6E+03	3.5E+03	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	stormwater drain outlet from urban areas nearby; tidal influence	*E. coli*	2.0E+03		5.3E+02	3.4E+03	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	medium density urban (residential and industrial)	*enterococci*	5.0E+03		1900	8000	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	low intensity urban, some agriculture	*enterococci*	2.0E+03		1480	2500	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	medium density urban (residential and industrial)	*enterococci*	2.7E+03		2230	3110	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	medium density urban, some agriculture	*enterococci*	5.8E+03		3430	8100	cfu/100 ml	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	rural (cattle, horses, sheep)	*enterococci*	5.0E+03		11.2	9930	cfu/100 ml	Sidhu et al. 2012

Australia	2012	Creek receiving surface runoff	stormwater drain outlet from urban areas nearby; tidal influence	*enterococci*	1.0E+04		1930	18400	cfu/100 ml	Sidhu et al. 2012
United States	2012	Creeks receiving storm event runoff	low density development, mostly forest, some agriculture	*E. coli*	1.5E+03				cfu/100 ml	Rowny and Stewart 2012
United States	2012	Creeks receiving storm event runoff	high intensity urban	*E. coli*	5.4E+02				cfu/100 ml	Rowny and Stewart 2012
United States	2012	Creeks receiving storm event runoff	intermediate density, mix of forest, urban and agriculture	*E. coli*	5.2E+02				cfu/100 ml	Rowny and Stewart 2012
United States	2012	Creeks receiving storm event runoff	intermediate density, mix of forest and urban with some agriculture	*E. coli*	3.2E+02				cfu/100 ml	Rowny and Stewart 2012
United States	2012	Creeks receiving storm event runoff	intermediate density, mix of urban and forest with some agriculture	*E. coli*	4.0E+02				cfu/100 ml	Rowny and Stewart 2012
United States	2012	Creeks receiving storm event runoff	high intensity urban, with some forest	*E. coli*	1.1E+03				cfu/100 ml	Rowny and Stewart 2012
United States	2012	Creeks receiving storm event runoff	high intensity urban with some forest	*E. coli*	1.1E+03				cfu/100 ml	Rowny and Stewart 2012
United States	2014	Constructed wetland	Student housing development	*E. coli*		1.0E+03			MPN/100 ml	Humphrey et al. 2014
United States	2014	Constructed wetland	Student housing development	*E. coli*		7.8E+02			MPN/100 ml	Humphrey et al. 2014
United States	2018	Surface water	Urban - residential 20%, open space 41%, roads 8%, commercial and	*Enterococcus*	854.1429	300.8961			cfu/100 ml	Steele et al. 2018

			industrial with low level agriculture in lower floodplain					
United States	2018	Surface water	As above	*Norovirus (GI and/or GII) (96%)*		97.3	gene copies/100 ml	Steele et al. 2018
United States	2018	Surface water	As above	*Adenovirus (22%)*				Steele et al. 2018
United States	2018	Surface water	As above	*Enterovirus (0%)*				Steele et al. 2018
United States	2018	Surface water	As above	*Campylobacter spp. (1%)*				Steele et al. 2018
United States	2018	Surface water	As above	*Campylobacter jejuni (17%)*		3.5	gene copies/100 ml	Steele et al. 2018
United States	2018	Surface water	As above	*Campylobacter coli (87%)*		61.4	gene copies/100 ml	Steele et al. 2018
United States	2018	Surface water	As above	*Campylobacter lari (78%)*		1.9E+01	gene copies/100 ml	Steele et al. 2018
United States	2018	Surface water	As above	*Salmonella (25%)*				Steele et al. 2018
United States	2018	Surface water	As above	*Human MST (100%)*		8.2E+01	gene copies/100 ml	Steele et al. 2018
United States	2018	Surface water	As above	*Avian MST (100%)*				Steele et al. 2018
United States	2018	Surface water	As above	*Canine MST (83%)*				Steele et al. 2018
United States	2008	Tributaries receiving runoff	Wetland	*Faecal colifoms*	527		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Wetland	*E. coli*	161		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Wetland	*Enterococci*	276		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Wetland	*Giardia*	3.5		(oo)cysts/100 mL	Cizek et al. 2008
United States	2008	As above	Wetland	*Cryptosporidium*	4.4		(oo)cysts/L	Cizek et al. 2008
United States	2008	As above	Wooded/forestry	*Faecal colifoms*	305		CFU/100 ml	Cizek et al. 2008

United States	2008	As above	Wooded/forestry	*E. coli*	179		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Wooded/forestry	*Enterococci*	372		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Wooded/forestry	*Giardia*	7.3		(oo)cysts/100 mL	Cizek et al. 2008
United States	2008	As above	Wooded/forestry	*Cryptosporidium*	6		(oo)cysts/L	Cizek et al. 2008
United States	2008	As above	Developed	*Faecal colifoms*	2398		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*E. coli*	2320		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*Enterococci*	1322		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*Giardia*	5.1		(oo)cysts/100 mL	Cizek et al. 2008
United States	2008	As above	Developed	*Cryptosporidium*	7.4		(oo)cysts/L	Cizek et al. 2008
United States	2008	As above	Developed	*Faecal colifoms*	1126		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*E. coli*	608		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*Enterococci*	1458		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*Giardia*	1.8		(oo)cysts/100 mL	Cizek et al. 2008
United States	2008	As above	Developed	*Cryptosporidium*	1.7		(oo)cysts/L	Cizek et al. 2008
United States	2008	As above	Developed	*Faecal colifoms*	955		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*E. coli*	485		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*Enterococci*	1923		CFU/100 ml	Cizek et al. 2008
United States	2008	As above	Developed	*Giardia*	1		(oo)cysts/100 mL	Cizek et al. 2008
United States	2008	As above	Developed	*Cryptosporidium*	nd		(oo)cysts/L	Cizek et al. 2008

Table 13: Prevalence of microorganisms in stormwater (concentration data not available, ordered by microorganism)

