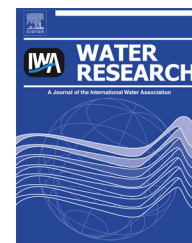


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# Quantitative assessment of infection risk from exposure to waterborne pathogens in urban floodwater

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## ABSTRACT

Flooding and heavy rainfall have been associated with waterborne infectious disease outbreaks, however, it is unclear to which extent they pose a risk for public health. Here, risks of infection from exposure to urban floodwater were assessed using quantitative microbial risk assessment (QMRA). To that aim, urban floodwaters were sampled in the Netherlands during 23 events in 2011 and 2012. The water contained *Campylobacter jejuni* (prevalence 61%, range 14– $>10^3$  MPN/l), *Giardia* spp. (35%, 0.1–142 cysts/l), *Cryptosporidium* (30%, 0.1–9.8 oocysts/l), noroviruses (29%,  $10^2$ – $10^4$  pdu/l) and enteroviruses (35%,  $10^3$ – $10^4$  pdu/l). Exposure data collected by questionnaire, revealed that children swallowed 1.7 ml (mean, 95% Confidence Interval 0–4.6 ml) per exposure event and adults swallowed 0.016 ml (mean, 95% CI 0–0.068 ml) due to hand–mouth contact. The mean risk of infection per event for children, who were exposed to floodwater originating from combined sewers, storm sewers and rainfall generated surface runoff was 33%, 23% and 3.5%, respectively, and for adults it was 3.9%, 0.58% and 0.039%. The annual risk of infection was calculated to compare flooding from different urban drainage systems. An exposure frequency of once every 10 years to flooding originating from combined sewers resulted in an annual risk of infection of 8%, which was equal to the risk of infection of flooding originating from rainfall generated surface runoff 2.3 times per year. However, these annual infection risks will increase with a higher frequency of urban flooding due to heavy rainfall as foreseen in climate change projections.

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## 1. Introduction

One of the major global concerns in climate change is the increased frequency of extreme events. Extreme rainfall events may occur more often and may cause flooding to occur

more often (Easterling et al., 2000). In addition, the risk of flooding may increase by ongoing urbanization and increased imperviousness of urban areas (Ten Veldhuis et al., 2010).

To prevent flooding, urban drainage systems are expanded with semi-natural devices, such as infiltration trenches,

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swales and ponds. These locations are often multi-functional, also operating as recreational areas and only filling up during exceptional storms (Butler and Davies, 2004). In The Netherlands, such locations are often combined with playgrounds, with the intention that children can play, swim or boat when these locations are filled.

Exposure to urban floodwater or water from sites that are intended to store or infiltrate rainwater may pose a health risk in humans. Such water may contain a variety of contaminants depending on the origin of the floodwater. Floodwater originating from rainfall-generated surface runoff may be contaminated by dirt from paved surfaces (including dog feces and bird droppings), while floodwater originating from flooded storm sewers may be contaminated by illicit connections to sanitary sewers (Marsalek and Rochfort, 2004) and floodwater originating from backflow from a combined sewer system will be contaminated with wastewater (Smith et al., 2007). As a result, floodwater may contain human enteric pathogens such as norovirus and enterovirus, which are prevalent in urban wastewater (Lodder and De Roda Husman, 2005), or *Campylobacter*, *Giardia* and *Cryptosporidium*, which have been frequently reported in both animal feces and human wastewater (Schets et al., 2008; Koenraad et al., 1994). These enteric pathogens account for a large proportion of all gastrointestinal illnesses in the Netherlands and the US (De Wit et al., 2001; Mead et al., 1999) and may cause outbreaks when people are exposed to floodwater. The waterborne pathogens *Campylobacter*, *Cryptosporidium*, *Giardia*, norovirus and enterovirus can be seen as representative of the fate and transport of other pathogens potentially of concern from the waterborne route of exposure (Ferguson et al., 2003).

