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Modelling the mechanistic determinants of antimicrobial resistant *Escherichia coli* and *Pseudomonas aeruginosa* within private groundwater systems in the Republic of Ireland

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Antimicrobial resistant organisms and genes are now recognised as emerging water contaminants with significant potential adverse human and ecological health impacts. For example, the World Health Organisation have recently estimated that the global human health burden associated with antimicrobial infection will likely outstrip cancer mortalities by the year 2050, with >10 million deaths predicted due to these infections. The presence of antimicrobial resistant bacteria in drinking water supplies represents a particular concern due to daily associated exposures, with untreated groundwater consumption posing a substantial risk due to its unregulated nature. In the Republic of Ireland, high reliance on unregulated, private water wells and on-site domestic wastewater treatment in concurrence with a unique agricultural profile and diverse (hydro)geological settings, has resulted in the 'perfect storm' with respect to the relative ubiquity of sources and hydrological pathways for microbiological contamination, including antimicrobial resistant bacteria.

The current study sought to identify the occurrence of antimicrobial resistant bacteria in the Irish subsurface environment, and apply spatiotemporal statistical modelling to identify environmental (e.g., hydrogeological, climatic, etc.) and anthropogenic (e.g., antimicrobial use, bacterial sources, etc.) drivers, and thus hydrological mechanisms associated with this occurrence. Private (unregulated) wells ($n = 132$) in 21/26 administrative counties were assessed and temporally sampled relative to periods of varying (human and veterinary) antimicrobial usage. Samples were analysed for bacterial (*Escherichia coli* and *Pseudomonas aeruginosa*) presence and, where isolated, antimicrobial resistance profiles were quantified. Data pertaining to well location, design and condition, adjacent (< 100 m) contamination sources, groundwater vulnerability and antecedent meteorology were geospatially collated to identify resistance hotspots and associated climatic, hydrogeological and anthropogenic risk factors. Preliminary results highlight the prevalence of bacterial contamination in Irish groundwater wells; 35 (26.5%) and 8 (6%) of the 132 supplies analysed during the first round of sampling (Autumn 2019) tested positive for *E. coli* and *P. aeruginosa*, respectively. While *P. aeruginosa* (an opportunistic soil/water resident) were only found in supplies from high ($H=6.5\%$) and extreme ($E=6.5\%$; $X=14.3\%$) groundwater vulnerability

categories, *E. coli* (faecal indicator) were found across all vulnerability categories. Differences in antimicrobial resistance levels across and within these two bacterial species will be used to provide insights into hydrological contamination pathways (i.e. 'traditional' recharge, direct ingress/preferential flow, or a combination depending on hydrogeological setting). Findings will provide evidence of the extent of antimicrobial resistance in domestic groundwater supplies, and valuable insights into the hydrogeological and microbiological mechanisms governing the potential public health risks associated with untreated groundwater consumption.