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Transport and fate of manure-borne pathogens: Modeling perspective

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ABSTRACT

Among other constituents, manure contains pathogenic microorganisms that can cause serious illness and death in humans. The objective of this work is to review the status and challenges in modeling fate and water transport of manure-borne pathogens (MBP) and organisms-indicators of fecal contamination at pedon, hillslope, and watershed scales. Approaches used to model various aspects are critically evaluated, including (a) release of microorganisms from manure, (b) microorganism survival and inactivation in manure, soil, and surface water, (c) partitioning and attachment of pathogenic and indicator organisms to solid particles in runoff, soil, and sediment, and (d) transport with straining or entrapment in overland flow and in streams. The current challenges and research needs are outlined that include (a) the paucity of experimental data about the transport of pathogenic micro-organisms, (b) the need to quantify potential and actual input of pathogens from wildlife, (c) uncertainty in background concentrations of indicator microorganisms, (d) better under-standing of the effect of manure particulates on the MBP fate and transport, (e) relating the microorganism fate and transport parameters to environmental variables, such as soil and vegetation properties and weather parameters, (e) evaluating natural tracers with the transport behavior similar to microorganisms, e.g., manure-borne phosphorus, (f) under-standing the uncertainty of the stream sampling data, (g) developing a process-based model of microorganism resuspension during the rainfall events, (i) developing upscaling techni-ques to utilize pedon and hillslope scale measurements and models in the watershed modeling, (j) a better insight into filtering function of vegetated buffer strips and riparian zones. Ensembles of simulations have to be made to estimate the possible distribution of simulation results and risks associated with a specific allocation of manure and manure management practices.

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1.   Introduction

The best estimate of total amount of agricultural animal manure produced in the World is anywhere between 10^{10} and 10^{11} tons annually (Fayer and Trout, 2005). Manure abundance brings a mixed blessing for humanity, being an important source of plant nutrients and energy if used properly, but causing substantial pollution of water or produce if managed improperly. Pathogenic microorganisms that are found in manure can cause serious illness and death in humans (Cotruvo et al., 2004). By the frequency of being the cause of water quality impairment, pathogens rank first and second among five leading pollutants in estuaries and rivers, respectively, in the United States (EPA, 2004).

The major manure-borne pathogens (MBP) are bacteria, such as *Campylobacter*, several strains of *Escherichia coli*, *Listeria monocytogenes*, *Salmonella*, *Yersinia enterocolitica*; and protozoa *Cryptosporidium parvum* and *Giardia*. Many other MBPs exist, however, they are less common. The infectious doses of bacterial pathogens vary widely; for example, the infectious dose for enterohemorragic *E. coli* is estimated to be as few as 10 cells, 500 cells for *Campylobacter*, 10^5 for *Salmonella*, as high as 10^8 for some strains of pathogenic *E. coli*. The infectitious doses are much smaller for protozoa: less than 10 organisms for the *C. parvum* and 10–25 for *Giardia*. Massive disease outbreaks have been caused by MBPs, the most notable being in Milwaukee when more than 400,000 persons were infected with *Cryptosporidium* oocysts via the public water supply (MacKenzie et al., 1994).

Size and shape, density, surface properties, and biological activities of pathogenic microorganisms set them uniquely apart from other contaminants that are transported in surface and subsurface water environments. Pathogenic microorganisms have sizes in the range of fine silt particles and only slightly exceed the 1 μm threshold value defining colloidal particles, and the 2 μm threshold value defining clay particles. Pathogenic bacteria are usually rod-shaped with a length between 2 and 6 μm, and a width from 0.5 to 2 μm. *C. parvum* oocysts are typically almost spherical with diameters mostly within the range from 2 to 6 μm. *Giardia lamblia* oocysts are ellipsoidal with typical numbers of moderate eccentricity between 1.1 and 1.5 and a large diameter of between 9 and 15 μm (Medema et al., 1998). The density of pathogenic microorganisms is very close to the density of water, and mostly varies between 1.01 and 1.07 g cm^{-3}. The organisms are suspended rather than dissolved in water. Most pathogenic microorganisms have a low net negative surface charge over a wide range of pH values; therefore, charge-based attachment to negatively charged soil, sediment, or rock surfaces is likely to be hindered. However, for the same reason, microorganisms and protozoa oocysts can approach a positively charged inorganic surface and establish specific chemical interactions, which may be beneficial for survival. For example, outer walls of *C. parvum* oocysts contain glycoproteins that promote adhesion to inorganic surfaces (Nanduri et al., 1999). Bacteria adhering onto a surface frequently secrete extracellular polymeric materials in order to attach themselves to the surface. Another behavioral pattern of many bacteria is motility, i.e., the ability to move using the viscous drag in water in search of more favorable conditions (Berg, 2000).

MBPs are released to the environment along with manure particles that can serve as carriers, abode, and food for microbes. Manure has been reported to enhance the transport of microorganisms in soils (Gagliardi and Karns, 2000; Guber et al., 2005a). In the presence of manure colloids, MBP transport becomes colloid-facilitated, as evidenced by similar breakthrough for manure particulates and *E. coli* in soils (Shelton et al., 2003). Finally, pathogenic microorganisms are always a part of the microbial community, and their survival is controlled by both chemical and physical factors, such as temperature, water content, pH, ionic strength, etc., and the overall microbial community dynamics.

