

A Consensus: Microbial Source Tracking in Water

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A consensus: microbial source tracking (MST) in water



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Traditionally, water quality regulation and protection of public health has relied on culture-based methods that quantify faecal indicators such as the coliforms. Since *Escherichia coli* represents over 97% of the thermotolerant coliforms, it has been used extensively as a key indicator of faecal contamination in water testing industry. However the presence of *E. coli* or other coliforms (and more recently enterococci) does not provide any information regarding the source of contamination and therefore is not always an effective indicator of actual risk to humans. While human/animal faecal contamination of water can pose a serious health risk to public, the risk can be managed more efficiently and effectively if the source is known. In this respect, microbial source tracking (MST) can be used as an efficient tool by water managers to improve management of public health.

Indeed, there has been a growing interest in applying MST methods to identify the sources of human/animal faecal contamination over the past 10 years; more than 100 papers being published in this area over the last 3 years alone (Figure 1). These

reports all demonstrate how MST methods have been utilised to differentiate groups of microorganisms, usually faecal indicator organisms, for the purpose of tracking sources of faecal pollution. Ecological studies using these methods, alone or in combination, have yielded varying results, sometimes contradictory to each other, leaving water management authorities wondering as to what extent they can rely on the outcome of these methods.

Surface waters are constantly receiving pathogenic microorganisms through defecation of humans (via septic tanks or due to sewage overflow) and animals. Identification of major sources of potential pathogens in water is therefore necessary to minimise the public health risks associated with such contamination. To trace the source of contamination, several MST methods have been used to establish a database of faecal indicator bacteria from known host groups (database-dependent methods). These methods, however, are either not sufficiently discriminatory to differentiate between indicator bacteria in the same species or are not sufficiently reproducible. In addition, some of the currently used methods are either complicated and require special trained personnel, or are costly and labour intensive, therefore not suitable for routine

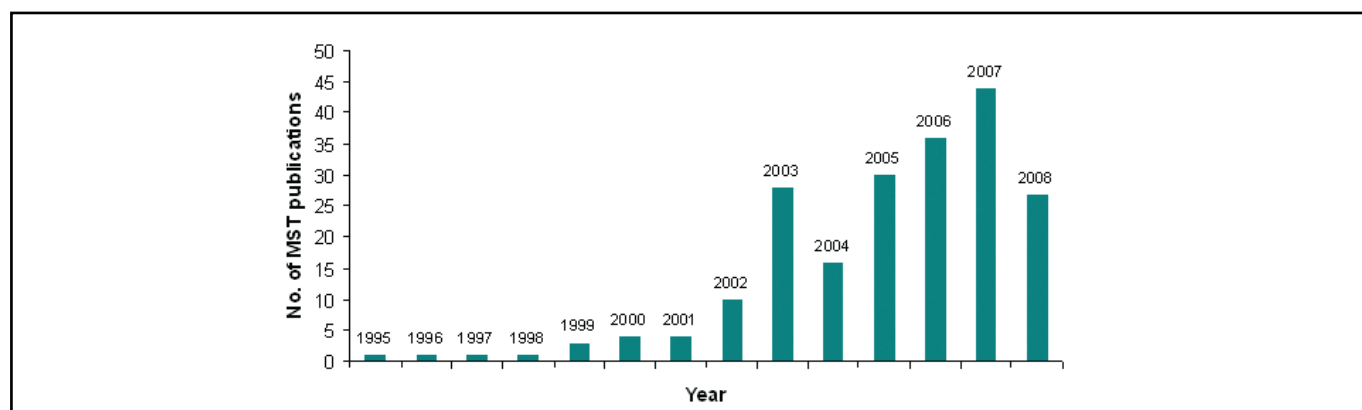


Figure 1. A representation of the increasing interest in microbial source tracking by the number of refereed publications.

water quality monitoring. The current literature also suggests that database-dependent methods require further evaluation in terms of their size and representativeness. Stability of faecal indicator bacteria in the environment is another important factor, which needs to be addressed. Finally, it is not known whether a database developed for a given catchment can be used in another catchment within the same geographical region.

