

Human health risks of faecal  
pollution from different sources:  
A review of the literature




**E/S/R**

THE SCIENCE  
BEHIND THE  
TRUTH

---

**December 2015**



**PREPARED FOR:** Environment Canterbury, Community & Public Health,  
Christchurch City Council and the Ministry of Health

**CLIENT REPORT No:** CSC15019

**PREPARED BY:** Megan Devane and Brent Gilpin

**REVIEWED BY:** Elaine Moriarty

## DISCLAIMER

The Institute of Environmental Science and Research Limited (ESR) has used all reasonable endeavours to ensure that the information contained in this client report is accurate. However ESR does not give any express or implied warranty as to the completeness of the information contained in this client report or that it will be suitable for any purposes other than those specifically contemplated during the Project or agreed by ESR and the Client.

# ACKNOWLEDGEMENTS

---

We are grateful for funding for this project from Ministry of Health, Environment Canterbury, Christchurch City Council and Clean Water Productive Land.

Author



**Megan Devane**

Senior Scientist

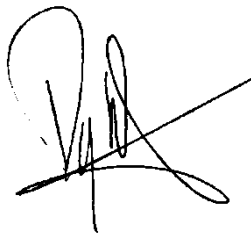
Author



**Brent Gilpin**

Science Leader

Manager



**Wim Nijhof**

Group Manager

Peer reviewer



**Elaine Moriarty**

Senior Scientist



# CONTENTS

---

ABBREVIATIONS.....	VII
EXECUTIVE SUMMARY .....	1
1. INTRODUCTION.....	3
2. ANIMAL FAECES .....	4
2.1 AVERAGE DAILY FAECAL OUTPUTS .....	4
2.2 BOVINE SOURCES – DAIRY COWS AND BEEF CATTLE .....	5
2.4 SHEEP AND LAMB FAECES .....	8
2.5 GOAT FAECES.....	9
2.6 DOG FAECES.....	10
2.7 CAT FAECES.....	12
2.8 WILDFOWL FAECES .....	13
3. HUMAN SEWAGE .....	16
3.1 STUDIES THAT DIRECTLY COMPARED REDUCTION VALUES FOR RAW AND TREATED WASTEWATER.....	16
4. COMPARISON BETWEEN SOURCES.....	21
5. CONCLUSIONS.....	26
REFERENCES .....	29

---

## LIST OF TABLES

TABLE 1: PUBLISHED DAILY FAECAL OUTPUTS FROM A RANGE OF ANIMALS .....	4
TABLE 2: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN DAIRY COW AND BEEF CATTLE FAECES.....	5
TABLE 3: PREVALENCE DATA FOR INDICATORS AND PATHOGENS IN DAIRY COW FAECES .....	6
TABLE 4: PRESENCE/ABSENCE DATA INDICATORS AND PATHOGENS IN BEEF CATTLE FAECES.....	6
TABLE 5: INDICATORS AND PATHOGENS IN CALF FAECES.....	7
TABLE 6: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN SHEEP FAECES .....	8
TABLE 7: PREVALENCE DATA INDICATORS AND PATHOGENS IN SHEEP FAECES ....	8
TABLE 8: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN LAMB FAECES.....	9
TABLE 9: PRESENCE/ABSENCE DATA INDICATORS AND PATHOGENS IN LAMB FAECES .....	9
TABLE 10: QUANTITATIVE DATA ON LEVELS OF PATHOGENS IN GOAT FAECES .....	9
TABLE 11: QUANTITATIVE DATA ON LEVELS OF ENTEROCOCCI IN DOG FAECES ...	10
TABLE 12: PRESENCE/ABSENCE DATA ON PATHOGENS IN DOG FAECES.....	10
TABLE 13: QUANTITATIVE DATA ON LEVELS OF PATHOGENS IN CAT FAECES .....	12
TABLE 14: PRESENCE/ABSENCE DATA ON PATHOGENS IN CAT FAECES.....	12
TABLE 15: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN BLACK SWAN FAECES .....	13
TABLE 16: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN DUCK FAECES .....	13
TABLE 17: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN CANADA GEESE FAECES.....	14
TABLE 18: PRESENCE/ABSENCE AND QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN SEAGULL FAECES .....	15

TABLE 19: PRESENCE/ABSENCE DATA INDICATORS AND PATHOGENS IN PIGEON FAECES .....	15
TABLE 20: DATA ON LEVELS AND PREVALENCE OF INDICATORS AND PATHOGENS IN UNSPECIFIED WILDFOWL FAECES .....	15
TABLE 21: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN UNTREATED HUMAN SEWAGE.....	17
TABLE 22: QUANTITATIVE DATA ON LEVELS OF INDICATORS AND PATHOGENS IN TREATED SEWAGE.....	18
TABLE 23: COMPARISON STUDIES OF INFLUENT AND EFFLUENT AT SEWAGE TREATMENT PLANTS .....	19
TABLE 24: QUANTITATIVE DATA ON AVERAGE DAILY OUTPUT PER ANIMAL OF INDICATORS AND PATHOGENS IN MAMMALS AND BIRDS.....	24
TABLE 25: LEVELS OF INDICATORS AND PATHOGENS RELATIVE TO <i>E. COLI</i> CONCENTRATION NORMALISED TO 1000 CFU/G.....	25
TABLE 26: COMPARISON OF PREVALENCE OF INDICATORS AND PATHOGENS IN ANIMAL FAECES .....	25
TABLE 27: PREDICTED MEDIAN ENTEROCOCCI DENSITIES THAT CORRESPOND TO GI ILLNESS LEVELS OF 0.036, ANALOGOUS TO 36 PEOPLE OUT OF 1000 BECOMING ILL IF THEY INGEST RECREATIONAL WATER CONTAINING THESE LEVELS OF ENTEROCOCCI (REPRODUCED FROM SOLLER ET AL., 2010) .....	28

## LIST OF FIGURES

FIGURE 1. PROBABILITY OF GI ILLNESS FROM INGESTION OF WATER CONTAINING FRESH FAECAL POLLUTION AT DENSITIES OF 35 CFU 100ML <sup>-1</sup> ENT (3A) AND 126 CFU 100ML <sup>-1</sup> <i>E. COLI</i> FROM A RANGE OF SOURCES. FIGURE REPRODUCED FROM SOLLER ET AL. (2010).....	27
-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	----

# ABBREVIATIONS

---

CFU	Colony forming unit
EHEC	Enterohaemorrhagic <i>Escherichia coli</i>
EPEC	Enteropathogenic <i>E. coli</i>
ESBL	Extended-spectrum beta-lactamase
ESC	Cephalosporinase <i>E. coli</i>
FIB	Faecal indicator bacteria
GC	Gene copies
MPN	Most probable number
PCR	Polymerase Chain Reaction
PFU	Plaque forming unit
RT-PCR	Reverse-transcriptase Polymerase Chain Reaction
STEC	Shiga-toxin-producing <i>E. coli</i>
Stx1	Shiga toxin 1 gene
Stx2	Shiga toxin 2 gene



# EXECUTIVE SUMMARY

---

Faecal pollution of surface water can come from a number of sources including raw human sewage, treated sewage, farm animals such as cows and sheep, domestic animals, wildfowl and many other sources. The aim of this project was to explore the evidence available in the literature as to how contact with surface water contaminated with these sources of pollution may affect human health risk (e.g. during swimming or secondary contact activities, such as boating). In particular, the goal was to assess whether non-human sources (e.g. wildfowl) could affect human health, given that previous research has shown high levels of non-human pathogen sources in Christchurch waterways (Moriarty & Gilpin 2015). The first approach taken in this project was to explore the presence and levels of indicator bacteria (such as *Escherichia coli* and enterococci) and pathogens in a range of animal faeces relevant to the New Zealand environment. We then evaluated published Quantitative Microbial Risk Assessments (QMRA) of the risk to human health of water contaminated with faeces from different sources.

All animal and wildfowl faeces are potential human health risks. Many studies of pathogens in animal faeces have been presence/absence based, and have used methods that detect all species or subtypes of a particular genus or species without differentiating between the pathogenic and non-pathogenic types. Future studies will increasingly make greater use of molecular techniques to identify pathogenicity which will build a clearer picture of the risk to human health of microorganisms from different species. In addition differences in methodology, regional differences, and the small number of samples analysed in many studies, limits the robustness of comparisons between sources. With these caveats in mind, we make the following observations:

- *Campylobacter* have been identified in human, sheep, cattle, dairy cow, dog, cat, black swan, duck, canada geese, and gull faeces.
- *Cryptosporidium* have been identified in human, sheep, cattle, dairy cow, dog, cat, goats, duck and geese faeces.
- *Giardia* have been identified in human, sheep, cattle, dairy cow, dog, cat, goat, duck and geese faeces.
- *Salmonella* have been identified in human, sheep, cattle, dairy cow, dog, cat, duck, pigeon and geese faeces.
- Pathogenic *Escherichia coli* have been identified in human, sheep, cattle, dairy cow, dog, cat, pigeon and geese faeces.

- Viruses of importance to human health are only found in human faeces.

There is a requirement for on-going monitoring of faecal sources for the emergence of new pathogens or changes in virulence or prevalence of existing pathogens, which will impact human health risk.

Published Quantitative Microbial Risk Assessment (QMRA) studies suggest that human faeces has the greatest health risk, including when it is only a minor component of faecal pollution in water. Keeping human faeces out of recreational and drinking water must remain a priority. Treated human sewage needs to be evaluated on the basis of individual treatment processes to assess the pathogen inactivation rates and likely impacts on the ratio of indicator to pathogen.

All animal and wildfowl faeces are potential human health risks, particularly to children and immunocompromised individuals. Amongst the animals characterised by risk modelling in international studies, cattle/dairy cow sources appear to have the highest risk, which is driven by the presence of *Campylobacter*, pathogenic *E. coli* and *Cryptosporidium*. The health risk associated with poultry appears to be mainly driven by *Campylobacter*, making poultry of lower risk than human and cattle/dairy cow source, but higher risk than wildfowl. Notable in these QMRA studies, is the absence of information on health risks from sheep and lambs which represent a significant portion of the faecal contamination observed in rural NZ rivers and streams. The QMRA studies have also only been undertaken using gull faeces as a wildfowl source.

A key conclusion from these QMRA studies is that in water containing the same level of faecal indicator from different sources, there is potentially a lower risk of human illness when the water is impacted by chicken, gull and pig faecal material, than human or cattle faeces. Further extrapolation of this work suggests that if the indicator organisms in water are **entirely** from chicken, pig or gull sources, acceptable levels of indicator organisms could be three to 50 times higher than if from a human source.

# 1. INTRODUCTION

---

Faecal pollution of water can come from a number of sources including raw human sewage, treated sewage, farm animals such as cows and sheep, wildfowl and many other sources.

The aim of this report was to review the published literature on levels of indicators and pathogens in a range of sources potentially polluting water in New Zealand.

The scope of this review was restricted to the following sources:

- human sewage (Raw and Treated);
- sheep and cows;
- dogs and cats;
- wildfowl.

During the course of reviewing the literature, information regarding goat faeces was also found and is included. In each of these sources we wanted to identify the presence and levels in faeces of faecal indicator bacteria (*E. coli* and enterococci), and pathogens (*Campylobacter*, *Salmonella*, STEC, Viruses, *Cryptosporidium* and *Giardia*). There was an emphasis on those pathogens known for their zoonotic potential. The European Academies Science Advisory council (EASAC) defines zoonoses as an infection that is naturally transmissible, directly or indirectly, between vertebrate animals and humans. Some zoonoses cause disease in the animal and human, while others are commensal in the animal host.