The peer-reviewed body of literature on MBP transport and fate has emerged relatively recently, and has experienced an exponential growth since 1996. Several excellent reviews have been published lately (Jamieson et al., 2002; Ferguson et al., 2003; Tyrrel and Quinton, 2003; Unc and Goss, 2004; Oliver et al., 2005), summarizing the status of research and identifying significant gaps in knowledge about transport and fate mechanisms of MBP. The reviews describe MBP transport as a phenomenon occurring after microorganisms have been released, along with manure particulates, into flowing water. Once suspended in water, the microorganisms can be transported with surface and/or subsurface water flow, and partition to soil particles. Microorganisms can travel in water as free cells, be attached to suspended manure particulates, or be attached to soil particles. They can be trapped in soils and sediment, can be attached to subsurface solids and eventually can be detached from them, and can be retained in litter and micro-ponds at the soil surface or at soil textural interfaces. During transport and after retention in the soil, the microorganisms are affected by environmental conditions, such as availability of nutrients and predation. Only a small part of the pore space may be available to microorganisms in the subsurface environments, and only a small part of the soil surface may be conducting almost all of the overland transport. The level of detail about the aforementioned processes depends on the scale at which a study or predictions have to be made and the factors that control the migration behavior. In recent years, MBP fate and transport has been researched at several scales (Fig. 1), corresponding to the range of scales considered in hydrology (Blöschl and Sivapalan, 1995). Research issues and hypotheses are different at the various scales. The fine-scale studies are concerned mostly with uncovering mechanisms of transport and survival, whereas intermediate scale research allows for evaluating the relative importance of these mechanisms in real-life conditions and indicates possible directions to lump mechanisms in coarse-scale models. The utility of results in decision-making and management evaluation increases as the scale increases. The pedon scale and hillslope scale, for example, can provide information about the efficiency of specific agricultural practices; in particular, the utility of vegetated buffer strips between fields or pastures and streams, and efficacy of wetlands in preventing MBPs from entering the streams. The watershed scale research provides information for ranking sources of microbial contamination and recommending management practices to improve the quality of the water resources in the watershed.
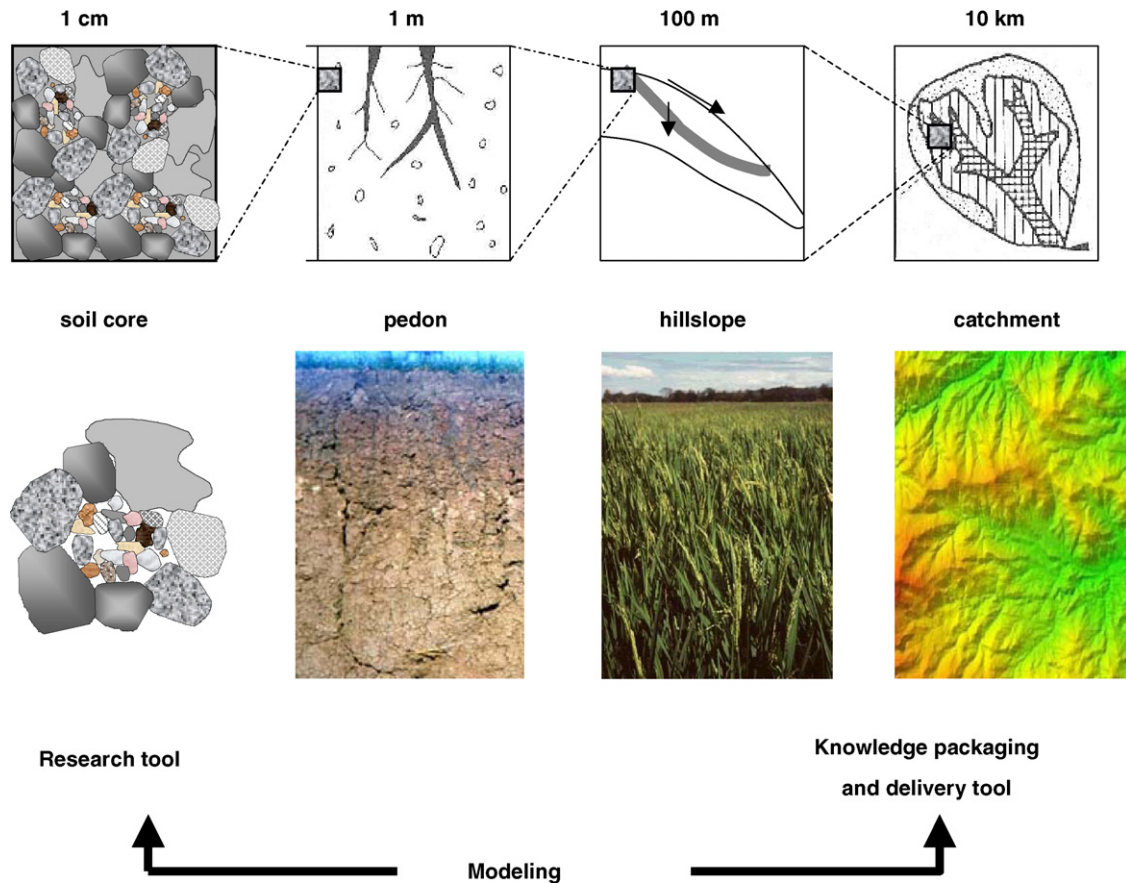
Fig. 1 – Different scales of researching and modeling manure-borne pathogen fate and transport.

To design and evaluate manure management practices, interactions of infiltration, partitioning, adsorption/detachment, straining, and biological die-off/regrowth have to be integrated in conjunction with projected flow regimes and pathogen loads. Because of the complexity of these interactions, there exists a need for the development of simulation models accounting for these interactions. At the soil core and pedon scales, modeling serves as a research tool to test hypotheses about mechanisms and factors of pathogen transport and fate. At hillslope and watershed scales, modeling serves as a knowledge packaging and delivery tool to address issues of public interest. At these scales, it is not possible to include as much detail about the interacting processes and factors, but the level of complexity in the interactions remains quite high (Fig. 2). Any explanatory or predictive MBP transport model has to incorporate the effects of soil, vegetation, management, and weather on microorganism fate and transport processes with a scale-appropriate detail. The first generation of models was developed in the 1980s and was concerned mostly with pedon and hillslope scales (Springer et al., 1983; Overcash et al., 1983; Crane and Moore, 1986; Moore et al., 1988). Currently, much of the emphasis is being placed on modeling at the watershed scale.

