

# SWAT-SIR Model for Predicting Fate and Transport of Manure-borne Pathogens in Fragmented Agriculture-Forest Ecosystems

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**Abstract:** The objective of this study was to develop and qualitatively evaluate a model predicting transmission of manure-borne pathogens between co-grazing cattle and wildlife. The developed add-on module SIR that we coupled with SWAT model included the following new components: wildlife population changes, resource selection, dose-response, compartmental susceptible-infectious-recovered (SIR) module and pathogen shedding. Probabilities of the wild and domestic animal infection by pathogens and numbers of infected animals were computed based on a dose-response approach, which included beta-Poisson and exponential models. Land use and plant biomass predicted with watershed-scale model SWAT were used as the input for the deer resource selection and foliage consumption. Pathogen shedding by wild and domestic animals was computed in the add-on module SIR based on the number of infected animals, daily shedding rates and duration of grazing. The developed model was implemented to define scenarios and identify mechanisms of *E.coli* O157:H7 transmission between co-grazing white-tailed deer and cattle for a small watershed. Introducing SIR component into SWAT model allowed prediction of increasing *E.coli* O157:H7 load on farmlands in spring and summer months as a result of increasing numbers of infected cattle and deer. This increase can potentially be caused by the infection spreading among cattle due to grooming as well as deer infection by pathogens ingested with foliage after surface manure application or released to foliage from cattle fecal deposits. The model output linked with ARC-GIS allowed spatial and temporal analysis of pathogen distribution across the watershed for specific weather and management scenarios. Overall, the developed SWAT-SIR model is a useful tool for assessment of pathogen transport and for development of better management practices in mixed agriculture-forest ecosystems.

**Keywords:** *Watershed scale, pathogen transport; domestic-wildlife interaction.*

## 1. Introduction

Manure-borne pathogens such as *E. coli* O157:H7, *Salmonella*, *Campylobacter* and *Cryptosporidium*, have become of increasing concern due to continuously increasing number of waterborne disease outbreaks in the United States and Canada (Besser et al., 1993; Cieslak et al., 1993; Jackson et al., 1998). Multiple outbreaks have prompted enhanced research of possible interaction and pathogen transmission between co-grazing domestic and wild animals (Rice et al., 1995, 2003; Sargeant et al., 1999). McGee et al. (2002) have shown that *E. coli* O157:H7 could survive in field water for 14 days at temperatures over 15°C and calves could become colonized with *E. coli* O157 after drinking from water sources fecally contaminated 183 days earlier (LeJeune et al., 2001). Branham et al. (2005) concluded that wildlife consuming water from cattle troughs could potentially become infected with the bacteria, and conversely spread the bacteria to livestock and other wildlife.

Several models have been recently used to predict bacteria fate and transport originated from livestock and wildlife at watershed scale. Among such models are Hydrological Simulation Program-FORTRAN (HSPF) (Bicknell et al., 1997), and Soil and Water Assessment Tool (SWAT) (Sadeghi and Arnold, 2002; Neitsch et al., 2005). Moyer and Hyer (2003) used HSPF model to simulate source-

specific contributions of fecal coliform bacteria to instream load from beaver, cats, cattle, deer, dogs, ducks, geese, horses, humans, muskrats, poultry, raccoons, and sheep for Christians Creek watershed in Virginia. Coffey et al. (2010) analysed the effects of various source scenarios on pathogen outputs in Irish catchments using SWAT model. Different approaches to modeling pathogen transport and risk assessment found their further development in an Integrated Environmental Modeling Framework (IEM) (Whelan et al, 2014).

