Developing a characterization factor framework for microbial contamination

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Abstract. Life Cycle Impact Assessment (LCIA) can be used as a method to assess environmental impact of pathogen contamination in several stages. This paper attempts to determine the characterization factor (CF) for microbial contamination from livestock emission in surface water on a global scale. CF was defined as the change in Disability Adjusted Life Years (dDALY in yr) due to a marginal change in emission of a pathogen (dOocyst/day). This CF consists of intake fraction, effect factor and damage factor. The average intake fraction per river basin specific is 0.003, meaning that 0.3% of the emitted oocysts is emitted by the human population via drinking water and swimming. The effect factor value has a range from 0.0022-0736 case/oocyst, with the average 0.29 case/oocyst. The final characterization factor has a range between 0 to 1.2 x 10-5 DALY/oocyst in a river basin scale. In this study, CFs was determined for pathogen contamination for the first time. It was shown how these can be derived for *Cryptosporidium* and other pathogen with similar cause-impact pathways.

1 Introduction

Life Cycle Assessment (LCA) is a method to assess environmental impact from a particular product, services or sources which conducted in several stages [1]. The Life Cycle Impact Assessment (LCIA) is the third stage of the LCA after goal and scope definition and inventory analysis. In impact assessment, the resource use and emissions gathered in the inventory step are translated into potential environmental impacts [2]. While the frameworks for some categories are already established in LCA (e.g climate change, global warming, acidification), the frameworks for some impact categories are still to be included.

Exposures related to drinking, non-potable water, and wastewater systems can lead to contact with various pathogens. Both enteric and environmental pathogens may result in health outcomes when ingested or inhaled, ranging from risk of infection and mortality [3]. *Cryptosporidium* is one of the most common pathogen found in surface water [4]. The oocysts of *Cryptosporidium* can survive for several months in surface water before being ingested by humans [5]. The oocysts of *Cryptosporidium* can infect both animals and

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humans even in a low dose condition [6]. Moreover, outbreaks of cryptosporidiosis have been reported worldwide [7].

Increasing waterborne disease related to climate change [8] and induced by human activities, such as massive livestock production and rapid agricultural production. Consequently, the effect of pathogens on human health damage has become more important. While the health damage related to pathogen infections can be quantified in disability-adjusted life years (DALYs) as commonly being done in risk assessment, it is often neglected in life cycle assessment methods. Although previous research has included the effects of pathogen in LCA [1], the existing research has not yet investigated the full cause-effect pathway to systematically include impact assessment factors in LCA. Therefore, an impact assessment framework for microbial contamination is inevitably needed.

