

2012-10-03-149 CGN minireviews on mycobacteria: (07) Mycobacteria in potable water
To: (04) Food-borne, water-borne and air-borne diseases; (05) Zoonoses, general; (08) Mycobacterial diseases; (22) Veterinary administration (27) Scientific information

CGN minireviews on mycobacteria as a public health risk

A new series, aimed at stimulating discussion on published literature dealing with the threat to public health posed by mycobacteria. Although some information of global significance has been known for decades, the risk posed by mycobacteria remains underestimated.

Edited by the [Reference Laboratory for Paratuberculosis and Avian Tuberculosis](#) World Organization for Animal Health (OIE) and [Biomedical Technology, Epidemiology and Food Safety Global Network](#) operating in the Veterinary Research Institute, Brno, Czech Republic

We support the [One Health Initiative](#)

(07) Mycobacteria in potable water (B. Klanicova, Brno)

Environmental mycobacteria, common in diverse aquatic habitats like natural waters, can enter drinking water distribution systems, where they persist in biofilms. They are more resistant to disinfection methods like chlorination, ozonation or UV irradiation than are common bacteria (Falkinham, 2009; Whiley et al., 2012). In a study by Falkinham (2011) it was shown that 17 (46%) of 37 households from patients with lung disease were contaminated with *M. avium* and that 7 (41%) of 17 had the same DNA fingerprint as the patient. One patient isolate from sputum corresponded with an isolate from the shower water. Environmental mycobacteria include *Mycobacterium avium* subsp. *paratuberculosis* (MAP) which is widely discussed as one of the possible factors in the development of Crohn's disease. Aboagye and Rowe (2010) detected MAP culture-positive sample in the final treated water from a freshwater lake. Beumer et al. (2010) detected MAP-specific DNA using PCR in 81% of drinking water and biofilm samples in the USA. The study of Pierce (2009) is the first report of a possible link between Crohn's disease and the consumption of fully treated drinking water. Those infected were three unrelated individuals. Drinking water and biofilms from drinkers are important environmental sources of mycobacteria which cause non-tuberculous mycobacteriosis in pigs (Matlova et al., 2003). According to Pavlik et al. (2005) the most prevalent mycobacteria isolated from tuberculous lesions in slaughtered pigs (*M. a. avium* and *M. a. hominissuis*) originate from free living birds and contaminated drinking water, feeds, and feed supplements. Water tubing and reservoirs for medicated drinking water can be heavily contaminated and pathological lesions are efficiently controlled by sanitation.

From the Web of Science database 297 records are retrieved using the following search profile:
Topic=((mycobact* AND water) AND (drinking OR potable OR household OR bottled OR mineral))

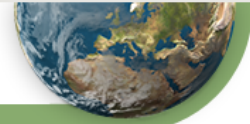
Selected references

Aboagye, G., Rowe, M.T. (2011)

Occurrence of *Mycobacterium avium* subsp *paratuberculosis* in raw water and water treatment operations for the production of potable water

Water Research, 45, 3271-3278

Mycobacterium avium subsp. *paratuberculosis* (Map) causes Johne's disease of cattle and is implicated as a cause of Crohn's disease in humans. The organism is excreted in animal faeces and can contaminate water catchment areas. This coupled with Map's survival in the environment means that water destined for domestic use may be a source of exposure. This work was designed to determine the occurrence of Map in Lough Neagh (the largest freshwater lake in the British Isles), used as a reservoir, and in two water treatment works (WTW1 and WTW2) which abstract from the lough and which have slow sand filtration (SSF) and dissolved air flotation respectively as their principal treatment regimes. The organism was not detected in lough water samples by culture (n = 70) but 29% (20/70) were positive by PCR. In the raw water to WTW1 and WTW2 no culture positives were detected but 54% (13/24) and 58% (14/24) respectively were PCR positive. In WTW1 there were no culture positives at the SSF or final water but 31% (8/26) and 45% (9/20) respectively were PCR positive. In WTW2 similar results were obtained with 26% (6/23) and 48% (11/23) in the floccules and final water respectively. At WTW2 however one culture positive was detected in the final water. This latter finding is of concern. The inability to reach definitive conclusions indicates the need for further research, particularly in the detection methods for viable Map.



Beumer, A., King, D., Donohue, M., Mistry, J., Covert, T., Pfaller, S. (2010)

Detection of *Mycobacterium avium* subsp. *paratuberculosis* in Drinking Water and Biofilms by Quantitative PCR

Applied and Environmental Microbiology, 76, 7367-7370

It has been suggested that *Mycobacterium avium* subspecies *paratuberculosis* has a role in Crohn's disease. The organism may be acquired but is difficult to culture from the environment. We describe a quantitative PCR (qPCR) method to detect *M. avium* subsp. *paratuberculosis* in drinking water and the results of its application to drinking water and faucet biofilm samples collected in the United States.