According to a systematic review (Cann et al., 2013), the most common waterborne pathogens that were identified during outbreaks after extreme water events, such as flooding and heavy rainfall were *Vibrio* spp. (24%), *Leptospira* spp. (19%), *Campylobacter* 9%), *Cryptosporidium* spp. (9%) and norovirus (6%). However, it is unclear to which extent flooding pose a risk for public health.

Health risks from exposure to water from the flooding of different urban drainage systems such as combined sewers, storm sewers and infiltration fields can be quantified using the quantitative microbial risk assessment (QMRA) framework. QMRA requires information on the concentration of pathogens in the water or on the correlation between indicator bacteria and pathogens in the water, the exposure of people to these pathogens and dose–response relations for different pathogens.

In the present study, we aimed to assess health risks due to ingestion of urban floodwater by determining the risk of infection for a set of waterborne pathogens that can cause gastrointestinal diseases. The waterborne pathogens *Campylobacter*, *Cryptosporidium*, *Giardia*, norovirus and enterovirus were quantified in urban floodwater. Questionnaires were used to gather data to be able to estimate the volume of floodwater ingested by people during exposure. The generated pathogen data and exposure data were used to calculate the risk of infection for flooding originating from combined sewers, storm sewers and rainfall generated surface runoff. As a result, this study provides insight into health risks

resulting from the flooding of different urban drainage systems.

## 2. Material and methods

### 2.1. Sampling

Samples were taken from June 2011 until May 2012 by a sampling team that drove to locations where flooding was expected according to a Dutch meteorological website ([www.weerplaza.nl](http://www.weerplaza.nl)). At location, they checked their smartphone for emergency calls to the fire brigade about flooding ([www.112meldingen.nl](http://www.112meldingen.nl)) and went to those addresses. Samples were taken where buildings were flooded, infiltration fields had filled or at least 100 m<sup>2</sup> of the street was flooded (in order to prevent sampling of small rainwater puddles). One grab sample of approximately 20 L was collected per sampling location according to ISO 5667-2 (Anonymous, 2006a) and analyzed within 24 h after sampling. On the site, the duration of flooding until sampling was estimated by collecting information from residents. Furthermore, a distinction was made between three different origins of floodwater, using the following classification system:

- 1) Flooding originating from overflowing combined sewers;
  - a. The floodwater had a typical smell of sewage;
  - b. Toilets in houses were flooded;
  - c. Manhole covers of the combined sewer system were floated or displaced;
- 2) Flooding originating from overflowing storm sewers;
  - a. A storm sewer drained into a rainwater infiltration field;
  - b. Manhole covers of the storm sewer system were floated or displaced;
- 3) Flooding originating from rainfall generated surface runoff
  - a. A connection to an urban drainage system was absent;
  - b. Rainfall generated surface runoff drained into a rainwater infiltration field.

### 2.2. Fecal indicator bacteria

Volumes of 40 ml, 10 ml, 1 ml, 0.1 ml, 0.01 ml and 0.001 ml were analyzed for fecal indicator bacteria *Escherichia coli* was enumerated using the Rapid Test on Tryptone Soy Agar (996292, Oxoid, Wesel, Germany) and Tryptone Bile Agar (806567, Oxoid) according to ISO9308-1 (Anonymous, 2000a). Colonies were confirmed with James Reagens (BioMerieux, Marcy l'Étoile, France) according to the manufacturer's instructions. Intestinal enterococci were enumerated according to ISO7899-2 (Anonymous, 2000b) on Slanetz and Bartley Agar (1005125, Oxoid) and confirmation on Bile Esculin Azide Agar (726007, Remel).

### 2.3. *Campylobacter*

The presence of *Campylobacter* in volumes of 50 ml, 5 ml and 0.5 ml volumes was determined using the method described in ISO 17995 (Anonymous, 2005). This method was extended by PCR on the Preston Broth and the typical colonies to be able

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