The deficiency of existing pathogen transport models risk assessment tools that may result in a low predictive accuracy and high uncertainty is that the pathogen loads are generally unknown and vary appreciably in time and space. This partly occurs due to the lack of accounting for interactions and pathogen transmission within grazing animals and between co-grazing wildlife and domestic animals. It is generally assumed that distributions of ill animal across habitat are known and concentration of pathogens in the shed fecal material is constant. Absence of a mechanism of pathogen transmission between grazing animals in the models may result in inaccurate predictions of pathogen fate and transport particularly in fragmented agriculture-forest ecosystems, where the abundance of grazing wild animals is prone to seasonal changes depending on many factors, e.g. forage availability, predation, hunting, etc. This abundance in turn affects probability of animal interaction, disease transmission and pathogen shedding by ill animals. The seasonal habitat of wild animals may also vary from year to year depending on interannual weather variability and farm management practices. Therefore there is a need for accounting for pathogen transmission between co-grazing domestic and wild animals in temporally and spatially variable wildlife habitats in order to achieve reliable pathogen risk assessments and development of better management practices.

The objective of this study was to develop an add-on module that predicts pathogen transmission between co-grazing wild and domestic animals. During module development special attention was paid to: (i) seasonal variations in habitat and abundance of wild animals; (ii) pathogen transmission with water, forage and via grooming; (iii) animal infection and recovery; and (iv) pathogen shedding, survival and transport.

## 2. Materials and Methods

### 2.1 Modeled processes and structure of the SIR module

Modified version of SWAT2012 (Kim et al., 2010) was used as a main process-based model in this study, since it has well developed interface; it is linked to ArcGIS (ESRI® ArcGIS™); and it supports commonly used soil (SSURGO, NRCS) and land-use (NLCD2006) databases. SWAT model includes following bacterial processes:

- deposition on soil and foliage by grazing animals and manure fertilization;
- die-off/re-growth in soil, water and on foliage;
- wash-off from soil and foliage;
- leaching from soil;
- subsurface, overland and instream transport;
- bacteria resuspension from streambed sediment.

An add-on module SIR (Susceptible - Infected - Recovered) was developed and coupled with SWAT to improve the model's capacity in predicting pathogen fate and transport in fragmented agriculture-forest ecosystems, where ignorance of interaction between wildlife and domestic animals may lead to considerable underestimation of pathogen load on steams and farm lands. New add-on module includes processes shown in Fig.1. Infection of co-grazing domestic and wild animals occurs through pathogen ingestion with water, foliage and via grooming soiled hide. A dose-response component of the SIR computes the probability of animal infection based on the ingested daily dose of pathogens. The infected animals shed pathogens at grazing area until full recovery. These pathogens can grow, die-off, and be released into the soil and foliage with rainfall water. Initiated runoff can wash pathogens off the soil, manure, and fecal deposits and transport them toward surface water. During high flow events survived microorganisms can be resuspended from the bottom sediment and be transported with stream water to tributaries of higher order. Pathogens in the stream can be ingested by domestic and wild animals in pathogen free areas and potentially cause animal infection and further pathogen spreading.