Falkinham, J.O. (2009)

Surrounded by mycobacteria: nontuberculous mycobacteria in the human environment

Journal of Applied Microbiology, 107, 356-367

A majority of the *Mycobacterium* species, called the nontuberculous mycobacteria (NTM), are natural inhabitants of natural waters, engineered water systems, and soils. As a consequence of their ubiquitous distribution, humans are surrounded by these opportunistic pathogens. A cardinal feature of mycobacterial cells is the presence of a hydrophobic, lipid-rich outer membrane. The hydrophobicity of NTM is a major determinant of aerosolization, surface adherence, biofilm-formation, and disinfectant- and antibiotic resistance. The NTM are oligotrophs, able to grow at low carbon levels [$> 50 \mu\text{g}$ assimilable organic carbon (AOC) l(-1)], making them effective competitors in low nutrient, and disinfected environments (drinking water). Biofilm formation and oligotrophy lead to survival, persistence, and growth in drinking water distribution systems. In addition to their role as human and animal pathogens, the widespread distribution of NTM in the environment, coupled with their ability to degrade and metabolize a variety of complex hydrocarbons including pollutants, suggests that NTM may be agents of nutrient cycling.

Falkinham, J.O. (2011)

Nontuberculous Mycobacteria from Household Plumbing of Patients with Nontuberculous Mycobacteria Disease

Emerging Infectious Diseases, 17, 419-424

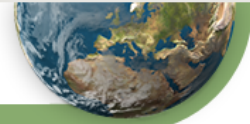
To determine whether plumbing could be a source of nontuberculous mycobacteria (NTM) infection, during 2007-2009 I isolated NTM from samples from household water systems of NTM patients. Samples from 22/37 (59%) households and 109/394 (28%) total samples yielded NTM. Seventeen (46%) of the 37 households yielded ≥ 1 *Mycobacterium* spp. isolate of the same species as that found in the patient; in 7 of those households, the patient isolate and 1 plumbing isolate exhibited the same repetitive sequence-based PCR DNA fingerprint. Households with water heater temperatures ≤ 125 degrees C (≤ 50 degrees C) were significantly more likely to harbor NTM compared with households with hot water temperatures ≥ 130 degrees F (≥ 55 degrees C) ($p = 0.0107$). Although households with water from public or private water systems serving multiple households were more likely to have NTM (19/27, 70%) compared with households with a well providing water to only 1 household (5/12, 42%), that difference was not significant ($p = 0.1532$).

Matlova, L., Dvorska, L., Bartl, J., Bartos, M., Ayele, W.Y., Alexa, M., Pavlik, I. (2003)

Mycobacteria isolated from the environment of pig farms in the Czech Republic during the years 1996 to 2002

Veterinarni Medicina, 48, 343-357

Sources of mycobacterial infections in 50 pig herds in the Czech Republic were investigated during the years 1996 to 2002. A total of 2412 samples from the external environment (feeds, bedding materials, drinking water, biofilms on drinkers, scrapings from the walls, floors and pen barriers, dust, spider webs, peat, kaolin, faeces, organs of rodents, and birds, etc.) were examined. After staining by the Ziehl-Neelsen technique, acid-fast rods were detected in 95 (3.9%) samples by direct microscopic examination and mycobacteria were cultured from 575 (23.8%) samples. From *Mycobacterium avium* complex (MAC), *M. avium* subsp. *hominissuis* (genotype IS901-, IS1245+) of serotypes 4, 6, 8, and 9 (272; 47.0%

