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Numerical modeling and simulation to monitor dispersion pressure on the deposition of halobacterium in slight heterogeneous semi confined bed

Abstract

This paper monitor the rate of Halobacterium deposition in semi confined bed, the study observed the transport of this contaminant to be influenced by high deposition of porosity in the study area. The study has monitored the behavior of Halobacterium expressing the pressure from high degree of porosity in the deltaic formations. Application of numerical modeling and simulation were applied and it generated different concentration that ranged from 0.0334-0.8854, 0.111-0.67824, 4.0200-0.0012, 0.8720-7.400, and 0.1256-0.8793 few locations that observed higher concentration are definitely influenced by the deposition of high porosity, the study applying numerical simulation has monitored the contaminants more discrete generated through exact deposition of change in concentration with respect to depth, the predictive results were subjected to model validation with experimental values and both parameters developed faviourable fits.

Keywords: numerical modeling, dispersion, halobacterium, heterogeneous, semi confined bed

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Abbreviations: EPA, environmental protection agency; LMERS, lake michigan ecological research station; UTI, urinary tract infections

Introduction

Groundwater is considered to be of excellent quality because of the soil barrier providing effective isolation of this high quality source water from surface pollutants. This is true for most groundwater resources a lthough we know that many aquifers all over the world are polluted and/or is being polluted.[1–4] Habitats containing only a single kind of microorganism are found only in the laboratory. Natural habitats contain many kinds of organisms which interact in complex ways. The great reservoir of bacteria in nature is the soil, which contains both the largest population and the greatest variety of species. Most bacteria that are found in surface waters are derived from the soil. However, the quality of subsurface waters may be impacted both by naturally occurring processes as well as by actions directly attributable to human activities. The number and variety of the microorganisms in natural waters vary greatly in different places and under different conditions. Bacteria are washed into the water from the air, the soil and from almost every conceivable object. Significant numbers of bacteria can be removing through media even when the percentage retained is very high. The faeces of animals contain vast numbers of bacteria and many enter natural water systems. The sizes of openings in subsurface material can be assumed to be variable and are generally not measured, but porosity and permeability measurements on aquifer sediments indicate that adequate spaces for bacteria exist in many sediment types, even in some rather dense porous rocks.[5–8] The interstices of the shallow aquifer sediments can easily accommodate bacteria and probably protozoa and fungi as well. Larger organisms will be excluded from most subsurface formations, except for gravelly and cavernous aquifers[2,3,6] Microbiological pollution derived mostly from human and animal activities such as unsewered settlements; on-site sanitation; cemeteries; waste disposal; waste disposal; feedlots; etc. Microorganisms certainly will be the dominant forms of life and, in most cases; they will be the only forms of life present in aquifers. However, with very few exceptions the only waterborne microbial pathogens of man are essentially human bacteria, viruses and protozoa, and in considering the safety of drinking water from the point of view of infectious diseases one can almost completely ignore any source of infectious agents except human excreta. In relation to microbial pollution of groundwater it is therefore only necessary to ensure that at the point of extraction no contamination with human excreta occurs[1,3,5,8] bacteria are the bacteria most commonly associated with well water.

The United States environmental protection agency (EPA) standard for drinking water is a total coliforms count of zero. Coliforms bacteria are a large group of various rod-shaped species and strains of bacteria. The group includes bacteria that occur naturally in the intestines of warm-blooded animals (fecal coliforms) and no fecal coliforms. Non-fecal coliforms bacteria are very common and are found virtually everywhere on soil particles, insects, plants, animals, walls and furniture in homes and on your skin and clothes. Fecal coliforms can include disease causing (pathogen species) and non-disease causing species. Over 200 types of non-disease causing bacteria have been found in human digestive tracts. Most arrive on the food and drink we consume. Many yogurt cultures include coliforms bacteria. *Lactobacillus* acidophilus is the most common bacteria strain used in commercial yogurts and some studies show it creates an acidic environment that inhibits harmful bacteria in the digestive tract. *Escherichia* coli (*E. coli*), often listed in water quality analyses, is one species of fecal coliforms bacteria. A single *E. Coli* is 2 microns long