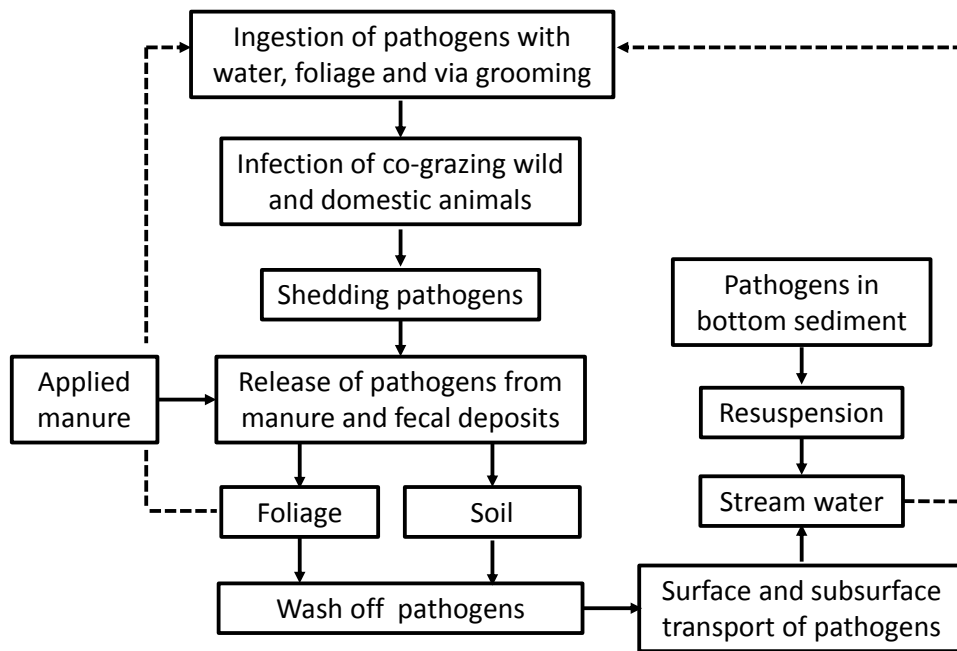


Figure 1. Modelled processes and structure of the SIR module

New processes considered in SIR module include:

- seasonal changes in wildlife population and habitat;
- resource selection and seasonal changes in foliage consumption;
- ingestion of pathogens with water, foliage and via grooming soiled hide;
- infection and recovery of co-grazing wild and domestic animals;
- pathogen shedding by infected animals;
- survival of pathogens in manure;
- kinetic release of pathogens from applied manure and fecal material.

These processes are coupled with the processes simulated in SWAT2012 to produce daily values per unit area of hydrological response units (HRUs) and subbasins, which are defined in SWAT as groups of HRUs bordering the same stream:

- number of infected animals;
- number of pathogenic and nonpathogenic cells ingested and shed by wild and domestic animals;
- number of non-pathogenic and pathogenic cells in soil, on foliage and in runoff water;
- total number of non-pathogenic and pathogenic cells transported with overland and subsurface flow from each HRU to streams;
- instream concentrations of non-pathogenic and pathogenic cells.

Results of SWAT-SIR simulations transferred to SWAT database using a standalone postprocessor can be used for further spatial analysis in ArcGIS. Another option for data visualization is transferring results in ASCII format into any standard software that supports graphical analysis.

## 2.2 Population dynamics and pathogen transmission between animals

The population component of the add-on SIR module describes seasonal changes in wildlife abundance at each subbasin. The changes are modeled using forcing functions that account for birth ( $b$ ), recruitments ( $r$ ), and mortality ( $d$ ) caused by diseases, predation, hunting, accidents, and etc. (Fig. 2). These functions and their parameters may be specific for the modeled species and geographic area of their distribution, and can potentially be affected by the modeled pathogens.

A three-compartment SIR model (Keeling and Rohani, 2008) was implemented in the add-on module to predict infection and recovery of co-grazing wild and domestic animals. Infection of a susceptible group of animals ( $S$ ) occurs through water and foliage consumption with probability computed using a

dose response-model. Two dose-response models are currently used in the add-on SIR module, i.e. exponential and beta-Poisson model (Haas et al., 2000). Fraction of susceptible animals  $\beta$  computed based on the daily dose of ingested pathogens constitutes the infected group of animals ( $I$ ), the fraction that recovers at a daily rate  $\alpha$  constitutes the Recovered group ( $R$ ). Transition of recovered animals  $R$  into the group  $S$  occurs at a daily rate  $w$ . Infected animals shed pathogens at rates specific for species, gender, age, season and ranging conditions, but constant during the whole infection period of time. Generally, the pathogen content in feces of infected animals tends to decrease over time, but it appeared impractical to simulate the infection and recovery of each animal at subbasin scale.

