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Development of a relative risk model for drinking water regulation and design recommendations for a peri urban region of Argentina



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ABSTRACT

Argentina is a developing Latin American nation that has an aim of achieving the United Nations Millennium Development Goals for potable water supplies. Their current regulations however, limit the continued development of improved potable water quality and infrastructure from a microbiological viewpoint. This is since the current regulations are focused solely to pathogenic Eschericia coli (E. coli), Pseudomonas aeruginosa (P. aeruginosa) and fecal indicators. Regions of lower socioeconomic status such as peri-urban areas are particularly at risk due to lessened financial and political ability to influence their environmental quality and infrastructure needs. Therefore, a combined microbiological sampling, analvsis and quantitative microbial risk assessment (OMRA) modeling effort were engaged for a peri-urban area of Salta Argentina. Drinking water samples from home taps were analyzed and a QMRA model was developed, results of which were compared against a general 1:10,000 risk level for lack of a current Argentinian standard. This QMRA model was able to demonstrate that the current regulations were being achieved for E. coli but were less than acceptable for P. aeruginosa in some instances. Appropriate health protections are far from acceptable for *Giardia* for almost all water sources. Untreated water sources were sampled and analyzed then QMRA modeled as well, since a significant number of the community (\sim 9%) still use them for potable water supplies. For untreated water E. coli risks were near 1:10,000, however, P. aeruginosa and Giardia risks failed to be acceptable in almost all instances. The OMRA model and microbiological analyses demonstrate the need for improved regulatory efforts for the peri-urban area along with improved investment in their water infrastructure.

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Introduction

Motivation and purpose of study

The essential nature of water means that a consistent source of high quality water is vital to the survival and thriving of a community. Therefore, poor microbiological water quality poses a serious and immediate problem for human health. Some communities

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http://dx.doi.org/10.1016/j.ijheh.2015.06.007 1438-4639/© 2015 Elsevier GmbH. All rights reserved. do not have access to either appropriate sanitation or potable water facilities, thus complicating the already poor water quality conditions. This lack of infrastructure is known to allow these communities to be exposed to pathogenically contaminated water (Razzollini et al., 2011). Additionally even if some water infrastructure is equipped, a significant fraction of waterborne disease burden can still be attributed to the way water resources are managed (Prüss-Ustün et al., 2014; Wolf et al., 2014).

The last report of the Joint Monitoring Programme for Water Supply and Sanitation (JMP; WHO/UNICEF, 2014a) indicate that 116 countries have already met the Millennium Development Goal (MDG) related to water between 1990 and 2012. This achievement resulted in 2.3 billion people gaining access to improved drinking water. While this is an important achievement, it is important to note that the MDG indicators do not take water quality measurements into account. Therefore it is increasingly recognized that water from improved sources does not guarantee increased water quality or safety. Bain et al. (2014) provides evidence of the presence of fecal contamination in sources considered improved in Low- and Middle-Income countries and suggest that, by equating *improved* with *safe*, the number of people with access to a microbiologically and chemically safe water have been greatly overstated. In this context, JMP indicated that one of the objectives for 2030 is to halve the proportion of the population without access at home to safe drinking water and progressively eliminate inequalities to its access (WHO/UNICEF, 2014b).

Water standards in Argentina are governed by the Argentine Food Code (Código Alimentario Argentino) (CAA, 2014). While this is a good step in developing safe drinking water standards and regulations, there are some potentially hazardous omissions in the development of these regulations. Namely microbiological quality of water is ascertained using indicator organisms, coliform bacteria, *Escherichia coli* (*E. coli*) and *Pseudomonas aeruginosa* (*P. aeruginosa*). Considering that potable water engineering design most typically follows pertinent regulations, there exists the potential for known pathogens other than those regulated to cause waterborne disease burden. Therefore, this study was designed to compare the relative differences in pathogenic hazard and controls through the lens of quantitative microbial risk assessment (QMRA).

QMRA is a powerful tool to project an estimated likelihood of deleterious health effects from exposure to pathogenic hazards. Even if high risks can be surmised the quantification of these risks gives weight of evidence to decisions and designs to address these risks. The QMRA paradigm has progressively been relied upon in regulatory and engineering design fields (Gale, 1996; Haas et al., 2014; Weir et al., 2011). The QMRA developed utilizes the Monte Carlo method to develop confidence intervals for the risk values, and account for variable uncertainty in the model.