Between 5 May and 25 June, 2015 we carried out a literature search using Science direct and University of Canterbury database using the following search terms:

- *Cryptosporidium*
- *Giardia*
- Beef cattle
- Dairy
- Sheep
- Lambs
- Cats
- Dogs
- Wildfowl
- Avian
- Birds
- Pets
- Companion animals
- Faecal indicator bacteria
- *Escherichia coli*
- STEC/VTEC
- Enterococci
- Viruses, enterovirus
- Zoonotic/zoonoses
- Toxoplasmosis
- Human wastewater
- Treated wastewater
- New Zealand

We reviewed online abstracts for over 300 papers, and retrieved and reviewed full papers from approximately 100 papers.

## 2. ANIMAL FAECES

---

This section describes the results of literature searches for the presence and levels of indicator bacteria and pathogens in a range of sources.

### 2.1 AVERAGE DAILY FAECAL OUTPUTS

To enable calculation of the daily output of any microorganism from a particular source requires an estimate of the daily output of faecal material from that source. These varied from between 24.8 kg per day for dairy cows down to 0.05 kg per day for seagulls (TABLE 1). Estimates of daily faecal load were not found for cats or pigs.

**TABLE 1: Published daily faecal outputs from a range of animals**

Microorganism	Prevalence	References
Dairy Cow	24.8 kg day <sup>-1</sup>	Muirhead et al. (2011)
Dairy calf	1.65 kg day <sup>-1</sup>	Atwill et al. (2012)
Beef cattle	14.4 kg day <sup>-1</sup>	
Sheep	1.5 kg day <sup>-1</sup>	Moriarty et al. (2011a)
Large dog	52 g dw day <sup>-1</sup>	Wright et al. (2009)
Small dog	7.6 g dw day <sup>-1</sup>	
Gull	0.05 kg day <sup>-1</sup>	
Canada geese	0.250 kg day <sup>-1</sup>	

## 2.2 BOVINE SOURCES – DAIRY COWS AND BEEF CATTLE

Quantitative data in dairy cow faeces is primarily based on New Zealand studies, with *Campylobacter* frequently detected at high levels, while *Salmonella* were not detected in either of the NZ studies undertaken (TABLE 2). A number of other studies reported the presence/absence of a range of pathogens (TABLE 3).

**TABLE 2: Quantitative data on levels of indicators and pathogens in dairy cow and beef cattle faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size (No. of animals)?	Daily Output/cow	Country	References
<i>E. coli</i>	8.20E+04	99.5	155	2.01E+09	NZ	Moriarty et al. (2008)
Enterococci	4.50E+02	93.3	155	1.04E+07		
<i>Campylobacter</i>	4.30E+02	63.9	155	6.81E+06		
<i>Salmonella</i>	0.00E+00	0		-		
<i>Campylobacter</i> (thermophilic)	1.3E+02	9	120	2.90E+05	Denmark	Nielsen (2002)
includes <i>C. jejuni</i> and <i>C. coli</i>	6.1E+02	89.4	360	7.85E+06	UK	Stanley et al. (1998)
STEC <i>E. coli</i>	1.0E+05 to 1.0E+08	15.9	605	2.3E+08 to 2.3E+11	Japan	Fukushima and Seki (2004)
<i>Cryptosporidium parvum</i>	3.38E+00	0.71		5.95E+04	USA	Atwill et al. (2003)

Mean CFU/MPN /((oo)cysts g<sup>-1</sup>) – Mean CFU (colony forming units), MPN (Most probable number) or oocysts (in case of protozoa).

**TABLE 3: Prevalence data for indicators and pathogens in dairy cow faeces**

Microorganism	Prevalence %	Study size (No of animals)?	Country	References
<i>Campylobacter</i> spp.	36	161	NZ	Grinberg et al. (2005)
<i>C. jejuni</i>	6.8	161		
<i>Campylobacter</i> spp.	40	pooled n = 496	UK	Brown et al. (2004)
<i>C. jejuni</i>	31	311	USA	Bae et al. (2005)
<i>C. coli</i>	6			
<i>Salmonella enterica</i>	9.6	960	USA	Callaway et al. (2005)
<i>Salmonella enterica</i>	56			
STEC <i>E. coli</i>	1.3	155	NZ	Moriarty et al. (2008)
STEC <i>E. coli</i>	stx1 4 stx2 6 eae 7	72	NZ	Cookson et al. (2006a)
STEC <i>E. coli</i>	100 in all farms	Per Farm Organic (n = 60) and Conventional farms (n =60)	Switzerland	Kuhnert et al. (2005)
<i>E. coli</i> O157	25 organic 17 conventional			
STEC- <i>E. coli</i> O157-	58 4.6			
non <i>E. coli</i> O157 STECs	20.7	82 herds	Spain	Oporto et al. 2008
<i>E. coli</i> O157 :H7	7	82 herds		
STEC <i>E. coli</i>	stx1 30-47 stx2 30-53 eae 64-76	Approx. 9000 faecal samples	USA	Lambertini et al., (2015)
<i>Cryptosporidium</i> spp.	5.2	155	NZ	Moriarty et al. 2008
<i>Cryptosporidium</i> spp.	7.3	288	Ireland	Moriarty et al. 2005
<i>C. parvum</i>	0.6	354	NZ	Learmonth et al. 2003

**TABLE 4: Presence/Absence data indicators and pathogens in beef cattle faeces**

Microorganism	Prevalence %	Study size	Country	References
<i>E. coli</i> O157 :H7	6.70	30	Spain	Oporto et al. 2008
<i>E. coli</i> O157 :H8	1.60	124 herds	Spain	Oporto et al. 2008
Shiga toxin <i>E. coli</i> (STEC) non <i>E. coli</i> O157	46	124 herds	Spain	Oporto et al. 2008
<i>Salmonella</i>	6.20	130	Italy	European Food Safety Agency, 2010
<i>Salmonella</i>	5.40	707	Italy	
<i>Salmonella</i>	0.3- 1.3	199-386 animal per year over 12 years	Slovenia	
<i>Cryptosporidium parvum</i>	8.4	379	Spain	Castro-Hermida et al. 2007
<i>Giardia duodenalis</i> (Assemblage A)	7.30	110	Germany	Gillhuber et al. 2013
<i>Giardia enteris</i> (zoonotic)	0			
<i>Giardia duodenalis</i>	26.6	379	Spain	Castro-Hermida et al. 2007

Younger animals have been found to have higher levels of *Cryptosporidium* and higher prevalence of both *Cryptosporidium* and *Giardia* (TABLE 5).

**TABLE 5: Indicators and pathogens in calf faeces**

Microorganism	Mean CFU/MPN / (oo)cysts g <sup>-1</sup>	Prevalence %	Study size	Daily Output/ calf	Country	References
<i>Campylobacter</i> (thermophilic) includes <i>C. jejuni</i> and <i>C. coli</i>	≤4 months old 2.5E+04	42	107	1.73E+06	Denmark	Nielsen (2002)
	>4 months old 7.90E+02	20	105	1.36E+06		
<i>C. jejuni</i> <i>C. coli</i>		24 20	105		USA	Bae et al. (2005)
<i>Salmonella</i>	0.00E+00	0	156	0	NZ	Grinberg et al. 2005
<i>E. coli</i> O157:H7		23-26	52		Canada	(Gannon et al., 2002)
STEC <i>E. coli</i> and enteropathogenic <i>E. coli</i> (EPEC)( <i>eae</i> gene)		<i>stx1</i> 2 <i>stx2</i> 19 <i>eae</i> 44	91		NZ	Cookson et al. (2006a)
STEC <i>E. coli</i> and <i>E. coli</i> (EPEC)( <i>eae</i> gene)		STEC 2.6 Atypical EPEC 12.3	299		NZ	Irshad et al. (2014)
<i>E. coli</i> O157		17.7 and 23.8 farms	309 calves, Farms n=197		NZ	Irshad et al., (2012)
<i>C. parvum</i>	3.00E+06	10-80		1.50E+10		Atwill et al. (2012)
<i>C. parvum</i>		10.9	304		NZ	Learmonth et al. (2003)
<i>C. parvum</i>		21.2	156		NZ	Grinberg et al. (2005)
<i>Giardia</i>		4.5		1.00E+03	NZ	Moriarty et al. (2008)

## 2.4 SHEEP AND LAMB FAECES

A number of studies have been completed on indicators and pathogens in sheep and lamb faeces (TABLES 6-9).

**TABLE 6: Quantitative data on levels of indicators and pathogens in sheep faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size	Daily Output/sheep	Country	References
<i>E. coli</i>	1.67E+07	100	220	2.51E+10	NZ	Moriarty et al. (2011a)
Enterococci	6.80E+05	100	220	1.02E+09		
Enterococci	1.20E+04	100	7	1.80E+07	NZ	Anderson et al. (1997)
<i>Campylobacter</i>	2.08E+03	30.4	220	9.48E+05	NZ	Moriarty et al. (2011a)
<i>E. coli</i> O157	Range <100-1.0E+06	6.5	15 farms ~50 sheep/farm	9.8E+03 to 9.8E+07	Scotland	Ogden et al. (2005)
<i>C. parvum</i>	5.30E+01	5.3	446	4.21E+03	Spain	Castro-Hermida et al. (2007)
<i>Giardia duodenalis</i>	3.24E+02	19.2	446	9.33E+04		

**TABLE 7: Prevalence data indicators and pathogens in sheep faeces**

Microorganism	Prevalence %	Study size	Country	References
<i>C. jejuni</i>	25	24	UK	Brown et al. (2004)
<i>C. coli</i>	21	24		
<i>Cryptosporidium</i> spp.	3.6	220	NZ	Moriarty et al. (2011a)
<i>Cryptosporidium</i> spp.	9.4 - 25.0	32	USA	Santin et al. (2007)
<i>C. parvum</i>	3.1	32		
<i>Cryptosporidium</i> spp.	26	500	Australia	Ryan et al (2005)
<i>C. parvum</i>	0			
<i>C. hominis</i>	0.02			
<i>Giardia</i> Assemblage A*	11	500	Australia	Ryan et al (2005)
<i>Giardia</i>	18.8-37.5	32	USA	Santin et al. (2007)
<i>E. coli</i> O157:H7	7.3	278 individuals	Spain	Oporto et al. (2008)
<i>E. coli</i> O157:H7	8.7	122 herds		
Shiga toxin <i>E. coli</i> (STEC) but non <i>E. coli</i> O157:H7	50.8	122 herds		
STEC <i>E. coli</i>	<i>stx1</i> 56 <i>stx2</i> 18 <i>eae</i> 22	50	NZ	Cookson et al. (2006a)
Shiga toxin <i>E. coli</i> (STEC)	1	220	NZ	Moriarty et al. (2011a)
<i>Salmonella</i>	0	220		

\*Human infective form of *G. duodenalis*



**TABLE 8: Quantitative data on levels of indicators and pathogens in lamb faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size	Daily Output/ lamb	Country	References
<i>E. coli</i>	6.04E+08	100	105	4.53E+11	NZ	Moriarty et al. (2011a)
Enterococci	1.44E+07	100	105	1.08E+10		
<i>Campylobacter</i>	3.33E+05	80.9		2.02E+08		
<i>Cryptosporidium</i> spp.	6.83E+03	0.9	137	4.61E+06	Belgium	Geurden et al., (2008)
<i>Cryptosporidium</i> - cervine genotype	8.90E+03	28.6	105	1.91E+06	NZ	Moriarty et al. (2011a)
<i>Giardia</i> spp.	2.80E+01	37.1	105	7.79E+03		
<i>Giardia</i>	3.60E+04	4.8	3142	1.31E+06	Australia	Yang et al. (2014)
<i>Giardia</i> spp.	4.58E+03	25.5	137	5.84E+05	Belgium	Geurden et al., (2008)

**TABLE 9: Presence/Absence data indicators and pathogens in lamb faeces**

Microorganism	Prevalence %	Study size	Country	References
<i>C. parvum</i>	13	477	Australia	Yang et al. (2009)
<i>Cryptosporidium</i> spp.	33-77	31	USA	Santin et al. (2007)
<i>C. parvum</i>	3.2	31		
<i>Giardia</i> spp.	11.6	477	Australia	Yang et al. (2009)
<i>Giardia</i> Assemblage A	1.1	477		
<i>Giardia</i>	6.5-12.9	31	USA	Santin et al. (2007)
STEC <i>E. coli</i>	stx1 48 stx2 9 eae 13	46	NZ	Cookson et al. (2006a)
non <i>E. coli</i> O157 STEC	3.8	105	NZ	Moriarty et al. (2011a)
<i>Salmonella</i>	1.9	105		

## 2.5 GOAT FAECES

While we found data from Spain and Belgium on the levels of *Giardia* and *Cryptosporidium* in goat faeces (TABLE 10), we saw no data on levels of faecal indicator bacteria and bacterial pathogens from this source.