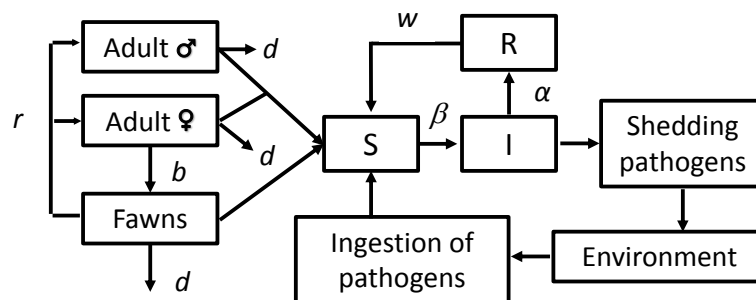


Figure 2. Wildlife population changes, infection and recovery in SIR add-on module

The pathogens shed into environment can be released with precipitation from the fecal deposits and survive on foliage, in soil and water. Daily ingestion of pathogens by domestic and wild animals is proportional to water and foliage consumption, fecal material groomed from soiled hide, and pathogen content in the consumed products in the add-on module. The foliage consumption for domestic animals is defined by the grazing time at a range land, while for wildlife it is computed as a sum of foliage consumed at farm, range, and forested areas as well as lawns or gardens at residential areas on daily basis. Fractions of days that wild animals spend at each area are computed from odds ratios that indicate the prevalence of different food sources in the daily foliage consumption. The odds ratios specific for wildlife species, season, and geographical area of distribution should be estimated based on monitoring or publically available data prior to simulations.

### 2.3 Bacteria survival and release from fecal material and applied manure

The existing bacteria survival component of SWAT was extended to model growth and die-off of bacteria in fecal deposits and in applied manure. Bacteria growth/die-off was modeled using Chick's first order decay equation with manure- and feces-specific parameters modified for temperature similarly to SWAT model.

Release of nonpathogenic and pathogenic bacteria from applied manure and fecal material deposited by domestic and wild animals was modeled using Bradford-Schijven (2002) equation with modifications of Guber et al. (2013). The release model was implemented for daily time step based on daily precipitation and accumulated mass of fecal deposits.

### 2.4 Model implementation to a fragmented agriculture-forest watershed

The developed add-on SIR module for SWAT software was implemented to estimate the hypothetical impact of *E. coli* O157:H7 transmission between livestock and white-tailed deer on pathogen spread at the Little Cove Creek watershed located in Franklin County, Southern Pennsylvania. Land-use within the 75.2 km<sup>2</sup> watershed includes forest (74%), hay (15.6), pasture (6.5%) and urban lands (3.8%). SWAT model has been calibrated on data of *E. coli* instream monitoring at three sites located along the watershed with contribution areas of 18.8 km<sup>2</sup>, 36.8 km<sup>2</sup>, and 68.0 km<sup>2</sup>, respectively (Kim et al., 2010). We used SWAT parameters obtained by Kim et al. (2010) authors to model overland, subsurface, and instream transport of total *E. coli* and *E. coli* O157:H7.

New model parameters for the add-on SIR module were estimated from our previous studies and publically available data. There are several sources for estimating deer abundance, i.e. annual censuses of the deer herd conducted by the U.S. Fish and Wildlife Service (USFWS), the State Departments of Natural Resources, the State Departments of Game and Fish, and Quality Deer Management Association (QDMA). The initial abundance was set to 2 heads per ha of deciduous forest in our simulations and then changed in time as a result of birth, recruitment and mortality. The parameters of the forcing functions describing birth, recruitment and mortality were estimated from deer population monitoring conducted in central New York.

SWAT-SIR simulations were conducted for weather conditions of 2007 with the total amount of precipitation of 669 mm. Solid and liquid manure was applied in spring on hay fields adjacent to two dairy facilities at rates of 48 and 3 ton/ha, respectively. All pasture lands received 14 ton/ha of solid manure. *E. coli* O157:H7 constituted 1% of total *E. coli* content in the applied manure in the simulations. Grazing season started when biomass of the foliage was sufficient to provide food for cattle density of 4 head/ha. In the cattle herd 4% of animals were shedding *E. coli* O157:H7 at the beginning of the grazing season. Values of parameters in the dose-response models (Haas et al., 2000) for cattle and deer infection by *E. coli* O157:H7 are generally unknown. Therefore three hypothetical infection and recovery scenarios were considered in this study that included: (a) epidemic, (b) gradual increase in numbers of infected animals (b), and recovery (c). These scenarios were set by different values of the dose of *E. coli* O157:H7 that would infect 50% of the exposed animals. The dose was the smallest for the epidemic scenario and the largest for the recovery scenario.

