



**Agricultural  
Research  
Service**



**UNIVERSITY OF  
MARYLAND**

# **Microbial Water Quality Simulation Using Agricultural Policy Environmental eXtender (APEX)**

Oct 23, 2025

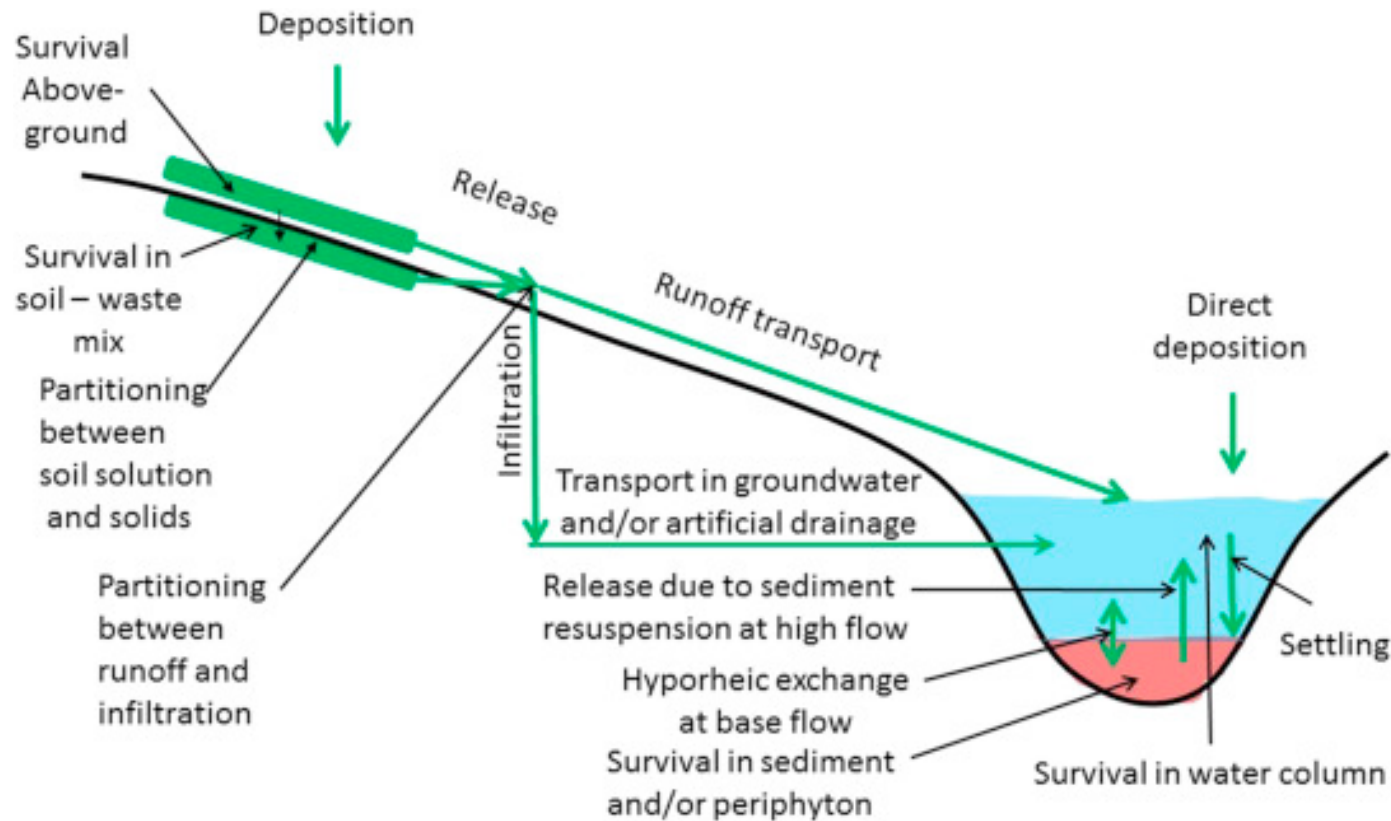
Jiye Lee



**DEPARTMENT OF  
ENVIRONMENTAL  
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# Microbial module development

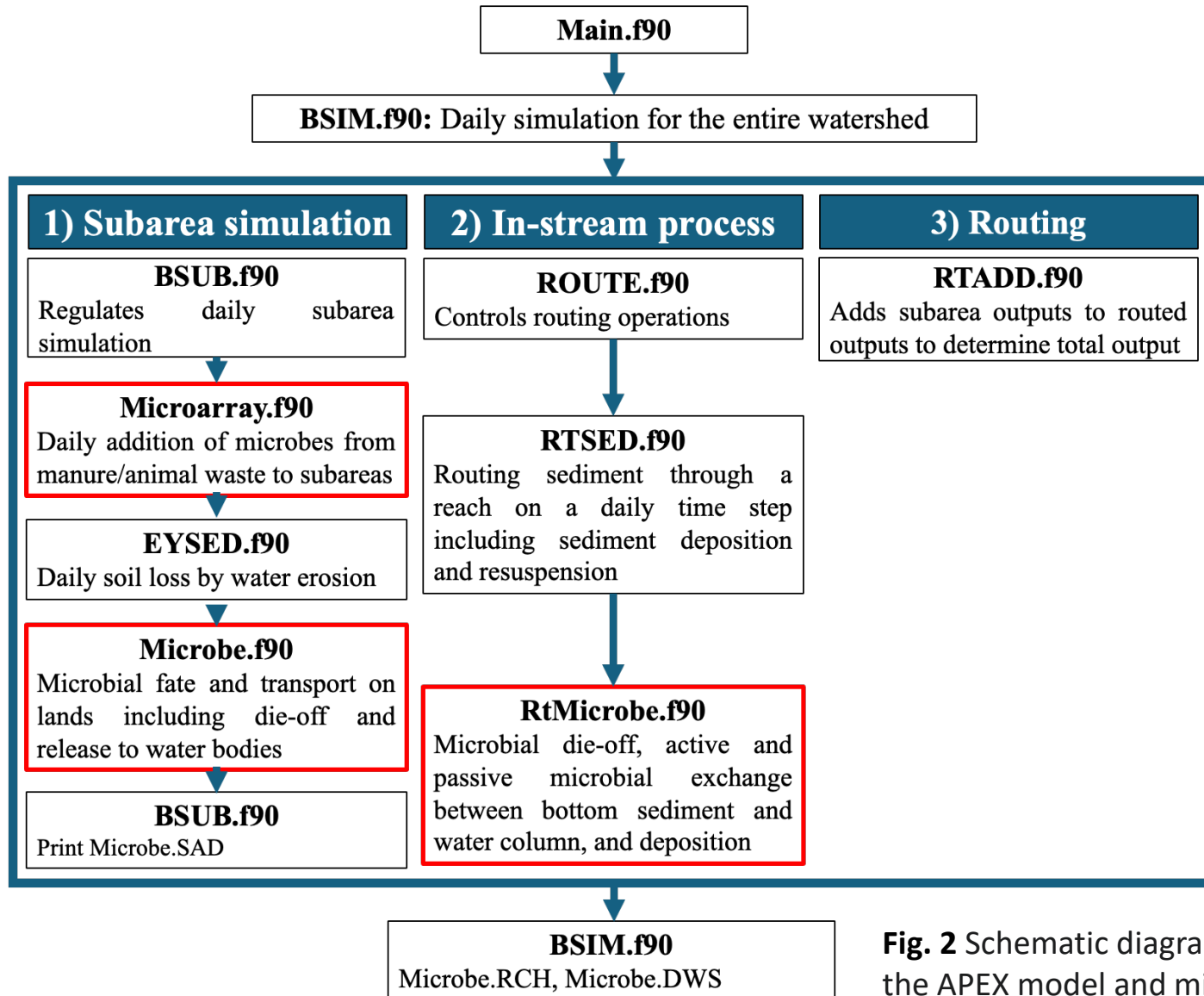
## Key microbial processes on land and in water bodies



- 1) Animal waste (manure) deposition
- 2) Die-off on soil
- 3) Release with runoff
- 4) Die-off in water
- 5) Resuspension during high/low flow periods
- 6) Settling

**Fig. 1** Key microbial fate and transport on land and in water bodies

# Microbial module development



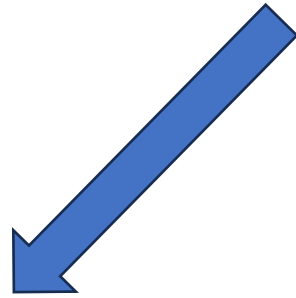
## Main subroutines for microbial module

- 1) **Microarray.f90**  
Addition of microbes on lands from manure from the APEX model
- 2) **Microbe.f90**  
Microbial release with runoff to water bodies
- 3) **RtMicrobe.f90**  
Microbial process in water and bottom sediment including die-off passive and active transport, and deposition

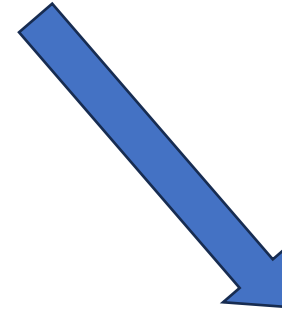
**Fig. 2** Schematic diagram of linkage of the APEX model and microbial module

# Microbial module development

**Applications of APEX-M**



**Research questions**



**Management questions**

# Sub-models for microbial inactivation and release

*Can we distinguish between microbial sub-models with the monitoring data?*

## Sub-model evaluation and selection for simulating generic *E. coli*

### 1. Inactivation sub-model comparison

- Chick's law
- Q10-model
- With vs without lag phase, drastic/gradual decrease

### 2. Microbial release models comparison

- Exponential model
- Bradford-Schijven model
- Vadas-Kleinman-Sharpley model

### 3. With vs without active transport between bottom sediments and water column

# Microbial sub-models

**Table 1.** Models for microbial inactivation and microbial release.