The goal of this work is to review the status and challenges in modeling the fate and water transport of manure-borne pathogens in the environment. We have limited the scope of the work by considering the pedon, the hillslope, and the watershed scales. The voluminous literature on core scale modeling deserves a separate in-depth review.

2. Modeling processes of fate and transport of manure-borne microorganisms

An important feature of pathogenic microorganisms that distinguishes them from other water-borne contaminants is the difficulty of enumeration. Collecting quantitative data on concentrations of pathogenic bacteria or protozoa oocysts in natural water is much more costly (one to three orders of magnitude) as compared with inorganic and organic contaminants. This creates substantial difficulties for detailed experimental studies and modeling of manure-borne pathogen transport in the environment because the contaminant transport studies are always based on concentration variations in space and time, and the natural spatial variability of bacteria and protozoa oocyst concentration is very high. Indicators of fecal contaminations rather than manure-borne pathogenic microorganisms are most often measured, simulated, and regulated. Two commonly used indicators are the total numbers of viable *E. coli* and *Enteroccci*. In addition, *Clostridium perfringens* and F-specific coliphages have been suggested as useful indicators. The concept behind using indicators is that, although large numbers of indicator organisms do not necessarily signify the presence of pathogenic organisms, their
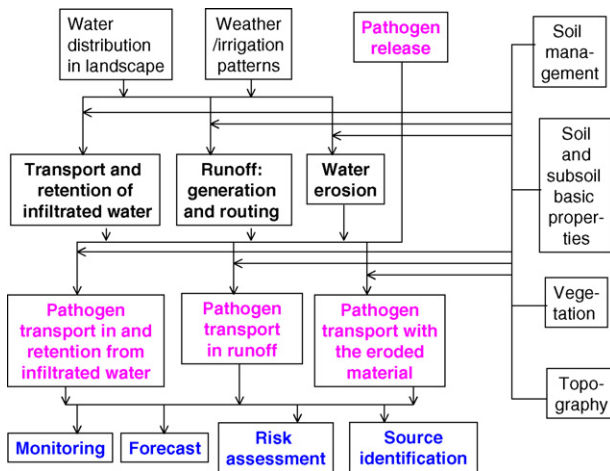
Fig. 2 – Information flow in coarse-scale models of manure-borne pathogen fate and transport.

absence almost surely shows that pathogenic organisms are not present. Until now, the majority of fate and transport models have been developed and tested for indicator organisms rather than for pathogens *per se*.

Most of the modeling efforts are based on the process-based approach that considers separately the release of manure-borne organisms, their overland transport with water and sediment, infiltration into soil, and transport in the vadose zone and groundwater, die-off at the source and during the transport, and in-stream die-off and growth. As for other agricultural contaminants, correct simulation of water and sediment transport in the process-based approach is critical for obtaining accurate predictions of indicator fate and transport (Muñoz-Carpena et al., 1999). All indicator fate and transport models are developed using some existing hydrologic model as the vehicle for transport calculations.

2.1. Release from the source

Several models have been proposed and tested to simulate the release of manure-borne microorganisms. The assumption of the exponential release is frequently used in watershed scale models such as SWAT (Soil and Water Assessment Tool, Sadeghi and Arnold, 2002)

$$\Delta M_R = M_S k_1 \Delta Q \tag{1}$$

and HSPF (Hydrological Simulation Program – FORTRAN, Bicknell et al., 1997).

$$\Delta M_R = M_S[1 - \exp(-k_2 \Delta Q)] \tag{2}$$

Here ΔM_R is the count of microorganisms released during a runoff event; M_S is the count of microorganisms in the manure storage layer of soil in the beginning of the runoff event, ΔQ is the runoff yield during the runoff event, cm, k_1 and k_2 are the release rate parameters, cm^{-1}.

The research at finer scales reveals more complex dependencies of the released microorganisms on time or on runoff yield than models (1) and (2) can predict (Guber et al.,

submitted). These dependences were successfully simulated with two-parametric models; one such model was derived from the work of Vadas et al. (2004) as

$$M_r = M_m a \left(\frac{\rho_w q}{M_d} t\right)^b, \tag{3}$$

and another model was modified after Bradford and Schijven (2002)

$$M_r = M_m \left[1 - \frac{1}{(1 + \alpha\beta t)^{1/\beta}}\right]. \tag{4}$$

In Eqs. (3) and (4), M_R is the count of microorganisms released during the runoff event; M_m is the count of microorganisms in the surface-applied manure before the runoff event; M_d is the mass of the applied manure per unit area, g (dry mass) cm^{-2}; ρ_w is the water density equal to 1 g cm^{-3}; q is the runoff rate, cm h^{-1}; α, h^{-1}, and a, b, β are dimensionless fitting parameters.

Models (3) and (4), as compared with (1) and (2), provided a substantially better description of the release kinetics of *E. coli* observed in plot-scale experiments with the surface-applied bovine manure (Guber et al., submitted). In this work, a 10-fold difference in root mean square error of model (2) compared with model (4) was observed. When model (4) was fitted to the experimental data on *E. coli* release from manure applied on the bare soil and on the grassland, the parameter α linearly depended on the irrigation rate, and the dependence was the same at vegetated and bare plots, whereas the parameter β was 10 times larger at grass plots as compared with the bare plot.