### 3. RESULTS AND DISCUSSION

Simulated deer abundance changes at the watershed had a seasonal trend with the maximum value in June due to new fawns birth, and the minimum in spring as a result of hunting and winter starvation (Fig. 3). Overall, does dominated in deer populations in the course of the year followed by fawns. The summer increase in deer abundance corresponded to grazing season of cattle and the prevalence of deer grazing on hay fields and pastures. The changes in habitat and population increased probability of deer infection by the pathogens released from the applied manure and fecal material deposited by infected cattle on pastures. Figure 4 illustrates hypothetical infection of deer by *E. coli* O157:H7 at a pasture. The first peak in the deer infection occurred at 130 DOY and was associated with the manure application on the pasture. The second peak occurred at 166 DOY and was caused by *E. coli* O157:H7 ingestion with the foliage contaminated by co-grazing cattle. This peak was more pronounced for the cattle epidemic scenario (Fig. 4a) as compared to the scenario with a gradual increase in the number of infected animals (Fig. 4b) and the cattle recovery scenarios (Fig. 4c). Among deer groups the percentage of infected does was the highest during the first infection period (131 DOY), while the percentage was the highest for fawns during the second infection period (166 DOY). These percentages were consistent with the seasonal changes in the deer population shown in Fig. 3.

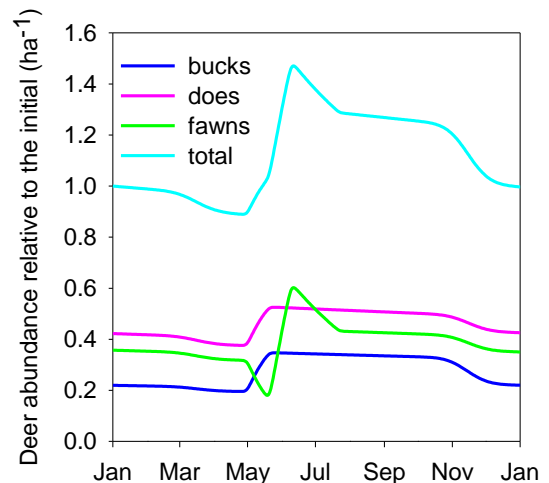


Figure 3. Seasonal changes in deer population

Interestingly, *E. coli* O157:H7 in the applied manure did not infect the cattle that started grazing two weeks after the manure application. That occurred due to bacteria die-off in manure and on foliage as well as bacteria wash off the foliage by rainfall water. Both processes resulted in a decrease in the pathogen content below the infection level. The simulated number of *E. coli* O157:H7 cells shed by the cattle was from 3 to 5 orders of magnitude greater than that shed by deer. This difference was less for the recovery scenario (Fig. 5c) and the highest for the cattle epidemic scenario (Fig. 5a). Relatively low loads of *E. coli* O157:H7 were attributed to lower deer abundance on pastures, and smaller mass of deer fecal deposits compared to the cattle. The number of infected deer affected the

pathogen loads but concentrations of *E. coli* O157:H7 produced by deer were too low to infect co-grazing cattle.