| Inactivation sub-model                                                                                                                                                                                                                                               | Equation                                                                     | Microbial release models                        | Equation                                                    |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|-------------------------------------------------|-------------------------------------------------------------|
| Chick’s law                                                                                                                                                                                                                                                          | $N = N_0 e^{-kt}$ $k = k_r \theta^{T-T_r}$                                   | Exponential (Bicknell et al., 1997)             | $\frac{N}{N_0} = 1 - \exp(-k_e W)$                          |
| Q <sub>10</sub> model                                                                                                                                                                                                                                                | $k = k_r Q_{10}^{(T-T_r)/10}$ <p>Q<sub>10</sub>: temperature coefficient</p> | Bradford-Schijven (Bradford and Schijven, 2002) | $\frac{N}{N_0} = 1 - \frac{1}{(1 + k_p \beta W)^{1/\beta}}$ |
|                                                                                                                                                                                                                                                                      |                                                                              | Vadas-Kleinman-Sharpley (Vadas et al., 2004)    | $\frac{N}{N_0} = AW^n$                                      |
| N, total count of microorganisms; N <sub>0</sub> , initial total count of microorganisms; t, time (days). T: temperature; T <sub>r</sub> : reference temperature (often 20 °C), A, k <sub>e</sub> , k <sub>p</sub> , and n are release parameters; W, rainfall depth |                                                                              |                                                 |                                                             |