and about 0.5 microns in diameter. There are hundreds strains of *E. Coli* bacteria that differ only in the type of toxin or enzyme that they produce. Despite the fact that they originate in the digestive system of a warm-blooded creature, most *E. Coli* strains are not harmful to humans. *E. Coli* can be easily cultured in a laboratory and therefore, they are a good indicator species for bacterial contamination in water tests. Its presence in a water sample indicates that sewage material may be present and that if sewage is present, more harmful disease-causing organisms may also be present, and for example *Vibrio* cholerae that causes cholera.[9–12] Researchers today have discovered that *E. Coli* may not always be an effective indicator of water quality. While it is true that *E. Coli* is found in the intestines of warm blooded animals, scientists have recently revealed that *E. Coli* can also persist and perhaps thrive in many other natural environments.[13–15] Take soil for example. Research conducted at the USGS Lake Michigan Ecological Research Station (USGS LMERS) has shown that temperate forest soils in the Indiana Dunes harbor *E. Coli* throughout the entire year (winter included)! The sediments and soil in the watershed of Dunes Creek (a Lake Michigan tributary) contain *E. Coli*, and the persistently high *E. Coli* counts in Dunes Creek itself may be due to rainfall and stream flow eroding the sediment-borne bacteria into the water. In these cases there was no significant human fecal input, yet the *E. Coli* was there.[16,17] What about sand? *E. Coli* is found in beach sand as well! Bacteria harbored in sand may even persist longer than in water because the bacteria adhere to sediment particles, unlike bacteria that are free in the water.[12,15] Research has shown that *E. Coli* counts were higher in the near shore sand and submerged sand than in the beach water. Additionally, the *E. Coli* counts were typically several orders of magnitude higher in the sand than in the water. The geometric mean of *E. Coli* counted in the foreshore sand in a study on 63rd street beach in Chicago was 4,000 CFU's/ 100ml of water, as compared to only 43 CFU's /100ml water in the water.[12,15] How ironic that by closing the swimming waters that may have 240 colonies/100ml of water, we may actually be increasing the contact people have with even higher concentrations of *E. Coli* (sometimes as high as 11,000 CFU/100ml of water) in shallow water and sand.[12,14,15] Water samples for bacteria testing are collected and cultured, and then must incubate for 18hours before the colony growth is visible. Therefore, after a water sample is collected, results are not available until the next day." By that time, the bacteria levels in our beach waters may have changed significantly. In fact, most studies show little or no correlation between indicator levels from the sampling day to the next day when the results are actually used by the beach managers to make decisions about beach closings.[16] Urinary tract infections (UTI) are the most common nosocomial infections which accounts for 40% of hospital acquired infections.[10–12] *Escherichia coli* are the most frequently found bacteria in both community and hospital acquired UTIs.[14–16] In recent years antimicrobial resistance has emerged explosively in many diverse bacterial types largely as a consequence of unrestrained antimicrobial use in medicine.[7,8,10] This affects the management of UTI by increasing prevalence of multidrug resistant strains of *E. Coli*.[6,10] Therefore developing methods for accurate identification of multidrug resistant strains of *E .Coli* is mandatory.[6,9,10,13] In recent years several methods have been diffusion agar is a traditional and routine method of antimicrobial sensitivity testing. E-test provides a rapid and convenient means for determining minimal inhibitory concentration (MIC) for a variety of antimicrobial agents. Studies have shown that E-test shows good agreement with reference "agar dilution" susceptibility testing methods.[8,9] MIC determining methods like E-test, although provide quantitative measurement of antimicrobial sensitivity[11,16] because of their cost and limited availability in developing countries, their application is not as frequent as disk diffusion method.[14–16] Although, previous reports have compared E-test with disk diffusion in determining antimicrobial susceptibility, differences in their capabilities for selection of multidrug resistant strains of *E. Coli* in UTI has not been fully encountered. In this study we have compared E-test and disk diffusion results in finding out multidrug resistant strains of *E. Coli* in urinary tract infections.[6,7,17]

Governing equation

The Implicit Scheme Numerical Solution

$$\frac{\partial C}{\partial t}=\frac{Q}{A}\frac{\partial C}{\partial x}+D\frac{\partial^2 C}{\partial x^2}+\frac{qL_{IN}}{A}C \tag{1}$$

But $\frac{Q}{A}=$ Velocity, v in meter per second (m/s).

Thus equation (1) becomes:

$$\frac{\partial C}{\partial t}=v\frac{\partial C}{\partial x}+D\frac{\partial^2 C}{\partial x^2}+\frac{qL_{IN}}{A}C \tag{2}$$

Converting the PDE to its algebraic equivalent equation by applying the finite different approximation technique for the implicit scheme, we obtain as follows.

$$\frac{\partial C}{\partial t}=\frac{C_i^{j+1}-C_i^j}{\Delta t} \tag{3}$$

$$\frac{\partial C}{\partial x}=\frac{C_{i+1}^{j+1}-C_{i-1}^{j+1}}{2\Delta x} \tag{4}$$

$$\frac{\partial^2 C}{\partial x^2}=\frac{C_{i+1}^{j+1}-2C_i^{j+1}+C_{i-1}^{j+1}}{\Delta x^2} \tag{5}$$