2 Methods

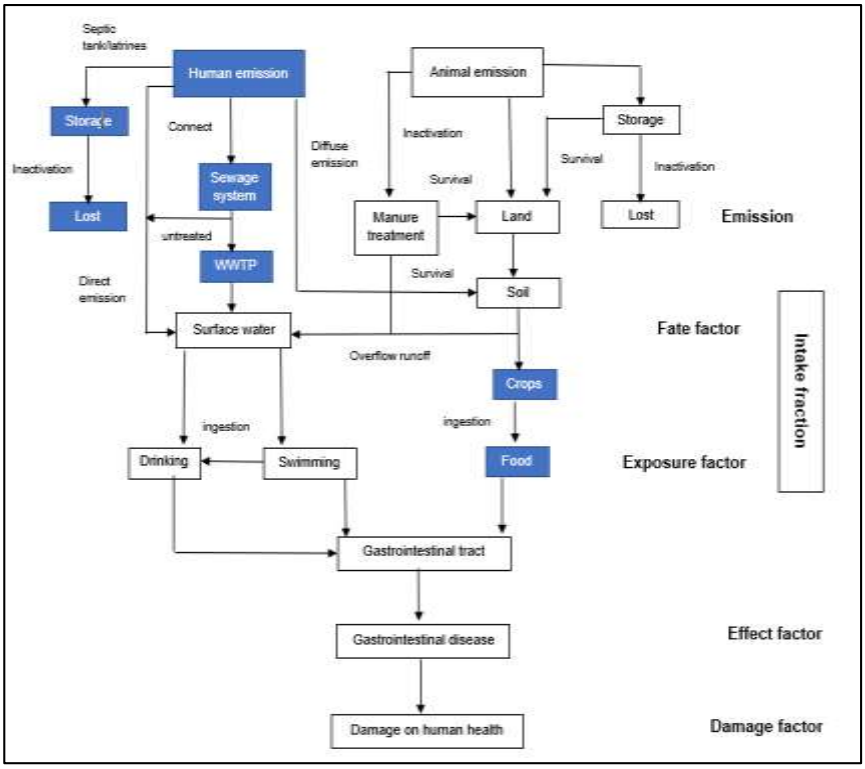

Fig. 1. Cause-impact pathway of *Cryptosporidium* infection (blue boxes are negligible in this study).

The CFs is defined as the change in Disability Adjusted Life Years of all population (dDALY in yr) due to a linear change in emission of pathogen (dOocyst/day) and was derived per river basin.

$$CF = IF \cdot EF \cdot DF \quad (1)$$

Where:

The intake fraction (IF) is the change of oocysts number in per number of oocysts released [-].

The effect factor (EF) is the linear change of risk due to the intake of oocysts (case/oocyst).
The damage factor [DALY/risk or DALY/probability of infection]

2.1 Intake fraction

The exposure of waterborne pathogen occurs through ingestion, inhalation and dermal contact [5]. However, this study only includes the possible intake of *Cryptosporidium* through ingestion pathway from drinking and swimming activities as a starting point due to lack of data from other exposure pathways. The change of emission was described as the emission of oocyst load from livestock emission per day. The load value (oocyst/day) was derived from the output of GlowPa-Crypto L1 model by Vermeulen et al. [9]. The intake fraction was determined by the change of intake rate due to the change of emission, as provided by a formulation below:

$$\mathrm{IF_r} = \frac{IR \cdot \sum(\Delta C_i \cdot Pop_i)}{\Delta M_{total}} \quad (2)$$

Where:

IF_r = River basin r specifc intake fraction [-]
C_i = Concentration of total oocyst per grid cell i [oocyst/m^3]
IR = Intake rate of contaminated water [m^3/person/day]
Pop_i = Population number per grid cell i [person]
ΔM_r = Change of total emission per river basin r per day [oocyst/day]

2.2 Effect factor

In this study, the effect factor of *Cryptosporidium* was determined as the linear change in risk (probability of infection) due to an increase of oocyst concentration where the risk is 0.5 probability of infection per day. This factor was determined as:

$$LEF = \frac{0.5}{I50} \quad (3)$$

Where:

LEF = Effect factor [case/oocysts]
I_{50} = Dose where the infection is 50% [oocysts]

A dose-response assessment determines the relation between the concentration of oocyst that enter the host' body (dose), and possible infection (risk). This study used six dose-response models for pathogen infection developed by Messner [10]. The order of models represents an increase of complexity, which are fractional Poisson model, an exponential model, exponential with immunity model, beta-Poisson model, hierarchical beta-Poisson model, and hierarchical logistic model.

2.3 Damage factor

The damage factor was determined based on the latest data from the World Health Organization (WHO) and the Global Burden of Disease [3]. The damage factor

[DALY/case] distinguishes between differences in the severity of disabilities caused by a disease in terms of affected life years.

Table 1. Estimation of DALY value for cryptosporidiosis [11].