**Active transport between bottom sediments and water column**

$$N = r \cdot A \cdot C_M$$

r: the bacteria release factor (ton·m<sup>-2</sup>·day<sup>-1</sup>)  
A: bottom area of the reach (m<sup>2</sup>)  
C<sub>M</sub> : bacteria concentration in the bottom sediment of the pond (CFU·ton<sup>-1</sup>)

# Differences between inactivation sub-models

## *E. coli* inactivation patterns: single stage and multiple stages

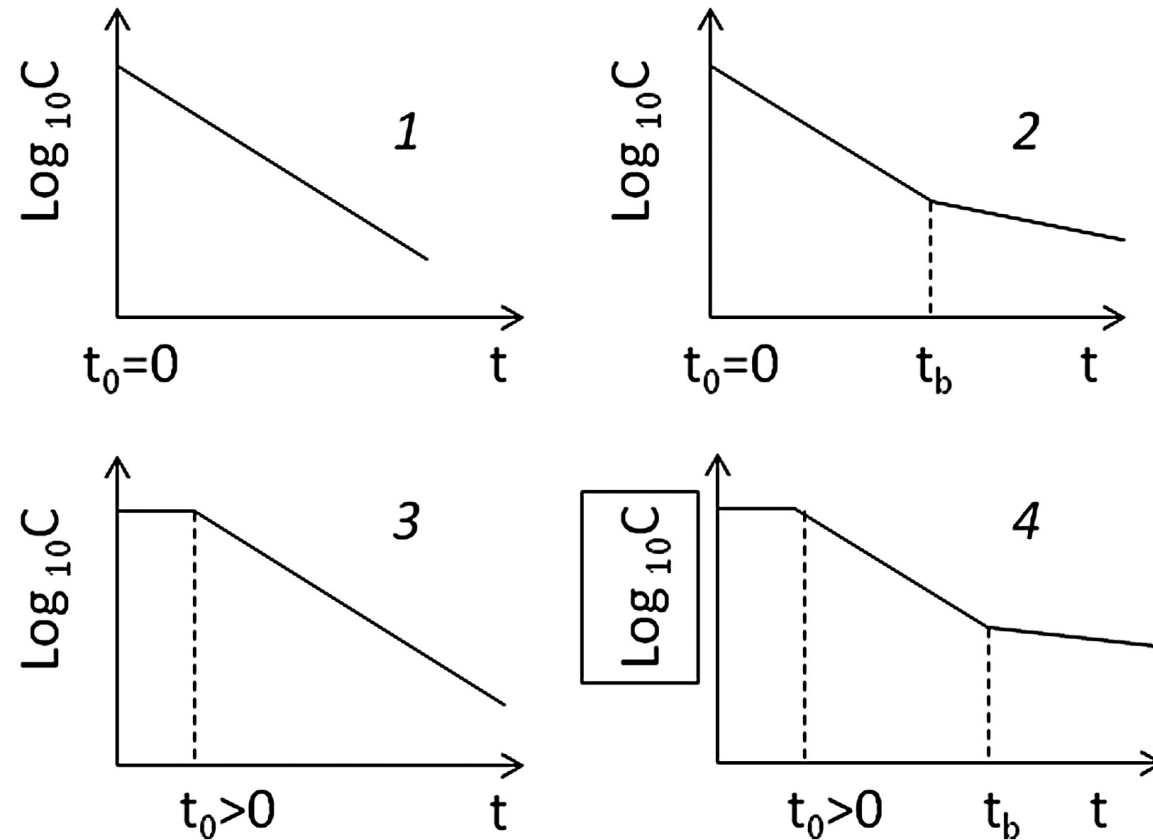


Fig. 3. Patterns found in data on *E. coli* inactivation in waters (Blaustein et al., 2013)