Substituting equation (3) through (5) into (2) gives:

$$\frac{C_i^{j=1}-C_i^j}{\Delta t}=v\left[\frac{C_{i+1}^{j+1}-C_{i-1}^{j+1}}{2\Delta x}\right]+D\left[\frac{C_{i+1}^{j+1}-2C_i^{j+1}+C_{i-1}^{j+1}}{\Delta x^2}\right]+\frac{qL_{IN}}{A}C_i^{j+1}$$

$$C_i^{j+1}-C_i^j=\frac{\Delta t}{2\Delta x}v\left[C_{i+1}^{j+1}-C_{i-1}^{j+1}\right]+\frac{\Delta tD}{\Delta x^2}\left[C_{i+1}^{j+1}-2C_i^{j+1}+C_{i-1}^{j+1}\right]+\frac{\Delta tqL_{IN}}{A}C_l^{j+1}$$

$$C_i^{j+1}-C_i^j=\lambda\left(C_{i+1}^{j+1}-C_{i-1}^{j+1}\right)+K\left(C_{i+1}^{j+1}-2C_i^{j+1}+C_{i-1}^{j+1}\right)+\alpha C_i^{j+1}$$

Or

$$C_i^j+(\alpha-\lambda-2K-1)C_i^{j+1}+(\lambda+K)C_{i+1}^{j+1}+KC_{i-1}^{j+1}=0 \tag{6}$$

For cases where the initial and final conditions are given, boundary condition at the first node can be expressed as:

$$C_0^{j+1}=f_0\left(t^{j+1}\right) \tag{7a}$$

Hence, first node equation is expressed as:

$$C_i^j+(\alpha-\lambda-2K-1)C_i^{j+1}+(\lambda+K)C_{i+1}^{j+1}=-Kf_0\left(t^{j+1}\right) \tag{7b}$$

Similarly, the last node boundary condition is:

$$C_l^{j+1} = f_{l+1}\left(t^{j+1}\right) \tag{8a}$$

$$C_l^j + (\alpha-\lambda-2K-1)C_l^{j+1} + KC_{l-1}^{j+1} = -(\lambda+K)f_{l+1}\left(t^{j+1}\right) \tag{8b}$$

For

$1 \le x \le 9$ *and* $0 \le t \le 4$; and for the first instance, we obtain as follows:

At time=0(*i.e j*=0) :

$i = 1$,

$$C_1^0 + KC_0^1 + (\alpha-\lambda-2K-1)C_1^1 + (\lambda+K)C_2^1 = 0$$

$$C_1^0 + (\alpha-\lambda-2K-1)C_1^1 + (\lambda+K)C_2^1 = -Kf_0\left(t^1\right) \tag{9a}$$

$i = 2$,

$$C_2^0 + KC_1^1 + (\alpha-\lambda-2K-1)C_2^1 + (\lambda+K)C_3^1 = 0 \tag{9b}$$

$i = 3$,

$$C_3^0 + KC_2^1 + (\alpha-\lambda-2K-1)C_3^1 + (\lambda+K)C_4^1 = 0 \tag{9c}$$

$i = 4$,

$$C_4^0 + KC_3^1 + (\alpha-\lambda-2K-1)C_4^1 + (\lambda+K)C_5^1 = 0 \tag{9d}$$

$i = 5$,

$$C_5^0 + KC_4^1 + (\alpha-\lambda-2K-1)C_5^1 + (\lambda+K)C_6^1 = 0 \tag{9e}$$

$i = 6$,

$$C_6^0 + KC_5^1 + (\alpha-\lambda-2K-1)C_6^1 + (\lambda+K)C_7^1 = 0 \tag{9f}$$

$i = 7$,

$$C_7^0 + KC_6^1 + (\alpha-\lambda-2K-1)C_7^1 + (\lambda+K)C_8^1 = 0 \tag{9g}$$

$i = 8$,

$$C_8^0 + KC_7^1 + (\alpha-\lambda-2K-1)C_8^1 + (\lambda+K)C_9^1 = 0 \tag{9h}$$

$i = 9$,

$$C_9^0 + KC_8^1 + (\alpha-\lambda-2K-1)C_9^1 = -(\lambda+K)f_{10}\left(t^1\right) \tag{9i}$$

$$Atime, t = 0, C_1^0 = C_2^0 = C_3^0 = C_4^0 = C_5^0 = C_6^0 = C_7^0 = C_8^0 = C_9^0 = 0$$

