



The Impact of Traditional Septic Tank Soakaway Systems and the Effects of Remediation on Water Quality in Ireland

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In Ireland the domestic wastewater of over 1/3 of the population is treated by on-site systems. These systems are based on a traditional design for disposal of domestic wastewater and rely on the surrounding subsoil for further treatment. Inefficient treatment is often associated with these systems and can cause pollution of local aquifers and waterways. The effluent nutrient load can contribute to eutrophication, depletion of dissolved oxygen and excessive algae growth in surface water bodies. Human enteric pathogens associated with faecal pollution of water sources may promote the outbreak of disease through contamination of drinking water supplies. The subsoil attenuation plays an important role in the protection of groundwater from effluent pollution. Therefore, as over 25% of the countries domestic water supplies are provided by groundwater, the protection of groundwater resources is crucial.

This project involves both the assessment of traditional septic tank soakaway systems and the effects of remediation in low permeability subsoil settings on water quality in Ireland. The study aims to confirm by microbial source tracking (MST), the source (human and/or animal) of faecal microorganisms detected in groundwater, surface water and effluent samples, and to monitor the transport of pathogens specific to on-site wastewater outflows. In combination with MST, the evaluation of nitrification and denitrification in surrounding soil and effluent samples aims to assess nitrogen removal at specific intervals; pre-remediation and post-remediation.

Two experimental sites have been routinely sampled for effluent, soil and groundwater samples as well as soil moisture samples using suction lysimeters located at various depths.

A robust and reproducible DNA extraction method was developed, applicable to both sites. MST markers based on host-specific Bacteroidales bacteria for universal, human and cow-derived faecal matter are being employed to determine quantitative target occurrence using real-time Polymerase Chain Reaction (qPCR) assays (Kildare et al., 2007). The abundance of both archaeal and bacterial 16S rRNA and of several functional nitrification and denitrification genes (i.e. *amoA*, *nirS*, *nirK*, and *nosZ*) is also being determined and compared in both sites. Ultimately, this novel project aims to assess the effectiveness of remediation at reducing the risk of pathogen transport and nitrate loading to local ground and surface waters.

Results from both sites suggest low permeability subsoil prevents the even distribution of effluent through the receiving subsoil, forcing it instead to flow laterally via distinct pathways such as sand lenses and nearby drainage routes. This affects the ability of the subsoil to sufficiently treat the percolating effluent. Initial results from the remediation of the existing systems to alternative low pressure systems indicate a positive impact towards the groundwater quality of both sites. This step towards a better understanding of the factors influencing microbial denitrification and the behaviour of pathogens in sensitive environments aids in identifying management options for reducing nitrous oxide (N₂O) emissions and nitrate (NO₃⁻) leaching; and for enhanced protection of public health.