

1. Executive Summary

- 1.1 This study has investigated parts of water distribution systems where *Mycobacterium* spp. and *Helicobacter* are likely to survive if they gain access to water distribution systems. The study assesses the ability of these organisms to survive within water distribution systems and colonise biofilms and deposits from water mains and domestic plumbing, particularly those subject to intermittent flow and localised heating. The prevalence and significance of any *Mycobacterium avium* Complex (MAC), *Mycobacterium avium* subsp. *paratuberculosis* (MAP) and *Helicobacter pylori* isolated from distribution are reported. This is the first study to examine the survival of *H. pylori* in water supply systems in England.
- 1.2 Three distribution systems, a treated lowland river (area EL), upland impounding reservoir (area NW) and groundwater source (area RG) were selected and domestic properties served by these distribution systems were examined. Water (102 samples), biofilm (43) and deposit (42) samples were taken, giving a total of 187 samples. The majority of samples (140) were taken from 18 different domestic properties (houses and school premises). In addition there were 36 samples taken from nine hydrants on the three different distribution systems, five water meters samples were taken from area NW and six deposit samples taken from a service reservoir in area NW.
- 1.3 All 187 samples were analysed for *Mycobacterium* spp. and 151 samples (excluding the 36 hot water samples taken at the domestic properties, which would be unlikely to yield *Helicobacter* spp.) were analysed for *Helicobacter* spp.
- 1.4 There were no *Helicobacter* spp. cultured from the 151 samples, however, there was evidence of *Helicobacter* spp. DNA in 39 (26%) samples overall. Of the 18 domestic properties 16 (89%) had samples positive in one or more of the PCR assays; 33 of 115 (29%) samples from these properties were *Helicobacter* spp. positive and six of the positives were identified as *H. pylori*. Three of these six *H. pylori* were confirmed by direct sequencing. By PCR *H. pylori* were only detected in biofilm or deposit samples from five properties. The six reservoir deposit samples and five water meter samples were

negative for both culture and PCR. However four of the nine water hydrants were DNA positive in at least one of the PCR assays, yielding six positive samples. Overall *Helicobacter* spp. and *H. pylori* DNA were detected more frequently in biofilm samples (42%) and were more prevalent in area NW (31%) than areas RG (26%) and EL (20%).

- 1.5 The absence of culturable *H. pylori* in samples suggests that although these organisms can gain access to water distribution systems there is no evidence that they can survive disinfection.
- 1.6 The methods for the isolation of *Mycobacterium* spp. were refined from those used for the previous project; to improve detection large volumes of water were sampled, decontamination procedures were optimised, *Mycobacterium* spp. were enumerated and the identification of mixed cultures of *Mycobacterium* spp. was improved. The results suggest that *Mycobacterium* spp. were only present in low numbers. Although relatively few sites yielded MAC and no MAP were found, other *Mycobacterium* spp. were isolated from a wide range of domestic sites. Mycobacteria were isolated from every type of sample, most commonly isolated from showers (67%) and least commonly from tap net deposits (17%). Ten samples were positive for MAC and these were from shower (three samples) and hot water (four samples) in properties and from reservoir (one sample) and water meter (two samples) deposits. Overall *Mycobacterium* spp. were more prevalent in area EL (60%) compared to both NW (45%) and RG (43%). However MAC appeared to be more common in area NW (11%) upland impounding reservoir, than the other areas RG (2%) and EL (2%).
- 1.7 It is clear that there is widespread public exposure to mycobacteria in general and to *M. avium* in particular. Reported clinical cases of non-tuberculosis mycobacterial infections in the UK remain relatively low. There is no conclusive evidence for the presence of *M. avium* subspecies *paratuberculosis* in drinking water itself.
- 1.8 The detection of MAC in water samples is further evidence that these organisms can survive water treatment and grow within distribution. It is likely that in some domestic and institutional settings much larger numbers of MAC may grow. It is also likely that the risk of acquiring MAC in an

immunocompromised patient is likely to be increased where the number of MAC present in water is increased. There is obviously widespread exposure of people to MAC and this does not appear to have caused a major public health problem. There would be no need for control measures in most cases.

- 1.9 MAP was not detected in any samples. Its common presence in animal faeces suggests that it can get into source waters. The absence of MAP detection in any samples may reflect a genuine absence or a continuing problem with the technology for detecting this very slow- growing organism. As there is no conclusive evidence of the presence of MAP the exact public health consequences are unclear.
- 1.10 These results demonstrate the strengths and inadequacies of the methodologies for isolating MAC, MAP and *H. pylori*. Further work on method development is required for an assured position on the significance of these results.
- 1.11 The rare occurrence of MAP (0%), MAC (5%) and *H. pylori* (4%) within water distribution and properties in England are unlikely to be a major public health concern.