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A catchment-scale model to predict spatial and temporal burden of *E. coli* on pasture from grazing livestock

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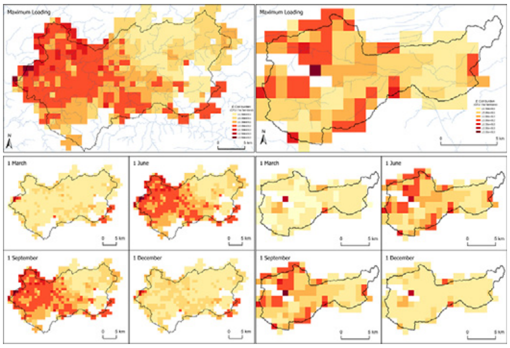
HIGHLIGHTS

- The ViPER model is applied to two contrasting catchments.
- Outputs represent spatially distributed maps of predicted *E. coli* burden to land.
- Model shows how *E. coli* burden varies by catchment type and land use composition.
- ViPER enables spatially targeted decision-making for managing *E. coli* in catchments.

GRAPHICAL ABSTRACT



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ABSTRACT

Effective management of diffuse microbial water pollution from agriculture requires a fundamental understanding of how spatial patterns of microbial pollutants, e.g. *E. coli*, vary over time at the landscape scale. The aim of this study was to apply the **Vi**sualising **P**athogen & **E**nvironmental **R**isk (ViPER) model, developed to predict *E. coli* burden on agricultural land, in a spatially distributed manner to two contrasting catchments in order to map and understand changes in *E. coli* burden contributed to land from grazing livestock. The model was applied to the River Ayr and Lunan Water catchments, with significant correlations observed between area of improved grassland and the maximum total *E. coli* per 1 km^2 grid cell (Ayr: $r = 0.57$; $p < 0.001$, Lunan: $r = 0.32$; $p < 0.001$). There was a significant difference in the predicted maximum *E. coli* burden between seasons in both catchments, with summer and autumn predicted to accrue higher *E. coli* contributions relative to spring and winter ($P < 0.001$), driven largely by livestock presence. The ViPER model thus describes, at the landscape scale, spatial nuances in the vulnerability of *E. coli* loading to land as driven by stocking density and livestock grazing regimes. Resulting risk maps therefore provide the underpinning evidence to inform spatially-targeted decision-making with respect to managing sources of *E. coli* in agricultural environments.

1. Introduction

Diffuse water pollution from agriculture represents a significant threat to the water quality and biodiversity of aquatic ecosystems

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around the world (Flávio et al., 2017). Spatially targeted decision-making and deployment of mitigation is therefore critical for effective and efficient water resource management, thus helping to reduce agricultural impacts on surface waters (Vinten et al., 2017; Greene et al., 2015). Developments in nutrient management planning and efforts to limit nitrogen (N) and phosphorus (P) export from land to water have highlighted the importance of critical source areas (CSAs), defined as zones in the landscape where high sources of nutrients coincide with high potential for hydrological transfer (Heathwaite et al., 2000). The CSA approach thus represents a powerful tool for conceptualising pollutant risk in agricultural systems and, importantly, it is not restricted to the management of nutrient pollution. Indeed, a significant proportion of surface water contamination with faecal indicator organisms (FIOs), of which *Escherichia coli* is one of the most common, can be attributed to CSAs of microbial pollution (Oliver et al., 2012).

The detection of waterborne *E. coli*, and other FIOs (such as intestinal enterococci), indicates that at some point faecal material has been delivered to the aquatic environment. This delivery can occur via diffuse inputs from agricultural or urban runoff, from point source inputs such as leaking septic tanks or sewage outflows, from the direct deposition of faeces into receiving waters from livestock, or from wildlife that commonly frequent riparian corridors, e.g. deer, birds (Neill et al., 2018; Pattis et al., 2017; Schijven et al., 2015). Much effort has focused on targeting point source inputs, given that this ‘end-of-pipe’ spatial location is often easily identifiable. In contrast, the management of diffuse and wildlife contributions of microbial pollution to receiving waters represents a more difficult challenge for the policy and regulatory community.

There are examples of national-scale screening tools and models that attempt to identify relative contributions of microbial loads from catchments under high and low river discharge, and the importance of urban versus agricultural land use (Kay et al., 2010; Palazón et al., 2017). These studies provide useful information at the national level as to where and why FIO loads are likely to be generated, and help to highlight potential areas of coastline that are vulnerable to microbial pollution from contaminated catchment discharge. However, such screening tools do not provide information on the nuances in spatial variation of where *within* a catchment FIOs are likely to originate (Dymond et al., 2016). They cannot, therefore, guide finer-scale decision-making concerning where management and mitigation should be prioritised to reduce delivery of FIOs from land to water. Clearly, this represents a different spatial scale of interest; approaches that aim to identify high-risk catchments at a national-scale, coupled with the mapping of spatial variations of relative risk across a landscape within those catchments can provide a more integrated, complementary risk assessment (Heathwaite et al., 2005).