Arranging equations (6a) through (6i) in vector matrix gives:

$$\begin{bmatrix} \omega & \lambda+K & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ K & \omega & \lambda+K & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & K & \omega & \lambda+K & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & K & \omega & \lambda+K & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & K & \omega & \lambda+K & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & K & \omega & \lambda+K & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & K & \omega & \lambda+K & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & K & \omega & \lambda+K \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & K & \omega \end{bmatrix} \begin{Bmatrix} C_1^1 \\ C_2^1 \\ C_3^1 \\ C_4^1 \\ C_5^1 \\ C_6^1 \\ C_7^1 \\ C_8^1 \\ C_9^1 \end{Bmatrix} = \begin{Bmatrix} -Kf_0\left(t^1\right) \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ -(\lambda+K)f_{10}\left(t^1\right) \end{Bmatrix}$$

Where:

$$\omega = (\alpha-\lambda-2K-1)$$

Hence, at any point with time, the general form of the above equation is presented as:

$$\begin{bmatrix} \omega & \lambda+K & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ K & \omega & \lambda+K & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & K & \omega & \lambda+K & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & K & \omega & \lambda+K & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & K & \omega & \lambda+K & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & K & \omega & \lambda+K & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & K & \omega & \lambda+K & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & K & \omega & \lambda+K \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & K & \omega \end{bmatrix} \begin{Bmatrix} C_1^{j+1} \\ C_2^{j+1} \\ C_3^{j+1} \\ C_4^{j+1} \\ C_5^{j+1} \\ C_6^{j+1} \\ C_7^{j+1} \\ C_8^{j+1} \\ C_9^{j+1} \end{Bmatrix} = \begin{Bmatrix} -Kf_0\left(t^{j+1}\right) \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ -(\lambda+K)f_{l+1}\left(t^{j+1}\right) \end{Bmatrix}$$

Method of application

numerical Method were applied through the developed system to generate the governing equations, derived solution generated the derived model solution, this were simulated to monitor the contaminants at different depth, values of contaminant known as concentration at different depth were generated, this results are within the values of concentration from other experimental values from the same contaminant by other experts, validation of the developed through is concept is for monitoring such microbes in deltaic environment.

Results and discussion

Results and discussion are presented in tables including graphical representation for Acetobacter stated below. The study express these values through graphical representation as it monitor the Halobacterium at different deposition. Figure 1 shows that the behavior of the microbes migrates under exponential phase with sudden slight decrease between 10-15m thus rapidly increase to the optimum values at 30m, Figure 2 developed rapid exponential migration to the optimum level recorded at 30m, Figure 3 observed the migration experiencing degradation with respect to depth, high to low concentration of Halobacterium were observed in the study location, Figure 4 experiences sudden increase from initial Concentration and rapidly experienced increase were it observed slight decrease between 20-25m, fluctuating to maximum rate at 30m, Figure 5 observed Halobacterium with linear homogeneous increase to the optimum level recorded at 30m while Figures 6-10 where compared with experimental values for model validation and bother parameters developed faviourable fits (Tables 1-10).

Citation: Eluozo SN, Amagbo LG, Afiibor B. Numerical modeling and simulation to monitor dispersion pressure on the deposition of halobacterium in slight heterogeneous semi confined bed. *MOJ App Bio Biomech.* 2017;1(4):153–159. DOI: 10.15406/mojabb.2017.01.00024

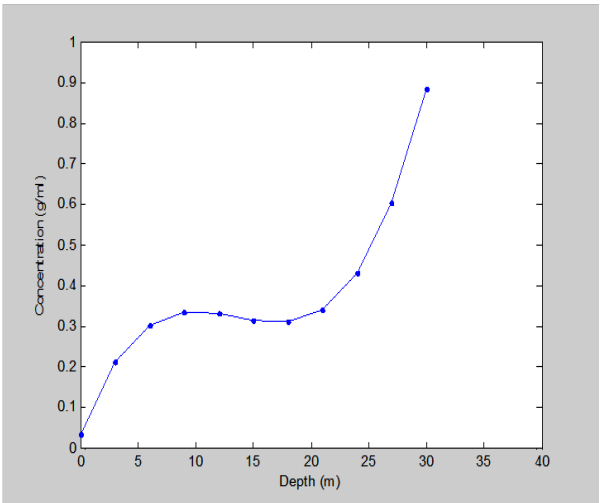

Figure 1 Simulation Values from Halobacterium Concentration at Different Depth.