At the watershed scale, the release parameters k_1 and k_2 in (1) and (2), respectively, are often related to the land use (Virginia Department of Environmental Quality, 2003). Parameter k_2 ranged from 2 cm^{-1} at pastures to 5 cm^{-1} for impervious surfaces (Moyer and Hyer, 2003). Smaller values of k_2 (up to 0.5 cm^{-1}) were encountered in some HSPF calibrations (Virginia Department of Environmental Quality, 2003). Other factors influencing bacteria release from manure were noted, such as manure age (e.g., Springer et al., 1983; Hutchison et al., 2004), manure application methods (e.g., Soupir et al., 2003; Drapcho and Hubbs, 2003).

At the plot scale with surface manure application, the release parameters are lower than at the hillslope scale. Values of k_2 were between 0.5 and 1 cm^{-1} in the work of Guber et al. (submitted) where manure was surface-applied on small plots. Values of k_2 were even smaller – less than 0.1 cm^{-1} – in experiments on rainfall-induced manure dissolution and infiltration in soil monoliths (Shelton et al., 2003). A scale effect seems apparent in the values of the release rate parameters, and it appears that direct use of small-scale parameters at large scales is not appropriate.

The difference between the models is illustrated in Fig. 3. In this figure, parameters k_1, k_2, a, and α were found assuming that a 1 cm runoff removed 50% bacteria after a 1 h rainfall event, and parameters b and β have been varied. For the next hour, model (2) estimates the removal to be 75%, models (3) and (4) can predict various removal values depending on values of parameters b and β. Models (3) and (4) predict much faster release in the beginning of the runoff event than in the end (Fig. 3). If this is true for coarser scales, then models (1) and
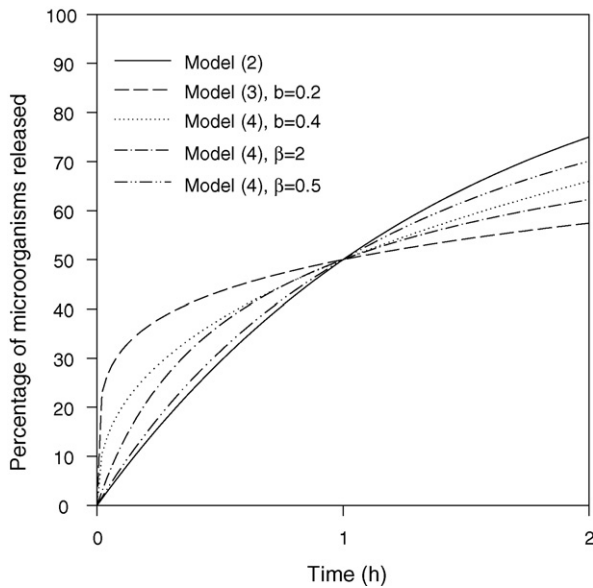
Fig. 3 – Release of manure-borne microorganisms simulated with different models.

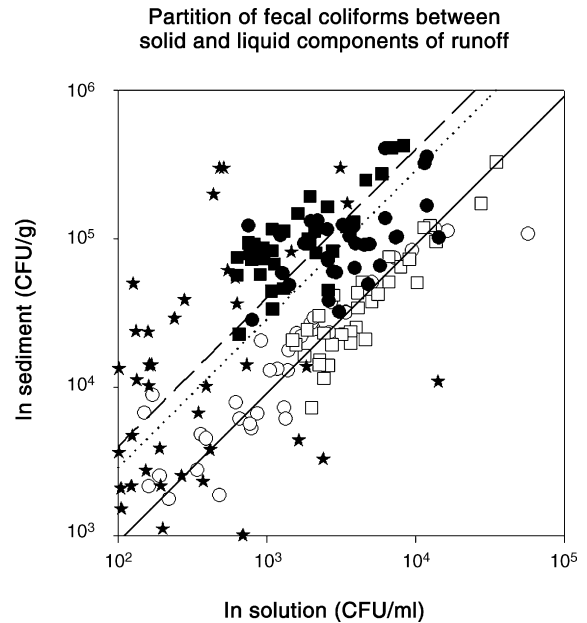Partition of fecal coliforms between solid and liquid components of runoff

Fig. 4 – Partitioning of *E. coli* between sediment and runoff (○, □, ●, ■) in a plot-scale rain simulation in Beltsville, Maryland, 2003, and between stream sediment and stream water (★) in Cove Mountain Creek, Pennsylvania; (○) sandy loam, spring, (□) silt loam, spring, (●) sandy loam, fall, (■) silt loam, fall.

(2) may need to be corrected for the duration of the runoff event or replaced with properly upscaled versions of (3) or (4). Otherwise short early microbial flushes may be encountered that will not be accurately predicted by (1) or (2) when calibrated with longer rainfall events.

2.2. Partitioning and attachment of pathogenic and indicator organisms

Partitioning submodels are used in three different components of manure-borne microorganism modeling. First, partitioning between runoff and sediment affects transport of released MBP. Second, partitioning between pore solution and solid phases in soils and sediments affects the subsurface transport and fate of released MBP. Third, after reaching streams, microorganisms can survive and thrive in stream bottom and bank sediments where their existence is affected by possible adsorption. Partitioning is simulated with the linear isotherm (Sadeghi and Arnold, 2002; Bicknell et al., 1997):

$$S = K_d C \tag{5}$$

where S is the amount of microorganisms in runoff, count g^{-1}, C is the concentration in runoff, count mL^{-1}, and K_d is the partitioning coefficient. Eq. (5) assumes an instantaneous equilibrium. Several kinetic adsorption-desorption equations have been suggested to simulate transport of indicator organisms at the core scale. None of them were deemed to be practical at coarser scales.

