



# Model of pathogen transmission between livestock and white-tailed deer in fragmented agricultural and forest landscapes



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## ABSTRACT

The study summarizes the current knowledge on infection and recovery of white-tailed deer and cattle, and integrates this knowledge into the Soil and Water Assessment Tool (SWAT) via a new add-on module SIR (Susceptible - Infected - Recovered) for predicting pathogen transmission between livestock and deer. New processes modeled by the SWAT-SIR model include: (a) seasonal changes in deer population and habitat; (b) resource selection and seasonal changes in foliage consumption by deer; (c) ingestion of pathogens with water, foliage and via grooming soiled hide by deer and grazing cattle; (d) infection and recovery of deer and co-grazing cattle; (e) pathogen shedding by infected animals; (f) survival of pathogens in manure; (g) kinetic release of pathogens from applied manure and fecal material. The model output is linked with ARC-GIS to allow spatial and temporal analysis of pathogen distribution across the watershed for specific land use, weather and management scenarios.

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## Software and/or data availability

The SWAT-SIR module with example of SWAT ARC GIS project can be obtained from the first author upon request.

## 1. Introduction

Manure-borne pathogens such as *Escherichia coli* O157:H7, *Salmonella*, *Campylobacter* and *Cryptosporidium* have become a subject of growing concerns due to continuous water body impairment causing increased number of waterborne disease outbreaks in the United States and Canada (Besser et al., 1993; Cieslak et al., 1993; Jackson et al., 1998). In 2014, the U.S. Environmental Protection Agency reported 3451 impaired water bodies in the United States based on *E. coli* monitoring (U.S. EPA, 2014). Livestock is commonly considered among the major sources of fecal contamination (Jones, 1999; Chapman, 2000; Gallagher et al., 2012) with cattle as a principal reservoir of *E. coli* O157:H7 (Borczyk et al., 1987; Ørskov

et al., 1987; Zhao et al., 1995). However, in fragmented agricultural and forest landscapes, wildlife can also serve as a reservoir for pathogens, thus contributing a considerable portion of the fecal pollution (Daszal et al., 2000; Ishii et al., 2007; Parajuli, 2007; Harmel et al., 2010). Several recent *E. coli* O157:H7 outbreaks were associated with deer. Specifically, 15 illness cases, including two deaths in Oregon in July–August 2011 were caused by strawberry-transmitted infection of *E. coli* O157:H7 produced by black-tailed deer (Laidler et al., 2013). Consumption of unpasteurized apple juice caused infection of at least seventy people by *E. coli* O157:H7 in the western United States and British Columbia, Canada, in October 1996. This outbreak of *E. coli* O157:H7 infection was suspected to be associated with apples coming from orchards frequented by deer (Cody et al., 1999). Since *E. coli* O157:H7 is spread via a fecal-oral route and both cattle and deer may harbor this pathogen, there is a possibility for the pathogen transmission between the two groups of animals through exposure to contaminated water and foliage (Branham et al., 2005). This possibility was supported by the results of Rice et al. (1995), Sargeant et al. (1999), and Renter et al. (2001) who isolated *E. coli* O157:H7 from feces of white-tailed deer co-grazing with cattle.

Multiple outbreaks associated with deer have prompted enhanced research of possible interaction and pathogen transmission between co-grazing domestic and wild animals (Rice et al.,

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1995; Sargeant et al., 1999). Lejeune et al. (2001) showed that calves could become colonized with *E. coli* O157 after drinking from water sources that were fecally contaminated 183 days earlier. Branham et al. (2005) concluded that white-tailed deer could potentially become infected by *E. coli* O157:H7 and *Salmonella* spp. via consumption of water from cattle troughs, and conversely spread the pathogens to livestock and other wildlife.

Modeling is commonly used to evaluate risk of surface water contamination by fecal bacteria. Several models have been recently used to predict fate and transport of manure-borne bacteria produced by livestock and wildlife at the watershed scale. For example, Hydrological Simulation Program—FORTRAN (HSPF) (Bicknell et al., 1997) was used to simulate total and source-specific contributions of fecal coliform bacteria to instream load from domestic and wild animals by Yagow et al. (2001), Moyer and Hyer (2003), Benham et al. (2006), Chin et al. (2009), and other studies. Soil and Water Assessment Tool (SWAT) (Sadeghi and Arnold, 2002; Neitsch et al., 2005) was used for bacteria source tracking by Baffaut and Benson (2003), Parajuli (2007), Parajuli et al. (2009), Coffey et al. (2010), Frey et al. (2013), and for predicting *E. coli* and fecal coliform concentrations in stream water by Baffaut and Sadeghi (2010), Kim et al. (2010), Cho et al. (2012), Iudicello and Chin (2013), and Jayakody et al. (2013). A relatively simple tool for bacteria source characterization, BSLC (Bacteria Source Load Calculator), was developed by Zeckoski et al. (2005) to characterize the bacteria sources and loads for development of the TMDL (Total Maximum Daily Load) allocation scenarios. TMDL is a program established by U.S. Environment Protection Agency (EPA) in 1992 in response to Clean Water Act of 1972 describing the maximum amount of pollutants that a body of water can receive while still meeting water quality standards. Dorney et al. (2006) coupled a microbial fate and transport model with the WATFLOOD/SPL9, a watershed hydrology modeling system, to determine the primary sources of pathogenic contamination in a watershed in Southwestern Ontario, Canada. Ferguson et al. (2007) developed a process-based mathematical model PCB (pathogen catchment budgets) to predict *Cryptosporidium*, *Giardia* and *E. coli* loads generated within and exported from drinking water catchments and applied this model for the Wingecarribee catchment located approximately 200 km south west of Sydney, Australia. Park et al. (2014) recently extended the Agricultural Policy/Environmental eXtender (APEX) model to predict microbial fate and transport at farm and small watershed scales.