Study area and description

Argentina is a developing country of Latin America and the Caribbean region with 91–100% of the population using improved sources of drinking water and is among the countries that met the MDG for water (WHO/UNICEF, 2014a). Nevertheless, there is evidence of improved water sources with presence of waterborne pathogens (Abramovich et al., 2001; Basualdo et al., 2000, 2007; Lurá et al., 2000; Costamagna et al., 2005; Gamboa et al., 2011; Vidaurre et al., 2010). In Salta, a province in the northwest region of Argentina, more than half of the total population of infants is affected by diarrhea annually by infectious pathogens. Seasonal trends can be observed as well with bacteria predominating in spring and summer, viruses particularly in the winter and parasites being endemic year round in some areas (Rajal et al., 2010). Public health monitoring is limited by poor epidemiological records, exacerbated by the lack of diarrhea cases having the etiological agent assayed (only in 4% studied in 2013; Ministerio de Salud, 2014). This lack of records also means that monitoring for water quality or treatment faults through epidemiological evidence (monitoring for the clusters of similar symptoms) cannot be reliably performed. The determination of etiological agent is also important for increased weight of evidence to target specific pathogens in future regulations or changes to current regulations. Therefore a QMRA model developed to describe the potential water quality impacts for a set of treatment options will be valuable to start addressing some of these knowledge gaps.

The indicators and pathogens for microbiological drinking water control under current regulations in the CAA (2014) are limited to coliform bacteria, *E. coli* and *P. aeruginosa*. With these bacteria as the only design criteria for a treatment plant obviously the efficiency of pathogenic protozoa and virus removal in water treatment systems is being overlooked. This leads to the treatment systems allowing for waterborne disease outbreaks, sometimes without corresponding evidence of microbiological contamination of drinking water (CEPIS/OPS, 2004; Hrudey and Hrudey, 2004).

Seghezzo et al. (2013) outlined the commitment of the water utility of Salta to improving water treatment efficiency with the implementation of an initial Water Safety Plan (WSP). Important results showed there is need for improvement namely: (1) define health based targets, (2) assess whether the treatment is appropriate to achieve health based targets, and (3) define required sample sizes and frequency. These improvements to the WSP can be addressed by utilizing a QMRA approach (Medema and Ashbolt, 2006). Both methodologies, WSP and QMRA, are useful to evaluate and improve the microbial safety of drinking water and are recommended by the third and fourth editions of the Guidelines for Water Quality (WHO, 2008, 2011). Importantly by using a WSP and QMRA together more weight of evidence can be used for regulatory reform, water treatment process selection and system maintenance prioritization. Actual adaptations to the scope of the WSP are outside the bounds of this work but are currently underwav.

Since QMRA is computationally intensive there is occasional reluctance to engage in such a significant quantitative effort. Additionally as Argentina has no history of developing or using QMRA models in the drinking water industry there is the possibility for trepidation and need of regulator education. In this work we outline the development of a QMRA model and outline the general decisions and recommendations that can be made from the results. This model will also serve to help educate Argentine utilities and regulatory agencies on the applicability and use of QMRA models, particularly in drinking water.

The QMRA is developed using data from an intensive drinking water sampling and assay research (here in termed drinking water assessment). The drinking water assessment was developed for a peri-urban area near Salta, Argentina. This area has two water treatment plants that have been designed and developed based on the current regulations. Therefore to compare the risks under current regulations and for an additional known hazard three pathogens were chosen for assay and QMRA modeling: enteropathogenic *E. coli*, *P. aeruginosa* and *Giardia* subspecies. Viruses were not sampled for due to costs of analysis as well as parasites being prioritized since they are a known source water hazard.

There are at least four types of *E. coli* pathogenic to humans: enterotoxigenic (ETEC), enterohemorrhagic (EHEC), enteropathogenic (EPEC), and enteroinvasive (EIEC). The organisms are excreted in the feces of warm-blooded animals (including humans) and transmitted by direct contact or via contaminated food and water. Ingestion of *E. coli* results in a wide range of possible outcomes, from asymptomatic infection to death particularly due to EHEC most typically via hemolytic uremic syndrome (HUS) (Rubino et al., 2011). Further details about the other strains are well outlined in Percival et al. (2004). *E. coli* is sensitive to chlorine and other oxidant disinfectants, therefore it is known that adequate chlorination effectively reduces infection and illness risks (Hunter, 2003). However, if the chlorination process is not designed, optimized or maintained properly then health risks will increase if this is the primary or sole means of microbial control.

P. aeruginosa is part of a large group of free-living bacteria that are ubiquitous in the environment, often found in natural waters such us lakes or rivers but not often found in drinking water (Mena and Gerba, 2009). Occasional occurrence in drinking water is typically indicative of water quality deterioration, if present in drinking water, the population is potentially exposed to a pathogen capable of ocular infections, especially the immunocompromised communities (Percival et al., 2004). *P. aeruginosa* does not exhibit resistance Download English Version:

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