# Differences between release sub-models

## *E. coli* release models: exponential, B-S, and VKS

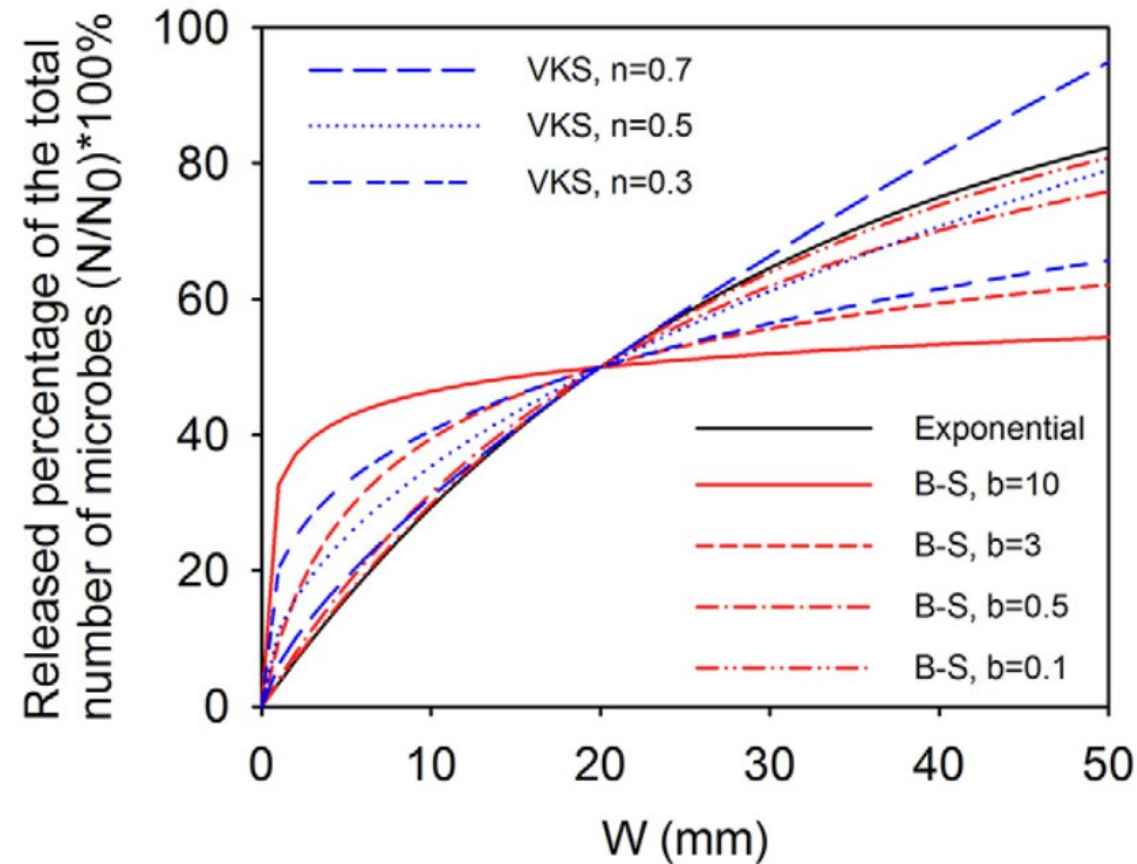


Fig.4. Difference in shapes of release curves simulated with three release models: exponential, Bradford-Schijven (B-S), and Vadas-Kleinman-Sharpley (VKS)

# Microbial module development

*Can we distinguish between microbial sub-models with the monitoring data?*

## Sub-model evaluation and selection for simulating generic *E. coli*

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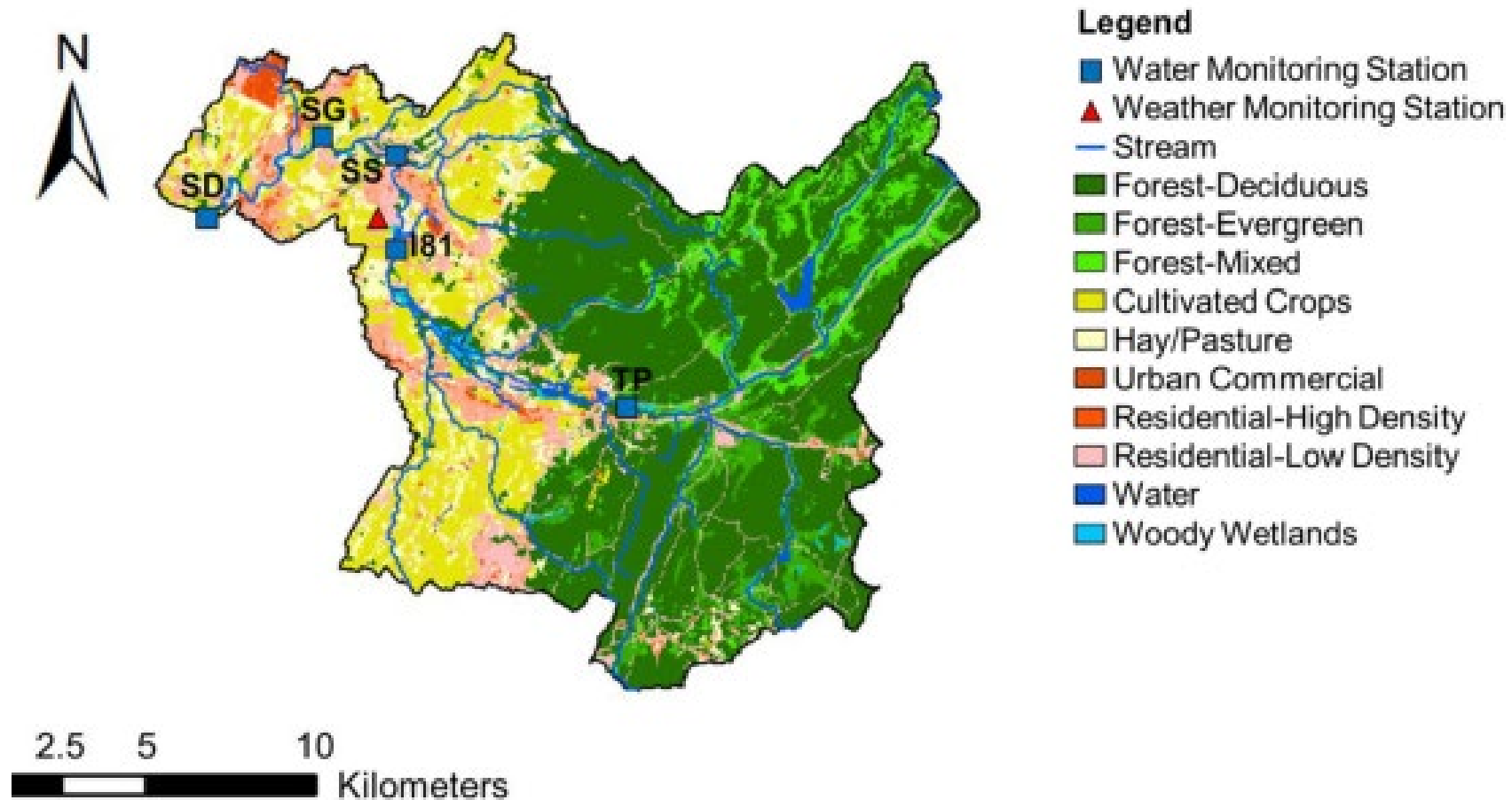
### 2. Microbial release models comparison