The first step in pinpointing potential CSAs of diffuse microbial water pollution associated with grazing ruminant livestock is the spatial identification of high FIO sources (e.g. *E. coli*) on pasture, hereafter termed burden. The overall burden of *E. coli* derived from grazing activity is governed by the number and type of livestock, and their associated faecal excretion rates and *E. coli* shedding potential (Coffey et al., 2016). In addition, the grazing duration will dictate the rate of replenishment of fresh faeces and associated *E. coli* content to pasture. Post defecation, the concentration of *E. coli* is influenced by a number of environmental factors (Tian et al., 2002), e.g. temperature, UV irradiance and rainfall, which can directly moderate the moisture content of the faecal habitat and indirectly impact on availability of nutrients within the faecal matrix (Oliver and Page, 2016). Ultimately, the coupling of spatial patterns of *E. coli* burden hotspots with an understanding of the likelihood of cell mobilisation from faeces following rainfall and their onward hydrological transfer through the catchment is an essential pre-requisite to enable identification of grazed pasture most vulnerable for contributing diffuse microbial pollution to water (Oliver et al., 2010).

The development of a catchment-scale model of *E. coli* burden is therefore required to map spatial patterns of *E. coli* accumulation on land, but can be challenging given the potential variability in rates of faecal excretion and *E. coli* shedding across and within livestock types. Others have avoided this issue by attributing a set value of *E. coli* shedding per livestock unit, with no differentiation of *E. coli* content or die-off associated with different livestock types (Tian et al., 2002). However, logical structuring of a simple empirical model accounting for differential *E. coli* behaviour by livestock type, which can be applied spatially, will provide a first approximation of relative risk of *E. coli* accumulation across agricultural catchments. In response, the overall aim of this study was to evaluate the recently developed **Vi**sualising **P**athogen & **E**nvironmental **R**isk (ViPER) model, which was created to predict *E. coli* burden on agricultural land (Oliver et al., 2017). The objectives of this study were to: (i) apply the ViPER model in a spatially distributed manner to two contrasting catchments where livestock numbers were known to represent relatively high and low grazing densities; and (ii) use outputs from the model to explore where, when and why *E. coli* burden varies within these two contrasting catchments, thus demonstrating value to catchment managers.

2. Materials and methods

2.1. Case study catchments

To demonstrate the potential of the ViPER model to operate in a spatially distributed manner, we selected two contrasting test catchments in Scotland (Fig. 1) where knowledge and understanding of agricultural practices are relatively well reported (Aitken, 2003; Vinten et al., 2017). The River Ayr and the Lunan Water catchments were selected because they represent different and distinct agricultural regions, and both have designated EU bathing waters at the catchment outlet. The spatial

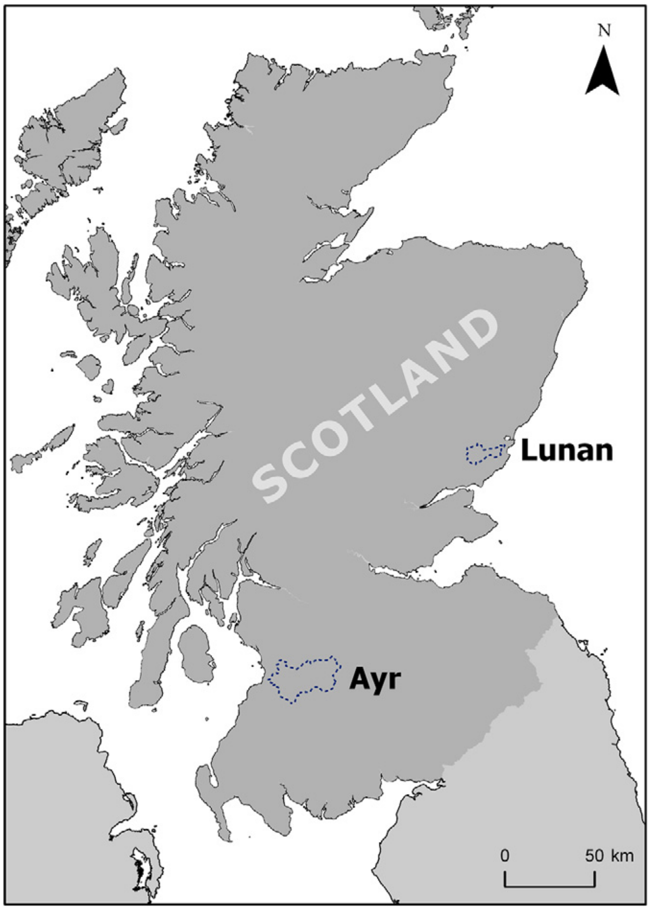

Fig. 1. Spatial locations of the River Ayr catchment and the Lunan Water catchment in Scotland.