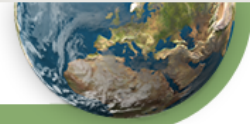


isolates), *M. a. avium* (genotype IS901+, IS1245+) of serotype 2 (13; 2.2% isolates) and *M. intracellulare* (genotype IS901-, IS1245-) of different serotypes (2; 0.3% isolates) were detected most frequently. Other isolates from among 14 other mycobacterial species ranked as follows: 64 *M. gordonae*, 47 *M. fortuitum*, 17 *M. chelonae*, 14 *M. flavescens*, 11 *M. terrae*, seven *M. phlei*, seven *M. scrofulaceum*, three *M. diernhoferi*, three *M. triviale*, three *M. smegmatis*, two *M. xenopi*, one *M. szulgai*, one *M. gastri*, and one *M. ulcerans*. The remaining 111 isolates of unidentified species did not contain specific sequences IS901 and IS1245 characteristic for the pathogenic members of MAC (*M. a. avium* and *M. a. hominissuis*). Peat, drinking water, biofilms on drinkers, bedding materials, feeds, free living birds, kaolin and charcoal were identified as potential sources of mycobacterial infections for pigs. Peat given to piglets as a feed supplement was the most important source of mycobacteria (65.1% positive of 327 examined samples); 81.2% of them were positive for *M. a. hominissuis* of serotypes 4, 6, 8, and 9. By contrast, mycobacteria of other species (*M. gordonae*, *M. fortuitum*, *M. chelonae*, *M. flavescens*, etc.) were the main isolates obtained from drinking water and biofilms on drinkers for pigs. By culture examination, the detection rate was higher in the biofilm samples (36.4%) than in the samples of drinking water (29.6%). The third group of sites with detected high levels (26.4%) of mycobacterial contamination were various types of beddings of woody material. *M. a. hominissuis* of serotypes 6, 8, and 9 were the most frequent isolates from sawdust; *M. a. avium* serotype 2 was sporadically detected. Mycobacterial findings in other samples from the external environment (wall and floor scrapings, dust, soil from the runs, and invertebrates) gave an indication of the pressure of infection in the herds. High contamination levels in faecal samples (15.6%) and in scrapings (18.4%) from respective parts of pens and stables indicated exposure of pigs to mycobacteria. In those materials, isolation of *M. a. hominissuis* of serotypes 4, 6, 8, and 9 prevailed. Mycobacteria were also detected in 7.9% of 430 samples of various invertebrate species. Various mycobacterial species were identified in the larvae and puparia of *Eristalis tenax* and *Musca* spp. and in imagoes of *Drosophila* spp., *Musca* spp., family Scatophagidae, *Stomoxys calcitrans*, *E. tenax*, and in earthworms. All of the constituents of the external environment that are potential sources of mycobacterial infections should be considered during implementation of preventative measures and the control of mycobacterial infections in pig herds

Pavlik, I., Matlova, L., Dvorska, L., Shitaye, J.E., Parmova, I. (2005)

Mycobacterial infections in cattle and pigs caused by *Mycobacterium avium* complex members and atypical mycobacteria in the Czech Republic during 2000-2004
Veterinari Medicina, 50, 281-290

Bovine tuberculosis was last detected in cattle and pigs in the Czech Republic in 1995. Since March, 31, 2004 (Commission Decision No. 2004/320/EC) the Czech Republic has been included amongst states free from bovine tuberculosis within the European Union. The purpose of the present study was to evaluate results of intravital and post-mortem diagnosis of mycobacterial infections in slaughtered cattle and pigs from 2000 to 2004. When bovine tuberculosis in cattle was investigated, a tuberculin skin test with bovine tuberculin was performed every year and a skin test with avian tuberculin was simultaneously conducted in the animals with a positive response. A total of 2 419 889 animals were examined with a positive response being found in 123 (0.005%) of them. After slaughter, bovine tuberculosis was not detected in any of these animals by gross and/or laboratory examinations. With avian tuberculin, 40 349 animals were tested and positive responses were detected in 43 (0.1%) of them; the incidence was similar in all the years monitored. Tuberculous lesions were detected in 209 (0.01%) of 1 967 211 slaughtered cattle. Mycobacteria were present in 40 (21.3%) of 188 animals examined by laboratory methods: 26 isolates of *Mycobacterium avium* subsp. *avium* (18 isolates of serotype 2 and 8 isolates not typeable), 11 isolates of *M. a. hominissuis* (1 isolate of serotype 8 and 10 isolates not typeable), and 3 isolates of atypical mycobacteria. Tuberculous lesions were detected in 49 312 (0.22%) of 22 312 580 slaughtered pigs by veterinary-meat inspection. During the 5-year-period monitored, the incidence of tuberculous lesions decreased from 0.37% in 2000 to 0.10% in 2004. The following mycobacteria were isolated from 757 (33.5%) of 2 261 animals whose organs were examined by culture: 203 isolates of *M. a. avium* (180 isolates of serotype 2, 3 isolates of serotype 2/8, and 20 isolates not typeable), 442 isolates of *M. a. hominissuis* (1 isolate of serotype 1, 262 isolates of serotype 8, 35 isolates of serotype 9, 1 isolate of mixed serotypes 8/9, and 143 isolates not typeable), and atypical mycobacteria (n = 112). In both animal species, *M. avium* complex members prevailed: *M. a. avium* was the most prevalent subspecies in cattle, *M. a. hominissuis* in pigs. The main sources of *M. a. avium* and



M. a. hominissuis are free living birds and contaminated external and stable environments (i.e. drinking water, feeds, and feed supplements), respectively. During the entire period monitored, miliary or generalized tuberculosis was not detected in any of the animals. The decreased incidence of tuberculous lesions in pigs was particularly a result of preventive measures adopted to control the occurrence of atypical mycobacteria.