Nonetheless, the objective of these methods is to overcome the limitations of traditional faecal indicator bacteria and more accurately identify the sources of faecal contamination (humans or animals or both). Indeed, some of these methods are designed to differentiate among animal species and to a large extent are capable of doing so¹; however, these methods require more validation before they can be adopted as a standard tool.

The MST methods can be broadly categorised as microbial and chemical methods. Microbial methods can be further categorised as genotypic and phenotypic methods. Genotypic methods include ribosomal DNA genetic markers of bacteroides, *Enterococcus faecium* enterococci surface protein (esp) marker, β -glucuronidase gene in *E. coli*, ribotyping, pulsed-field gel electrophoresis, repetitive extragenic palindromic polymerase chain reaction (REP-PCR), amplified fragment length polymorphism (AFLP), denaturing gradient gel electrophoresis (DGGE), terminal restriction fragment length polymorphism (T-RFLP), enterotoxin biomarkers and F⁺ coliphages genotyping. Phenotypic methods include multiple antibiotic resistance analysis, carbon source utilisation and biochemical fingerprinting.

Chemical methods have also been used as indicators of human or animal faecal pollutions. These methods include faecal sterols, optical brighteners, caffeine and pharmaceuticals, with faecal sterols being the most commonly used chemical method to trace the source of faecal contamination in surface waters. All of these methods have pros and cons that need to be taken into consideration when setting out to answer a specific question.

The field of MST has been the subject of many recent reviews^{2,3}, and the advantages and disadvantages of the existing methods have been summarised in other reviews^{1,4}. In Australia the application

of MST for understanding water quality issues has been very much restricted to the research arena and the methods have not been routinely applied in a practical sense. However, there have been a number of studies carried out in south east Queensland to answer various questions for water authorities⁵⁻⁸.

Implications for the water industry

The management, ie. regulation and legislation, of water quality totally focuses on enumerating faecal indicator organisms. Only recently some more specific pathogens or a wider group of indicator organisms have been added to the list. Water quality managers and those responsible for setting guidelines for water quality monitoring have largely lost sight of the actual pathogens.

Field and Samadpour² are sensible in their suggestion of a rational approach starting with epidemiological data that is available to identify the pathogens of concern and then use targeted pathogen monitoring, coupled with targeted faecal source tracking, to best manage water quality and public health. MST then would become a tool within a tool box that could be adapted and applied to answer specific questions. It is curious that this approach has been over sighted since the water industry in Australia and most developed countries have adopted a hazard analysis of critical control point (HACCP) approach to water quality management. MST goes a long way to identifying the critical control points in the water cycle by giving direct information about the source of the contamination.

The World Health Organization suggested that MST and analytical tools for measuring the infectivity and pathogenicity are priority research issues⁹. While the number of research papers has definitely increased since then (Figure 1), the uptake of the information in the water industry has been much slower. A drop off in the number of publications in MST in 2008 may also indicate that the interest, funding or both may not be sustainable in the research community.

Conclusion

MST has the potential to be an extremely useful tool for the management of public health for water supplies. Targeted



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risk management approaches to deal with specific sources of contamination can save on resources by reducing the pathogen load at the source through catchment management practices. Other identified advantages of tracking the origin of waterborne pathogens include: orient control activities to priority areas; managing animal presence in catchments; understanding emerging and re-emerging disease; tracking disease to source; support out-break investigations and response.

The consensus on MST by the authors and a number of our colleagues is that MST tools (including database-dependent methods) should continue to be developed, validated and utilised in a tool box approach. More importantly, the routine practice of these methods in water industry, to trace the source of human or animal faecal contamination in a catchment, should be highly encouraged. The choice of methods in such practices may vary and should be primarily based on the questions asked by water industry.

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