Outcomes	Severity	Duration	Burden of disease per case in DALYs	Disease burden (DALY) per 1000 cases
Watery diarrhoea	0.067	7 days	0.0013	1.34
Death	1	13.2 yrs	13.2	0.13
Total DALY/1000 cases				1.47

3 Results and discussion

3.1 Intake fraction

Figure 2 shows that the intake fraction of *Cryptosporidium* varies between 0 and 0.03 oocysts taken in per oocysts released. This implies that from 0 up to 3% oocysts is taken in by global population per number of oocyst released by livestock emission.

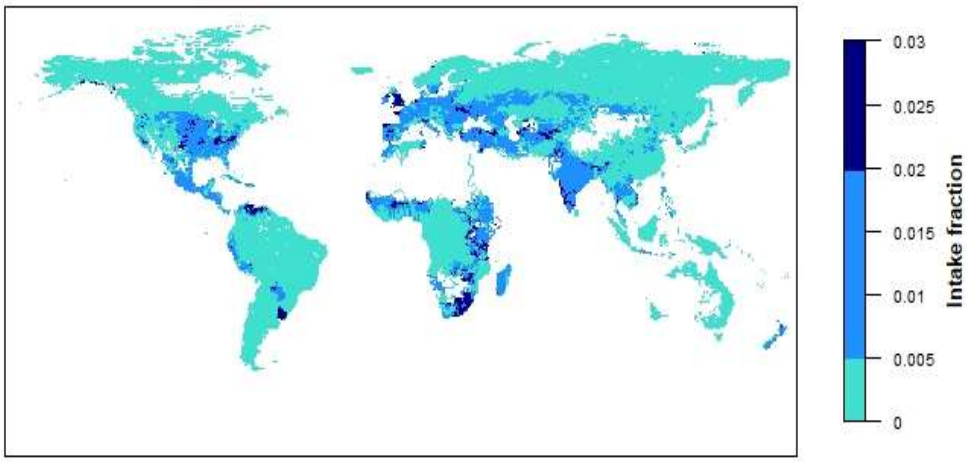

Fig. 2. River basin-specific intake fractions of *Cryptosporidium* worldwide

In Africa region, hotspots area can be seen in South Africa, Nigeria, Ethiopia, and Kenya (along Nile River and Euphrate and Tigris River). Meanwhile, in America continent, high intake fraction can be seen in some part of USA, Venezuela and Uruguay (along Mississippi River, Amazon River and Parana River). In Europe continent, a high intake fraction can be seen in United Kingdom (along Thames River). These results are in accordance with the global pathogen model by Hofstra [12] where the hotspots of oocyst loads found in India, Latin America and big cities in China.

The intake fraction was calculated only based on the livestock emission so that it might underestimate the result. However, human emission could contribute until 40% for *Cryptosporidium* emission to surface water [12]. In addition, the other exposure route like ingestion from crops was also neglected in this study. The value of intake fraction also

varies per region due to variability in river discharge [13] and pathogen behaviour before entering the surface water [14]. A higher discharge may decrease oocyst concentrations due to dilution [15] or increase the microorganism concentration due to resuspension from sediments and increased runoff [8].

3.2 Effect factor

Figure 3 below shows the effect factor value from six different dose-response models by Messner [10]. The effect factor value ranges from 0.0022 to 0736 cases/oocyst. A minimum value was obtained by using an exponential dose-response model (0.0022 case/oocyst); while a maximum value was obtained by using fraction Poisson model (0.736 case/oocyst). The Beta Poisson and an exponential with immunity model give slightly different effect factor values, as 0.534 and 0.442 case/oocyst respectively. Both hierarchical models also give slightly different values, with 0.026 and 0.014 case/oocyst respectively.