- Exponential model
- Bradford-Schijven model
- Vadas-Kleinman-Sharpley model

### 3. With vs without active transport between bottom sediments and water column

# Do we need to account for additional microbial processes?

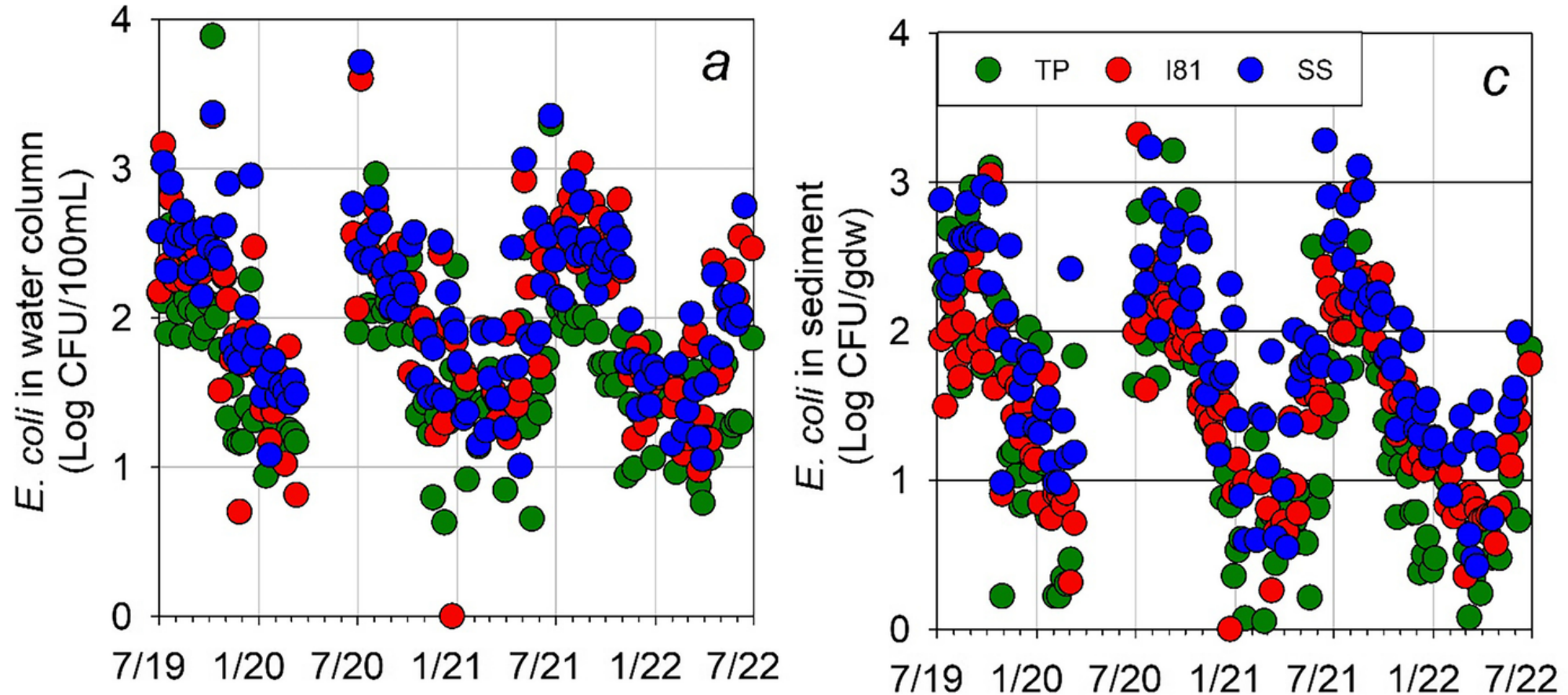