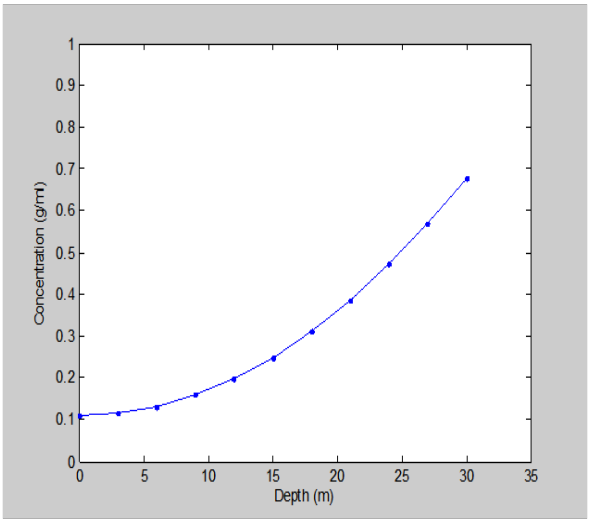

Figure 2 Simulation Values from Halobacterium Concentration at Different Depth.

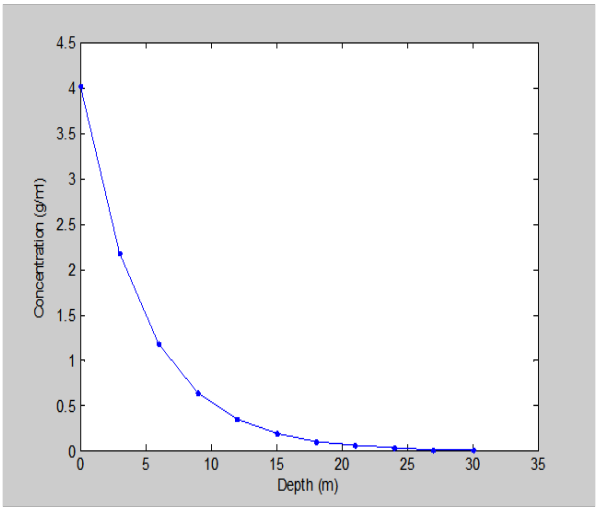

Figure 3 Simulation Values from Halobacterium Concentration at Different Depth.

Table 1 Simulation Values from Halobacterium Concentration at Different Depth

Depth(m)	Concentration(g/ml)
0	0.0334
3	0.2106
6	0.3034
9	0.3359
12	0.3319
15	0.3154
18	0.3105
21	0.341
24	0.431
27	0.6045
30	0.8854

Table 2 Simulation Values from Halobacterium Concentration at Different Depth

Depth(m)	Concentration(g/ml)
0	0.111
3	0.115074
6	0.130848
9	0.158322
12	0.197496
15	0.24837
18	0.310944
21	0.385218
24	0.471192
27	0.568866
30	0.67824

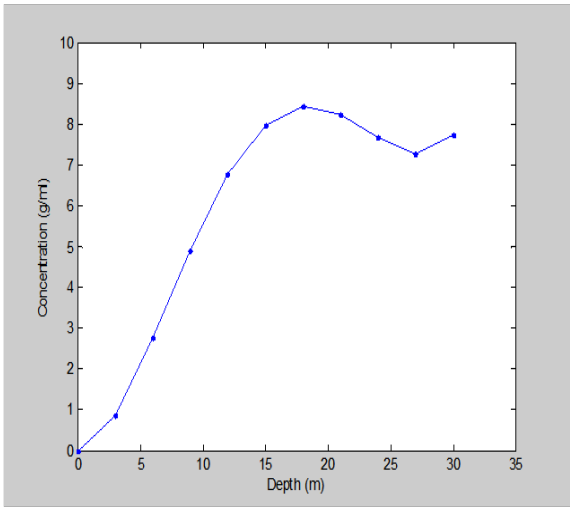

Figure 4 Simulation Values from Halobacterium Concentration at Different Depth.

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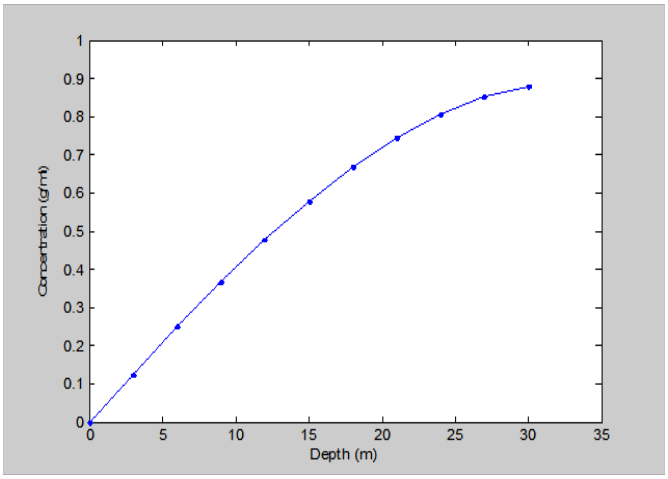

Figure 5 Simulation Values from Halobacterium Concentration at Different Depth.

