



Detection and quantification of soil-transmitted helminths in environmental samples: A review of current state-of-the-art and future perspectives



Isaac Dennis Amoah^{a,b,*}, Gulshan Singh^a, Thor Axel Stenström^a, Poovendhree Reddy^b

^a Institute for Water and Wastewater Technology (IWWT), Durban University of Technology, PO Box 1334, Durban, 4000, South Africa

^b Department of Community Health Studies, Faculty of Health Sciences Durban University of Technology, PO Box 1334, Durban, 4000, South Africa

ARTICLE INFO

Article history:

Received 25 October 2016

Received in revised form 6 February 2017

Accepted 10 February 2017

Available online 15 February 2017

Keywords:

Soil-transmitted helminths

Wastewater

Sludge

qPCR

Digital PCR

BacLight Live/Dead

Flow cytometry

LAMP

ABSTRACT

It is estimated that over a billion people are infected with soil-transmitted helminths (STHs) globally with majority occurring in tropical and subtropical regions of the world. The roundworm (*Ascaris lumbricoides*), whipworm (*Trichuris trichiura*), and hookworms (*Ancylostoma duodenale* and *Necator americanus*) are the main species infecting people. These infections are mostly gained through exposure to faecally contaminated water, soil or contaminated food and with an increase in the risk of infections due to wastewater and sludge reuse in agriculture. Different methods have been developed for the detection and quantification of STHs eggs in environmental samples. However, there is a lack of a universally accepted technique which creates a challenge for comparative assessments of helminths egg concentrations both in different samples matrices as well as between locations. This review presents a comparison of reported methodologies for the detection of STHs eggs, an assessment of the relative performance of available detection methods and a discussion of new emerging techniques that could be applied for detection and quantification. It is based on a literature search using PubMed and Science Direct considering all geographical locations. Original research articles were selected based on their methodology and results sections. Methods reported in these articles were grouped into conventional, molecular and emerging techniques, the main steps in each method were then compared and discussed. The inclusion of a dissociation step aimed at detaching helminth eggs from particulate matter was found to improve the recovery of eggs. Additionally the selection and application of flotation solutions that take into account the relative densities of the eggs of different species of STHs also results in higher egg recovery. Generally the use of conventional methods was shown to be laborious and time consuming and prone to human error. The alternate use of nucleic acid-based techniques has improved the sensitivity of detection and made species specific identification possible. However, these nucleic acid based methods are expensive and less suitable in regions with limited resources and skill. The loop mediated isothermal amplification method shows promise for application in these settings due to its simplicity and use of basic equipment. In addition, the development of imaging soft-ware for the detection and quantification of STHs shows promise to further reduce human error associated with the analysis of environmental samples. It may be concluded that there is a need to comparatively assess the performance of different methods to determine their applicability in different settings as well as for use with different sample matrices (wastewater, sludge, compost, soil, vegetables etc.).

© 2017 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Contents

1. Introduction	188
2. Methodology	189
2.1. Search strategy	189
3. Conventional methods	189

* Corresponding author at: Institute for Water and Wastewater Technology (IWWT), Durban University of Technology, PO BOX 1334, Durban 4000, South Africa.
E-mail address: amoahkid@gmail.com (I.D. Amoah).

3.1.	Sample types and quantity	189
3.1.1.	Wastewater/water	189
3.1.2.	Sludge/Compost/Biosolids	189
3.1.3.	Soil	189
3.1.4.	Plants	190
3.2.	Egg recovery	191
3.2.1.	Separation of eggs from particles	191
3.2.2.	Filtration of samples	191
3.3.	Concentration	193
3.3.1.	Sedimentation	193
3.3.2.	Flotation	193
3.3.3.	Phase extraction	193
3.4.	Viability determination	194
3.4.1.	BacLight Dead/Live method	194
4.	Nucleic acid based techniques	194
4.1.	Nucleic acid extraction	194
4.2.	Polymerase chain reactions	195
4.3.	Loop-mediated isothermal amplification	196
5.	Emerging techniques	196
5.1.	Digital PCR	196
5.2.	Parasite identification using image analysis software	196
6.	Future prospects	197
6.1.	Flow cytometry	197
7.	Conclusion	197
	Acknowledgements	198
	References	198