## Conococheague Creek watershed, PA



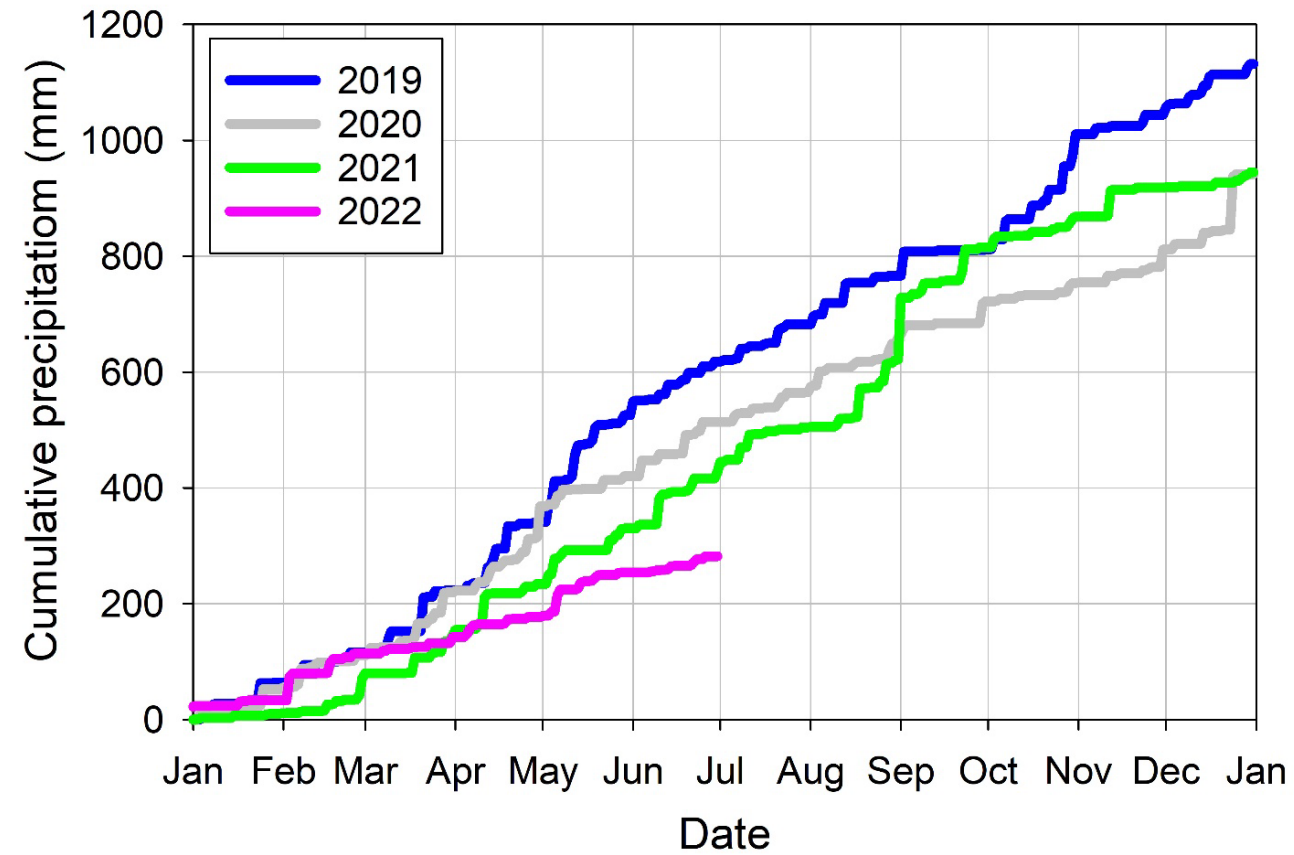
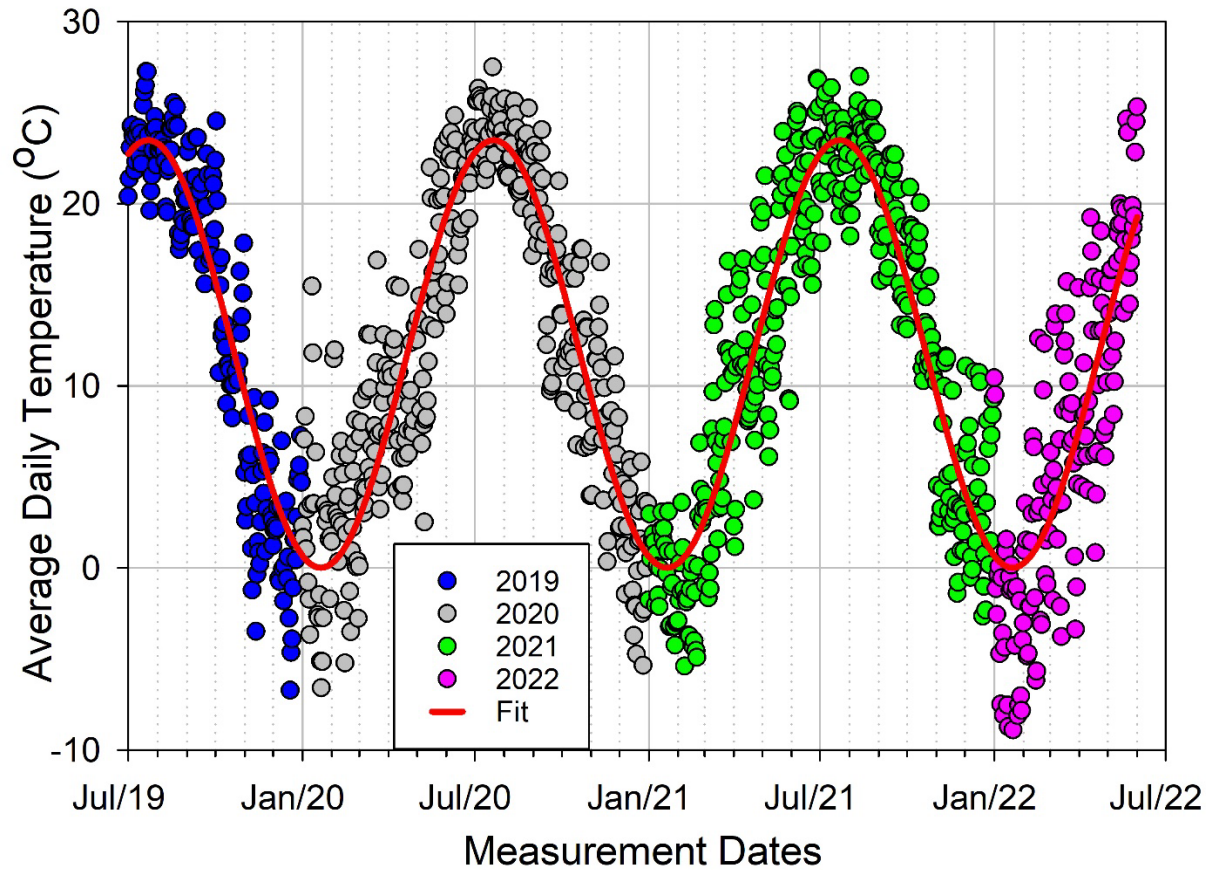
**Fig. 5** Land use map of upstream area of the Conococheague Creek watershed and monitoring locations (treatment plant [TP], Interstate 81 [I81], Scotland school [SS], Sycamore Grove [SG], and Silon Dam [SD])