Table 3 Simulation Values from Halobacterium Concentration at Different Depth

Depth(m)	Concentration(g/ml)
0	4.02
3	2.1723
6	1.1738
9	0.6342
12	0.3426
15	0.1849
18	0.0995
21	0.0529
24	0.0271
27	0.0118
30	0.0012

Table 4 Simulation Values from Halobacterium Concentration at Different Depth

Depth(m)	Concentration(g/ml)
0	0
3	0.872
6	2.7634
9	4.9094
12	6.7594
15	7.9763
18	8.437
21	8.2322
24	7.6666
27	7.2584
30	7.74

Table 5 Simulation Values from Halobacterium Concentration at Different Depth

Depth(m)	Concentration(g/ml)
0	0
3	0.1256
6	0.2487
9	0.3668
12	0.4776
15	0.5788
18	0.6684
21	0.7446
24	0.806
27	0.8512
30	0.8793

Table 6 Predictive and Experimental Values from Halobacterium Concentration at Different Depth

Depth(m)	Predictive conc. (g/ml)	Experimental values conc.(g/ml)
0	0.0334	0.032
3	0.2106	0.244
6	0.3034	0.398
9	0.3359	0.352
12	0.3319	0.306
15	0.3154	0.362
18	0.3105	0.414
21	0.341	0.468
24	0.431	0.522
27	0.6045	0.676
30	0.8854	0.831

Table 7 Predictive and Experimental Values from Halobacterium Concentration at Different Depth

Depth(m)	Predictive conc. (g/ml)	Experimental values Conc. (g/ml)
0	0.111	0.023
3	0.115074	0.077
6	0.130848	0.131
9	0.158322	0.185
12	0.197496	0.239
15	0.24837	0.293
18	0.310944	0.247
21	0.385218	0.401
24	0.471192	0.455
27	0.568866	0.509
30	0.67824	0.563

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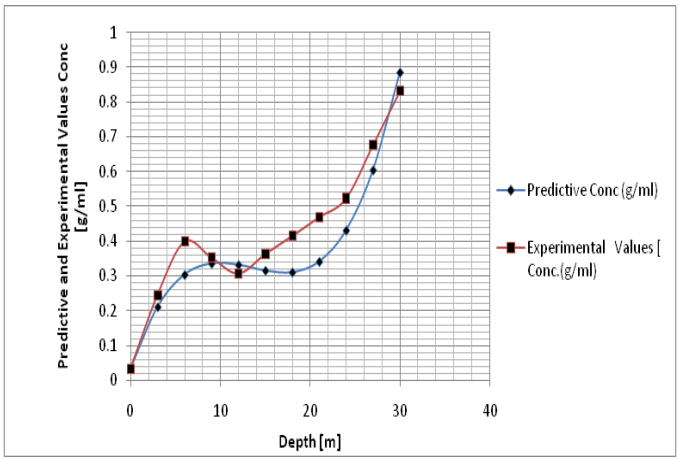

Figure 6 Predictive and Experimental Values from Halobacterium Concentration at Different Depth.

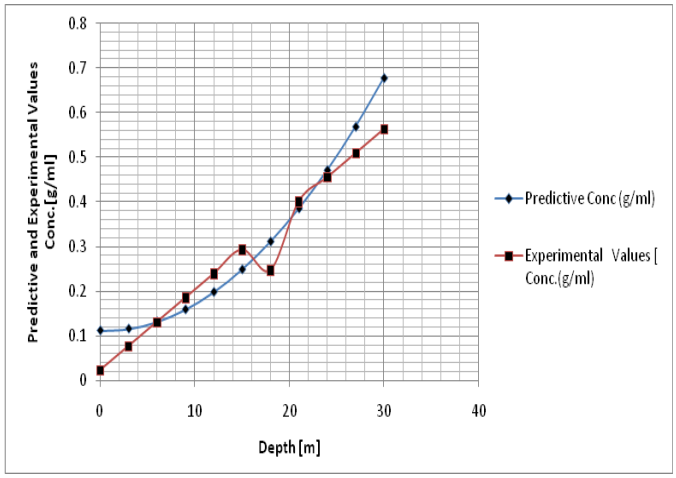

Figure 7 Predictive and Experimental Values from Halobacterium Concentration at Different Depth.