Country of origin	Year of publication	Source	Catchment land use	Microorganism	Prevalence	References
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Adenovirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Low intensity urban, some agriculture	*Adenovirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Adenovirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban, some agriculture	*Adenovirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Rural (cattle, horses, sheep)	*Adenovirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Stormwater drain outlet from urban areas nearby; tidal influence	*Adenovirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Campylobacter spp.*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Low intensity urban, some agriculture	*Campylobacter spp.*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Campylobacter spp.*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban, some agriculture	*Campylobacter spp.*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Rural (cattle, horses, sheep)	*Campylobacter spp.*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Stormwater drain outlet from urban areas nearby; tidal influence	*Campylobacter spp.*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*HF183 biomarker*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Low intensity urban, some agriculture	*HF183 biomarker*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*HF183 biomarker*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban, some agriculture	*HF183 biomarker*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Rural (cattle, horses, sheep)	*HF183 biomarker*	Present	Sidhu et al. 2012

Australia	2012	Creek receiving surface runoff	Stormwater drain outlet from urban areas nearby; tidal influence	*HF183 biomarker*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Polyomavirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Low intensity urban, some agriculture	*Polyomavirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Polyomavirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban, some agriculture	*Polyomavirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Rural (cattle, horses, sheep)	*Polyomavirus*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Stormwater drain outlet from urban areas nearby; tidal influence	*Polyomavirus*	Absent	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Salmonella enterica*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Low intensity urban, some agriculture	*Salmonella enterica*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban (residential and industrial)	*Salmonella enterica*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Medium density urban, some agriculture	*Salmonella enterica*	Present	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Rural (cattle, horses, sheep)	*Salmonella enterica*	Absent	Sidhu et al. 2012
Australia	2012	Creek receiving surface runoff	Stormwater drain outlet from urban areas nearby; tidal influence	*Salmonella enterica*	Present	Sidhu et al. 2012

3.7 STOCKYARDS

Stockyards are premises wherein livestock are held or contained for a range of purposes, including sale, receipt, transport, exhibition, husbandry, weaning, and slaughter (Fotheringham 1995, Department of Water 2015). They may be temporary or permanent in nature, and used continuously or occasionally. They may differ significantly in size and scale, from small on-site or community pens, to slaughterhouses with capacity for more than 250-1000 head at a time (e.g. Kiermeier et al. 2006). The largest stockyard in the Southern Hemisphere is the Fielding Sale Yards in Manawatū, at 70,000 square meters. Thousands of head of cattle and sheep are sold each week, with the animals retained in permanent pens. Volume and management of effluent will differ between yards of different scale. Small or temporary systems may simply manually remove solid manure, while larger systems will likely dispose of wastes through a treatment system. For example, at the Fielding Sale Yards, all effluent deposited through the day is hosed down through a series of drains that connects to a sump, which in turn is connected to the Manawatū District Council waste stream and on to the treatment plant.

There was no specific information was found on the microbial loading from stockyards during the literature review. A loading rate however could be estimated using the loading rates from the various farmed animals detailed in this report, factoring in the capacity of stockyard, its function (short- or longer-term housing) and what, if any, waste treatment or management exists on site.

3.8 ANIMAL EFFLUENT/MANURE APPLICATION TO LAND

Sources of microorganisms from dairy farming include the diffuse discharge of Farming Dairy Effluent (FDE) to land. The on-farm dairy effluent is typically collected at the diary shed, stored in a holding facility (e.g. effluent storage pond) with no or several forms of treatment before its application to land via an irrigation system (i.e. travelling irrigator). Specific notes on animal effluent/manure application to land include:

- Travelling irrigators typically have high instantaneous rates of application, >100 mm/hr. Assuming the average depth of FDE is divided by the time for a complete pass, average application rate is approximately 20-30 mm/h.
- Low rate applicators apply at rates of <10mm/h therefore reduce the chance of exceeding the soils infiltration capacity, preventing ponding and surface runoff.
- Application of effluent should include consideration of soil type - whether they exhibit overland flow or preferential flow risk, as well as the presence of any artificial preferential channels.
- Recommended that FDE management practices are matched with soil and landscape features in order to prevent direct losses of effluent contaminants.
- Application can be made at field capacity on well drained soils with little or no connection to surface water and that pose lowest risk for direct losses of applied effluents (high infiltration rate, high drainage fluxes, large degree of matrix flow) Deferred application not necessary but storage should be available to avoid application to saturated soils. Land slope should be less than 7 degrees.
- Deferred irrigation or storage capacity needed to allow for FDE to be applied at an average rate less than infiltration rate to prevent ponding in soils with impeded drainage or low infiltration.

FDE pond storage calculator measures farm-specific storage requirements using data including catchment rainfall, shed water use, number of cows, irrigation hardware and management and soil information.

Table 14: Animal effluent/manure application to land microbial loading rates (grouped by study and only includes data on dairy cattle).

Country of origin	Year of paper	Microorganism	FDE [2]Median	FDE Geometric mean	FDE Arithmetic mean	FDE Min	FDE Max	FDE Units	Average microbial loading rate	Units	References
NZ	2011	*E. coli*	8,600,000		8,600,000			MPN/100 ml			Donnison et al. 2011
NZ	2011	*Campylobacter*	9,300		55,000			MPN/100 ml			Donnison et al. 2011
NZ	2011	*E. coli*	22,000		77,000			MPN/100 ml	67,000,000	*E. coli*/cow/day	Donnison et al. 2011
NZ	2011	*Campylobacter*	200		1,000			MPN/100 ml	860,000	*Campylobacter*/cow/day	Donnison et al. 2011
NZ	2011	*E. coli*	12,000,000		12,000,000			MPN/100 ml			Donnison et al. 2011
NZ	2011	*Campylobacter*	6,000		36,000			MPN/100 ml			Donnison et al. 2011
NZ	2011	*E. coli*	140,000		190,000			MPN/100 ml			Donnison et al. 2011
NZ	2011	*Campylobacter*	93		1,700			MPN/100 ml			Donnison et al. 2011
NZ	2011	*E. coli*							300,000,000	*E. coli*/cow/day	Donnison et al. 2011
NZ	2011	*Campylobacter*							2,800,000	*Campylobacter*/cow/day	Donnison et al. 2011

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[2] Farm Dairy Effluent = FDE

