

Characterisation of sources and pathways of microbiological pollutants to protect remote private water supplies

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In order to comply with legislation such as the Water Framework Directive and to safeguard public health, there is a critical need to maintain the quality of water sources that are used to supply drinking water. Private water supplies (PWS) are still common in many rural areas in the UK, and are especially vulnerable to poor water quality, owing to the limited treatment they often receive and variable raw water quality in groundwater and surface water sources. A significant issue affecting PWS quality is contamination by faecal pathogens derived from grazing animals or agricultural practices. In Scotland, approximately 20,000 PWS serve around 200,000 people, with a number of these PWS consistently failing to meet water quality targets relating to coliform bacteria and *E. coli*, both of which can be indicative of faecal contamination (faecal indicator organisms - FIOs).

The purpose of our study was to employ integrated empirical and modelling approaches from hydrology and microbiology to elucidate the nature of the still poorly-understood interplay between hydrological flow pathways which connect sources of pathogens to PWS sources, antecedent conditions, seasonality and pathogen transfer risk, for two catchments with contrasting land uses in Scotland: an agricultural catchment (Tarland Burn) and a montane catchment (Bruntland Burn). In the Tarland Burn, 15 years of spatially-distributed samples collected at the catchment-scale of FIO counts were analysed alongside hydrometric data to identify “hot spots” of faecal pathogen transfer risk and possible spatial and temporal controls. We also used a combination of tracer-based and numerical modelling approaches to identify the relationship between hydrological connectivity, flow pathways, and the mobilisation of faecal pathogens from different sources. In the Bruntland Burn, we coupled a pathogen storage, mobilisation and transport scheme to a previously developed tracer-informed hydrological model for the catchment to investigate temporal patterns and controls of pathogen transfer risk from different hydrological source areas identified from extensive past tracer and numerical modelling work: groundwater, hillslopes and the dynamic riparian zone.