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 favourable fits.

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

Abbreviations: EPA, environmental protection agency; LMER8, 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 though 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 aquifers5,6. 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 occurs5,6.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

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Governing equation

The Implicit Scheme Numerical Solution

\[
\frac{\partial C}{\partial t} = \frac{Q \partial C}{A \partial x} + D \frac{\partial^2 C}{\partial x^2} + \frac{qL_{IN}}{A} \frac{C}{C_j^{i+1}}
\]

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

Thus equation (1) becomes:

\[
\frac{\partial C}{\partial t} = \frac{\partial^2 C}{\partial x^2} + \frac{qL_{IN}}{A} \frac{C}{C_j^{i+1}}
\]

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

\[
\frac{C_j^{i+1} - C_j^{i}}{\Delta t} = \frac{C_j^{i} - C_j^{i+1}}{2\Delta x} + D \frac{C_j^{i+1} - 2C_j^{i} + C_j^{i-1}}{\Delta x^2} + \frac{qL_{IN}}{A} \frac{C}{C_j^{i+1}}
\]

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

\[
\frac{C_j^{i+1} - C_j^{i}}{\Delta t} = \frac{C_j^{i} - C_j^{i+1}}{2\Delta x} + D \left[ \frac{C_j^{i+1} - 2C_j^{i} + C_j^{i-1}}{\Delta x^2} \right] + \frac{qL_{IN}}{A} \frac{C}{C_j^{i+1}}
\]

Or

\[
C_j^{i+1} = \frac{\Delta t}{2\Delta x} \left( C_j^{i+1} - C_j^{i} \right) + D \left[ \frac{C_j^{i+1} - 2C_j^{i} + C_j^{i-1}}{\Delta x^2} \right] + \frac{qL_{IN}}{A} \frac{C}{C_j^{i+1}}
\]

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

\[
C_j^{i+1} = f_i \left( t^{i+1} \right)
\]

Hence, first node equation is expressed as:

\[
C_j^{i+1} = \left( \alpha - \lambda - 2K - 1 \right) C_j^{i+1} + (\lambda + K) C_j^{i+1} = 0
\]
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Similarly, the last node boundary condition is:

\[
C_{i}^{j+1} = f_{i}^{j+1} (t^{j+1}) \quad (8a)
\]

\[
C_{i}^{j} + (\alpha - \lambda - 2K - 1) C_{i}^{j+1} + KC_{i-1}^{j+1} = - (\lambda + K) f_{i}^{j+1} (t^{j+1}) \quad (8b)
\]

For

\[1 \leq x \leq 9 \text{ and } 0 \leq t \leq 4; \]

and for the first instance, we obtain as follows:

At time \(t = 0\) (i.e. \(j = 0\)):

\[i = 1,\]

\[
C_{1}^{0} + KC_{0}^{0} + (\alpha - \lambda - 2K - 1) C_{1}^{1} + (\lambda + K) C_{1}^{1} = 0 \quad (9a)
\]

\[i = 2,\]

\[
C_{2}^{0} + KC_{1}^{0} + (\alpha - \lambda - 2K - 1) C_{2}^{1} + (\lambda + K) C_{2}^{1} = 0 \quad (9b)
\]

\[i = 3,\]

\[
C_{3}^{0} + KC_{2}^{0} + (\alpha - \lambda - 2K - 1) C_{3}^{1} + (\lambda + K) C_{3}^{1} = 0 \quad (9c)
\]

\[i = 4,\]

\[
C_{4}^{0} + KC_{3}^{0} + (\alpha - \lambda - 2K - 1) C_{4}^{1} + (\lambda + K) C_{4}^{1} = 0 \quad (9d)
\]

\[i = 5,\]

\[
C_{5}^{0} + KC_{4}^{0} + (\alpha - \lambda - 2K - 1) C_{5}^{1} + (\lambda + K) C_{5}^{1} = 0 \quad (9e)
\]

\[i = 6,\]

\[
C_{6}^{0} + KC_{5}^{0} + (\alpha - \lambda - 2K - 1) C_{6}^{1} + (\lambda + K) C_{6}^{1} = 0 \quad (9f)
\]

\[i = 7,\]

\[
C_{7}^{0} + KC_{6}^{0} + (\alpha - \lambda - 2K - 1) C_{7}^{1} + (\lambda + K) C_{7}^{1} = 0 \quad (9g)
\]

\[i = 8,\]

\[
C_{8}^{0} + KC_{7}^{0} + (\alpha - \lambda - 2K - 1) C_{8}^{1} + (\lambda + K) C_{8}^{1} = 0 \quad (9h)
\]

\[i = 9,\]

\[
C_{9}^{0} + KC_{8}^{0} + (\alpha - \lambda - 2K - 1) C_{9}^{1} = - (\lambda + K) f_{i}^{10} (t^{j}) \quad (9i)
\]

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

\[
\begin{pmatrix}
C_{1}^{0} \\
C_{2}^{0} \\
C_{3}^{0} \\
C_{4}^{0} \\
C_{5}^{0} \\
C_{6}^{0} \\
C_{7}^{0} \\
C_{8}^{0} \\
C_{9}^{0}
\end{pmatrix}
= \begin{pmatrix}
- KC_{1}^{1} \\
- KC_{2}^{1} \\
- KC_{3}^{1} \\
- KC_{4}^{1} \\
- KC_{5}^{1} \\
- KC_{6}^{1} \\
- KC_{7}^{1} \\
- KC_{8}^{1} \\
- KC_{9}^{1}
\end{pmatrix}
\]

\[
C_{1}^{0} = C_{2}^{0} = C_{3}^{0} = C_{4}^{0} = C_{5}^{0} = C_{6}^{0} = C_{7}^{0} = C_{8}^{0} = C_{9}^{0} = 0 \quad (10)
\]

\[
\omega = (\alpha - \lambda - 2K - 1)
\]

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

\[
\begin{pmatrix}
C_{1}^{0} \\
C_{2}^{0} \\
C_{3}^{0} \\
C_{4}^{0} \\
C_{5}^{0} \\
C_{6}^{0} \\
C_{7}^{0} \\
C_{8}^{0} \\
C_{9}^{0}
\end{pmatrix}
= \begin{pmatrix}
- KC_{1}^{1} \\
- KC_{2}^{1} \\
- KC_{3}^{1} \\
- KC_{4}^{1} \\
- KC_{5}^{1} \\
- KC_{6}^{1} \\
- KC_{7}^{1} \\
- KC_{8}^{1} \\
- KC_{9}^{1}
\end{pmatrix}
\]

\[
C_{1}^{0} = C_{2}^{0} = C_{3}^{0} = C_{4}^{0} = C_{5}^{0} = C_{6}^{0} = C_{7}^{0} = C_{8}^{0} = C_{9}^{0} = 0 \quad (11)
\]

**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 contaminant 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 favourable fits (Tables 1-10).

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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 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.

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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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                          |

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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                   | 8.064                            |
| 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 deposition in the study locations, the transport process were thoroughly observed to migrates through the rates of Halobacterium depositions in the study locations, the depositional structure of the formation, these conditions explained the rates of Halobacterium were observed to be influences by various depositional structure of the formation, these conditions explained the rates of Halobacterium deposition in the study locations, the transport process were thoroughly observed to migrates through the rates of Halobacterium depositions in the study locations, the depositional structure of the formation, these conditions explained.

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None.

Conflicts of interest

Author declares that there is no conflict of interest.

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