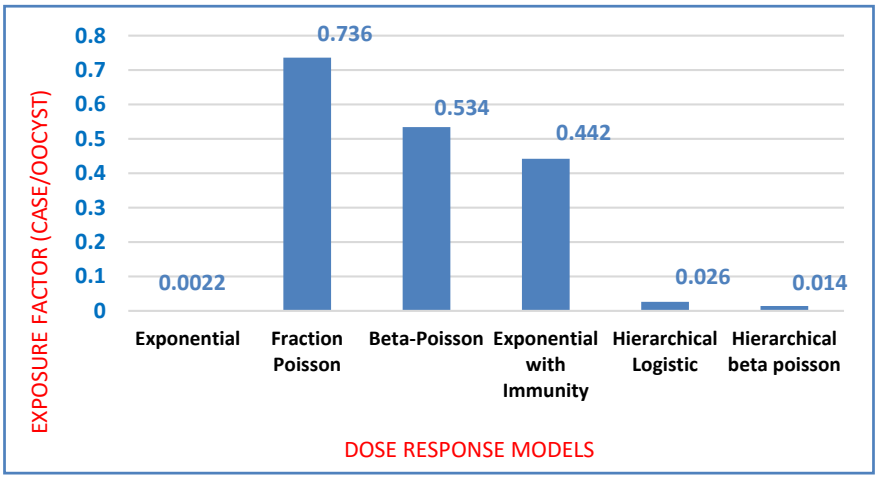

Fig. 3. Effect factors from different dose-response models of Cryptosporidium.

Linear effect factor (LEF) was chosen in this study due to the linearity factor fit the ID_{50} curve better rather than marginal effect factor or average effect factor. In addition, the usage of LEF also made the differences of various dose-response models more visible. Among these models, the fraction Poisson model is the only one-parameter model and assumes that all oocyst included in the study were capable to initiate an infection. Thus, the linear effect factor value using this model is the highest among six different dose-response models. In contrast, an exponential dose-response model has the lowest linear effect value despite has the same number of a parameter as Fraction Poisson. This is due to an exponential model has an assumption that there is also a probability of not becoming infected from a successfully ingested oocyst.

3.3 Final characterization factor

Figure 4 depicts DALY value per number of oocyst released in a river basin scale. The characterization value ranges from 0 to 1.2 x 10^{-5} DALY/oocyst. The magnitude of characterisation factor is equal to the intake fraction because the average value of effect factor was being used to estimate the results.

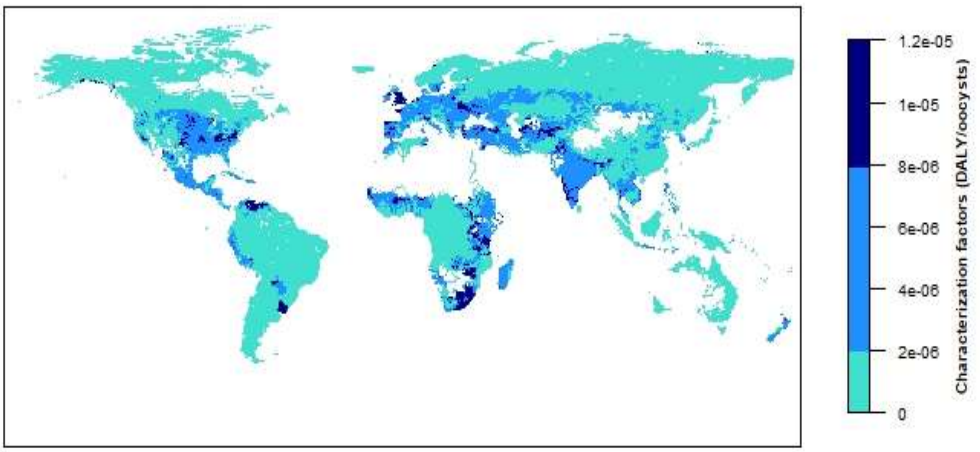

Fig. 4. River basin specific characterization factor of *Cryptosporidium* worldwide.

Most of the CF for human health damage expressed as DALY per kg emission. In this study, we used oocyst unit since most of the pathogen models also use this unit to express pathogen concentration or pathogen load. In fact, it will be more understandable for an LCA practitioner to have the final characterization factor per unit of production. However, an LCA practitioner is not able to derive the number of oocyst from certain product. Nevertheless, as the first step this framework can be used to link the life cycle inventory and impact assessment.