1. Introduction

It is estimated that over 1.5 billion people are infected with at least one species of soil-transmitted helminths (STHs) worldwide (WHO, 2015), with the majority of these infections caused by the roundworms (*Ascaris lumbricoides* and *Strongyloides stercoralis*), whipworms (*Trichuris trichiura*) and hookworms (*Necator americanus* or *Ancylostoma duodenale*) (Strunz et al., 2014). Ascariasis is reported in 771.7–891.6 million people, while 429.6–508.0 million people have trichuriasis and 406.3–480.2 million are infected with hookworm (Pullan et al., 2014). Most of these infections occur in tropical and subtropical regions of the world where poverty results in poor sanitary conditions (Stolk et al., 2016). STHs infections are mostly caused by exposure to faecally contaminated water, soil or contaminated food (Keraita and Amoah, 2011). Wastewater and sludge reuse is reported to contribute significantly to the high risk of infections. In endemic areas, wastewater is estimated to contain up to ~3000 eggs/L (Kamizoulis, 2008; Mara and Sleigh, 2010).

The association between ascariasis and wastewater use among farmers has been reported by several studies (Seidu et al., 2008; Blumenthal et al., 2001; Pham-Duc et al., 2013; Rutkowski et al., 2007; Trang et al., 2006; Habbari et al., 1999), where consumers of the farm produce are also at risk of infection. The highest health risks for consumers of wastewater irrigated produce are with crops which are eaten raw, for example, salad crops and some root crops or crops grown close to the soil surface (e.g. lettuce) (WHO, 2006). Wastewater for unrestricted reuse in agriculture should contain ≤1 helminth egg per liter to reduce the risk of STHs infections to below the WHO guidelines target level (WHO, 2006). This requires sensitive detection and a consistent quantification of STHs eggs in wastewater, sludge or other sample matrices. Accurate detection and quantification of STHs eggs in environmental samples is challenging. The heterogeneity of the occurrence of STHs in environmental samples is problematic for laboratory testing due to varying amounts of moisture, solids, quantity of samples and soil particles (Collender et al., 2015). Another challenge with environmental

samples is the need to recover small numbers of STHs eggs from large volumes of samples (Maya et al., 2006; Mes, 2003).

Over the last few years, different techniques for detecting and quantifying the total number and the viable and non-viable fractions of STHs eggs in environmental samples has been developed and applied. The choice of technique used is largely influenced by the different types of samples (Maya et al., 2006). One reason for this may be the lack of published quality assurance/quality control (QA/QC) data on the various methods (Bowman et al., 2003). In addition to the more traditional methods based on sedimentation and/or flotation, which mainly involves the separation and concentration of eggs and the microscopical identification and quantification of these eggs, several new techniques have been developed. These new techniques make the identification and quantification of helminth eggs more efficient and sensitive. The advent of genomic sequencing and the wealth of data generated have markedly increased the feasibility of developing polymerase chain reaction (PCR)-based methods as diagnostic tools for helminth parasites (Gyawali et al., 2015). Defined gene sequences of STHs eggs can be detected with PCR, quantitative PCR (qPCR) and other nucleic acid based methods from small quantities of samples (Gordon et al., 2011). These techniques can also identify STHs eggs to species level (Gordon et al., 2011). Furthermore advanced nucleic acid based techniques (like multiplex PCR) makes it possible to target more than one species at a time (Pontes et al., 2002). The reliable quantification of viable eggs is essential both related to risk based target values and for the validation of sanitation system performance.

The lack of a globally accepted method for the detection and quantification of STHs eggs in environmental samples poses a challenge for comparative assessments of egg concentrations both in different sample matrices as well as between locations. This article presents a review of commonly used methods for the detection and quantification of STHs eggs in environmental samples, with a comparison of the advantages and disadvantages of each technique. We also review new and emerging techniques that may be applied for the detection and quantification of STHs eggs in the environment.

Download English Version:

<https://daneshyari.com/en/article/5670852>

Download Persian Version:

<https://daneshyari.com/article/5670852>

[Daneshyari.com](https://daneshyari.com)