NZ	2011	*E. coli*							12,000,000	*E. coli*/cow/day	Donnison et al. 2011
NZ	2011	*Campylobacter*							17,000	*Campylobacter*/cow/day	Donnison et al. 2011
NZ	2003	*Campylobacter*			1000			MPN/100ml			Ross and Donnison 2003
NZ	2003	*Campylobacter*			1000000			MPN/100ml			Ross and Donnison 2003
NZ	2003	*Campylobacter*			100000			MPN/100ml			Ross and Donnison 2003
NZ	1989	Total coliforms	80,000	57,000				MPN/100ml			Hickey et al. 1989
NZ	1989	Faecal coliforms	70,000	40,000				MPN/100ml			Hickey et al. 1989
NZ	1989	Total coliforms		70,000				MPN/100ml			Hickey et al. 1989
NZ	1989	Faecal coliforms		49,000				MPN/100ml			Hickey et al. 1989
NZ	2001	Faecal coliform			910,000			MPN/g wet weight			Roach et al. 2001
NZ	2004	Faecal coliform			100000			cfu/100ml			McLeod et al. 2004
USA	2011	Enterococci	300		870	8.3	4800	MPN/ml			Dungan et al. 2012
USA	2011	Total Coliforms	3100		5500	270	28000	MPN/ml			Dungan et al. 2012
USA	2011	*E. coli*	1600		3500	10	13000	MPN/ml			Dungan et al. 2012
USA	2011	*C. perfringens*	640		880	11	5000	cfu/ml			Dungan et al. 2012
USA	2011	*Campylobacter jejuni*			4800	<770	27000	cells/ml (estimated by qPCR)			Dungan et al. 2012
USA	2011	*E. coli stx1*			2000	<1200	6300	cells/ml (estimated by qPCR)			Dungan et al. 2012

USA	2011	*E. coli eaeA*		2000	150	6300	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*L. monocytogenes*		4000	1400	6600	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*M. avium*		2900	<16	71000	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*S. enterica*		21000	3000	83000	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*Cryptosporidium spp.*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*Giardia spp.*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*L. interrogans*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	Enterococci	530	1100	5.2	7800	MPN/ml	Dungan et al. 2012
USA	2011	Total Coliforms	5000	600000	380	17000000	MPN/ml	Dungan et al. 2012
USA	2011	*E. coli*	950	3600	<1	55000	MPN/ml	Dungan et al. 2012
USA	2011	*C. perfringens*	620	1100	<1	6400	cfu/ml	Dungan et al. 2012
USA	2011	*Campylobacter jejuni*		2500	<770	18000	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*E. coli stx1*		6800	3600	9900	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*E. coli eaeA*		3300	2400	4200	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*L. monocytogenes*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012

USA	2011	*M. avium*		150	<16	1300	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*S. enterica*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*Cryptosporidium spp.*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*Giardia spp.*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*L. interrogans*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	Enterococci	810	1600	1.6	7400	MPN/ml	Dungan et al. 2012
USA	2011	Total Coliforms	16000	57000	140	430000	MPN/ml	Dungan et al. 2012
USA	2011	*E. coli*	4200	17000	<1	72000	MPN/ml	Dungan et al. 2012
USA	2011	*C. perfringens*	360	3100	<1	55000	cfu/ml	Dungan et al. 2012
USA	2011	*Campylobacter jejuni*		3400	<770	25000	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*E. coli stx1*		1,000	<1,200	2,700	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*E. coli eaeA*		140	140	140	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*L. monocytogenes*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*M. avium*		220	<16	1400	cells/ml (estimated by qPCR)	Dungan et al. 2012
USA	2011	*S. enterica*				ND	cells/ml (estimated by qPCR)	Dungan et al. 2012

USA	2011	*Cryptosporidium spp.*			ND	cells/ml (estimated by qPCR)			Dungan et al. 2012
USA	2011	*Giardia spp.*			ND	cells/ml (estimated by qPCR)			Dungan et al. 2012
USA	2011	*L. interrogans*			ND	cells/ml (estimated by qPCR)			Dungan et al. 2012
NZ	2003	*E. coli*	122,000			MPN/100 ml			Craggs et al. 2003
NZ	2003	*E. coli*	16,200			MPN/100 ml			Craggs et al. 2003
NZ	2003	*E. coli*	146			MPN/100 ml			Craggs et al. 2003
NZ	1996	Faecal coliforms		20,000,000		cfu/100ml			Ledgard et al.1996
NZ	1996	Faecal coliforms		100,000,000		cfu/100ml			Ledgard et al.1996
NZ	1996	Faecal coliforms		3000		cfu/100ml			Ledgard et al.1996
NZ	1996	Faecal coliforms		200		cfu/100ml			Ledgard et al.1996
NZ	2004	*E. coli*		1,600,000		cfu/100 ml			Monaghan and Smith 2004
NZ	2011	*E. coli*		63,096			100000000	*E. coli*/ha/da	Muirhead et al. 2011
NZ	2011	*E. coli*		794			1000000	*E. coli*/ha/da	Muirhead et al. 2011
NZ	2011	*E. coli*					100000000 (95th percentile)	*E. coli*/ha/da	Muirhead et al. 2011
NZ	2011	*E. coli*					1000000 (95th percentile)	*E. coli*/ha/da	Muirhead et al. 2011

NZ	2019	*E. coli*	247,718			cfu/100 ml	Cameron and Di 2019
NZ	2018	*E. coli*	181,333			cfu/100 ml	Wang et al. 2019
NZ	2018	*E. coli*	1,146,667			cfu/100 ml	Wang et al. 2019
Canada	1982	Total coliforms	478,630			cfu/gram	Culley and Phillips 1982
Canada	1982	Faecal coliforms	204,174			cfu/gram	Culley and Phillips 1982
Canada	1982	Faecal streptococci	208,930			cfu/gram	Culley and Phillips 1982
NZ	2014	*E. coli*	5,800,000	2000000	13000000	MPN/100 ml	McLeod et al. 2014
NZ	1996	Total coliforms	250,000			*E. coli*/100 ml	Selvarajah 1996
NZ	1996	Faecal coliforms	350,000			*E. coli*/100 ml	Selvarajah 1996
NZ	1996	Total coliforms	0.00063			*E. coli*/100 ml	Selvarajah 1996
NZ	1996	Faecal coliforms	34,000			*E. coli*/100 ml	Selvarajah 1996
NZ	1996	Total coliforms	230,000			*E. coli*/100 ml	Selvarajah 1996
NZ	1996	Faecal coliforms	51,000			*E. coli*/100 ml	Selvarajah 1996
NZ	2010	*E. coli*	9,700			MPN/100 ml	Monaghan et al. 2010
NZ	2010	*E. coli*	170,000			MPN/100 ml	Monaghan et al. 2010
NZ	2010	*E. coli*	690,000			MPN/100 ml	Monaghan et al. 2010
NZ	2010	*E. coli*	270,000			MPN/100 ml	Monaghan et al. 2010
NZ	2010	*E. coli*	280,000			MPN/100 ml	Monaghan et al. 2010
NZ	2010	*E. coli*	240,000			MPN/100 ml	Monaghan et al. 2010
NZ	2010	*E. coli*	10,000			MPN/100 ml	Monaghan et al. 2010