To our knowledge, this is the first study that explores the characterization framework of health damage due to pathogen contamination. Previous studies mostly investigate the health damage impact due to the chemical substance (GHG emission, human toxicity) or physical substance (i.e. particulate matter). Our CF results have the same unit for human health damage (DALY) and can therefore directly be included in LCA case studies.

4 Conclusion

A clear impact assessment framework which showed how characterization factor of microbial contamination can be derived had been developed through this study. A cause impact pathway has already been made for both livestock and human emission. Since this study only covers the livestock emission, a prospect research ahead could be including human emission into the characterization factor development. In addition, some of the required data is neither available per grid cell or per river basin specific, for instance, exposure pathway per age category. The DALY data for *Cryptosporidiosis* is not available per country or region. When those data are available the final characterization factor can be developed more specific per grid or country level. A health target or a preferred environmental state condition also can be set for certain pathogen for further develop other effect factors besides the linear effect model. Furthermore, the framework also can be assigned to different kind of pathogen that causes major waterborne disease, for instance, *Campylobacter, Giardia* or *Rotavirus*. Lastly, for an LCA practitioner, the development of characterization factor per unit production, for example as DALY/kg of milk or DALY/kg of meat production will be inevitably useful.

References

1. L. Corominas, J. Foley, J. Guest, S. Hospido, A. Larsen, H. F. Morera, A. Shaw, Water Research **47**, 5480–5492 (2013)
2. M.Z. Hauschild, & M.A.J. Huijbregts. *Life Cycle Impact Assessment* (Springer, 2015)
3. S.S. Lim, et al., The Lancet **380**, 2224–2260 (2012)
4. U.S. Environmental Protection Agency (EPA), *Cryptosporidium: Drinking Water Health Advisory* (Environmental Protection, 2001)
5. G. Medema. *Risk Assessment of Cryptosporidium in Drinking Water Risk Assessment of Cryptosporidium in Drinking Water.* 134. (Public Health, 2009)
6. E.K.. Lipp, J.A. Patz, S.M. Bernard, B.J. Rose, P.R. Epstein, B.H. Sherman. *and Change in the United States : Potential Impacts on Water- Climate Variability and Foodborne Diseases Caused by Microbiologic Agents* (2001)
7. M.C. Hlavsa, D.M. Roellig, H. Matthew, *Healthy and Safe Swimming Week — Using Molecular Characterization to Support Investigations of Aquatic Facility – Associated Outbreaks of Cryptosporidiosis — Alabama , Arizona , and Ohio* (2017)
8. N. Hofstra, *Quantifying the impact of climate change on enteric waterborne pathogen concentrations in surface water* (Current Opinion in Environmental Sustainability, 2011)
9. L.C. Vermeulen, J. Benders, G. Medema, N. Hofstra, Environmental Science and Technology **51,** 8663–8671 (2017)
10. M.J. Messner, P. Berger, Risk Analysis **36,** 1969–1982 (2016)
11. A.H. Havelaar, J.M. Melse, *Quantifying public health risk in the WHO Guidelines for Drinking Water Quality: a burden of disease approach.* 1–49 (RIVM Report 734301022, 2003)
12. N. Hofstra, A.F. Bouwman, A.H.W. Beusen, G.J. Medema, Science of the Total Environment **442,** 10–19 (2013)
13. L.C. Vermeulen, N. Hofstra, Regional Environmental Change **14**, 307–319 (2014)
14. W. An, D. Zhang, S. Xiao, J. Yu, M. Yang, Environmental Science & Technology **45**, 4951–4958 (2011)
15. M.M. Islam. *Assessing the Impact of Socio-economic Development and Climate Change on Faecal Indicator Bacteria in the Betna River , Bangladesh Table of Contents* (Wageningen University and Research, 2017)