**TABLE 10: Quantitative data on levels of pathogens in goat faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size	Daily Output/ goat	Country	References
<i>C. parvum</i>	1.84E+02	7.7	116	2.13E+04	Spain	Castro-Hermida et al. (2007)
<i>Cryptosporidium</i> spp.	2.30E+05	9.5	148	3.28E+07	Belgium	Geurden et al., (2008)
<i>Giardia duodenalis</i>	1.13E+02	19.8	116	3.36E+04	Spain	Castro-Hermida et al. (2007)
<i>Giardia</i> spp.	1.80E+04	35.8	148	9.67E+06	Belgium	Geurden et al., (2008)

## 2.6 DOG FAECES

We were unable to find any data on *E. coli* levels in dog faeces. While there were some information on enterococci in dog faeces, the results are based on a total of 10 animals (TABLE 11), so again are limited. There are much more data on the presence or absence of pathogens in dog faeces, with a range of pathogenic *E. coli*, *Campylobacter*, *Cryptosporidium*, *Giardia*, *Clostridium* and *Salmonella* all reported in dog faeces (TABLE 12).

**TABLE 11: Quantitative data on levels of Enterococci in dog faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size	Daily Output/ dog	Country	References
Enterococci	6.40E+07	100	6 medium-large dogs	3.30E+09	USA	Wright et al. (2009)
Enterococci	5.90E+06	100	3 small dogs	4.50E+06		
Enterococci	2.30E+04	100	1	1.20E+06	NZ	Anderson et al. (1997)

**TABLE 12: Presence/absence data on pathogens in dog faeces**

Microorganism	Prevalence %	Study size	Country	References
Pathogenic <i>E. coli</i>	83	52	USA	Holland et al. (1999)
Pathogenic <i>E. coli</i> (eae)	7.3	153	Germany	Krause et al. (2005)
ESC* <i>E. coli</i>	3	102	Canada	Lefebvre et al. (2006)
ESBL** <i>E. coli</i>	1			
ESBL <i>E. coli</i>	14	100	Germany	Schaufler et al. (2015)
<i>C. jejuni</i>	7	289	Australia	Baker et al. (1999)
<i>C. coli</i>	2			
<i>C. upsaliensis</i>	34			
<i>C. jejuni</i>	11	4	Denmark	Damborg et al. (2004)
<i>C. jejuni</i>	7	70 healthy dogs	Canada	Chaban et al. (2010)
<i>C. coli</i>	0			
<i>C. lari</i>	0			
<i>C. upsaliensis</i>	43			
<i>C. jejuni</i>	46	65 diarrhoeic dogs		
<i>C. coli</i>	25			
<i>C. lari</i>	9			
<i>C. upsaliensis</i>	85			
<i>Campylobacter</i>	0	102	Canada	Lefebvre et al. (2006)
<i>C. jejuni</i>	1	249	UK	Parsons et al. (2010)
<i>C. upsaliensis</i>	37			

Microorganism	Prevalence %	Study size	Country	References
<i>Staphylococcus aureus</i> (methicillin-resistant)	0	102	Canada	Lefebvre et al. (2006)
<i>Salmonella</i> (healthy dogs)	Range 0-3.5	N/A	USA	Marks et al., (2011)
<i>Salmonella</i> (diarrhoeic dogs)	Range 0-3.6			
<i>Salmonella</i>	3	102	Canada	Lefebvre et al. (2006)
Vancomycin-resistant enterococci	0	102		
<i>Giardia</i>	15.2	Estimate of 4.3 million dogs	UK	Bouزيد et al. (2015)
<i>Giardia</i>	4	129	USA	Wang et al. (2012)
<i>Giardia</i>	2.6	77	Japan	Yoshiuchi et al. (2010)
<i>Giardia duodenalis</i>	Pet store 39	69	Canada	Uehlinger et al. (2013)
<i>Giardia duodenalis</i>	Vet clinic 38	78		
<i>Giardia duodenalis</i>	Shelter 6	62		
<i>Cryptosporidium</i>	2	129	USA	Wang et al. (2012)
<i>Cryptosporidium</i>	3.9	77	Japan	Yoshiuchi et al. (2010)
<i>Cryptosporidium</i>	Pet store 10	78	Canada	Uehlinger et al., (2013)
<i>Cryptosporidium</i>	Vet clinic 8	62		
<i>Clostridium perfringens</i>	34	95	USA	Minamoto et al. (2014)
Enterotoxigenic <i>E. coli</i>	48	104		
<i>Clostridium perfringens</i>	84 healthy	105	Canada	Goldstein et al. (2012)
<i>Clostridium perfringens</i>	91 diarrhoeic	54		
<i>Clostridium difficile</i>	Range 10-21	N/A	USA	Marks et al. (2011)
<i>Clostridium difficile</i>	8	102	Canada	Lefebvre et al. (2006)

\*ESC = Cephalosporinase *E. coli*

\*\*ESBL = Extended-spectrum beta-lactamase

## 2.7 CAT FAECES

We were unable to find any data on *E. coli* or enterococci levels in cat faeces. There are some data on pathogens found in cat faeces, with a range of pathogenic *E. coli*, *Campylobacter*, *Cryptosporidium*, *Giardia*, *Clostridium*, *Salmonella* and *Toxoplasma gondii* all reported in cat faeces (TABLE 13 and TABLE 14 ). We could not find an estimate of daily faecal outputs per cat.

**TABLE 13: Quantitative data on levels of pathogens in cat faeces**

Microorganism	Mean CFU/MPN / (oo)cysts g <sup>-1</sup>	Prevalence %	Study size	Daily Output	Country	References
<i>Giardia</i>	2.00E+04	10.1	345	N/A	Australia	Yang et al. (2015)
<i>Cryptosporidium</i>	3.50E+03	10		N/A		

**TABLE 14: Presence/absence data on pathogens in cat faeces**

Microorganism	Prevalence %	Study size	Country	References
<i>C. jejuni</i>	4	195	Australia	Baker et al., (1999)
<i>C. coli</i>	0			
<i>C. upsaliensis</i>	11			
<i>C. jejuni</i>	33	4	Denmark	Damborg et al. (2004)
Pathogenic <i>E. coli</i>	6.5	62	Germany	Krause et al. (2005)
<i>Clostridium perfringens</i>	> 80 healthy & diarrhoeic	N/A	USA	Marks et al., (2011),
<i>Salmonella</i>	Range 0-8.6	N/A		
<i>Giardia</i>	12	Estimate of 250, 000	UK	Bouزيد et al. (2015)
<i>Giardia</i>	44	18	USA	Fayer et al. (2006)
<i>Giardia</i>	2	55		Yoshiuchi et al. (2010)
<i>Cryptosporidium</i>	12	250	USA	Ballweber et al. (2009)
<i>Cryptosporidium</i>	100	18	USA	Fayer et al. (2006)
<i>Cryptosporidium</i>	13	55	Japan	Yoshiuchi et al. (2010)
<i>Toxoplasma gondii</i>	0.4	252	Switzerland	Berger-Schoch et al. (2011)
<i>Toxoplasma gondii</i>	30	123	USA	Dabritz et al. (2007)
<i>Toxoplasma gondii</i>	1	326	USA	Dabritz (2006)
<i>Toxoplasma gondii</i>	0	63	NZ	Langham and Charleston, (1990).

## 2.8 WILDFOWL FAECES

The faeces of a range of wildfowl have been examined for indicators and pathogens including black swans (TABLE 15), ducks (TABLE 16), Canada geese (TABLE 17), seagulls (TABLE 17), pigeons (TABLE 19), and some unspecified wildfowl (TABLE 20).

**TABLE 15: Quantitative data on levels of indicators and pathogens in black swan faeces**

Microorganism	Mean CFU/MPN / (oo)cysts g <sup>-1</sup>	Prevalence %	Study size	Daily Output/ swan	Country	References
<i>E. coli</i>	1.91E+06	94	80	7.50E+08	NZ	Moriarty et al. (2011b)
Enterococci	1.10E+06	79		3.63E+08		
<i>Campylobacter</i>	2.04E+02	45		3.84E+04		

**TABLE 16: Quantitative data on levels of indicators and pathogens in duck faeces**

Microorganism	Mean CFU/MPN / (oo)cysts g <sup>-1</sup>	Prevalence %	Study size	Daily Output/ duck	Country	References
<i>E. coli</i>	9.40E+07	95	80	3.00E+10	NZ	Moriarty et al. (2011b)
<i>E. coli</i>		89	82		USA	Fallacara et al. (2001)
<i>E. coli</i>	1.00E+06		1 composite of 4 duck faeces	3.36E+08	NZ	Murphy et al. (2005)
<i>E. coli</i>	1.40E+07		16	4.70E+09	USA	Haack et al. (2003)
Faecal coliforms	3.30E+07		Not specified	1.11E+10	England	Gould and Fletcher (1978)
Faecal streptococci	5.40E+07			1.81E+10		
Enterococci	1.01E+08	100	80	3.39E+10	NZ	Moriarty et al. (2011b)
Enterococci	5.00E+07		13	1.68E+10	USA	Haack et al. (2003)
Enterococci	3.40E+05		2	1.14E+08	NZ	Anderson et al. (1997)
<i>Campylobacter</i>	5.92E+01	29	80	5.77E+03	NZ	Moriarty et al. (2011b)
<i>C. jejuni</i>		40	82		USA	Fallacara et al. (2001)
<i>Salmonella</i>		1				
<i>Cryptosporidium</i>	4.80E+01	49	69	7.90E+03	USA	Kuhn et al. (2002)
<i>Giardia</i>	4.36E+02	28		4.10E+04		

**TABLE 17: Quantitative data on levels of indicators and pathogens in canada geese faeces**

Microorganism	Mean CFU/MPN / (oo)cysts g <sup>-1</sup>	Prevalence %	Study size	Daily Output/ bird	Country	References
<i>E. coli</i>	3.62E+04	95	80	8.60E+06	NZ	Moriarty et al. (2011b)
<i>E. coli</i>		63	357		USA	Fallacara et al. (2001)
<i>E. coli</i>	3.60E+05		63	6.71E+07	USA	Middleton and Ambrose (2005)
<i>E. coli</i>	4.20E+03		16		USA	Haack et al. (2003)
Enterococci	5.00E+02		13			
Enterococci	2.51E+04		80	6.15E+08	NZ	Moriarty et al. (2011b)
Enterococci	7.30E+05		63	1.83E+08	USA	Middleton and Ambrose (2005)
<i>Campylobacter</i>	4.84E+03	40	80	4.84E+05	NZ	Moriarty et al. (2011b)
<i>C. jejuni</i>		5 and 16 over two years	318		USA	Rutledge et al. (2013)
<i>C. jejuni</i>		52	357		USA	Fallacara et al. (2001)
<i>Salmonella</i>		0				
<i>Cryptosporidium</i> spp.		5	80		NZ	Moriarty et al (2011b)
<i>Cryptosporidium</i> spp.		82 and 90	11 and 10 sites			Kassa et al. (2004)
<i>Cryptosporidium</i> spp.		23	209		USA	Zhou et al. (2004)
<i>C. parvum</i>		2				
<i>C. hominis</i>		1				
<i>Cryptosporidium</i> spp. (infectious <i>C. parvum</i> identified)	3.7E+02	78% of sites	9 sites		USA	Graczyk et al. (1998)
<i>Giardia</i> spp.	4.1E+02	100% of sites				

