**Research article** 

## MODELING AND SIMULATION OF ENTEROMOBACTER INFLUENCED BY HOMOGENEOUS POROSITY IN PENETRATING SEMI CONFINED BED IN COASTAL AREA OF OKIRIKA, RIVERS STATE OF NIGERIA

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#### Abstract

Enteromobacter were predominantly deposited in the study location, such region deposit semi confined bed with high degree of porosity in homogenous stratification, the rate of Enteromobacter in the study environments where found to deposit high percentage from every investigation, solution to engineer this contaminant out proof abortive from previous investigation and recommendations. The study generated theoretical values from the model simulated, graphical representations shows exponential migration on rapid state of the microbes at different concentration, the structure of the formation developed slight variation in concentration but with fast degree of migration, theoretical results were compared with experimental values, both parameters produced a best fits validating the developed model for the study. Experts will fine this model favorable through the application of this conceptual frame work to prevent further migration of the Enteromobacter in semi confined beds.

Keywords: simulation, Enteromobacter, homogenous porosity and semi confined bed

#### 1. Introduction

There are lots of characteristics that affect the survival of pathogens in water, mainly bacteria and viruses, comprise temperature, pH, dissolved oxygen, water hardness, presence of organic material, exposure to sunlight,

the existence of other micro-organisms and water conductivity (O'Brien & Newman, 1977; Lund, 1978; Melnick & Gerba, 1980; Davies-Colley et al. 1994). Protozoan cysts live above a wide variety of Ph values and are opposed to to osmotic pressures. *Cryptosporidium* oocysts can survive for over one year in isotonic the solutions are from laboratory; this may remain viable for long time in aquatic environments (Smith et al. 1991). The foremost issue affecting cyst and also helminth egg survival in water temperature is the higher temperatures resulting in faster death (Feachem et al. 1983; O'Donohue, 1995: Eluozo, 2013). Pathogens are carried through water over quite large distances. Analysis done in Zambezi River express that the bacteria were still detected 18.6 km downstream from the source of pollution at levels at 1.4 x

103 E. coli/100 ml (Feresu & Van Sickle, 1990). Lund (1978) similarly observations were pressed in tropical waters. Too much quantity of fecal bacteria in surface water, these were found to increase the risk of bacteria-induced illness to humans (Frenzel and Couvillion, 2002). Payment et al. (2000) found that the presence of pathogenic microorganisms (human enteric virus, Cryptosporidium, and Giardia) deposited in Saint Lawrence River in Canada; this was comprehensively correlated with bacterial indicators (total coliform, fecal coliform, and Clostridium perfringens). Concentration rate of fecal coliform from 200 colony-forming units (cfu) per 100 mL of water was established as a water-quality standard by the Federal Water Pollution Control Administration of the Department of the Interior in 1968 (USEPA, 1986). Current research, however, established that fecal coliforms confound to deposit less correlation to swimming-associated gastroenteritis than the other two common indicator bacteria (Escherichia coli and enterococci), prompting a shift in the suggested indicator organisms (USEPA, 1998, 2002:Eluozo, 2013). Total coliform, fecal coliform, fecal streptococci, enterococci, and E. coli bacteria shows the existence of species used to recognize the potential presence of pathogens. Preferably indicators for pathogens exist in much greater concentrations, demonstrate similar die-off and re-growth formations, and are connected with the equivalent sources (Moore et al., 1982). The first indicator used to examine pollution of drinking water by human waste was total coliform. Since exact pathogens are very complicated to collect and culture, the total coliform assembly was initially selected as an indicator because it was easy to detect, easy to culture, and typically is connected with fecal pollution from warm-blooded animals (Larsen et al., 1994). However, total coliforms include several organisms exists in non-fecal sources, making this indicator group too broad to be a steadfast indicator of fecal pathogens (Rosen, 2000). Fecal coliforms are a subgroup of total coliforms that originate specifically from the intestinal tracts of warm- blooded animals. Fecal coliforms are the predominant indicator used to assess human health hazards in streams (Rosen, 2000), but E. coli and enterococci are thought to have a higher degree of association with outbreaks of gastrointestinal illness (USEPA, 1986). E. coli is a constituent of the fecal coliform group and includes the toxin-producing O157:H7 strain. Enterococci is a subgroup of fecal streptococci that belongs to the genus Streptococcus and differs from fecal coliforms in that enterococci are less abundant in feces, are not known to replicate in the environment, and are more resistant to environmental stress (Maier et al., 2000). Land application of waste from confined animal production facilities is an effective method of disposing of animal waste while supplying nutrients to crops and pastureland. However, it has been well-documented that runoff from agricultural livestock and poultry litter applied areas is a source of fecal contamination in water (Crowther