The example of Fig. 4 shows the performance of the Eq. (5) with data on *E. coli* partitioning between runoff and sediment. Two groups of data in this figure represent the results of our 1-h triplicated experiments on the rainfall-induced *E. coli* release from a bovine manure strip placed on the top of 6-m long bare plots having 20% slope and either sandy loam or silt loam soil texture. Given the scatter in the data, the linear

approximation given by (5) appears to be reasonable. Similar to the results of Borst and Selvakumar (2003), soil texture did not affect this relationship. Values of K_d in spring and fall were 10 and 70 mL g^{-1}, respectively.

Batch experiments on partitioning between soil pore solution and solid phase show the non-linearity of the relationship between free and attached *E. coli*. Both Freundlich and Langmuir isotherms were suggested to simulate the equilibrium relationships (e.g., Gantzer et al., 2001). Partitioning of microorganisms in batch experiments is usually studied using centrifugation to separate solid and liquid particles. Duration and speed of centrifugation affects the distributions of *E. coli* between solids in sediment and supernatant (e.g., Ling et al., 2003). It is currently unclear whether the kinetics of attachment or the kinetics of straining of bacteria bombarded by settling soil particles is the factor affecting the solid–liquid distribution. With the long centrifugation, the attachment of bacteria to soil particles can be efficiently simulated with Eq. (5) when K_d is assumed to be a function of the clay content in soil (Ling et al., 2003). Data of these authors can be approximated as:

$$K_d = A(CLAY)^B \tag{6}$$

where CLAY is the percentage of clay particles <0.002 mm in soil, Eq. (6) was developed for $2 < CLAY < 50$, and parameters $A = 10^{-1.6 \pm 0.9}$, and $B = 1.98 \pm 0.7$ are the slope and the intercept of the regression in log-log coordinates. Clay content is generally thought to be the leading factor affecting K_d (Hagedorn et al., 1978; Bengtsson, 1989). Effects of other factors influencing bacterial attachment to soil, including soil hydrophobicity (Lindqvist and Bengtsson, 1991), presence of other bacteria

(Marshall et al., 1971), ions (Gilbert et al., 1976; Gannon et al., 1991; Jackson et al., 1994) and electrostatic interactions (Sharma et al., 1985), have all been previously documented. Attachment of the protozoan oocysts to soil particles currently is the subject of controversy in the literature. Recently, Guber et al. (2005b) and Kuczynska et al. (2005a) demonstrated that the presence of manure drastically affects the attachment of bacteria and *Cryptosporidium* oocysts to soil. The degree of equilibrium attained in attachment of pathogens and indicator microorganisms in different environments is a largely unexplored topic. Kinetics of equilibrium is affected by the time of contact, mixing intensity and access to different parts of pore space. Bradford et al. (2006) did not need to include attachment of *Giardia* cyst to solid grains in their simulated column transport studies through aquifer sands. Kuczynska et al. (2005b) demonstrated that either straining or attachment can explain the distribution of oocysts in disturbed soil columns.

Overall the applicability of batch K_d values to field conditions remains unclear. Bacteria and oocyst breakthrough in undisturbed soil through macropores has been well documented (e.g., Ferguson et al., 2003; Darnault et al., 2004). Diameters and continuity of macropores rather than the attachment affected such breakthrough, therefore, the presence of macroporosity should be accounted for in models of manure-borne microorganism transport and fate.

Sediment in streams may present a favorable environment for bacteria attachment to soil particles. Very little is known about the extent and mechanisms of this attachment (Ferguson et al., 2003). Fig. 4 summarizes our data on the relationship between *E. coli* contents in creek sediment and in the creek water collected during weekly grab sampling at six observation sites along the Cove Mountain creek, Pennsylvania. The sites represent forested gameland, pastureland, and cropland types of land use. The scatter in these data is much higher than in the superimposed runoff data. Given the scatter, model (5) seems to be a reasonable approximation. The K_d value in this case was 30 mL g^{-1}. The re-suspension of the sediment during and after rainfall events may cause a substantial release of bacteria from the sediment.

2.3. Survival and inactivation

The exponential model suggested by Chick (1908),

$$N = N_0 \exp(-\mu t) \tag{9}$$

is the predominant model used to describe the survival of manure-borne microorganisms in stored manure, soil, land applied manure, streams, and groundwater. Here N is the number of indicator bacteria at the time t, N_0 is the original number of indicator bacteria, and μ is the die-off rate constant.

The die-off rates of fecal coliforms and *E. coli* in soils are affected by a multiplicity of factors. Crane and Moore (1986) reviewed multiple sources of data and found a wide distribution of μ values in soils ranging from 0.1 to 2 day^{-1} (Fig. 5). An increase in soil water content causes a decrease in die-off rate constants (i.e., Reddy et al., 1981; Mubiru et al., 2000). Enteric bacteria have a shorter survival period in acid soils (Gerba et al., 1975; Ellis and McCalla, 1976), with a pH of 6–7 being the most favorable for bacterial survival (Cuthbert et al., 1955;
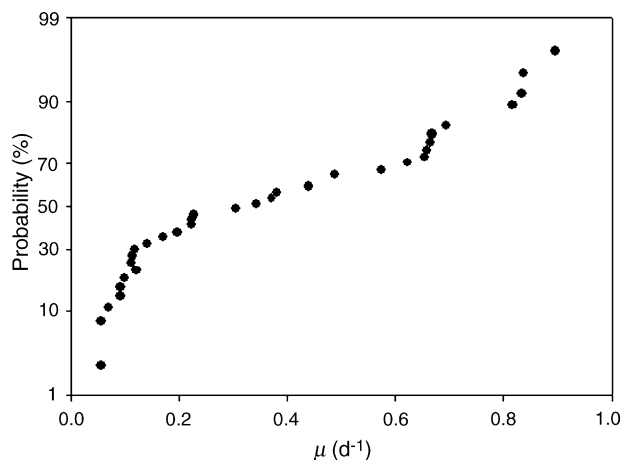

Fig. 5 – Distribution of the E. coli inactivation rate constants (data from Crane and Moore, 1986).