**TABLE 18: Presence/Absence and quantitative data on levels of indicators and pathogens in seagull faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size	Daily Output	Country	References
<i>E. coli</i>	1.87E+07		80	8.98E+08	NZ	Moriarty et al. (2011b)
<i>E. coli</i>	1.00E+07		Not specified	5.00E+08	USA	Fogarty et al. (2003)
Enterococci	1.00E+06			5.00E+07		
Enterococci	4.20E+03		2	2.10E+05	NZ	Anderson et al., (1997)
Enterococci	8.96E+06	99	80	4.44E+08	NZ	Moriarty et al. (2011b)
<i>Campylobacter</i>	7.66E+02	59		2.26E+04		
<i>C. lari</i>		2	205		Northern Ireland	Moore et al., (2002)
Urease-positive thermophilic <i>Campylobacter</i>		10	205			
<i>C. jejuni</i>		1	205			
<i>Cryptosporidium</i> spp.		0	205			

**TABLE 19: Presence/Absence data indicators and pathogens in pigeon faeces**

Microorganism	Prevalence %	Study size	Country	References
<i>Salmonella enterica</i>	3	277	USA	Pedersen et al. (2006)
Shiga toxin <i>E. coli</i> (STEC)	0	466		
Shiga toxin <i>E. coli</i> (STEC) virulence genes	8	466		

**TABLE 20: Data on levels and prevalence of indicators and pathogens in unspecified wildfowl faeces**

Microorganism	Mean CFU/MPN /((oo)cysts g <sup>-1</sup> )	Prevalence %	Study size	Daily Output	Country	References
Enterococci	2.00E+04		26		USA	Wright et al. (2009)
<i>C. jejuni</i>		26	180		UK	Brown et al. (2004)
<i>Campylobacter</i> spp.		50	449		USA	Fallacara et al. (2001)

## 3. HUMAN SEWAGE

---

There are many studies of pathogens in both influent (raw sewage) and effluent (treated sewage) and only a sample of results from such studies are provided in this report in TABLE 21 and TABLE 22. Additional examples of concentration and prevalence are presented in TABLE 23, which looks at comparative studies between raw and treated sewage to assess removal rates of indicators and pathogens. We believe that there is additional unpublished data in New Zealand generated by district councils, regional councils and thesis dissertations, which future work should attempt to obtain.

### 3.1 STUDIES THAT DIRECTLY COMPARED REDUCTION VALUES FOR RAW AND TREATED WASTEWATER

Estimating the prevalence and abundance of pathogens in human sewage is complex and dependent on whether the sewage is raw or treated effluent and also the type of effluent treatment undertaken before discharge into the environment (Soller et al., 2010). TABLE 23 provides examples of the effect of treatment on various indicators and pathogens by presenting the  $\log_{10}$  reduction in concentration of these microbes as they pass through the treatment process. In the study of Kitajima et al. (2014) the prevalence of viruses decreased with  $\log_{10}$  reductions ( $<\log_{10} 2.9$ ). In addition, the potentially pathogenic viruses were still prevalent (range 25 to 92%) in effluent samples. Decrease in FIB levels ranged from removal rates of  $\log_{10} 3.15$  to  $3.98$  in a Canadian study by Shannon et al. (2007). A Swedish treatment site trialled three different types of treatment for removal of microbes from wastewater: T1) tertiary filtration, T2) membrane bioreactor (MBR), and T3) upflow anaerobic sludge blankets (UASB) (Ottoson et al., 2006). Treatment 2, the MBR, showed the highest log removal of indicators and viruses while Treatment 3, the USAB, showed the lowest removal rates for these organisms. The T2, MBR, produced an almost  $\log_{10} 5.0$  removal of *E. coli* and similar for enterococci. The removal rates for viruses were much lower, at less than  $\log_{10} 2.0$  removal even in the MBR system and viruses were still detected in effluent streams, ranging from 18 to 80% prevalence. Pathogenic protozoa showed the most effective removal rates for pathogens in the study with no *Giardia* or *Cryptosporidium* detected in the effluent from Treatments 2 and 3, even though *Giardia* was detected at 100% prevalence in influent.

As is evident from the removal rates outlined in TABLE 23, secondary treated effluent has the potential for a higher risk of illness than raw sewage due to the higher removal of indicator organisms during treatment compared with the greater resistance of pathogens such as viruses and protozoa. Therefore, the concentration of microbial indicators may be



within water quality guidelines but there is still the potential for infection by pathogens when treated wastewater is identified as the source of contamination (MfE and MoH 2003).

**TABLE 21: Quantitative data on levels of indicators and pathogens in untreated human sewage**

Microorganism	Mean CFU/MPN/PFU 100 mL <sup>-1</sup> virus/(oo)cyst L <sup>-1</sup>	Range CFU/MPN/PFU 100 mL <sup>-1</sup> (oo)cyst L <sup>-1</sup>	Pre- Valence %	Study size	Country	References
<i>E. coli</i>	1.00E+08		100	13	Honolulu	Yang et al. (2014)
<i>E. coli</i>	3.60E+06			1	Spain	Marín et al. (2015)
<i>Salmonella</i> spp	0.00E+00			1		
<i>Cryptosporidium</i> spp.	0.00E+00			1		
Faecal coliforms (Baseflow)	1.70E+07		100	252	UK	Kay et al. (2008)
Faecal coliforms (Highflow)	2.80E+06		100	279		
Enterococci	5.00E+06	1.0E+06- 1.0E+07	100		NZ	Anderson et al. (1997)
F-specific coliphage	1.58E+05		100		Japan	Haramoto et al. (2015)
Enteropathogenic <i>E. coli</i> (EPEC) eae:	3.99E+02		100	13	Honolulu	Yang et al. (2014)
Enterohemorrhagic <i>E. coli</i> (EHEC) stx <sub>1</sub> :	1.5E+00		15.40			
<i>E. coli</i> (EHEC) stx <sub>2</sub> :	2.1E+00		23.1			
*ESBL <i>Enterobacteriaceae</i>	2.40E+08	1.9-2.9E+08	100	21	Poland	Korzeniewska and Harnisz (2013)
<i>Cryptosporidium</i> spp.	8.7E+01	7.4E+01 – 1.0E+02	92	24	USA	Kitajima et al. (2014a)
<i>Giardia</i> spp.	5.60E+03	4.8 E+03 – 6.4 E+03	100 <i>G. intestinalis</i> ** 17 Plant A; 67 Plant B			
<i>Cyclospora</i> spp.	1.20E+04 copies		25			
Human adenovirus	5.01E+05		100	10	Japan	Haramoto et al. (2015)
Norovirus Genogroup I:	1.45E+05		90			
Norovirus Genogroup II:	7.94E+06		60			

\*ESBL = Extended spectrum beta-lactamase

**TABLE 22: Quantitative data on levels of indicators and pathogens in treated sewage**

Treatment type	Microorganism	Mean CFU/PFU/MPN 100 mL <sup>-1</sup> (oo)cyst L <sup>-1</sup> virus GCL <sup>-1</sup>	Prevalence %	Study size	Country	References
Final effluent	<i>E. coli</i>	1.70E+04		1	Spain	Marín et al. (2015)
Primary settled sewage	Faecal coliforms	1.80E+07	100	60	UK	Kay et al. (2008)
Settled septic tank	Faecal coliforms	7.20E+06	100	42		
Trickling filter	Faecal coliforms	4.30E+05	100	477		
Tricking/sand filter	Faecal coliforms	2.10E+05	100	11		
Activated sludge	Faecal coliforms	2.80E+05	100	261		
oxidation ditch	Faecal coliforms	2.00E+05	100	35		
UV disinfection	Faecal coliforms	2.80E+02	100	108		
Reedbed /grass plot	Faecal coliforms	1.30E+04	100	71		
Treated wastewater	<i>E. coli</i>	1.84E+02	75	24	USA	Kitajima et al. (2014b)
oxidation pond effluent	Enterococci	1.00E+03			NZ	Anderson et al. (1997)
Treated wastewater	F-specific coliphage	3.2E+02		10	Japan	Haramoto et al. (2015)
effluent (clarifiers)	<i>E. coli</i> O157	-	7	44	France	Bertrand and Roig (2007)
Treated Sewage	ESBL isolates of <i>Enterobacteriaceae</i>	Range 6.0E+01-3.5E+06	100	21	Poland	Korzeniewska and Harnisz (2013)
Activated sludge or biological trickling filter	<i>Cryptosporidium</i> spp.	1.25E+01	83	24	USA	Kitajima et al. (2014a) (oo)cyst L <sup>-1</sup>
	<i>Giardia</i>	1.12E+02	100			
	<i>Cyclospora</i> spp.	-	13			
Treated Sewage Virus concentrations reported in log <sub>10</sub> gene copies L <sup>-1</sup>	Human adenovirus	1.29E+04	100	10	Japan	Haramoto et al. (2015)
	Norovirus Genogroup I	1.82E+03	70			
	Norovirus Genogroup II	5.25E+04	30			

**TABLE 23: Comparison studies of influent and effluent at sewage treatment plants**

Microorganisms	Mean log <sub>10</sub> gene copies 100 mL <sup>-1</sup> Or comparable prevalence	Reference and Comments
Viruses	Norovirus <b>Influent</b> Genogroup (G) I and II ~100% in both Plant A and B <b>effluent</b> Genogroup (G) I and II, 75% in both A and B, G IV: 67% Plant A; 25% Plant B	<p><b>Kitajima et al. (2014)</b> US study of two wastewater treatment plants with influent (n = 12 from each plant) and effluent samples (n = 12 from each plant) collected monthly over a one year period. Plant A used activated sludge process and Plant B a biological trickling filter tower, and both used chlorination for disinfection. Isolation was by an electronegative filter method and identification by quantitative PCR for 11 viruses which included rotavirus, adenovirus, enterovirus, polyomaviruses and the genogroups of norovirus.</p> <p>Norovirus had the highest viral reduction during treatment at both plants (GII log<sub>10</sub> reduction 2.1 at A and 2.9 at B; followed by GIV norovirus, log<sub>10</sub> reduction 1.7 at A and 2.7 at B) compared with all other viruses. Both treatment plants had statistically similar reduction rates for all viruses, with the exception of enterovirus which had greater reduction at Plant B (bio trickling filter).</p>
	Enterovirus <b>Influent</b> 100% Plants A and B; <b>Effluent</b> 58% (A); 92% (B)	
	Adenovirus <b>Influent</b> 100% (A) and 83% (B); <b>Effluent</b> 58% (A); 92% (B)	
<i>E. coli</i>	<b>Influent:</b> 7.18 <b>Final Effluent:</b> 3.20 Log <sub>10</sub> reduction range: 3.52-3.98	
<i>C. perfringens</i>	<b>Influent:</b> 5.85 <b>Final Effluent:</b> 2.70 Log <sub>10</sub> reduction range: 3.15-3.39	<p><b>Shannon et al. (2007)</b> Canadian study of five stages of one wastewater treatment plant using real-time qPCR methods. Concentrations measured in log<sub>10</sub> gene copies (GC)/100 mL.</p> <p><i>Listeria monocytogenes</i> (no data given) and <i>Aeromonas hydrophila</i> (4.32 log<sub>10</sub> GC/100 mL) were only detected in influent, thereafter, not detected at any stage in treatment process. <i>E. coli</i> O157:H7, <i>Salmonella</i> spp., <i>Staphylococcus aureus</i>, <i>Legionella monocytogenes</i> and <i>Helicobacter pylori</i> were not detected in influent or at any stage of treatment</p>
<i>Enterococcus faecalis</i>	<b>Influent:</b> 4.66 <b>Final Effluent:</b> 1.42 Log <sub>10</sub> reduction: 3.24	
<i>Pseudomonas aeruginosa</i>	<b>Influent:</b> 4.38; <b>Primary effluent:</b> 2.22. Thereafter, not detected during treatment process or final effluent	