Table 8 Predictive and Experimental Values from Halobacterium Concentration at Different Depth

Depth(m)	Predictive conc.(g/ml)	Experimental values conc.(g/ml)
0	4.02	3.403
3	2.1723	2.45
6	1.1738	1.637
9	0.6342	0.968
12	0.3426	0.443
15	0.1849	0.062
18	0.0995	-0.175
21	0.0529	-0.268
24	0.0271	-0.217
27	0.0118	-0.022
30	0.0012	0.317

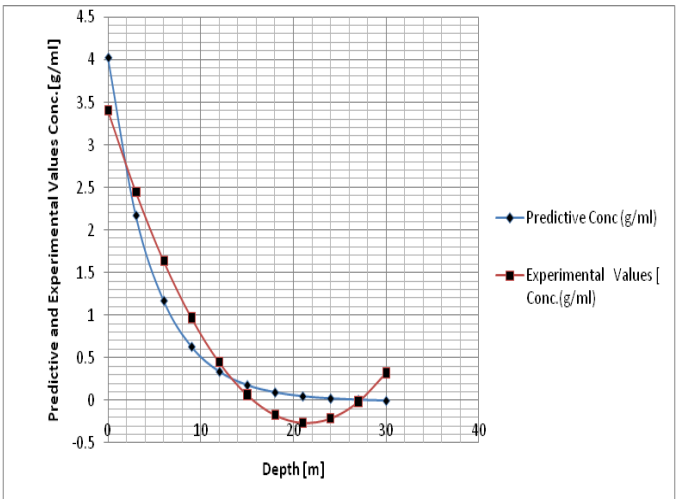

Figure 8 Predictive and Experimental Values from Halobacterium Concentration at Different Depth.

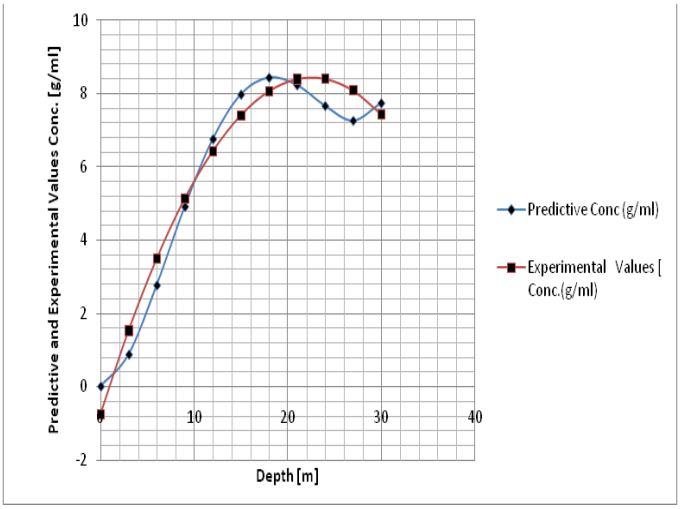

Figure 9 Predictive and Experimental Values from Halobacterium Concentration at Different Depth.

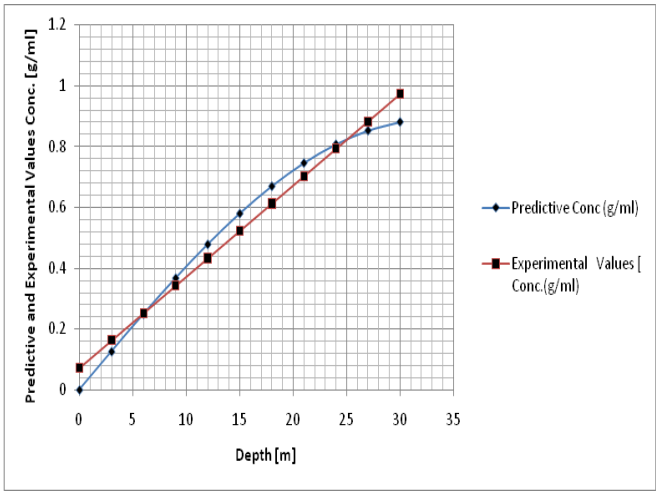

Figure 10 Predictive and Experimental Values from Halobacterium Concentration at Different Depth.

