

MICROBIOLOGICAL EVIDENCE OF SEPTIC SYSTEM FAILURE: IS THE ON-SITE VISUAL INSPECTION ENOUGH?

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EXTENDED ABSTRACT

Faecal contamination from humans and animals is believed to be a major cause of increased microbiological and nutrient loads in coastal and inland waterways. On-site wastewater treatment systems such as septic systems, aerobic wastewater and prevent biological and nutrient contaminants from entering surface and ground waters. Such systems are common in non-sewered urban and rural residential areas. In Australia around 12% of people rely on septic systems alone. A septic system consists of a tank that provides preliminary treatment of domestic household wastes, comprising sedimentation of solids and flotation of fats and greases and a soil absorption field where final treatment including biological stabilization and pathogen removal process takes place.

Septic systems may fail and release nutrients and pathogens into the environment. The failure rate is reported to be considerably high and is believed to be more than 40% in Australia. However, the rate may vary in different communities. Septic systems are thought to be a potential source of contamination of lakes, rivers and coastal waters. Identification of major contaminating source is therefore necessary for the management of surface and ground water quality. This can be done by typing of faecal indicator bacteria such as *Escherichia coli*, and enterococci that may come from warm-blooded animals, on-site or municipal wastewater treatment systems. Several studies have identified human versus non-human sources of faecal contamination by using different typing methods. These methods, although quite discriminatory, are either laborious and/or expensive, or cannot be used for the large number of isolates involved in ecological studies.

In this study, we used a metabolic fingerprinting technique (the PhPlate system) to compare *E. coli* and enterococci strains isolated from septic tanks in Eudlo Township in the Sunshine Coast region with those found in water samples collected from upstream (6 samples) and downstream (15 samples) of two adjacent tributaries of the Eudlo Creek. An additional 7 samples were also collected from a control site located 5km upstream of the study area with a very low density of septic systems.

Of the 48 septic systems surveyed in the township, 32 (67%) tanks needed cleaning out during the survey, and 23 (72%) of these systems had soggy absorption fields. Four (8%) tanks had structural problems such as broken baffles or lids. Two (4%) systems had technical faults such as the absorption field being located close to a water bore, or the tanks were installed below the flood level. Three (6%) tanks had insufficient capacity for the household wastes, and only seven (15%) systems were found well maintained. Eventually, nine septic systems were not included because the properties were vacant during the survey and/or they were located in areas not accessible for sampling.

From each septic tank up to 3 samples were collected at different time intervals and from each sample up to 40 colonies of each indicator bacteria were typed. Strains with similar metabolic fingerprints were regarded as identical and assigned to the same biochemical phenotypes (BPTs). Phenotypic diversity (maximum 1) of enterococci (0.5 ± 0.3) and *E. coli* (0.5 ± 0.3) in septic tanks were significantly lower than those found in water samples (0.8 ± 0.1 ; $p < 0.0001$ for enterococci and 0.9 ± 0.1 ; $p < 0.0001$ for *E. coli*) indicating that surface waters receive different indicator bacteria from several sources. While some septic tanks contained strains with the identical metabolic fingerprint, each septic tank also contained unique BPTs of both faecal indicator bacteria different from those found in other septic tanks. Unique BPTs from 22 septic tanks (including 1 well maintained tank) were found in water samples. None of these unique BPTs were found in samples from the control site or in faecal samples of animals when they were compared with our recently developed databank from 9 different animal species. High similarities between the populations of both indicator bacteria were also found between septic tanks and downstream water samples further indicating the contamination of both tributaries by defective septic systems. To our knowledge, this is the first study that provides direct evidence of septic system failure by identifying identical bacterial isolates in water samples. Based on our findings, we suggest that the performance evaluation of a septic system in accordance with the established guidelines should be accompanied by direct bacterial analysis of septic tanks and water samples before a final judgement is made on septic system performance. We further conclude that the biochemical fingerprinting method used in this study can provide

additional information about the percentage and level of faecal indicator bacteria and their presence in septic systems and water samples.