TABLE 23 continued: Comparison studies of influent and effluent at sewage treatment plants

Microorganisms	Mean MPN L <sup>-1</sup>	Prevalence	Reference and Comments
<i>Giardia</i>	Influent 1.3E+03 cysts Effluent T1: 0.4 cysts	Influent 100%; Effluent T1 11%; T2 0%; T3 0%	<p><b>Ottoson et al. (2006)</b> Swedish study of the inlet wastewater and effluent from an experimental treatment plant using one of three treatment (T1, T2, T3) regimes T1) tertiary filtration, T2) membrane bioreactor (MBR) T3) upflow anaerobic sludge blankets (UASB). Protozoan were analysed using immunofluorescence detection and viruses by RT-PCR. There was no speciation of protozoa to attribute sources to humans or to animals. The PCR method for enterovirus assayed all types of enteroviruses and is therefore an index of enterovirus removal rather than direct risk evaluator of pathogenic enteroviruses. Removal quantified as a log<sub>10</sub> reduction. Norovirus more frequently detected in winter samples (86%, n =7).</p> <p><u>Mean removal rates for indicators for each treatment regime</u></p> <p><i>E. coli</i>: log<sub>10</sub> removal T1, 3.23; T2, 4.97; T3 1.97</p> <p>Enterococci: log<sub>10</sub> removal T1,3.17; T2, 4.52; T3 1.75</p> <p><i>C. perfringens</i>: log<sub>10</sub> removal T1, 2.38; T2, 3.04; T3 0.66</p> <p>Somatic coliphages: log<sub>10</sub> removal T1, 2.32; T2, 3.08; T3 0.76</p> <p>F-RNA phage: log<sub>10</sub> removal T1, 3.47; T2, 3.78; T3 2.38</p>
<i>Cryptosporidium</i>	Influent 5.0E+01 oocysts Effluent T1: 0.13 oocysts	Influent 21%; Effluent T1 6%; T2 0%; T3 0% T1 and T2 showed 97.4% and >96.4% removal (resp.)	
Enteroviruses	Influent 1E+04 Effluent T1 and T2 <2.1E+02 T3: 3.5E+03	Influent 78%, n =23 Effluent T1 36%; T2 29%; T3 80% T1 and T2 showed 98.0% and 98.4% removal whereas T3 showed 65% removal of viruses after treatment	
Norovirus	Influent 3.0E+02 Effluent T1 and T2 <3.5E+01 T3: 3.0E+02	Influent 36.4%, n = 22 Effluent T1 18%; T2 18%; T3 40% T1 and T2 showed 89 % and 93% (resp.) removal whereas T3 showed zero removal of viruses after treatment	

## 4. COMPARISON BETWEEN SOURCES

---

There are extensive data on microorganisms in livestock, particularly beef cattle and dairy cows, of which we have provided a subset. The data provided in sections 2 and 3, however, does highlight the limited knowledge we have on the presence and levels of microorganisms in many of the other animal sources of interest such as avian species. A full QMRA comparing sources is beyond the scope of this report and is, based on the data available, potentially misleading. However, we have in TABLE 24, presented a comparison of the levels of microorganisms from a range of sources expressed as microorganisms per animal per day. Young livestock (lambs and calves) have the highest daily shedding potential for *Campylobacter* and *Cryptosporidium* and sheep have greater daily shedding of these two pathogens compared with the larger dairy cows, although not in comparison with *Cryptosporidium* shed by beef cattle. In general, avian species have two to three orders of magnitude reduced daily outputs of *E. coli* and *Campylobacter* compared with livestock.

It should be noted that many studies report prevalence and quantitative data at the genus level, for example, *Cryptosporidium*, and then test a limited subset of the isolates for specific pathogens known to be zoonoses, such as *C. parvum*. Therefore, the data for prevalence and concentration of microorganism will include a proportion that are not zoonotic and potentially do not represent a human health risk. Another example is infections of cattle by *Giardia duodenalis*. Most of the *G. duodenalis* belong to the non-zoonotic Assemblage E compared with the human infective Assemblage A (Atwill et al., 2012).

In TABLE 25, the numbers from TABLE 24 have been normalised to represent the concentration of indicators and pathogens that could be associated with 1000 CFU/g *E. coli* identified in the faeces of a particular animal species. There are approximately ten to 200-fold higher *E. coli* levels in livestock, black swans and gulls compared with enterococci. In contrast, Canada geese have tenfold higher enterococci levels compared with *E. coli*. In general, there are 1000-fold lower levels of *Campylobacter* in livestock compared with *E. coli* and even lower levels in most avian species, except for Canada geese, which have approximately 100-fold lower *Campylobacter* than *E. coli*. The potential for faecal pollution from Canada geese to cause illness in humans has been highlighted in a recent review (Gorham and Lee, 2015). Levels of *Cryptosporidium* are at least  $10^4$  fold less than *E. coli* in livestock, and even less in ducks. *Giardia* are present in very low levels compared with *E. coli* ( $10^5$  and  $10^6$  fold less concentration in ducks and livestock, respectively).

The prevalence of indicators and pathogens in mammals and birds is presented in TABLE 26. *E. coli* and enterococci are identified in >93% of the faeces of all livestock, with a lower

overall prevalence in avian species ranging from 63 to 95% for *E. coli* and 79 to 100% for enterococci.

The highest prevalence of *Campylobacter* was seen in lambs at 84% with the next highest in dairy cows, which ranged from 7- 64%. Calves and lambs are born *Campylobacter*-free but are rapidly colonised from the farm environment after birth (Gannon et al., 2002; Stanley and Jones, 2003). In general, calves and lambs are identified as shedding higher concentrations of *Campylobacter* compared with adult animals.

*Campylobacter* in avian species ranged from 29-52%, except for gulls at 1% prevalence.

*Cryptosporidium* was identified in 12-100% of cat faeces, however the 100% prevalence was from a smaller study size compared with the lower prevalence (12 and 13%) from a larger study size. The next highest prevalence of *Cryptosporidium* was seen in young livestock with ranges of 0.9-77% in lambs and 10-80% in calves.

*Giardia* was identified in up to 37% of sheep and lambs, only 5% in calves and 0-26% in beef cattle with no data on dairy cows. Maximum prevalence of *Giardia* in dogs and cats was 39 and 44%, respectively. Ducks were identified as carriers of *Giardia* at 28% prevalence, but there were no data on other avian species.

Pathogenic *E. coli* were identified at a maximum prevalence of 83% in dogs and 46% in beef cattle and 21% in dairy cows but at less than 8% prevalence in individual sheep and lambs. *E. coli* O157:H7 has been identified in widely varying concentrations in the faeces of sheep and cattle and tends to be sporadic with levels fluctuating between <100 to 10<sup>6</sup> CFU/g of faeces (Atwill et al., 2012; Chase-Topping et al., 2007; Matthews et al., 2006). These fluctuations have led to the term “super-shedders” for those livestock that carry >10<sup>3</sup>-10<sup>4</sup> CFU/g of *E. coli* O157:H7. In addition, the duration of shedding varies widely, with individual animals shedding for a few days or weeks and others up to six months. It has been estimated that 80% of transmission of *E. coli* O157:H7 is from 20% of the most infectious livestock (Matthews et al., 2006). A study of shiga-toxin producing *E. coli* (STEC) identified that 58.3% of 319 sheep and cattle faeces in New Zealand carried an STEC gene (Cookson et al., 2006b). Another study identified the same genetic isolates of STEC from cattle and human clinical samples using molecular subtyping techniques, illustrating that livestock in NZ can be a reservoir of disease-causing STEC in the human population (Cookson et al., 2006a).

Data for pathogenic *E. coli* in avian species were limited to 8% prevalence in pigeons from one study. *Salmonella* prevalence in all mammals and birds was generally low for both NZ

and international studies, ranging from 0 - 9%, except for dairy cows, which ranged between 10 and 56% prevalence.

*Toxoplasma gondii* is a protozoan that completes its sexual life cycle phase in the intestinal tract of cats and other felines, resulting in the excretion of oocysts in faeces. Infections by *Toxoplasma* are usually asymptomatic but the immunocompromised can become seriously unwell. Pregnant women are particularly susceptible to toxoplasmosis and infection of the foetus may result in foetal death. *Toxoplasma* was identified in cats in four studies at a prevalence ranging between 0 - 30%. However, three of these studies with samples sizes ranging between 63 and 252 had a prevalence of  $\leq 1\%$ .

In general, viruses in animals are not considered to be zoonotic because it is believed that there are strong barriers to prevent viruses crossing between animal species. A brief search of zoonotic viruses in the literature revealed some concerns about the potential for zoonotic viruses (Cavirani, 2008; Kallio-Kokko et al., 2005). Many of these viruses are not of common concern in the New Zealand environment but have been shown to cause disease in Africa and other continents. The West Nile virus (WNV) is an example of a virus introduced to North America in the late 1990s, which had rapid dissemination via mosquito vectors from various animal hosts. The introduction of WNV led to 14,000 cases of illness and 586 deaths being recorded in the USA up till 2005 (Kallio-Kokko et al., 2005).

There has been a recent research focus on the zoonotic potential of several viruses that cause gastroenteritis illness (GI) in humans such as norovirus and rotavirus and whether the specific viral types found in animal reservoirs including dogs, cattle, pigs and sheep, have the potential to cross the host-species barrier and cause illness in humans (Medici et al., 2015; Widdowson et al., 2005; Wolf et al., 2009). Some studies have highlighted that these viral species with animal reservoirs have caused infection in humans (but not necessarily illness) as evidenced by the detection of antibodies against bovine norovirus in humans (Bank-Wolf et al., 2010; Widdowson et al., 2005).

**TABLE 24: Quantitative data on average daily output per animal of indicators and pathogens in mammals and birds**

	<i>E. coli</i>	Enterococci	<i>Campylobacter</i>	<i>Cryptosporidium</i>	<i>Giardia</i>
Sheep	2.51E+10	1.02E+09	1.80E+07	9.48E+05	4.21E+03
Lambs	4.53E+11	1.08E+10	2.02E+08	4.61E+06	1.00E+05
Dairy cows	2.01E+09	1.04E+07	6.81E+06	5.95E+04	
Calves				1.50E+10	1.00E+03
Beef cattle		2.66E+06		1.11E+06	6.63E+05
Dogs		3.30E+09			
Cats				2.00E+04	3.50E+03
Black swans	7.50E+08	3.63E+08	3.84E+04		
Ducks	1.17E+10	1.70E+10	5.77E+03	7.90E+03	4.10E+04
Canada geese	3.80E+07	3.99E+08	4.84E+05		
Gulls	7.00E+08	1.65E+08	2.26E+04		



**TABLE 25: Levels of indicators and pathogens relative to *E. coli* concentration normalised to 1000 CFU/g**

	<i>E. coli</i>	Enterococci	<i>Campylobacter</i>	<i>Cryptosporidium</i>	<i>Giardia</i>
Sheep	1000	41	0.72	0.038	0.0002
Lambs	1000	24	0.45	0.010	0.0002
Dairy cows	1000	5	3.39	0.030	0.0000
Black swans	1000	484	0.0511		
Ducks	1000	1453	0.0005	0.0007	0.0035
Canada geese	1000	10500	12.7		
Gulls	1000	236	0.0323		

**TABLE 26: Comparison of prevalence of indicators and pathogens in animal faeces**

	Sheep	Lambs	Dairy Cows	Calves	Beef cattle	Dogs	Cats	Goats	Black Swans	Ducks	Canada Geese	Gulls	Pigeons
<i>E. coli</i>	100%	100%	99.5%	100%					94%	89-95%	63-95%		
Enterococci	100%	100%	93.3%	100%					79%	100%			
<i>Campylobacter</i>	25-30%	81%	7-64%			0-46%	0-33%		45%	29-40%	40-52%	1%	
<i>Cryptosporidium</i>	3-25%	0.9-77%	0.6-7.3%	10-80%	8%	2-10%	12-100%	8-9.5%		49%	1-23%	0%	
<i>Giardia</i>	19%-37%	1-37%		4.5%	0-26%	2.6-39%	2-44%	20-36%		28%			
Pathogenic <i>E. coli</i>	1-7%	4%	1-21%		1.6-46%	1-83%							8%
<i>Salmonella</i>	0%	1.9%	9.6-56%		0.3- 6%	0-3.6%	0-8.6%			1%	0%		3%
<i>Toxoplasma gondii</i>							0-30%						

## 5. CONCLUSIONS

---

Epidemiological studies exploring the relationship between infectious illness and the microbial quality of recreational waters impacted by non-human faecal sources have produced ambiguous results. This uncertainty associated with non-human faecal pollution and its impact on human health has raised concern when epidemiological studies tried to assess health impacts based on the knowledge gained from the effects of human faecal contamination. This knowledge gap led to a seminal paper by Jeffrey Soller and colleagues on using quantitative microbial risk assessment (QMRA) to explore the human health risks from recreational water impacted by pollution from either human, gull, chicken, pig or cattle faeces (Soller et al. 2010). The figure reproduced below from that paper shows that in water containing the same level of faecal indicator from each source there is potentially a lower risk of illness when the water is impacted by chicken, gull and pig faecal material, than human faecal matter. In contrast, there are similar risks from illness between faecal contamination derived from cattle (beef and dairy) and that from humans.