Pierce, E.S. (2009)

Possible transmission of Mycobacterium avium subspecies paratuberculosis through potable water: lessons from an urban cluster of Crohn's disease

Gut Pathogens, 1, Article Number: 17 DOI: 10.1186/1757-4749-1-17

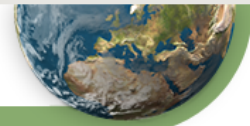
A "cluster" of patients refers to the geographic proximity of unrelated patients with the same disease and suggests a common environmental cause for that disease. Clusters of patients with Crohn's disease have been linked to the presence of an infectious microorganism in unpasteurized milk and cheese, untreated water supplied by wells or springs, animal manure used as fertilizer for family vegetable gardens, and bodies of water contaminated by agricultural runoff. Mycobacterium avium subspecies paratuberculosis (MAP) is the suspected cause of Crohn's disease. MAP causes a disease in dairy cows and other animals that is similar to Crohn's disease, called Johne's ('Yo-knees') disease or paratuberculosis. Dairy cows with Johne's disease secrete MAP into their milk and excrete MAP into their feces. MAP is present in untreated water such as well water, in bodies of water contaminated by agricultural runoff, and in unpasteurized milk and cheese. The "treatment" of "tap" water to make it "drinkable" or "potable" by the processes of sedimentation, filtration and chlorination has little to no effect on MAP. MAP is so resistant to chlorine disinfection that such disinfection actually selects for its growth. Other subspecies of Mycobacterium avium grow in biofilms present on tap water pipes. Despite the documented presence of MAP in tap water and its probable growth on tap water pipes, clusters of Crohn's disease have not previously been described in relationship to tap water pipes supplying patients' homes. This report describes three unrelated individuals who lived on the same block along a street in a midwestern American city and developed Crohn's disease within four years of each other in the 1960' s. A common tap water pipe supplied their homes. This is the first reported cluster of Crohn's disease possibly linked to fully treated drinking water, and is consistent with previously reported clusters of Crohn's disease linked to an infectious microorganism in water.

Whiley, H., Keegan, A., Giglio, S., Bentham, R. (2012)

Mycobacterium avium complex - the role of potable water in disease transmission

Journal of Applied Microbiology , 113, 223-232

Mycobacterium avium complex (MAC) is a group of opportunistic pathogens of major public health concern. It is responsible for a wide spectrum of disease dependent on subspecies, route of infection and patients pre-existing conditions. Presently, there is limited research on the incidence of MAC infection that considers both pulmonary and other clinical manifestations. MAC has been isolated from various terrestrial and aquatic environments including natural waters, engineered water systems and soils. Identifying the specific environmental sources responsible for human infection is essential in minimizing disease prevalence. This paper reviews current literature and case studies regarding the wide spectrum of disease caused by MAC and the role of potable water in disease transmission. Potable water was recognized as a putative pathway for MAC infection. Contaminated potable water sources associated with human infection included warm water distribution systems, showers, faucets, household drinking water, swimming pools and hot tub spas. MAC can maintain long-term contamination of potable water sources through its high resistance to disinfectants, association with biofilms and intracellular parasitism of free-living protozoa. Further research is required to investigate the efficiency of water treatment processes against MAC and into construction and maintenance of warm water distribution systems and the role they play in MAC proliferation.



Next minireviews

Mycobacteria ...

- ... are distributed in bottled water
- ... play a role in an Island story (ovine paratuberculosis and Crohn's disease)
- ... in the Czech Republic (Crohn's disease after the Iron Curtain had been risen)
- ... in Sardinia (T1D)
- ... in Cardiff (river Taff contaminated by MAP)
- ... in Mankanto (ill-fated swimming)
- ... can be found in every nook and cranny
- ... as secret agents (formula feeding, cold chain hypothesis, hygiene hypothesis)
- ... can, even after their death modulate inflammatory cytokines by means of their cell wall components
- ... were used for immunomodulation in Freund adjuvans already 65 years ago
- ... are pathogens as well as allergens or immunomodulators
- ... could be the missing environmental factor in many etiological hypotheses
- ... are considerably heat and chlorine resistant
- ... have unusual characteristics of food, water, and air borne pathogens or immunomodulators similar to allergens

See the introductory documents

- [Paratuberculosis and Crohn's disease: Premises and open questions](#)
- [Infectious diseases incorporated FUIDI premises](#)

**Follow the discussion at <http://centaur.vri.cz/?page=home>
[Please share your comments, opinions or suggestions.](#)**