Reddy et al., 1981). Animal diet substantially affects the die-off rates (Bach et al., 2005; Franz et al., 2005). Temperature is the only environmental variable that is currently used to modify the die-off rate constant μ in existing models for soil and manure. The ''T20 equation'' is used in the form (e.g., Sadeghi and Arnold, 2002):

$$\mu = \mu_{20}\theta^{T-20} \tag{10}$$

where μ_{20} is the die-off rate at 20 °C, T is the temperature, °C, θ is the temperature correction factor. For example, the data of Himathongkham et al. (1999) on die-off rate constants for the pathogenic *E. coli* O157:H7 in different types of cow manures can be approximated with the log-transformed Eq. (10):

$$\log \mu = (-0.063 \pm 0.005) + (0.028 \pm 0.004)(T-20)$$

Typically the value of θ is about 1.07 in all five environments of interest, i.e., in stored manure, soil, land applied manure and streams. The μ_{20} constant varies from one environment to another.

Yet another important reason for the wide range of values in Fig. 5 may be the limited applicability of the one-parametric Chick law (8) to actual data on survival. Experimental data on manure-borne microorganism die-off rarely follow Chick's law. Field experiments (e.g., Easton et al., 1999) show that the microorganism die-off actually occurs in two stages. The first stage may include some re-growth or, on the contrary, be very fast. Therefore a realistic die-off model should at least contain three parameters. One such model, known as the two-stage die-off model (Crane and Moore, 1986):

$$N = \begin{cases} N_0\exp(-\mu_1 t), & t < t_1 \\ N_0\exp(-\mu_1 t_1)\exp[-\mu_2(t-t_1)], & t \geq t_1 \end{cases} \tag{11}$$

was applied to simulate die-off in incubation experiments (e.g., Ogden et al., 2001). In Eq. (11), N is the number of indicator bacteria at the time t, N_0 is the original number of bacteria, μ_1 and μ_2 are die-off rate constants at the first and second stage of inactivation, and t_1 is the time when the first stage of inactiva-
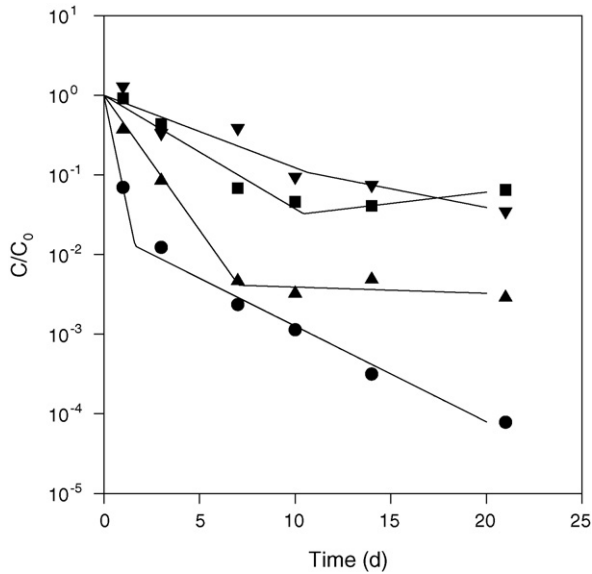
Fig. 6 – Application of model (11) to the data of Easton et al. (1999) on inactivation of pathogens and indicator bacteria in creek water; (●) E. coli O157: H7 (laboratory), (••) *Giardia* cysts (field chambers), (▲) E. coli (field chambers), (▼) *Enterococci* (field chambers).

tion ends. Fig. 6 shows the application of this model to the data of Easton et al. (1999) on survival of pathogenic organisms and indicator microorganisms in creek water. The two-stage inactivation is well-expressed for all organisms in this study, and relatively high concentrations are preserved for a long time. Initial regrowth of *E. coli* populations up to two orders of magnitude has been observed in several field and laboratory studies during first 1–2 weeks after deposition (Kudva et al., 1998; Wang et al., 2004; Bach et al., 2005; Muirhead et al., 2005). The predation by grazing protozoa or the parasitism by phages may alter the MTB die-off dynamics in many ways. Although these phenomena have been documented, prediction of their occurrence and dynamics is not currently possible.

Inactivation in natural waters has been shown to depend on solar radiation, and the equation

$$\mu = \frac{T}{a_{\mathrm{T}}} + \frac{I}{a_{\mathrm{I}}} \tag{12}$$

was suggested in Tian et al. (2002). Here T is the mean daily temperature, I is the daily solar radiation, and a_{T} and a_{I} are empirical parameters.

2.4. Transport models

Existing plot- and hillslope-scale models simulate overland MBP transport as a purely convective phenomenon (Fraser et al., 1998; Walker and Stedinger, 1999; Park and Huck, 2003; Sadeghi and Arnold, 2002; Bicknell et al., 1997; Collins and Rutherford, 2004; Barfield et al., 2003). The MBP flux is assumed to be proportional to the runoff water flux. Currently, no attempts have been made to simulate effects of differences in mobility of different parts and the heterogeneity of runoff flow on the MBP transport at the watershed and hillslope scales, although it has

been suggested to apply the advective-dispersive transport model (Davis et al., 2003). Such simulations assume that differences in accessibility of manure to the moving surface water can be emulated by calibrating the release rates.

The role of overland MBP transport with sediment is treated differently in different models. For example, Fraser et al. (1998) described a model in which MBP were transported while adsorbed to sediment and waste particles in overland flow. Applications of the HSPF model (Bicknell et al., 1997) usually ignore the transport with sediment and simulate the convective transport of freely floating bacteria. The SWAT model (Sadeghi and Arnold, 2002) simulates microorganism transport both with sediment and in the runoff water.