NZ	2011	*E. coli*	4,000,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	10,000,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	240,000,000	MPN/100 ml	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	960,000,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	910,000,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	2,400,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	500,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	140,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	18,000	MPN/100 ml	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	97,000	MPN/100g	Houlbrooke et al. 2011b
NZ	2011	*E. coli*	2,300,000	MPN/100g	Houlbrooke et al. 2011b

Concluding remarks

The report presents the truncated data for the key microbial species for the major land uses of concern in New Zealand. These will be used in the development of a Microbial Risk Assessment tool but will also be of great value and use for providing context regarding microbial contamination from various land uses. The data presented is up to date as at April 2020 and represents the past thirty years of studies and research. For further information on the extended data collated please contact ESR.

REFERENCES

Multiple domestic and community size OWMS

Borchardt, M.A., Bradbury, K.R., Calvin, A.E., Kolberg, R.J., Alexander, S.C., Archer, J.R. *et al*. (2011). *Norovirus* outbreak caused by a new septic system in a dolomite aquifer. Groundwater 49: 85–97.

DeBorde, D.C., Woessner, W.W., Lauerman, B. and Ball, P.N. (1998) Virus occurrence and transport in a school septic system and unconfined aquifer. Groundwater 36: 825-834.

Humphries, B., Weaver, L., Burbery, L., Webber, J., Morgan, L. and Gregor, J. (2019) Microbial pathogen removal from domestic effluent using coral sand in Kiribati. Journal of Applied Microbiology. 128(4): 1208-1220.

Keegan, M., Kilroy, K., Nolan, D., Dubber, D., Johnston, P.M., Misstear, B.D.R. *et al*. (2014). Assessment of the impact of traditional septic tank soakaway systems on water quality in Ireland. Water Science and Technology. 70: 634–641.

Jahne, M.A., Brinkman, N.E., Keely, S.P., Zimmerman, B.D., Wheaton, E.A and Garland, J.L. (2020). Droplet digital PCR quantification of norovirus and adenovirus in decentralized wastewater and graywater collections: Implications for onsite reuse. Water Research 169: 115213. https://doi.org/10.1016/j.watres.2019.115213

Pang, L., Close, M., Goltz, M., Sinton, L., Davies, H., Hall, C. Stanton, G (2004). Estimation of septic tank setback distances based on transport of *E. coli* and F-RNA phages. Environment International 29(7): 907-921.

Richards, S., Paterson, E., Withers, P.J.A. and Stutter, M. (2016). Septic tank discharges as multi-pollutant hotspots in catchments. Science of the Total Environment. 542: 854–863.

Schneeberger, C.L., O'Driscoll, M., Humphrey C., Henry, K., Deal, N., Seiber, K., Hill, V.R and Zarate-Bermudez, M (2015). Fate and transport of enteric microbes from septic systems in a coastal watershed. Journal of Environmental Health. 77(9): 22-30.

Dairy farming

Abeywardena, H., Jex, A.R., Nolan, M.J., Haydon, S.R., Stevens, M.A., McAnulty, R.W. and Gasser, R.B. (2012). Genetic characterisation of *Cryptosporidium* and *Giardia* from dairy calves: Discovery of species/genotypes consistent with those found in humans. Infection Genetics and Evolution 12(8): 1984-1993.

Al Mawly, J., Grinberg, A., Prattley, D., Moffat, J. and French, N. (2015a). Prevalence of endemic enteropathogens of calves in New Zealand dairy farms. New Zealand Veterinary Journal 63(3): 147-152.

Al Mawly, J., Grinberg, A., Prattley, D., Moffat, J., Marshall, J. and French, N. (2015b). Risk factors for neonatal calf diarrhoea and enteropathogen shedding in New Zealand dairy farms. Veterinary Journal 203(2): 155-160.

Browne, A.S., Midwinter, A.C., Withers, H., Cookson, A.L., Biggs, P.J., Marshall, J.C., Benschop, J., Hathaway, S., Haack, N.A., Akhter, R.N. and French, N.P. (2018). Molecular Epidemiology of Shiga Toxin-Producing *Escherichia coli* (STEC) on New Zealand Dairy Farms: Application of a Culture-Independent Assay and Whole-Genome Sequencing. Applied and Environmental Microbiology 84(14): e00481-18.

Castro-Hermida, J.A., Almeida, A., Gonzalez-Warleta, M., Da Costa, J.M.C., Rumbo-Lorenzo, C. and Mezo, M. (2007). Occurrence of *Cryptosporidium parvum* and *Giardia duodenalis* in healthy adult domestic ruminants. Parasitology Research 101(5): 1443-1448.

Cookson, A.L., Taylor, S.C., Bennett, J., Thomson-Carter, F. and Attwood, G.T. (2006). Serotypes and analysis of distribution of Shiga toxin producing *Escherichia coli* from cattle and sheep in the lower North Island, New Zealand. N Z Vet J 54: 78-84.

Donnison, A., Ross, C. and Clark, D. (2008). *Escherichia coli* shedding by dairy cows. New Zealand Journal of Agricultural Research 51(3): 273-278.

Fukushima, H. and Seki, R. (2004). High Numbers of Shiga Toxin-Producing *Escherichia Coli* found in bovine faeces collected at slaughter in Japan. FEMS Microbiology Letters 238(1): 189-197.