# Three years of monitoring for Conococheague creek watershed, PA

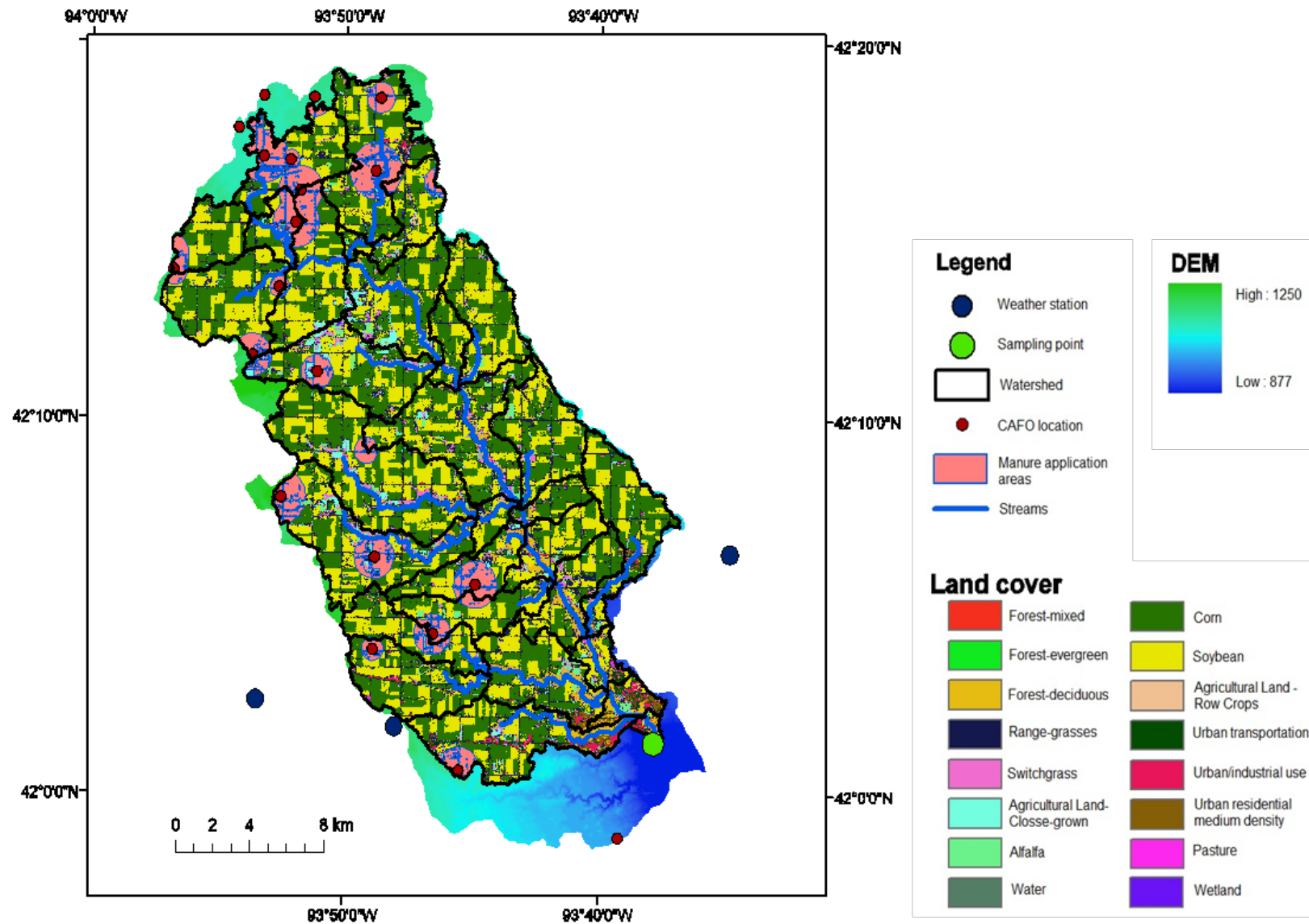
## Model evaluation and validation



**Fig. 6** Time series of *E. coli* concentrations in water column and sediment at TP, I81, and SS in Conococheague Creek Watershed (Pachepsky et al. 2023)



**Why did the differences in precipitation not affect the E. coli dynamics?**



**Fig 7.** Squaw Creek Watershed; Locations of Weather Stations, Gaging Station, Confined Feeding Operation Units, and Manure Application Areas Are Shown (Pandey et al., 2016).