*et al.*, 2002; Edwards *et al.*, 1994, 2000; Gerba and Smith, 2005; Tian *et al.*, 2002). The EPA's National Water Quality Inventory report (USEPA, 2000) identified bacteria as the leading cause of impairments in rivers and streams in the United States and agricultural practices were identified as the leading source of all bacterial impairments Transport of animal manures into surface water bodies can be detrimental to the health of humans, animals, and the ecosystem (USEPA, 2003). Animal waste contains many different types of organisms pathogenic to humans and animals which could be transported into streams when over-applied to agricultural lands. More than 150 pathogens found in livestock manure are associated with risks to humans, including *Campylobacter spp.*, *Salmonella spp.*, *Listeria* 

#### 2. Governing Equation

$\phi \frac{\partial c_3}{\partial t} = K_c \frac{\partial c_3}{\partial x} \qquad \dots$	(1)
Let $C_3 = TX$	
$\frac{\partial c_3}{\partial t} = XT^1$	(2)
$\frac{\partial c_3}{\partial x} = X^{1}T$	(3)
$\phi T^1 X = K X^1 T$	(4)
$\phi \frac{T^1}{T} = K_c \frac{X^1}{X} = \varphi^2$	(5)
$\phi \frac{T^1}{T} = \varphi^2$	
$\frac{T^1}{T} = \frac{\varphi}{\phi}$	(7)
$LnT = \frac{\varphi^2}{\phi}t + a_4$	
i.e. $T = C_4 \ell^{\frac{\varphi^2}{\phi^t}}$	(9)
$T = \ell^{\frac{\varphi^2}{\phi}t}$	
$\phi \frac{T^1}{T} = K_c \frac{X^1}{X} = \varphi^2$	

$$\frac{dx}{dx} - \frac{\varphi^2}{Kc}x = 0 \tag{12}$$

Auxiliary equation

$$M^2 - \varphi^2 = 0$$
 (13)

$$M = \pm i \frac{\varphi}{\sqrt{Kc}} \tag{14}$$

$$X = K_c \ell^{\frac{\varphi}{K_c}x} + E \ell^{\frac{-\varphi}{K_c}x}$$
(15)

Combining (10) and (15) yield

$$C_3 = TX$$

i.e. 
$$C_3 = C_4 \ell^{\frac{\varphi}{\phi}_t} \left( K_c \frac{\varphi}{\sqrt{Kc}} x + E \ell^{\frac{-\varphi}{\sqrt{Kc}} x} \right)$$
 (16)

The generated expressed model at this stage shows the level of inhibition that may be establish on the process of deposition in some region of the soil structure, it may deposit transitory flow base on minor deposition of porosity reflecting on the speed of transport flow. The percentage of porosity in this condition determine the tempo of inhibition from arsenic and fungi at this phase of the migration process, the pressure from degree of porosity strong-minded the deposition of arsenic and other substances inhibiting microbes in the stratification of the soil structure

Let $C = TY$	(17)
$\frac{\partial c}{\partial t} = T^1 Y$	(18)
$\frac{\partial^2 c}{\partial y^2} = TY^{11}$	
$\phi T^1 Y = K_d T Y^{11} = \alpha^2$	
$\int \frac{dT}{T} = \int \frac{-\alpha^2}{\phi} dt$	
$LnT = \frac{-\alpha^2}{\phi}t + a_5$	
$T = \ell^{\frac{-\alpha^2}{\phi}t + a_5}$	

$$\frac{\partial^2 y}{\partial y^2} + \frac{\alpha^2}{K_d} y = 0$$
(26)

Auxiliary equation is

$$M^{2} + \frac{\alpha^{2}}{K_{d}} = 0$$
 (27)

$$M = \pm i \frac{\alpha}{\sqrt{K_d}} \tag{28}$$

Combine (58) and (63), we have

$$C_4 = TY$$

If 
$$T = \frac{d}{v}$$
 and  $X = v.t$ 

Therefore the final equation will be of this form

$$C_4 = C_5 \ell^{\frac{-\alpha^2}{\phi} \frac{d}{\nu}} \left( A \cos \frac{\alpha}{\sqrt{K_d}} \nu t + A \sin \frac{\alpha}{\sqrt{K_d}} \nu t \right) \qquad (30)$$

#### 3. Materials and method

Soil samples from several different boring locations, were collected at intervals between three and thirty meters. Soil sample were collected in five different location, applying insitu method of sample collection, the soil sample were collected for analysis, standard laboratory analysis were carried out to determine the Enteromobacter concentration through column experiment, the result were analyzed to determine the influence of Enteromobacter in semi confined bed in the study area.

### **4 Results and Discussion**

Results and discussion from the expressed figures through the theoretical generated values are presented in tables and figures, the expression explain the rate of concentration through graphical representation for every condition assessed in the developed model equations.