Grinberg, A., Pomroy, W.E., Weston, J.F., Ayanegui-Alcerreca, A. and Knight, D. (2005). The occurrence of *Cryptosporidium parvum*, *Campylobacter* and *Salmonella* in newborn dairy calves in the Manawatu region of New Zealand. New Zealand Veterinary Journal 53(5): 315-320.

Hunt, C.L., Ionas, G. and Brown, T.J. (2000). Prevalence and strain differentiation of *Giardia intestinalis* in calves in the Manawatu and Waikato regions of North Island, New Zealand. Veterinary Parasitology 91(1-2): 7-13.

Irshad, H., Cookson, A.L., Hotter, G., Besser, T.E., On, S.L.W. and French, N.P. (2012). Epidemiology of Shiga toxin-producing *Escherichia coli* O157 in very young calves in the North Island of New Zealand. New Zealand Veterinary Journal 60(1): 21-26.

Krueger, N.A., Anderson, R.C., Krueger, W.K., Horne, W.J., Wesley, I.V., Callaway, T.R., Edrington, T.S., Carstens, G.E., Harvey, R.B. and Nisbet, D.J. (2008). Prevalence and concentration of *Campylobacter* in rumen contents and feces in pasture and feedlot-fed cattle. Foodborne Pathogens and Disease 5(5): 571-577.

Learmonth, J.J., Ionas, G., Pita, A.B. and Cowie, R.S. (2003). Identification and genetic characterisation of *Giardia* and *Cryptosporidium* strains in humans and dairy cattle in the Waikato Region of New Zealand. Water Science and Technology 47(3): 21-26.

Moriarty, E.M., Sinton, L.W., MacKenzie, M.L., Karki, N. and Wood, D.R. (2008). A survey of enteric bacteria and protozoans in fresh bovine faeces on New Zealand dairy farms. Journal of Applied Microbiology 105(6): 2015-2025.

Neilsen, EM. (2002). Occurrence and strain diversity of thermophilic campylobacters in cattle of different age groups in dairy herds. Letters in Applied Microbiology 35: 85–89.

Nydam, D.V., Wade, S.E., Schaaf, S.L. and Mohammed, H.O. (2001). Number of *Cryptosporidium parvum* oocysts or *Giardia* spp cysts shed by dairy calves after natural infection. American Journal of Veterinary Research 62(10): 1612-1615.

O'Handley, R.M., Cockwill, C., McAllister, T.A., Jelinski, M., Morck, D.W. and Olson, M.E. (1999). Duration of naturally acquired giardiosis and cryptosporidiosis in dairy calves and their association with diarrhea. Journal of the American Veterinary Medical Association 214(3): 391-396.

O'Handley, R.M., Olson, M.E., Fraser, D., Adams, P. and Thompson, R.C.A. (2000). Prevalence and genotypic characterisation of *Giardia* in dairy calves from Western Australia and Western Canada. Veterinary Parasitology 90(3): 193-200.

Rapp, D., Ross, C.M., Cave, V. and Muirhead, R.W. (2014). Prevalence, concentration and genotypes of *Campylobacter jejuni* in faeces from dairy herds managed in farm systems with or without housing. J Appl Microbiol 116(4): 1035-1043.

Uga, S., Matsuo, J., Kono, E., Kimura, K., Inoue, M., Rai, S.K. and Ono, K. (2000). Prevalence of *Cryptosporidium parvum* infection and pattern of oocyst shedding in calves in Japan. Veterinary Parasitology 94(1-2): 27-32.

Vanderholm DH (1984) Properties of agricultural wastes. In: Vanderholm DH ed. Agricultural waste manual. NZAEI Project Report No. 32. Lincoln University

Winkworth, C.L., Matthaei, C.D. and Townsend, C.R. (2008). Prevalence of *Giardia* and *Cryptosporidium* spp in calves from a region in New Zealand experiencing intensification of dairying. N Z Vet J 56(1): 15-20.

Zhao, T., Doyle, M.P., Shere, J. and Garber, L. (1995). Prevalence of enterohemorrhagic *Escherichia-coli* O157-H7 in a survey of dairy herds. Applied and Environmental Microbiology 61(4): 1290-1293.

Sheep farming

Anderson SA, Turner SJ, Lewis GD. (1997). Enterococci in the New Zealand environment: Implications for water quality monitoring. Water Science and Technology 35: 325-331.

Castro-Hermida JA, Almeida A, González-Warleta M, Correia da Costa JM, Rumbo-Lorenzo C, Mezo M. (2007). Occurrence of *Cryptosporidium parvum* and *Giardia duodenalis* in healthy adult domestic ruminants. Parasitology research 101: 1443-1448.

Cookson, A.L., Taylor, S.C., Bennett, J., Thomson-Carter, F. and Attwood, G.T. (2006). Serotypes and analysis of distribution of Shiga toxin producing *Escherichia coli* from cattle and sheep in the lower North Island, New Zealand. NZ Vet J 54(2): 78-84.

Geurden T, Thomas P, Casaert S, Vercruysse J, Claerebout E. (2008). Prevalence and molecular characterisation of *Cryptosporidium* and *Giardia* in lambs and goat kids in Belgium. Veterinary parasitology 155: 142.

Moriarty, E.M., McEwan, N., Mackenzie, M., Karki, N., Wood, D.R. and Sinton, L.W. (2011). Incidence and prevalence of microbial indicators and pathogens in ovine faeces in New Zealand. New Zealand Journal of Agricultural Research 54(2): 71-81.

Ogden, I.D., Macrae, M. and Strachan, N.J.C. (2005). Concentration and prevalence of *Escherichia Coli* O157 in sheep faeces at pasture in Scotland. Journal of Applied Microbiology 98(3): 646-651.

Ogden, I.D., Dallas, J.F., Macrae, M., Rotariu, O., Reay, K.W., Leitch, M., Thomson, A.P., Sheppard, S.K., Maiden, M., Forbes, K.J. and Strachan, N.J.C. (2009). *Campylobacter* excreted into the environment by animal sources: prevalence, concentration shed, and host association. Foodborne Pathogens and Disease 6(10): 1161-1170.