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Table 9 Predictive and Experimental Values from Halobacterium Concentration at Different Depth

Depth(m)	Predictive conc. (g/ml)	Experimental values conc. (g/ml)
0	0	-0.738
3	0.872	1.536
6	2.7634	3.486
9	4.9094	5.122
12	6.7594	6.414
15	7.9763	7.392
18	8.437	8.046
21	8.2322	8.376
24	7.6666	8.382
27	7.2584	8.064
30	7.74	7.422

Table 10 Predictive and Experimental Values from Halobacterium Concentration at Different Depth

Depth(m)	Predictive conc.(g/ml)	Experimental values[conc.(g/ml)
0	0	0.071
3	0.1256	0.161
6	0.2487	0.251
9	0.3668	0.341
12	0.4776	0.431
15	0.5788	0.521
18	0.6684	0.611
21	0.7446	0.701
24	0.806	0.791
27	0.8512	0.881
30	0.8793	0.971

Conclusion

The study of Halobacterium has been monitored at different simulation values expressed through graphical representation, the deposition of the Halobacterium were observed to be influences by various depositional structure of the formation, these conditions explained the rates of Halobacterium depositions in the study locations, the transport process were thoroughly observed to migrates through the behavior of the soil in semi confined bed. The results from these locations explain the depositions of the formation in semi confined under the pressure of high rate of porosity, this were observed to deposit at different structure of semi confined aquifers. The simulation values were subjected to model validation and both parameters developed faviourable fits.

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None.

Conflicts of interest

Author declares that there is no conflict of interest.

References

1. Whitman B, Shively, F. Growth Potential of Indicator Bacteria, E.coli and Enterococci, in Natural Temperate and Tropical Soils. *5th International Symposium on the Sediment Quality Assessment*. Aquatic Ecosystem and Health Management Society. USA; 2002. p. 16–18.
2. Engelbrecht JFP, Tredoux. *G bacteria in "unpolluted" groundwater Presented at the WISA 2000 Biennial Conference*. Sun City, South Africa; 2000. p. 1–2.
3. Engelbrecht JFP. *An assessment of health aspects of the impact of domestic and industrial waste disposal activities on groundwater resources*. USA; 1993.
4. Ghiores WC, Wilson JT. Microbial ecology of the Terrestrial Subsurface. *Advances in Applied Microbiology*. 1988;33:107–172.
5. American Ground Water Trust. *Coliform and E.Coli bacteria*. USA: well owner; 2002.
6. Whitman RL, Nevers MB. Foreshore Sand as a Source of *Escherichia coli* in Near shore Water of a Lake Michigan Beach. *Applied and Environmental Microbiol*. 2003;69(9):5555–5562.
7. Whitman RL, Nevers MB. Escherichia coli Sampling Reliability at a Frequently Closed Chicago Beach: Monitoring and Management Implications. *Environ Sci Technol*. 2004;38(16):4241–4246.
8. Whitman RL, Shively DA, Pawlik H, et al. Occurrence of Escherichia coli and Enterococci in Cladophora (Chlorophyta) in Near shore Water and Beach Sand of Lake Michigan. *Appl Environ Microbiol*. 2003;69(8):4714–4719.
9. Rabinovici SJ, Bernknopf RL, Wein AM, et al. Economic Trade-Offs of Swim Closures at a Lake Michigan Beach. *Environ Sci Technol*. 2004;38(10):2737–2745.
10. Erfani Y, Rasti A, Mirsalehian SM, et al. E-test versus disk diffusion method in determining multidrug resistant strains of *Escherichia coli* in urinary tract infection. *African Journal of Microbiology Research*. 2011;5(6):608–611.
11. Daza R, Gutierrez J, Piedrola G. Antibiotic susceptibility of bacterial strains isolated from patients with community-acquired urinary tract infections. *Int J Antimicrob Agents*. 2001;18(3):211–215.
12. Erfani Y, Choobineh H, Safdari R, et al. Comparison of E-test and Disk Diffusion Agar in amtibiotic Suseceptibility of *E. coli* Isolated from patients with urinary tract infections in Shariati Hospital(Iran). *Res J Biol Sci*. 2008;15(2):27–31.
13. Farrell DJ, Morrissey I, Robbins M, et al. A UK mulicenre sud of The Antimicrobial Susceptibility of Bacterial Pathogens Causing Urinary tract Infections. *J Infect*. 2003;46(2):94–100.
14. Giamarellou H, Poulakou G. Multidrug-resistant Gramnegative infections: what are the treatment options? *Drugs*. 2009;69(14):1879–1901.
15. Rahbar M, Yaghoobi M, Fattahi A. Comparison of different laboratory methods for detection of Methicillin Resistant *Staphylococcus aureus*. *Pak J Med Sci*. 2006;22(4):442–445.
16. Katz OT, Peled N, Yagupsky P. Evaluation of the current NCCLS guidelines for creening and confirming extended-spectrum beta-lactamase production in isolates of *E. Coli* and *Klebsiella* species from bacteremic patients. *Eur J Clin Microbiol Infect Dis*. 2004;23(11):813–817.
17. Eluozo SN. Predictive model to monitor the transport of *E. Coli* in homogeneous aquifers in port harcourt Niger delta of Nigeria. Scientific Journal of Pure and Applied Sciences 2013;2(3):140–150.