Transport of MBP in the vadose zone and ground water is usually neglected in watershed scale models (Sadeghi and Arnold, 2002; Tian et al., 2002). Soils are considered to be efficient filters, and it is thought that only cases of well-developed macroporosity or karst geology require simulations of MBP transport in the soil and subsoil. However, macropores are usually present in soils, and the extent to which they can transport MBPs is not well understood. Guber et al. (2005a) showed that large differences in soil hydraulic conductivity in undisturbed soil columns may occur with a negligibly small change in bulk density and porosity, and MBPs can be readily transmitted in saturated soil columns with high porosity.

The MBP transport in streams is most often considered as a result of the joint action of advection, dispersion, and inactivation. Tian et al. (2002) noted that the sediment of a stream can act as a transient reservoir for fecal pollution, absorbing microbial mass during periods of low flow and releasing mass during high-flow events. They suggested that simulations should consider in-stream mobilization caused by scour (resuspension). Resuspension occurs in turbulent water when the flow volume is higher than a certain threshold. Otherwise, under low-flow conditions, deposition takes place. The daily resuspension rate RS is defined as

$$\mathrm{RS} = \begin{cases} 1 - \exp\left[\dfrac{(V - V_0)}{Q_0}\right], & V > V_0 \\ 0, & V \leq V_0 \end{cases} \tag{13}$$

where V is the average daily flow volume, V_0 is the threshold flow volume for resuspension, and Q_0 is a parameter. Tian et al. (2002) estimated the resuspension rate to vary between 0.003 and 0.8 in their experimental settings.

Models of watershed and hillslope scales typically treat the vegetated buffer strips (VBSs) or wetlands as linear watershed boundary elements that remove MBP from the runoff water and trap the MBP associated with sediment particles. Sometimes the effect of VBS is not explicitly simulated but rather lumped in the delivery ratio depending on the distance from the stream (e.g., Tian et al., 2002). The removal efficiency is most often simulated as a simple function of the vegetated buffer strip width and slope, for example, with the equation of developed by Moore et al. (1988):

$$\mathrm{Pr} = 11.8 + 4.3R \tag{14}$$

where Pr is the percent removal of bacteria (not to exceed 75%), and R is the ratio of the filter strip width, m, to the slope, %.

The VBS have been shown to be highly variable in their effectiveness (Mawdsley et al., 1995; Tate et al., 2004; Fajardo et al., 2001). Coyne et al. (1998) demonstrated that between 55 and 95% of fecal coliforms are trapped by the VBS. A 10-m wide grass strip was sufficient to reduce fecal coliform contents in runoff by as much as 70% (Young et al., 1980; Walker et al., 1990) or in the case of Lim et al. (1998) complete removal of fecal coliform was possible. In contrast, Entry et al. (2000) reported little change in fecal coliform numbers after a pulse of applied pig wastewater moved down slope. Optimal design criteria for on-farm vegetated buffer strips currently do not exist for waterborne microbial contaminants (Atwill et al., 2002; Edwards, 2003).

Modeling has a potential to be an efficient tool in helping to explain the functioning of VBS and to develop design criteria. Sizes of VBS correspond to the plot scale and more detail must be included in the model. As MBPs begin to move with runoff, they partition between runoff and infiltration. The partitioning depends on local infiltration rates that tend to be highly variable (i.e., Gómez et al., 2001), and therefore the presence of relatively mobile and immobile transport zones in both surface and subsurface flow may need to be simulated. The amount of MBP entering soil during the runoff event is controlled by both soil infiltration rates and the status of vegetation. Fig. 7 shows the regression tree developed from data on E. coli contents in soil obtained after 1-h triplicated experiments on the rainfall-induced E. coli release from the bovine manure strip placed on the top of 6-m long bare plots having on average 20% slope and silt loam texture. The vegetation parameters serve as important splitting variables dividing the plot area into zones with relatively large and relatively small penetration of E. coli in soil.

The vegetation density may both enhance infiltration and create retention or trapping zones where runoff is filtered by saturated soils beneath these zones. Kuznetsov et al. (2006)
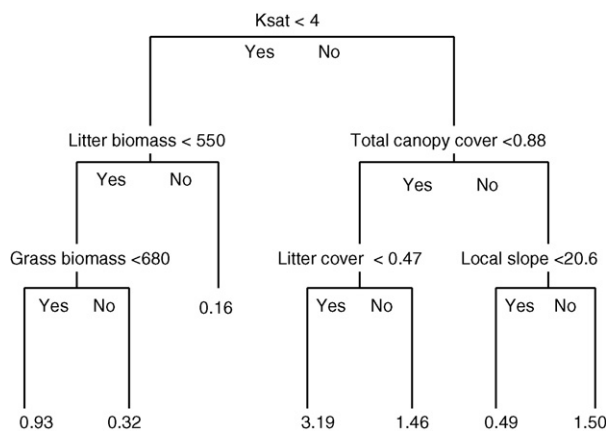

Fig. 7 – Dependence of the relative content of E. coli in soil after the runoff experiment with the release and overland transport of manure-borne E. coli on the soil saturated hydraulic conductivity (Ksat, cm h^{-1}), litter and grass biomasses, kg ha^{-1}, fractions of surface covered with plant canopy and litter, and the local slope, %. The E. coli relative contents are shown at the ends of the regression tree branches. The relative E. coli contents in soil are obtained by dividing local values by the area-averaged value.

developed the model Solute Transport with Infiltration and Runoff (STIR) that used the two-dimensional representation of the vegetation buffer strip in vertical cross-section to simulate the transport of manure-borne fecal coliforms and bromide added to manure. The advective-dispersive transport equation was used to simulate both the overland and the subsurface transport. The model was calibrated with data on bromide from manure and manure-borne fecal coliforms in runoff from 6-m long grass strips with manure strips placed on the top that were subjected to simulated rainfall. The dispersivity values for bromide and coliforms were close. The first-order surface retention rate was zero for bromide and had a substantial positive value for coliforms.