Yang, R.C., Jacobson, C., Gardner, G., Carmichael, I., Campbell, A.J.D. and Ryan, U. (2014). Development of a Quantitative PCR (QPCR) for *Giardia* and analysis of the prevalence, cyst shedding and genotypes of *Giardia* present in sheep across four states in Australia. Experimental Parasitology 137: 46-52.

Yang, R., Abraham, S., Gardner, G.E., Ryan, U. and Jacobson, C. (2017). Prevalence and pathogen load of *Campylobacter* Spp., *Salmonella Enterica* and *Escherichia coli* O157/O145 Serogroup in sheep faeces collected at sale yards and in abattoir effluent in Western Australia. Australian Veterinary Journal 95(5): 143-148.

Beef farming

Atwill, E.R., Hoar, B., Pereira, M.D.G.C., Tate, K.W., Rulofson, F. and Nader, G. (2003). Improved Quantitative Estimates of Low Environmental Loading and Sporadic Periparturient Shedding of *Cryptosporidium Parvum* in Adult Beef Cattle. Applied and Environmental Microbiology 69(8): 4604-4610.

Cookson, A.L., Taylor, S.C., Bennett, J., Thomson-Carter, F. and Attwood, G.T. (2006). Serotypes and analysis of distribution of Shiga toxin producing *Escherichia coli* from cattle and sheep in the lower North Island, New Zealand. NZ Vet J 54(2): 78-84.

Fukushima, H. and Seki, R. (2004). High Numbers of Shiga Toxin-Producing *Escherichia Coli* Found in Bovine Faeces Collected at Slaughter in Japan. FEMS Microbiology Letters 238(1): 189-197.

Hoar, B.R., Paul, R.R., Siembieda, J., Pereira, M.D.C. and Atwill, E.R. (2009). *Giardia Duodenalis* in Feedlot Cattle from the Central and Western United States. BMC Veterinary Research 5.

Irshad, H., Cookson, A.L., Prattley, D.J., Dufour, M. and French, N.P. (2014). Distribution of Escherichia coli strains harbouring Shiga toxin-producing E. coli (STEC)-associated virulence factors (stx1, stx2, eae, ehxA) from very young calves in the North Island of New Zealand. Epidemiol Infect 142(12): 2548-2558.

Krueger, N.A., Anderson, R.C., Krueger, W.K., Horne, W.J., Wesley, I.V., Callaway, T.R., Edrington, T.S., Carstens, G.E., Harvey, R.B. and Nisbet, D.J. (2008). Prevalence and Concentration of *Campylobacter* in Rumen Contents and Feces in Pasture and Feedlot-Fed Cattle. Foodborne Pathogens and Disease 5(5): 571-577.

Oates, S.C., Miller, M.A., Hardin, D., Conrad, P.A., Melli, A., Jessup, D.A., Dominik, C., Roug, A., Tinker, M.T. and Miller, W.A. (2012). Prevalence, Environmental Loading, and Molecular Characterization of *Cryptosporidium* and *Giardia* Isolates from Domestic and Wild Animals Along the Central California Coast. Applied and Environmental Microbiology 78(24): 8762-8772.

Ogden, I.D., Dallas, J.F., Macrae, M., Rotariu, O., Reay, K.W., Leitch, M., Thomson, A.P., Sheppard, S.K., Maiden, M., Forbes, K.J. and Strachan, N.J.C. (2009). *Campylobacter* Excreted into the Environment by Animal Sources: Prevalence, Concentration Shed, and Host Association. Foodborne Pathogens and Disease 6(10): 1161-1170.

Stanley, K.N., Wallace, J.S., Currie, J.E., Diggle, P.J. and Jones, K. (1998). The Seasonal Variation of Thermophilic Campylobacters in Beef Cattle, Dairy Cattle and Calves. Journal of Applied Microbiology 85(3): 472-480.

Wildfowl

Anderson, S.A., Turner, S.J. and Lewis, G.D. (1997). Enterococci in the New Zealand environment: Implications for water quality monitoring. Water Science and Technology 35(11-12): 325-331.

Gould, D.J. and Fletcher, M.R. (1978). Gull droppings and their effects on water quality. Water Research 12(9): 665-672.

Haack, S.K., Fogarty, L.R. and Wright, C. (2003). *Escherichia coli* and enterococci at beaches in the Grand Traverse Bay, Lake Michigan: Sources, characteristics, and environmental pathways. Environmental Science & Technology 37(15): 3275-3282.

Moriarty, E.M., Karki, N., Mackenzie, M., Sinton, L.W., Wood, D.R. and Gilpin, B.J. (2011). Faecal indicators and pathogens in selected New Zealand waterfowl. New Zealand Journal of Marine and Freshwater Research 45(4): 679-688.

Oates, S.C., Miller, M.A., Hardin, D., Conrad, P.A., Melli, A., Jessup, D.A., Dominik, C., Roug, A., Tinker, M.T. and Miller, W.A. (2012). Prevalence, environmental loading, and molecular characterization of *Cryptosporidium* and *Giardia* Isolates from domestic and wild animals along the Central California Coast. Applied and Environmental Microbiology 78(24): 8762-8772.

Ogden, I.D., Dallas, J.F., Macrae, M., Rotariu, O., Reay, K.W., Leitch, M., Thomson, A.P., Sheppard, S.K., Maiden, M., Forbes, K.J. and Strachan, N.J.C. (2009). *Campylobacter* Excreted into the Environment by Animal Sources: Prevalence, Concentration Shed, and Host Association. Foodborne Pathogens and Disease 6(10): 1161-1170.

Stormwater systems

Ahmed W, Hamilton K, Toze S, Cook S, Page, D. (2019). A review on microbial contaminants in stormwater runoff and outfalls: potential health risks and mitigation strategies. *Science of the Total Environment* 692: 1304-1321.

AWQC. 2008. *Pathogens in Stormwater.* Australian Water Quality Centre report prepared by P Monis for the NSW Department of Environment and Climate Change and the Sydney Metropolitan Catchment Management Authority.

Bambic DG, Hildare-Hann BJ, Rajal VB, Sturm BSM, Minton CB, Schriewer A, Wuertz S. 2015. Spatial and hydrologic variation of Bacteroidales, adenovirus and enterovirus in a semi-arid wastewater effluent-impacted watershed. *Water Research* 75: 85-94.