Different approaches to modeling pathogen transport and risk assessment were further developed in an Integrated Environmental Modeling Framework (IEM) (Whelan et al., 2014).

Current microbial transport models were developed for indicator organisms of fecal contamination and bacterial impairment of watersheds. The most commonly tested fecal bacteria indicators such as total coliforms, fecal coliforms, *E. coli*, fecal streptococci, and enterococci are relatively harmless. They indicate possibility of presence of pathogenic microorganisms, though the concentrations of the pathogens themselves are generally unknown. To extend the existing models to predict pathogen transport and assessment of pathogen water contamination, the models must include the mechanisms and processes of pathogen transmission within the same groups of animals as well as between different groups. These mechanisms are not well studied and information about pathogen transmission between animals is scarce. Moreover, infection and pathogen shedding by domestic and wild animals depend on different environmental factors that are difficult to account for due to their high spatial and temporal variability.

In this study we (i) summarized the current knowledge on infection and recovery of white-tailed deer and cattle, and (ii) integrated this knowledge into the SWAT model via a new add-on module SIR (Susceptible - Infected - Recovered) which can predict

pathogen transmission between livestock and deer. We demonstrated the SWAT-SIR features that can be helpful for analyzing pathogen sources and for development of better management practices for reducing pathogen loads on fragmented agricultural and forest landscapes.

## 2. Materials and methods

### 2.1. Theory

#### 2.1.1. Modeled processes and structure of the SIR module

As the basis for the development of our new SIR module, we used SWAT model. The SWAT software is frequently used to model bacteria fate and transport at a watershed scale, has a well-developed graphical user interface linked to ArcGIS (ESRI® ArcGIS™), and supports commonly used soil (SSURGO, NRCS) and land-use (NLCD2006) databases. Modified version of the SWAT2012 software (Kim et al., 2010) includes following bacterial processes:

- bacteria deposition on soil and foliage with applied manure or with fecal material of grazing animals;
- bacteria die-off/re-growth in soil, water and on foliage; bacteria wash-off from soil and foliage;
- bacteria leaching from soil; bacteria subsurface, overland and instream transport;
- bacteria deposition to and resuspension from streambed sediment.

This version of SWAT software was developed further to predict transmission of *E. coli* O157:H7 between livestock and grazing white-tailed deer. New add-on module SIR includes the processes shown in Fig. 1. A brief description of the modeled processes and SIR structure can be found in Guber et al. (2014). Here we present a complete description of the SIR module that includes governing equations, model parameters and simulation results.

Pathogens can be ingested by co-grazing cattle and deer with water, foliage and via grooming soiled hide and can cause animal infection (Fig. 1). The SIR module implements a dose–response approach to compute the probability of animal infection based on the ingested daily dose of pathogens. It is assumed that the infected animals shed pathogens at grazing areas in the amounts proportional to fecal material produced daily until their full recovery. The shed pathogens can grow, die-off in fecal material, and/or be

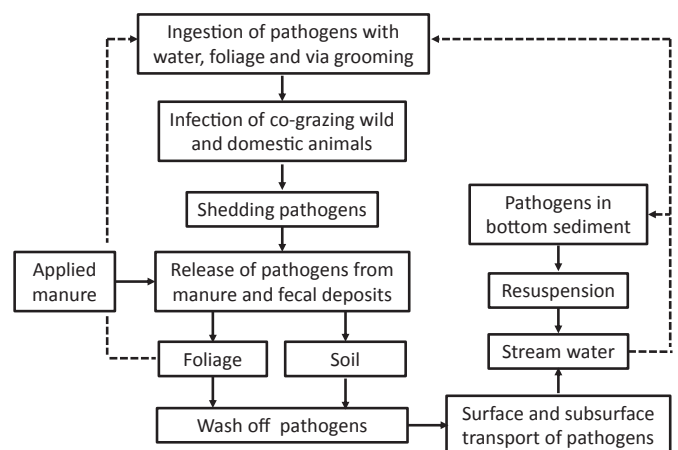


Fig. 1. Mechanism of pathogen transmission in the Susceptible - Infected - Recovered (SIR) add-on module.

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