Soller et al. (2010) noted that a key limitation in their study was the limited amount of data on the levels of indicator and pathogens in the sources they examined. This USA study (Soller et al., 2010) did not consider all of the sources important in New Zealand such as sheep, domestic pets, and a range of other wildfowl beyond seagulls. As this current report illustrates there are a lack of quality data on the levels of indicator organisms and pathogens in many of the faecal sources to New Zealand waters.

In a 2014 paper, Soller et al. extended their initial QMRA work. The starting point was that 35 enterococci /100ml provided an acceptable level of risk, and was based on the source of those enterococci being human faecal matter. The risk of illness was defined as 36 gastrointestinal illnesses (GI) per 1000 swimmers. Using QMRA modelling they estimated the level of enterococci that would provide an equivalent level of protection if those enterococci were from non-human sources. Their analysis suggested that if the enterococci are entirely from chicken, pig or gull sources, the equivalent level of enterococci that would provide the same protection, ranged from threefold to 50 times higher (TABLE 27).

Another key finding from the Soller et al. (2014) study was that where there are mixed sources of contamination identified, then the risk is dependent on the most potent source of faecal contamination. The risk of illness decreased as the contribution from human sources reduced from 100%, so that by 30% human attribution to FIB levels, the predicted risk of infection had lowered by 50% compared with the risk if all detected FIB were derived from human sources. Thereafter, the risk declined more rapidly, so that at  $\leq 20\%$  human

contribution to the mixed faecal source, the predicted risk was five times lower compared with a pure human source. These predictions were based on the faecal source being from recent faecal events and did not account for the differential die-off between FIB and pathogens. This preferential decay of FIB was seen in the treated wastewater data (TABLE 23), which illustrated higher log removal of FIB in comparison to pathogenic protozoa and viruses. The fact that the most potent faecal source (human or cattle, Soller et al. 2010) was the driver of predicted risk is of particular relevance to rural areas where ruminant agricultural sources are detected often in conjunction with avian sources. Therefore, unless the ruminant signal accounts for less than 30% of the mixed contamination, then the health risk is 50 to 100% of the risk associated with a solely ruminant faecal source.

Monitoring the research into the emergence of viral zoonoses in livestock and other animal reservoirs in the New Zealand environment, particularly for the GI causing norovirus and rotavirus species is required for the future.

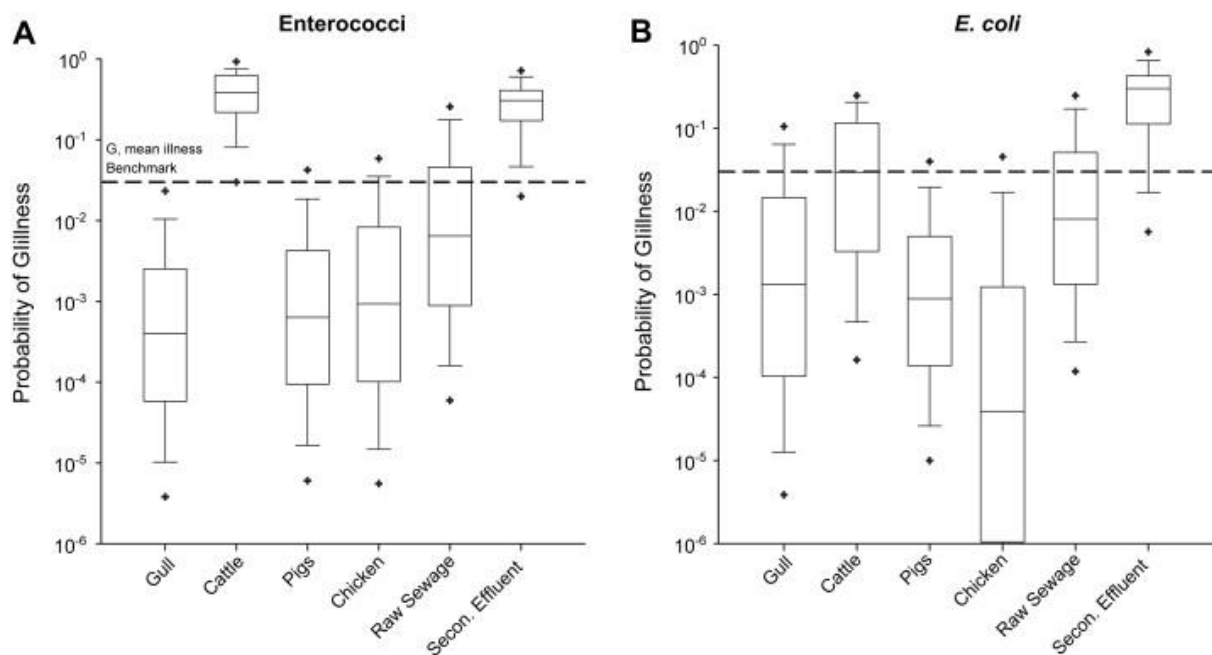


Figure 1. Probability of GI illness from ingestion of water containing fresh faecal pollution at densities of  $35 \text{ cfu } 100\text{mL}^{-1}$  ENT (3A) and  $126 \text{ cfu } 100\text{mL}^{-1}$  *E. coli* from a range of sources. Figure reproduced from Soller et al. (2010).

**TABLE 27: Predicted median enterococci densities that correspond to GI illness levels of 0.036, analogous to 36 people out of 1000 becoming ill if they ingest recreational water containing these levels of enterococci (reproduced from Soller et al., 2010)**

<b>Human contribution</b>	<b>0%</b>	<b>10%</b>	<b>20%</b>	<b>30%</b>	<b>50%</b>	<b>70%</b>	<b>100%</b>
<b>Non-human contribution</b>	<b>100%</b>	<b>90%</b>	<b>80%</b>	<b>70%</b>	<b>50%</b>	<b>30%</b>	<b>0%</b>
Pig	607	278	164	114	70	50	35
Chicken	103	95	87	79	62	49	35
Gull	1947	339	174	116	70	50	35
*Non-pathogenic source	-	350	175	117	70	50	35

\*For example, environmental or naturalised enterococci

# REFERENCES

---

- Anastasi EM, Matthews B, Gundogdu A, Vollmerhausen TL, Ramos NL, Stratton H, et al. Prevalence and persistence of *Escherichia coli* strains with uropathogenic virulence characteristics in sewage treatment plants. *Applied and Environmental Microbiology* 2010; 76: 5882-6.
- Anastasi EM, Matthews B, Stratton HM, Katouli M. Pathogenic *Escherichia coli* found in sewage treatment plants and environmental waters. *Applied and Environmental Microbiology* 2012; 78: 5536-41.
- Anderson SA, Turner SJ, Lewis GD. Enterococci in the New Zealand environment: Implications for water quality monitoring. *Water Science and Technology* 1997; 35: 325-31.
- Atwill ER, Hoar B, Pereira MdGC, Tate KW, Rulofson F, Nader G. Improved Quantitative Estimates of Low Environmental Loading and Sporadic Periparturient Shedding of *Cryptosporidium parvum* in Adult Beef Cattle. *Applied and Environmental Microbiology* 2003; 69: 4604-10.
- Atwill ER, Li X, Grace D, Gannon V. Zoonotic waterborne pathogen loads in livestock. In: Dufour A, Bartram J, Bos R, Gannon V, editors. *Animal waste, water quality and human health*. Published on behalf of WHO by IWA Publishing, Glasgow, 2012, pp. 115-56.
- Bae W, Kaya KN, Hancock DD, Call DR, Park YH, Besser TE. Prevalence and antimicrobial resistance of thermophilic *Campylobacter* spp. from cattle farms in Washington State. *Applied and Environmental Microbiology* 2005; 71: 169-74.
- Baker J, Barton MD, Lanser J. *Campylobacter* species in cats and dogs in South Australia. *Australian Veterinary Journal* 1999; 77: 662-6.
- Ballweber LR, Panuska C, Huston CL, Vasilopoulos R, Pharr GT, Mackin A. Prevalence of and risk factors associated with shedding of *Cryptosporidium felis* in domestic cats of Mississippi and Alabama. *Veterinary Parasitology* 2009; 160: 306-10.
- Bank-Wolf BR, König M, Thiel H-J. Zoonotic aspects of infections with noroviruses and sapoviruses. *Veterinary Microbiology* 2010; 140: 204-12.
- Berger-Schoch AE, Herrmann DC, Schares G, Müller N, Bernet D, Gottstein B, et al. Prevalence and genotypes of *Toxoplasma gondii* in feline faeces (oocysts) and meat from sheep, cattle and pigs in Switzerland. *Veterinary Parasitology* 2011; 177: 290-7.
- Bertrand R, Roig B. Evaluation of enrichment-free PCR-based detection on the rfbE gene of *Escherichia coli* O157—Application to municipal wastewater. *Water Research* 2007; 41: 1280-6.
- Bolton DJ, O'Neill CJ, Fanning S. A Preliminary Study of Salmonella, Verocytotoxigenic *Escherichia coli*/*Escherichia coli* O157 and *Campylobacter* on Four Mixed Farms. *Zoonoses and Public Health* 2012; 59: 217-28.
- Bouzid M, Halai K, Jeffreys D, Hunter PR. The prevalence of *Giardia* infection in dogs and cats, a systematic review and meta-analysis of prevalence studies from stool samples. *Veterinary Parasitology* 2015; 207: 181-202.
- Brown PE, Christensen OF, Clough HE, Diggle PJ, Hart CA, Hazel S, et al. Frequency and spatial distribution of environmental *Campylobacter* spp. *Applied and Environmental Microbiology* 2004; 70: 6501-11.
- Callaway TR, Keen JE, Edrington TS, Baumgard LH, et al. Fecal Prevalence and Diversity of Salmonella Species in Lactating Dairy Cattle in Four States\*. *Journal of Dairy Science* 2005; 88: 3603-8.
- Castro-Hermida JA, Almeida A, González-Warleta M, Correia da Costa JM, Rumbo-Lorenzo C, Mezo M. Occurrence of *Cryptosporidium parvum* and *Giardia duodenalis* in healthy adult domestic ruminants. *Parasitology research* 2007; 101: 1443-8.
- Cavirani S. Cattle industry and zoonotic risk. *Veterinary Research Communications* 2008; 32: 19-24.
- Chaban B, Ngeleka M, Hill JE. Detection and quantification of 14 *Campylobacter* species in pet dogs reveals an increase in species richness in feces of diarrheic animals. *BMC microbiology* 2010; 10: 73.