Brownwell MJ, Harwood VJ, Kurz RC, McQuaig SM, Lukasik J, Scott TM. 2007. Confirmation of a putative impact on stormwater quality at a Florida beach by microbial source tracking methods and structure of indicator organism populations. *Water Research* 41: 3747-3757.

Chandrasena GI, Deletic A, McCarthy DT. 2016. Biofiltration for stormwater harvesting: comparison of Campylobacter spp. and Escherichia coli removal under normal and challenging operational conditions. *Journal of Hydrology* 537: 248-259.

Cizek AR, Characklis GW, Krometis LA, Hayes JA, Simmons OD, Di Lonardo S, Alderisio KS, Sobsey MD. 2008. Comparing the partitioning behaviour of Giardia and Cryptosporidium with that of other indicator organisms in stormwater runoff. *Water Research* 42 (17): 4421-4438.

Gibson C, Stadterman K, States S, Sykora J. 1998. Combined sewer overflows: a source of *Cryptosporidium and Giardia*? *Water Science and Technology* 38 (12): 67-72.

Hathaway JM, Hunt WF, Jadlocki S. 2009. Indicator bacteria removal in storm-water Best Management Practices in Charlotte, North Carolina. *Journal of Environmental Engineering* 135 (12): 1275-1285.

Huang X, Rippy MA, Mehring AS, Winfrey BK, Jiang SC, Grant SB. 2018. Shift in dissolved organic matter and microbial community composition are associated with enhanced removal of fecal pollutants in urban stormwater wetlands. *Water Research* 137: 310-323.

Humphrey C, Chaplinski N, O'Driscoll M, Kelley T, Richards S. 2014. Nutrient and *E. coli* attenuation in a constructed stormwater wetland in the North Carolina coastal plain. *Environment and Natural Resources Research* 4: 12-22.

Jiang SC, LIM KY, Huang X, McCarthy D, Hamilton AJ. 2015. Human and environmental health risks and benefits associated with the use of urban stormwater. *WIREs Water* 2 (6): 683-699.

Kleinheinz GT, McDermott CM, Hughes S, Brown A. 2009. Effects of rainfall on *E. coli* concentrations at Door County, Wisconsin Beaches. *International Journal of Microbiology* 2009: 876050, 9p.

Noble RT, Griffith JF, Blackwood DA, Furham Gregory JB, Hernandez X, Liang X, Bera Angie A, Schiff K. 2006. Multitiered approach using quantitative PCR to track sources of faecal pollution affecting Santa Monica Bay, California. *Applied and Environmental Microbiology* 72 (2): 1604-1612.

Paule-Mercado, M.A., Ventura, J.S., Memon, S.A., Jahng, D., Kang, J.H., Lee, C.H., 2016. Monitoring and predicting the fecal indicator bacteria concentrations from agricultural, mixed land use and urban stormwater runoff. *Science of the Total Environment* 550: 1171–1181.

Rajal VB, McSwain BS, Thompson DE, Leutenegger CM, Wuertz S. 2007. Molecular quantitative analysis of human viruses in California stormwater. *Water Research* 41 (19): 4287-4298.

Rowny JG, Stewart JR. 2012. Characterisation of nonpoint source microbial contamination in an urbanising watershed serving as a municipal water supply. *Water Research* 46: 6143-6153.

Shen P, McCarthy DT, Chandrasena GI, Li Y, Deletic A. 2019. Validation and uncertainty analysis of a stormwater biofilter treatment model for faecal microorganisms. *Science of the Total Environment* https://doi.org/10.1016/j.scitotenv.2019.136157

Sidhu JPS, Hodgers L, Ahmed W, Chong MN, Toze S. 2012. Prevalence of human pathogens and indicators in stormwater runoff in Brisbane, Australia. *Water Research* 46 (20): 6652–6660.

States S, Stadterman S, Ammon L, Vogel P, Baldizar J, Wright D, Conley L, Sykora J. 1997. Protozoa in river water: sources, occurrence and treatment. *Journal of the American Water Works Association* 89 (9): 74-82.

Steele, JA, Blackwood D, Griffith JF, Noble RT, Schiff KC. 2018. Quantification of pathogens and markers of faecal contamination during storm events along popular surfing beaches in San Diego, California. *Water Research* 136: 137-149

Surbeck CQ, Jiang SC, Ahn JH, Grant SB. 2006. Flow fingerprinting fecal pollution and suspended solids in stormwater runoff from an urban coastal watershed. *Environmental Science and Technology* 40 (14): 4435-4441.

Stockyards

Department of Water. 2015. Water Quality Protection Note 80: Stockyards. Department of Water, Government of Western Australia: Perth.

Fotheringham VJC. 1995. Disinfection of stockyards. *Reviews in Science and Technology* 14(2): 293-307.

Galuszka J. 2019. Owners of Fielding Sale Yards fined more than $100,000 for letting effluent run into waterways. https://www.stuff.co.nz/business/farming/agribusiness/112035520/owners-of-feilding-sale-yards-fined-more-than-100000-for-letting-effluent-run-into-waterways.

Jain P, Cunningham D, Chesson J, Fabiansson S. 2003. *A Quantitative Risk Assessment of Microbial Emissions from Abattoirs.* Report PRMS.036. Prepared for Meat and Livestock Australia Limited. Bureau of Rural Sciences, Commonwealth of Australia, Canberra.

Kiermeier A, Bobbitt J, Vanderline P. Higgs G, Pointon A, Sumner J. 2006. Use of routine beef carcase *Escherichia coli* monitoring data to investigate the relationship between hygiene status of incoming stock and processing efficacy. *International Journal of Food Microbiology* 111: 263-269.

Ruane EM, Murphy PNC, Healy MG, French P, Rodgers M. 2011. On-farm treatment of dairy soiled water using aerobic woodchip filters. *Water Research* 45(20): 6668-6676**.**

Animal effluent/manure application to land

Bolan NS, Laurenson S, Lowe H, Luo J, Hill PH, Sukias J. 2009a. Treatment of farm effluents in New Zealand's dairy operations. *New Zealand Land Treatment Collective: Proceedings for the 2009 Annual Conference 120-*

Bolan NS, Laurenson S, Luo J, Sukias J. 2009b. Integrated treatment of farm effluents in New Zealand's dairy operations. Bioresource Technology 100: 5490-5497.