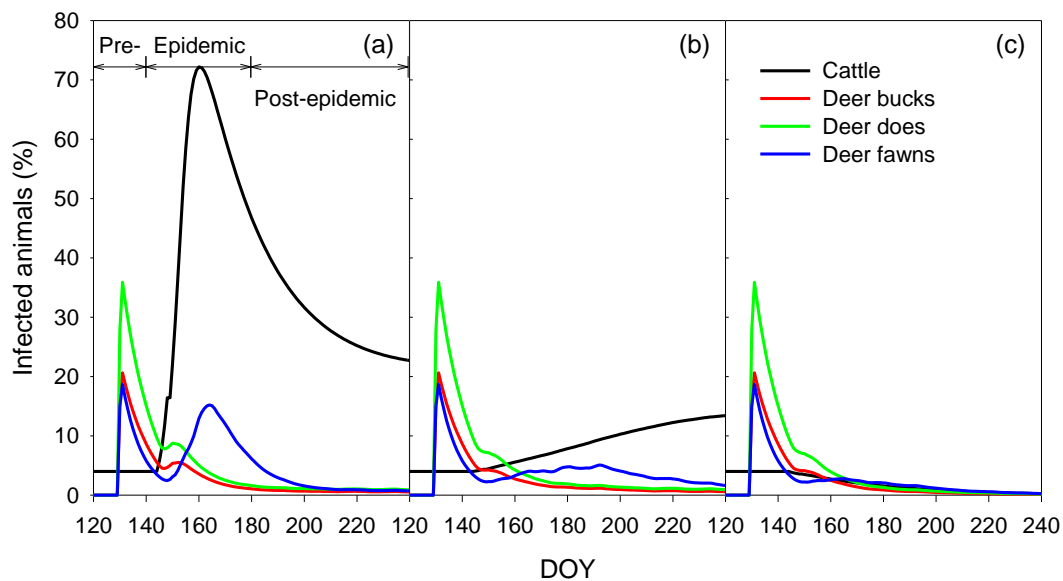


Figure 4. Simulated temporal dynamics of co-grazing cattle and deer infected by *E. coli* O157:H7 for cattle epidemic (a), gradual increase in the number of infected animals (b), and the recovery (c) scenarios. Note percentage for deer shows the ratio of infected animals within each group to the total deer population.

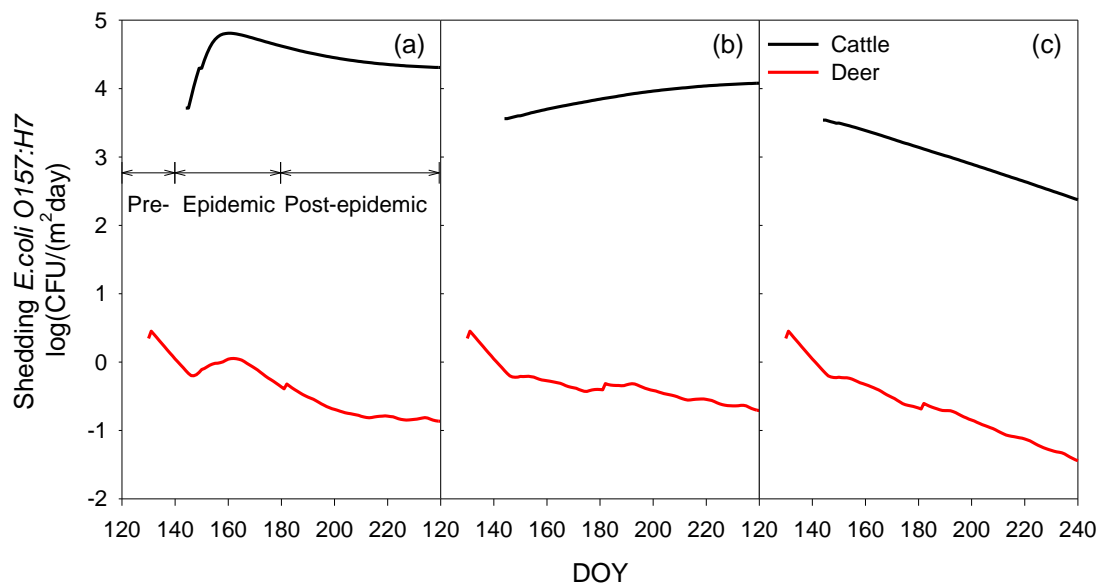


Figure 5. Simulated temporal dynamics of *E. coli* O157:H7 shedding by infected co-grazing cattle and deer for cattle epidemic (a), gradual increase in the number of infected animals (b), and the recovery (c) scenarios.