- Chase-Topping ME, McKendrick IJ, Pearce MC, MacDonald P, Matthews L, Halliday J, et al. Risk Factors for the Presence of High-Level Shedders of *Escherichia coli* O157 on Scottish Farms. *Journal of Clinical Microbiology* 2007; 45: 1594-603.
- Cookson AL, Croucher D, Pope C, Bennett J, Thomson-Carter F, Attwood GT. Isolation, characterization, and epidemiological assessment of shiga toxin-producing *Escherichia coli* O84 isolates from New Zealand. *Journal of Clinical Microbiology* 2006a; 44: 1863-6.
- Cookson AL, Taylor SC, Attwood GT. The prevalence of Shiga toxin-producing *Escherichia coli* in cattle and sheep in the lower North Island, New Zealand. *New Zealand Veterinary Journal* 2006 Feb;54(1):28-33. 2006b; 54: 28-33.
- Curtis T. Bacterial pathogen removal in wastewater treatment plants. In: Mara D, Horan N, editors. *Handbook of Water and Wastewater Microbiology*. Academic Press, London, 2003, pp. 477-90.
- Dabritz HA, Gardner IA, Miller MA, Lapping MR, Atwill ER, Packham AE, et al. Evaluation of Two *Toxoplasma gondii* Serologic Tests Used in a Serosurvey of Domestic Cats in California. *The Journal of Parasitology* 2007; 93: 806-16.
- Dabritz HA. The epidemiology of *Toxoplasma gondii* in cats and rodents from the Morro Bay area, California. Dissertation/Thesis. ProQuest, UMI Dissertations Publishing, 2006.
- Damborg P, Olsen KE, Moller Nielsen E, Guardabassi L. Occurrence of *Campylobacter jejuni* in pets living with human patients infected with *C. jejuni*. *J Clin Microbiol* 2004; 42: 1363-4.
- Dhama K, Chakrabort S, Tiwari R, Kumar A, Rahal A, Latheef SK, et al. Avian/Bird Flu Virus: Poultry Pathogen Having Zoonotic and Pandemic Threats: A Review. *Journal of Medical Sciences(Faisalabad)* 2013; 13: 301-15.
- Dubey JP, Jones JL. *Toxoplasma gondii* infection in humans and animals in the United States. *International Journal for Parasitology* 2008; 38: 1257-78.
- European Food Safety Agency E. The Community Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in the European Union in 2007. *EFSA Journal* 2009.
- European Food Safety Agency E. The Community Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in the European Union in 2008. *EFSA Journal* 2010; 8: 1496.
- Fallacara DM, Monahan CM, Morishita TY, Wack RF. Fecal shedding and antimicrobial susceptibility of selected bacterial pathogens and a survey of intestinal parasites in free-living waterfowl. *Avian Dis* 2001; 45: 128-35.
- Fayer R, Santín M, Trout JM, Dubey JP. Detection of *Cryptosporidium felis* and *Giardia duodenalis* Assemblage F in a cat colony. *Veterinary Parasitology* 2006; 140: 44-53.
- Fogarty LR, Haack SK, Wolcott MJ, Whitman RL. Abundance and characteristics of the recreational water quality indicator bacteria *Escherichia coli* and enterococci in gull faeces. *Journal of Applied Microbiology* 2003; 94: 865-78.
- Fujioka RS, Solo-Gabriele HM, Byappanahalli MN, Kirs M. U.S. Recreational water quality criteria: A vision for the future. *International Journal of Environmental Health Research* 2015; 12: 7752-76.
- Fukushima H, Seki R. High numbers of Shiga toxin-producing *Escherichia coli* found in bovine faeces collected at slaughter in Japan. *FEMS Microbiology Letters* 2004; 238: 189-97.
- Gannon VP, Graham TA, King R, Michel P, Read S, Ziebell K, et al. *Escherichia coli* O157:H7 infection in cows and calves in a beef cattle herd in Alberta, Canada. *Epidemiology and Infection* 2002; 129: 163-72.
- Geldreich EE. Sanitary significance of Faecal Coliforms in the environment. Federal Water Pollution Control administration, Publication WP-20-3., 1966. Geurden T. *Giardia* in Pets and Farm Animals, and Their Zoonotic Potential. Springer Vienna, Vienna, 2011, pp. 71-92.

- Geurden T, Thomas P, Casaert S, Vercruyse J, Claerebout E. Prevalence and molecular characterisation of *Cryptosporidium* and *Giardia* in lambs and goat kids in Belgium. *Veterinary Parasitology* 2008; 155: 142.
- Gillhuber J, Pallant L, Ash A, Thompson RCA, Pfister K, Scheuerle MC. Molecular identification of zoonotic and livestock-specific *Giardia*-species in faecal samples of calves in Southern Germany. *Parasites & Vectors* 2013; 6: 346.
- Goldstein MR, Kruth SA, Bersenas AME, Holowaychuk MK, Weese JS. Detection and characterization of *Clostridium perfringens* in the feces of healthy and diarrheic dogs. *Canadian journal of veterinary research = Revue canadienne de recherche vétérinaire* 2012; 76: 161-5.
- Gorham TJ, Lee J. Pathogen Loading From Canada Geese Faeces in Freshwater: Potential Risks to Human Health Through Recreational Water Exposure. *Zoonoses Public Health* 2015.
- Gould DJ, Fletcher MR. Gull droppings and their effects on water quality. *Water Research* 1978; 12: 665-72.
- Graczyk TK, Fayer R, Trout JM, Lewis EJ, Farley CA, Sulaiman I, et al. *Giardia* sp. Cysts and Infectious *Cryptosporidium parvum* Oocysts in the Feces of Migratory Canada Geese (*Branta canadensis*). *Applied and Environmental Microbiology* 1998; 64: 2736-2738.
- Grinberg A, Pomroy WE, Weston JF, Ayanegui-Alcerreca A, Knight D. The occurrence of *Cryptosporidium parvum*, *Campylobacter* and *Salmonella* in newborn dairy calves in the Manawatu region of New Zealand. *N Z Vet J* 2005; 53: 315-20.
- Haack SK, Fogarty LR, Wright C. *Escherichia coli* and enterococci at beaches in the Grand Traverse Bay, Lake Michigan: sources, characteristics, and environmental pathways. *Environmental Science & Technology* 2003; 37: 3275-82.
- Holland RE, Walker RD, Sriranganathan N, Wilson RA, Ruhl DC. Characterization of *Escherichia coli* isolated from healthy dogs. *Veterinary Microbiology* 1999; 70: 261-8.
- Hussong D, Damare JM, Limpert RJ, Sladen WJ, Weiner RM, Colwell RR. Microbial impact of Canada geese (*Branta canadensis*) and whistling swans (*Cygnus columbianus columbianus*) on aquatic ecosystems. *Applied and Environmental Microbiology* 1979; 37: 14-20.
- Irshad H, Cookson AL, Hotter G, Besser TE, On SL, French NP. Epidemiology of Shiga toxin-producing *Escherichia coli* O157 in very young calves in the North Island of New Zealand. *New Zealand Veterinary Journal* 2012; 60: 21-6.
- Irshad H, Cookson AL, Prattley DJ, Dufour M, French NP. 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. *Epidemiology and Infection* 2014; 142: 2548-58.
- Joffe DJ, Schlesinger DP. Preliminary assessment of the risk of *Salmonella* infection in dogs fed raw chicken diets. *Canadian Veterinary Journal-Revue Veterinaire Canadienne* 2002; 43: 441-2.
- Jones JL, Dubey JP. Waterborne toxoplasmosis--recent developments. *Experimental Physiology* 2010; 124: 10-25.
- Kallio-Kokko H, Uzcatogui N, Vapalahti O, Vaheri A. Viral zoonoses in Europe. *FEMS Microbiology Reviews* 2005; 29: 1051-1077.
- Kassa H, Harrington BJ, Bisesi MS. Cryptosporidiosis: a brief literature review and update regarding *Cryptosporidium* in feces of Canada geese (*Branta canadensis*). *Journal of environmental health* 2004; 66: 34.
- Kay D, Crowther J, Stapleton CM, Wyer MD, Fewtrell L, Edwards A, et al. Faecal indicator organism concentrations in sewage and treated effluents. *Water Research* 2008; 42: 442-54.
- Khan SI, Kamal N. Assessment of treatment efficiency by quantitative recovery of indicator bacteria and pathogens in sewage effluents. In: Satoh TMHT, editor. *Advances in Water and Wastewater Treatment Technology*. Elsevier Science B.V., Amsterdam, 2001, pp. 129-37.
- Kitajima M, Haramoto E, Iker BC, Gerba CP. Occurrence of *Cryptosporidium*, *Giardia*, and *Cyclospora* in influent and effluent water at wastewater treatment plants in Arizona. *Science of The Total Environment* 2014a; 484: 129-36.

- Kitajima M, Iker BC, Pepper IL, Gerba CP. Relative abundance and treatment reduction of viruses during wastewater treatment processes — Identification of potential viral indicators. *Science of The Total Environment* 2014b; 488–489: 290-6.
- Korzeniewska E, Harnisz M. Extended-spectrum beta-lactamase (ESBL)-positive *Enterobacteriaceae* in municipal sewage and their emission to the environment. *Journal of Environmental Management* 2013; 128: 904-11.
- Krause G, Zimmermann S, Beutin L. Investigation of domestic animals and pets as a reservoir for intimin- (eae) gene positive *Escherichia coli* types. *Veterinary Microbiology* 2005; 106: 87-95.
- Kuhn RC, Rock CM, Oshima KH. Occurrence of *Cryptosporidium* and *Giardia* in Wild Ducks along the Rio Grande River Valley in Southern New Mexico. *Applied and Environmental Microbiology* 2002; 68: 161-5.
- Kuhnert P, Dubosson CR, Roesch M, Homfeld E, Doherr MG, Blum JW. Prevalence and risk-factor analysis of Shiga toxin-producing *Escherichia coli* in faecal samples of organically and conventionally farmed dairy cattle. *Veterinary Microbiology* 2005; 109: 37-45.
- Kullas H, Coles M, Rhyan J, Clark L. Prevalence of *Escherichia coli* serogroups and human virulence factors in faeces of urban Canada geese (*Branta canadensis*). *International Journal of Environmental Health Research* 2002; 12: 153-62.
- Kwan PS, Birtles A, Bolton FJ, French NP, Robinson SE, Newbold LS, et al. Longitudinal study of the molecular epidemiology of *Campylobacter jejuni* in cattle on dairy farms. *Applied and Environmental Microbiology* 2008; 74: 3626-33.
- Lambertini E, Karns JS, Van Kessel JA, Cao H, Schukken YH, Wolfgang DR, et al. Dynamics of *Escherichia coli* Virulence Factors in Dairy Herds and Farm Environments in a Longitudinal Study in the United States. *Applied and Environmental Microbiology* 2015; 81: 4477-88.
- Langham NPE, Charleston WAG. An investigation of the potential for spread of *Sarcocystis* spp. and other parasites by feral cats New Zealand *Journal of Agriculture Research* 1990; 33: 429-35.
- Learmonth JJ, Ionas G, Pita AB, Cowie RS. 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 : a journal of the International Association on Water Pollution Research* 2003; 47: 21.
- Lefebvre SL, Waltner-Toews D, Peregrine AS, Reid-Smith R, Hodge L, Arroyo LG, et al. Prevalence of zoonotic agents in dogs visiting hospitalized people in Ontario: implications for infection control. *Journal of Hospital Infection* 2006; 62: 458-66.
- Lucio-Forster A, Griffiths JK, Cama VA, Xiao L, Bowman DD. Minimal zoonotic risk of cryptosporidiosis from pet dogs and cats. *Trends in Parasitology* 2010; 26: 174-9.
- Marín I, Goñi P, Lasheras AM, Ormad MP. Efficiency of a Spanish wastewater treatment plant for removal of potentially pathogenic bacteria and protozoa along water and sludge treatment lines. *Ecological Engineering* 2015; 74: 28-32.
- Markland SM, LeStrange KJ, Sharma M, Kniel KE. Old Friends in New Places: Exploring the Role of Extraintestinal *E. coli* in Intestinal Disease and Foodborne Illness. *Zoonoses and Public Health* 2015; 62: 491-496.
- Marks SL, Rankin SC, Byrne BA, Weese JS. Enteropathogenic bacteria in dogs and cats: diagnosis, epidemiology, treatment, and control. *Journal of Veterinary Internal Medicine* 2011; 25: 1195-208.
- Matthews L, Low JC, Gally DL, Pearce MC, Mellor DJ, Heesterbeek JA, et al. Heterogeneous shedding of *Escherichia coli* O157 in cattle and its implications for control. *Proceedings of the National Academy of Sciences of the United States of America* 2006; 103: 547-52.
- Medici MC, Tummolo F, Bonica MB, Heylen E, Zeller M, Calderaro A, et al. Genetic diversity in three bovine-like human G8P[14] and G10P[14] rotaviruses suggests independent interspecies transmission events. *The Journal of General Virology* 2015; 96: 1161.
- MfE and MoH. The New Zealand Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas Ministry for the Environment. 2003. 159 pages