Depths [M]	Concentration
3	0.012
6	0.024
9	0.036
12	0.043
15	0.06
18	0.072
21	0.084
24	0.096
27	0.11
30	0.12

## Table 1: Concentration of Enteromobacter at Different Depths

#### **Table 2: Concentration of Enteromobacter at Different Depths**

Time Per Day	Concentration
10	0.012
20	0.024
30	0.036
40	0.043
50	0.06
60	0.072
70	0.084
80	0.096
90	0.11
100	0.12

# Table 3: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at Different Depths

Depths [M]	Theoretical Values	<b>Experimental Values</b>
3	0.012	0.014
6	0.024	0.026
9	0.036	0.035
12	0.043	0.045
15	0.06	0.06
18	0.072	0.074
21	0.084	0.086
24	0.096	0.098
27	0.11	0.11
30	0.12	0.13

## Table 4: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at Different Time

Time Per Day	Theoretical Values	Experimental Values
10	0.012	0.014
20	0.024	0.026
30	0.036	0.035
40	0.043	0.045
50	0.06	0.06
60	0.072	0.074
70	0.084	0.086
80	0.096	0.098
90	0.11	0.11
100	0.12	0.13

#### **Table 5: Concentration of Enteromobacter at Different Depths**

Depths [M]	Concentration
2	2.40E-03
4	4.81E-03
6	7.22E-03
8	9.62E-03
10	0.012
12	0.014
14	0.016
16	0.019
18	0.021
20	0.024

 Table 6: Concentration of Enteromobacter at Different Time

Time Per Day	Concentration
2	2.40E-03
4	4.81E-03
6	7.22E-03
8	9.62E-03
10	0.012
12	0.014
14	0.016
16	0.019
18	0.021
20	0.024

Table 7: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at
Different Time

Depths [M]	Theoretical Values	Experimental Values
2	2.40E-03	2.38E-03
4	4.81E-03	<b>4.78E-03</b>
6	7.22E-03	7.24E-03
8	9.62E-03	9.77E-03
10	0.012	0.014
12	0.014	0.016
14	0.016	0.018
16	0.019	0.021
18	0.021	0.023
20	0.024	0.026

Table 8: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at
Different Time

Time Per Day	Theoretical Values	Experimental Values
2	2.40E-03	2.38E-03
4	4.81E-03	4.78E-03
6	7.22E-03	7.24E-03
8	9.62E-03	9.77E-03
10	0.012	0.014
12	0.014	0.016
14	0.016	0.018
16	0.019	0.021
18	0.021	0.023
20	0.024	0.026





Figure 1: Concentration of Enteromobacter at Different Depths

Figure 2: Concentration of Enteromobacter at Different Depths



 Table 3: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at Different Depths



Figure 4: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at Different Time



**Figure 5: Concentration of Enteromobacter at Different Depths** 

![](_page_10_Figure_1.jpeg)

Figure 6: Concentration of Enteromobacter at Different Time

![](_page_10_Figure_3.jpeg)

![](_page_10_Figure_4.jpeg)

![](_page_11_Figure_1.jpeg)

Figure 8: Comparison of Theoretical and Experimental Values of Enteromobacter concentration at Different Time

The figure with graphical representation shows that the concentration maintained progressive phase on every location, this condition are base several development, in most cases it can be attributed to several conditions, the rate homogeneous porosity in semi confined bed was predominant in the study locations, the stratifications were subject of concern, since homogeneous deposition were predominant, also reflecting on the concentration of Enteromobacter in the environment. depositing semi confined bed are base on some sand stone within the formation its disintegration was in signification in those region of the formation, the deposition of overburden pressure developed it to semi confined bed, such condition influences the deposition of Enteromobacter in the study environment, the behaviour of the microbes are reflected on the geological setting of the study area, the expressed influences from the state formation pressured the migration of concentration were observed, because of the pressured influences from the predominant high degree of porosity, the simulated results were compare with experimental values, both parameters developed a favuorable fits validating the derived model for the study.

#### **5.** Conclusion

Semi confined bed are base on the deposition of sand stone or porous rocks in soil formation. Such deposition were experiences in Okirika region of River State, homogenous porosity were observed in the stratification of the formation, the reflection of this formation characteristics influences were found to reflects on the migration way of the microbes, exponential phase were experiences from the graphical representation of the microbes, base on this factors it is obvious that the contaminant if not managed properly will definitely cause lots of harm

to aquiferous zone, the study centred on semi confined bed under homogenous porosity, it implies that the rate of concentration will linearly migrated to semi confined bed, it will not experiences some natural significant degradation, that can deposit in some regions were the microbes may be very few to be given little treatment, the graphical representation show rapid migration to the optimum values at thirty metres, the simulated model developed a best fit after comparison with experimental values. This expression has validated the developed model for the study area.

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