Brewer AJ, Cumby TR, Dimmock SJ. 1999. Dirty water from dairy farms: treatment and disposal options. *Biosource Technology* 67: 161-169.

Cameron KC, Di, HJ. 2019. A new method to treat farm dairy effluent to produce clarified water for recycling and to reduce environmental risks from the land application of effluent. *Journal of Soils and Sediments* 19: 2290-2302.

Cameron M, Trenouth C. 1999. *Resource Management Act – Practice and Performance. A case study of farm dairy effluent management*. Wellington, Ministry for the Environment.

Collins R, McLeod M, Hedley M, Donnison A, Close M, Hanly J, Horne D, Ross C, Davies-Colley R, Bagshaw C, Matthews L. 2007. Best management practices to mitigate faecal contamination by livestock in New Zealand waters. *New Zealand Journal of Agricultural Research* 50: 267-278.

Craggs RJ, Tanner CC, Sukias JPS, Davies-Colley RJ. 2003. Dairy farm wastewater treatment by an advanced pond system. *Water, Science and Technology* 48: 291-297.

Culley JLB, Phillips PA. 1982. Bacteriological quality of surface and subsurface runoff from manured sandy clay loam soil. *Journal of Environmental Quality* 11: 155-158.

Donnison A, Ross C, McGowan A. 2011. *Escherichia coli* and *Campylobacter* in two conventional Waikato dairy farm effluent ponds. *New Zealand Journal of Agricultural Research* 54, 97-104.

Dungan RS, Klein M, Leytem AB. 2012. Quantification of bacterial indicators and zoonotic pathogens in dairy wastewater ponds*. Applied and Environmental Microbiology* 78: 8089-8095.

Hawke RM and Summers SA. 2006. Effects of land application of farm dairy effluent on soil properties: a literature review. *New Zealand Journal of Agricultural Research* 49: 307-320.

Heatly P. 2001.Dairying and the environment: managing farm dairy effluent. New Zealand Dairy Research Institute, Palmerston North.

Hickey CW, Quinn JM, Davies-Colley RJ. 1989. Effluent characteristics of dairy shed oxidation ponds and their potential impacts on rivers. *New Zealand Journal of Marine and Freshwater Research* 23: 569-584.

Houlbrooke DJ. 2008. Best practice management of farm dairy effluent in the Manawatu-Wanganui region. Prepared for Horizons Regional Council. AgResearch, Hamilton. 44p.

Houlbrooke DJ, Horne DJ, Hedley MJ, Hanly JA, Snow VO. 2004. A review of literature on the land treatment of farm-dairy effluent in New Zealand and its impact on water quality. *New Zealand Journal of Agricultural Research* 47: 499-511.

Houlbrooke D, Laurenson S, Carrick S. 2011a. Categorising the environmental risk from land application of liquid wastes based on soil properties. Prepared for the Marlborough District Council. Joint publication of AgResearch and Landcare Research. Hamilton, New Zealand. 49p.

Houlbrooke D, Longhurst R, Orchiston T, Muirhead R. 2011b. *Characterising Dairy Manures and Slurries*. Envirolink tools report AGRX0901. Prepared for Surface Water Integrated Management (SWIM). AgResearch. 119p.

Longhurst RD, Robers AHC, O'Connor MB. 2000. Farm dairy effluent, a review of published data on the chemical and physical characteristics in New Zealand. *New Zealand Journal of Agricultural Research* 43: 7-143

Longhurst R, Houlbrooke D, Laurenson S. 2013. On-farm farm dairy effluent risk assessment. Report prepared for DairyNZ. RE500/2013/040. AgResearch.

McLeod M, Aislabie J, Ryburn J, McGill A. 2004. Microbial and chemical tracer movement through Granular, Ultic and Recent Soils. *New Zealand Journal of Agricultural Research* 47: 557-563.

Monaghan RM, Smith LC. 2004. Minimising surface water pollution resulting from farm-dairy effluent application to mole-pipe drained soils. II. The contribution of preferential flow of effluent to whole-farm pollutant losses in subsurface drainage from a West Otago fairy farm. *New Zealand Journal of Agricultural Research* 47: 417-428.

Monaghan RM, Hedley MJ, Di HJ, McDowell RW, Cameron KC, Ledgard SF. 2007. Nutrient management in New Zealand pastures – recent developments and future issues. *New Zealand Journal of Agricultural Research* 50: 181-201

Monaghan RM, Houlbrooke DJ, Smith LC. 2010. The use of low-rate sprinkler application systems for applying farm dairy effluent to land to reduce contaminant transfers. *New Zealand Journal of Agricultural Research* 53: 389-402.

Muirhead RW, Elliot AH, Monaghan RM. 2011. A model framework to assess the effect of dairy farms and wild fowl on microbial water quality during base flow conditions. *Water Research* 45: 2863-284.

Roach CG, Longhurst RD, Ledgard SF. 2001. Land application of farm dairy effluent for sustainable dairy farming. *Proceedings of the New Zealand Grassland Association* 63: 53-57.

Robb C, Barkle G. 2000. *New Zealand Guidelines for the Utilisation of Sewage Effluent on Land.* Whitehouse LJ, Wang H, Tomer M, eds. Joint publication of the New Zealand Land Treatment Collective and Forest Research. Rotorua, New Zealand.

Rollo M, Ledgard S, Longhurst B. 2017. Final report: trends in dairy effluent management. Final report prepared for the Ministry of Primary Industries. RE450/2017/041. AgResearch.

Ross C, Donnison A. 2003. *Campylobacter* and farm dairy effluent irrigation. *New Zealand Journal of Agricultural Research* 46: 255-262.

Selvarajah, N. 1996: Dairy farm effluent treatment pond performance in the Waikato region: a preliminary review of the regional survey. In: Mason, I. G. ed. *Tertiary treatment options for dairy shed and piggery wastewaters*. Proceedings of a Seminar, Massey University, 28 June. pp. 18-25.

Wang XM, Di HJ, Cameron KC, Li B. 2019. Effect of treated farm dairy effluent on E. coli, phosphorus, and nitrogen leaching and greenhouse gas emissions: a field lysimeter study. *Journal of Soils and Sediments* 19: 2303-2312.

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