# Microbial module application

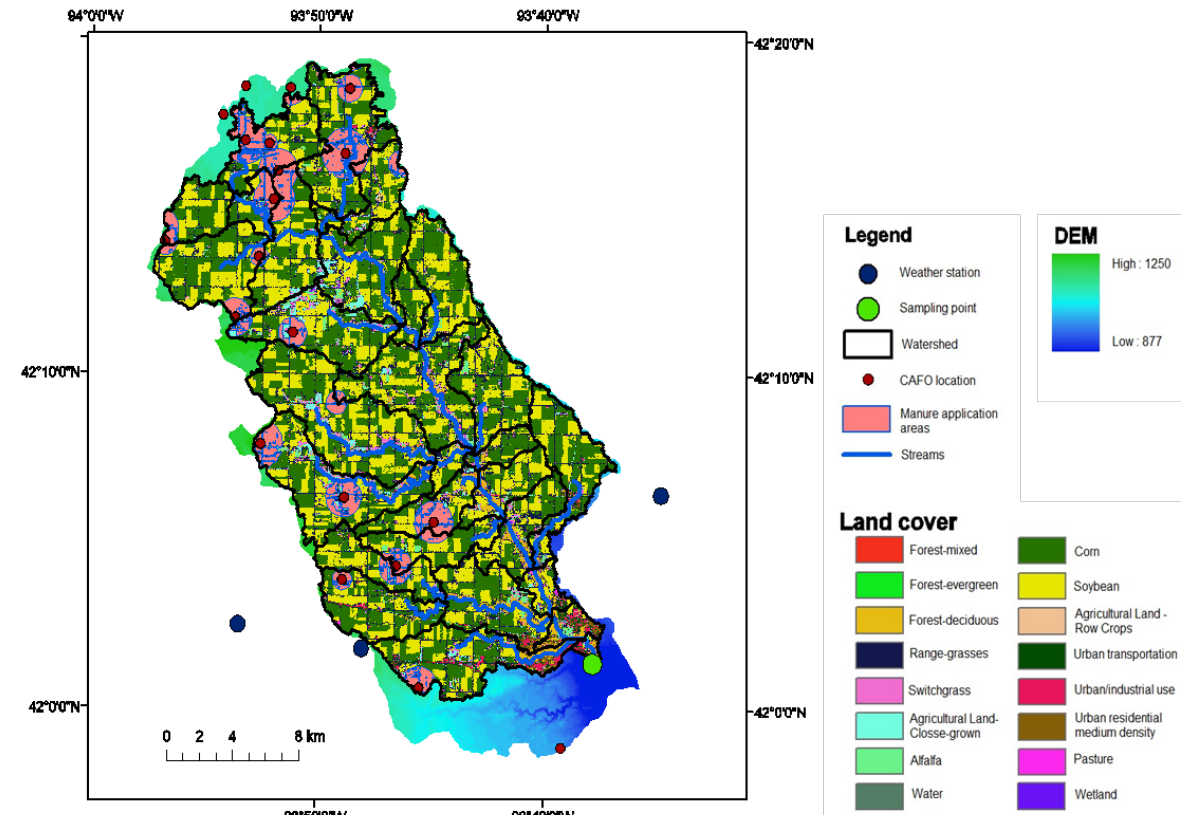
**How do variations in intra-annual precipitation and temperature affect microbial water quality?**

## Intra-annual weather patterns

- Rainfall intensity/precipitation/temperature

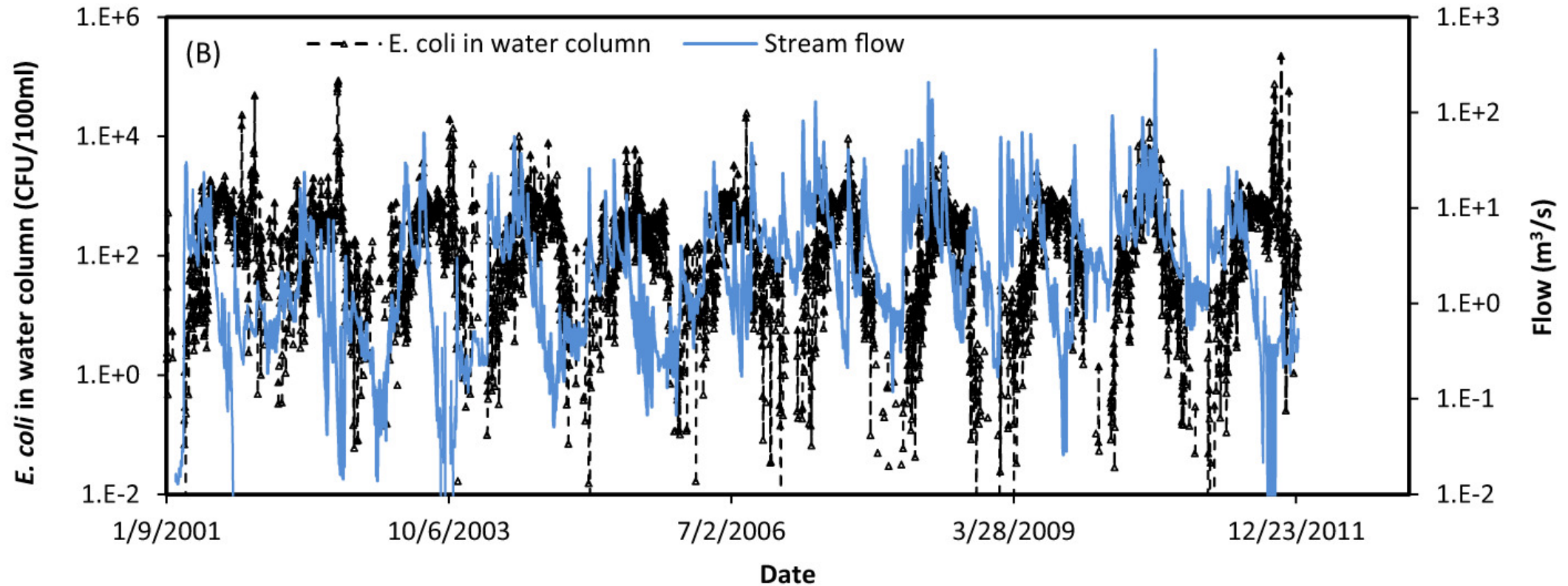
## Possible changes due to changing weather patterns

- 1) Release of manure with runoff into streams
- 2) Baseflow and surface runoff conditions
- 3) Water volume in streams
- 4) Microbial die-off on land and in streams



**Fig 7.** Squaw Creek Watershed; Locations of Weather Stations, Gaging Station, Confined Feeding Operation Units, and Manure Application Areas Are Shown (Pandey et al., 2016).

# How do variations in intra-annual precipitation and temperature affect microbial water quality?



**Fig 6.** *E. coli* Levels (CFU/100 g) in the water column and stream flow in Squaw Creek Watershed (Pandey et al., 2016).

*Intra-annual temperature and precipitation patterns will significantly affect microbial water quality under current watershed management practices.*

# Thank you!



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