Grooming appeared to dominate in the *E. coli* O157:H7 ingestion by cattle, while foliage consumption was a major cause of deer infection. This modeling result was partly due to scarce information about deer grooming and particularly manure presence on deer hide. Therefore deer grooming was not considered in the simulations. Grooming by cattle was also neglected in the recovery scenario (Fig. 6c). Overall, the results of the simulations indicated that infection of co-grazing deer and cattle by *E. coli* O157:H7 is unlikely through water consumption, less probable through foliage consumption for cattle and is most probable through foliage consumption for deer and via grooming for cattle for the three simulated scenarios.

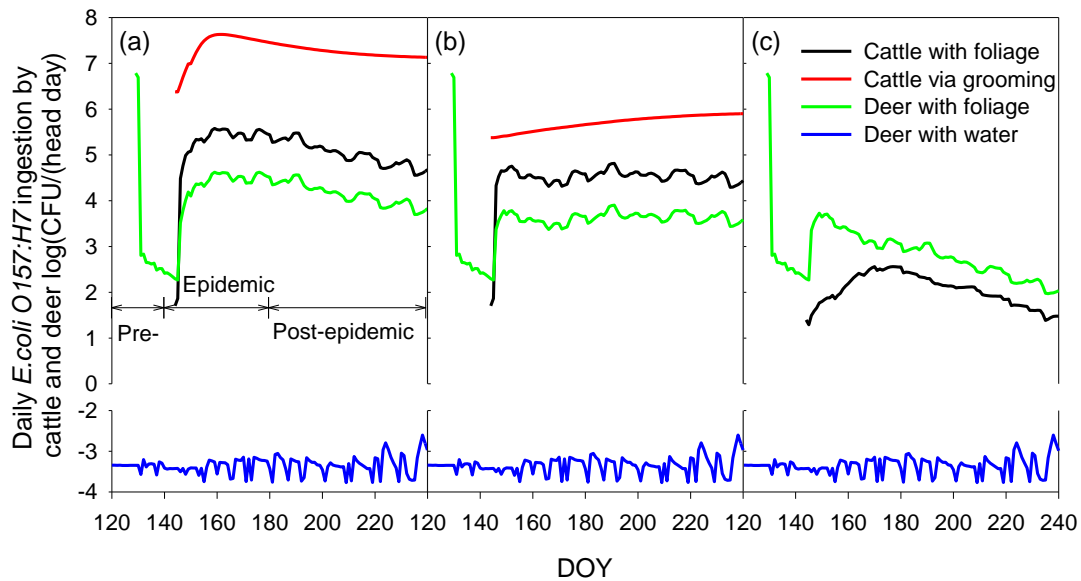


Figure 6. Ingestion of the *E. coli* O157:H7 by co-grazing cattle and deer simulated for three scenarios: cattle epidemic (a), gradual increase in the number of infected animals (b), and the recovery (c).

#### 4. CONCLUSIONS

Developed add-on module SIR for SWAT model is a useful tool for analysis of pathogen transmission between co-grazing cattle and white-tailed deer. Results obtained for the three studied scenarios, namely epidemic, gradual increase in the number of infected animals, and the recovery of grazing cattle, revealed seasonal trends in the cattle and deer infection by *E. coli* O157:H7 associated with spring manure application and sharing pasture by deer and cattle in summer months. Grooming appeared to be a major infection mechanism for cattle, while pathogen ingestion with foliage caused most deer infections in this study. Obtained results are likely specific to the species and scenarios considered in this study, however including processes of pathogen transmission and including wildlife interaction with livestock into a process based model of pathogen fate and transport opens a broad avenue for predicting impact of such interaction on water quality and pathogen contamination of crops, e.g. leafy greens in fragmented agriculture-forest ecosystems.

#### 5. ACKNOWLEDGMENTS

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