- Middleton JH, Ambrose A. Enumeration and antibiotic resistance patterns of fecal indicator organisms isolated from migratory Canada geese (*Branta canadensis*). *Journal of Wildlife Diseases* 2005; 41: 334.
- Minamoto Y, Dhanani N, Markel ME, Steiner JM, Suchodolski JS. Prevalence of *Clostridium perfringens*, *Clostridium perfringens* enterotoxin and dysbiosis in fecal samples of dogs with diarrhea. *Veterinary Microbiology* 2014; 174: 463-473.
- Mitchell SF, Wass RT. Food consumption and faecal deposition of plant nutrients by Black Swans (*Cygnus arratus* Latham) in a shallow New Zealand lake. *Hydrobiologica* 1995: 189-97.
- Moore JE, Gilpin D, Crothers E, Canney A, Kaneko A, Matsuda M. Occurrence of *Campylobacter* spp. and *Cryptosporidium* spp. in seagulls (*Larus* spp.). *Vector-Borne and Zoonotic Diseases* 2002; 2: 111-4.
- Moriarty EM, Karki N, Mackenzie M, Sinton LW, Wood DR, Gilpin BJ. Faecal indicators and pathogens in selected New Zealand waterfowl. *New Zealand Journal of Marine and Freshwater Research* 2011a: 1-10.
- Moriarty EM, McEvoy JM, Lowery CJ, Thompson HP, Finn M, Sheridan JJ, et al. Prevalence and characterisation of *Cryptosporidium* species in cattle faeces and on beef carcasses at slaughter. *The Veterinary Record* 2005; 156: 165.
- Moriarty EM, McEwan N, Mackenzie M, Karki N, Sinton LW, Wood DR. Incidence and prevalence of microbial indicators and pathogens in ovine faeces in New Zealand. *New Zealand Journal of Agricultural Research* 2011b; 54: 10.
- Moriarty EM, Sinton LW, Mackenzie ML, Karki N, Wood DR. A survey of enteric bacteria and protozoans in fresh bovine faeces on New Zealand dairy farms. *Journal of Applied Microbiology* 2008; 105: 2015-25.
- Muirhead RW, Elliott AH, Monaghan RM. A model framework to assess the effect of dairy farms and wild fowl on microbial water quality during base-flow conditions. *Water Research* 2011; 45: 2863-74.
- Murphy J, Devane ML, Robson B, Gilpin BJ. Genotypic characterization of bacteria cultured from duck faeces. *Journal of Applied Microbiology* 2005; 99: 301-9.
- Nielsen EM. Occurrence and strain diversity of thermophilic campylobacters in cattle of different age groups in dairy herds. *Letters in Applied Microbiology* 2002; 35: 85.
- Ogden ID, MacRae M, Strachan NJC. Concentration and prevalence of *Escherichia coli* O157 in sheep faeces at pasture in Scotland. *Journal of Applied Microbiology* 2005; 98: 646-651.
- Oporto B, Esteban JI, Aduriz G, Juste RA, Hurtado A. *Escherichia coli* O157:H7 and Non-O157 Shiga Toxin-producing *E. coli* in Healthy Cattle, Sheep and Swine Herds in Northern Spain. *Zoonoses and Public Health* 2008; 55: 73-81.
- Ottoson J, Hansen A, Björlenius B, Norder H, Stenström TA. Removal of viruses, parasitic protozoa and microbial indicators in conventional and membrane processes in a wastewater pilot plant. *Water Research* 2006; 40: 1449-57.
- Parsons BN, Porter CJ, Ryvar R, Stavisky J, Williams NJ, Pinchbeck GL, et al. Prevalence of *Campylobacter* spp. in a cross-sectional study of dogs attending veterinary practices in the UK and risk indicators associated with shedding. *The Veterinary Journal* 2010; 184: 66-70.
- Pedersen K, Clark L, Andelt WF, Salman MD. Prevalence of shiga toxin-producing *Escherichia coli* and *Salmonella enterica* in rock pigeons captured in Fort Collins, Colorado. *Journal of Wildlife Diseases* 2006; 42: 46.
- Roe WD, Howe L, Baker EJ, Burrows L, Hunter SA. An atypical genotype of *Toxoplasma gondii* as a cause of mortality in Hector's dolphins (*Cephalorhynchus hectori*). *Veterinary Parasitology* 2013; 192: 67-74.
- Rutledge ME, Siletzky RM, Gu W, Degernes LA, Moorman CE, DePerno CS, et al. Characterization of *Campylobacter* from resident Canada geese in an urban environment. *Journal of wildlife diseases* 2013; 49: 1.
- Ryan U. *Cryptosporidium* in birds, fish and amphibians. *Experimental Parasitology* 2010; 124: 113-20.

- Ryan UM, Bath C, Robertson I, Read C, Elliot A, McInnes L, et al. Sheep may not be an important zoonotic reservoir for *Cryptosporidium* and *Giardia* parasites. *Applied and Environmental Microbiology* 2005; 71: 4992-7.
- Santin M, Trout JM, Fayer R. Prevalence and molecular characterization of *Cryptosporidium* and *Giardia* species and genotypes in sheep in Maryland. *Veterinary Parasitology* 2007; 146: 17-24.
- Schaufler K, Bethe A, Lübke-Becker A, Ewers C, Kohn B, Wieler LH, et al. Putative connection between zoonotic multiresistant extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* in dog feces from a veterinary campus and clinical isolates from dogs. *Infection Ecology & Epidemiology* 2015; 5.
- Shannon KE, Lee DY, Trevors JT, Beaudette LA. Application of real-time quantitative PCR for the detection of selected bacterial pathogens during municipal wastewater treatment. *Science of The Total Environment* 2007; 382: 121-9.
- Soller JA, Schoen ME, Bartrand T, Ravenscroft JE, Ashbolt NJ. Estimated human health risks from exposure to recreational waters impacted by human and non-human sources of faecal contamination. *Water Research* 2010; 44: 4674-91.
- Soller JA, Schoen ME, Varghese A, Ichida AM, Boehm AB, Eftim S, et al. Human health risk implications of multiple sources of faecal indicator bacteria in a recreational waterbody. *Water research* 2014; 66: 254-264.
- Stanley K, Jones K. Cattle and sheep farms as reservoirs of *Campylobacter*. *Journal of Applied Microbiology* 2003; 94: 104-13.
- Stanley KN, Wallace JS, Currie JE, Diggle PJ, Jones K. The seasonal variation of thermophilic campylobacters in beef cattle, dairy cattle and calves. *Journal of Applied Microbiology* 1998; 85: 472-80.
- Teklehaimanot GZ, Genthe B, Kamika I, Momba MNB. Prevalence of enteropathogenic bacteria in treated effluents and receiving water bodies and their potential health risks. *Science of The Total Environment* 2015; 518–519: 441-9.
- Tweed SA, Skowronski DM, David ST, Larder A, Petric M, Lees W, et al. Human Illness from Avian Influenza H7N3, British Columbia. *Emerging Infectious Diseases* 2004; 10: 2196-9.
- Uehlinger FD, Greenwood SJ, McClure JT, Conboy G, O’Handley R, Barkema HW. Zoonotic potential of *Giardia duodenalis* and *Cryptosporidium* spp. and prevalence of intestinal parasites in young dogs from different populations on Prince Edward Island, Canada. *Veterinary Parasitology* 2013; 196: 509-14.
- Um MM, Barraud O, Kérourédan M, Gaschet M, Stalder T, Oswald E, et al. Comparison of the incidence of pathogenic and antibiotic-resistant *Escherichia coli* strains in adult cattle and veal calf slaughterhouse effluents highlighted different risks for public health. *Water Research* 2016; 88: 30-38.
- Wang A, Ruch-Gallie R, Scorza V, Lin P, Lappin MR. Prevalence of *Giardia* and *Cryptosporidium* species in dog park attending dogs compared to non-dog park attending dogs in one region of Colorado. *Veterinary Parasitology* 2012; 184: 335-40.
- Widdowson MA, Rockx B, Schepp R, van der Poel WHM, Vinje J, van Duynhoven YT, et al. Detection of serum antibodies to bovine norovirus in veterinarians and the general population in the Netherlands. *Journal of Medical Virology* 2005; 76: 119-28.
- Wolf S, Williamson W, Hewitt J, Lin S, Rivera-Aban M, Ball A, et al. Molecular detection of norovirus in sheep and pigs in New Zealand farms. *Veterinary Microbiology* 2009; 133: 184-9.
- Wood AJ, Trust TJ. Some qualitative and quantitative aspects of the intestinal microflora of the glaucous-winged gull (*Larus glaucescens*). *Canadian Journal of Microbiology* 1972; 18: 1577-83.
- Wright ME, Solo-Gabriele HM, Elmir S, Fleming LE. Microbial load from animal feces at a recreational beach. *Marine Pollution Bulletin* 2009; 58: 1649-56.

- Yang K, Pagaling E, Yan T. Estimating the prevalence of potential enteropathogenic *Escherichia coli* and intimin gene diversity in a human community by monitoring sanitary sewage. *Applied and Environmental Microbiology* 2014; 80: 119-27.
- Yang R, Jacobson C, Gordon C, Ryan U. Prevalence and molecular characterisation of *Cryptosporidium* and *Giardia* species in pre-weaned sheep in Australia. *Veterinary Parasitology* 2009; 161: 19-24.
- Yang R, Ying JIJ, Monis P, Ryan U. Molecular characterisation of *Cryptosporidium* and *Giardia* in cats (*Felis catus*) in Western Australia. *Experimental Parasitology* 2015; 155: 13-8.
- Yoshiuchi R, Matsubayashi M, Kimata I, Furuya M, Tani H, Sasai K. Survey and molecular characterization of *Cryptosporidium* and *Giardia* spp. in owned companion animal, dogs and cats, in Japan. *Veterinary Parasitology* 2010; 174: 313-6.
- Zhang Y, Chen Z, An W, Xiao S, Yuan H, Zhang D, et al. Risk assessment of *Giardia* from a full scale MBR sewage treatment plant caused by membrane integrity failure. *Journal of Environmental Sciences* 2015; 30: 252-8.
- Zhou L, Kassa H, Tischler ML, Xiao L. Host-adapted *Cryptosporidium* spp. in Canada geese (*Branta canadensis*). *Applied and Environmental Microbiology* 2004; 70: 4211-5.