3. Current challenges in fate and transport modeling

Substantial progress has been made in the modeling of MBP fate and transport in the last 10 years. Modeling results are being directly used to address issues of public concern, for example assessing TMDLs (total maximum daily loads) of MBPs and indicator organisms in the United States (EPA, 2005). As the model applications have accumulated, the need and urgency in answering several research questions has become apparent. The challenges that the face modeling studies also become more noticeable.

The comparison of the fate and transport between MBP and manure-borne indicator organisms is absent in the literature. Using indicator organisms has undoubtedly expanded our understanding of MBP fate and transport in the environment. However, the inactivation, partitioning, and transport properties of pathogenic manure-borne bacteria have only received limited research attention. There are indications that pathogenic E. coli may be inactivated faster than non-pathogenic E. coli strains (Fenlon et al., 2000), but there are also contradicting reports (Kudva et al., 1998). It is not known whether there are differences in attachment of pathogenic and indicator organisms to soil particles. The statement of Unc and Goss (2004) who conclude that "we know virtually nothing about how microorganisms may be partitioned between these states [water, manure particulates and sediment particles] whilst in transport" is fully applicable to pathogenic manure-borne microorganisms.

There exists a substantial body of experimental data on the fate and transport of manure-borne microorganisms in the environment. However, only a small fraction of this information can be used for the purposes of process-based modeling which is based on the mass conservation concept. Too often important components of the MBP mass balance have been and are being omitted in observations or not reported. The MBP fate and transport is primarily driven by the hydrology. Yet in many cases hydrologic observations have not been coupled with measurement of concentrations of microorganisms. Fortunately, existing fate and transport models function not only as simulations tools, but also create a framework for data collection. But such data collection has yet to happen.

Modeling of manure-borne pathogenic microorganisms has a built-in uncertainty related to the wildlife input (Ferguson et al., 2003). All wild animals shed microorganisms,

many of which belong to the same genera as manure-borne microorganisms and are pathogenic for humans. Loads of such microorganisms and the prevalence of them in the environment are typically not known. Providing abode and continuity corridors for wildlife is in many cases an important consideration in designing vegetated buffer strips and riparian zones. It is not known, however, what the deposition of pathogens from the wildlife is in the proximity to the streams that VBSs are supposed to shield from the MTB. In addition, the prevalence of pathogens in manures is not usually known.

Modeling of indicator organisms such as *E. coli* has the additional source of uncertainty related to the background concentrations of this organism in soils and sediments. Jenkins et al. (2005), for example, found background concentrations of *E. coli*, and fecal enterococci in soil higher than the concentrations of these microorganisms in runoff in all but one observation.

The uncertainty in model inputs and fate and transport observations does not preclude the fate and transport simulations. However, this uncertainty needs to be factored into simulations. An ensemble of simulations has to be made to estimate the possible distribution of simulation results and risks associated with a specific allocation of manure and best management practices (BMP). Such ensemble predictions require knowledge about the probability distributions of all uncertain model inputs. Data on typical ranges and frequency distributions of MBP modeling inputs have yet to be accumulated. One remedial strategy is to relate the uncertainty in model parameters and inputs to the environmental variables on which these parameters are known to be dependent. This is similar to the development of pedotransfer functions in soil hydrology that transform readily available soil attributes into hydraulic parameters that are more difficult to measure (e.g., Pachepsky and Rawls, 2004). Soil and vegetation parameters are the obvious first choice to be related to the parameters of MBP transport, partitioning and survival.

The scarcity of experimental data and the substantial cost of measurements of MBP transport imply the feasibility of using a natural tracer that would have some fate and transport patterns similar to those of MBP. Recently, similarities in transport of manure-borne phosphorus and fecal coliforms have been shown in controlled experiments for relatively short (1–6 m) transport distances (Stout et al., 2005). It remains to be seen to what extent these similarities hold for larger travel distances. The knowledge base of manure-borne P transport is substantially larger compared to MBP (e.g., Kleinman and Sharpley, 2003), and using it may be beneficial in MBP modeling.

Currently a substantial uncertainty exists in interpreting stream monitoring data on microorganisms, that are used to calibrate and test models. The spatial and temporal variability ranges have not been extensively studied, and it is not known how representative is a typical grab sample. A related knowledge gap is the absence of reliable data on survival of microorganisms in sediment and their resuspension. It is not really known how the increase of concentrations in a creek during a rainstorm event has to be partitioned between runoff and resuspension.

The problem of upscaling data on MBP fate and transport needs to be addressed. A field plot represents the smallest experimental scale at which the MBP fate and transport occurs in the same way as in the real world. Controlled experiments still can be designed and executed at this scale. Also, field plots can mimic the vegetative buffer strips that are currently in the spotlight as interest in the economic benefits of conservation practices grows. Translating the MBP fate and transport information from the plot scale to the hillslope and further to the watershed scale is not currently addressed, but needs to be pursued to improve coarse-scale modeling. No recommendations have been developed to select the cell grid size in modeling at the watershed scale. Results of such modeling studies are sensitive to the cell scale (e.g., Gupta et al., 2002). Scaling laws to change parameters of models from one size of cell to another may be possible, but have not yet been established.

Although MBP fate and transport process-based models are currently uncertain in their structure and limited in their knowledge base, no successful alternative has been suggested so far. Attempts to simulate indicator fate and transport using purely statistical approaches are inconclusive (Johnson et al., 2003) or untested (Bigras-Poulin et al., 2004). As attention to the health risks associated with manure-borne pathogenic microorganisms grows, the resources for the research will likely become available. The most important challenge then will be to use these resources to improve the knowledge base of fate and transport models of manure-borne pathogenic microorganisms.

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