

COMPARISON OF BACTERIA GROWTH SIMULATION RESULTS FOR WATER RECYCLING AND PLUG FLOW TYPE REACTOR

T. Juhna, A. Kolyshkin, I. Lukyanets, S. Nazarovs, J. Rubulis, A. Spalvins

1 INTRODUCTION

The quality of drinking water should not change during transport in water distribution networks from water treatment plant to the consumers. In particular, microbiological contamination should be minimized in order to avoid negative impact on human health. Although water is usually purified, bacteria may enter distribution networks in small amounts and if conditions are favourable they start to grow (regrow) in water phase and on the pipe surfaces to form biological sediments (biofilm). This process leads to deterioration of microbiological quality of drinking water. Regrowth of bacteria in drinking water distribution pipes has been analyzed by many authors [1,2,3,5,6]. Mathematical models were applied to simulate behaviour of bacteria in distribution networks. It has been found that there are several mechanisms involved in bacteria multiplication including bacteria attachment to the surfaces, growth on the surface in biofilm and bulk phase, biofilm detachment from pipe walls, nutrient uptake, bacteria growth inhibition by chlorine. To control bacteria regrowth in distribution networks, there is a need to better understand interaction between the regrowth governing mechanisms and how different factors are affecting them. Mathematical modelling of regrowth of microorganisms is much less time consuming approach than experimental research. The validation of mathematical model against experimental data is important step in model development. Due to complicated sampling procedure of water and biofilm samples, uncertainty of estimation of actual water residence time and influence of unspecified factors (corrosion, turbidity, loose deposits) verification of mathematical models in full scale is not always successful. Therefore, the first step in validation of mathematical models would be application of experimental devices which allow to mimic real water distribution network but under strictly control conditions. Two types of reactors are used: perfectly mixed with water recycling (PMWR) and plug flow (PF) reactors. Although flow conditions in both reactors are different both have been used to investigate biofilm formation in the real distribution networks. There are at least two major differences between PMWR and PF reactors. Firstly, boundary conditions used for a pipe are not applicable for PMWR, as water in reactor is recycled while water in a pipe is constantly replaced by a fresh one. Secondly, due to a limited length of PMWR reactor, the assumption of fully developed flow used in Zhang et al. [7] may be violated. If the flow is fully developed then the velocity vector has only one nonzero longitudinal component which is independent on a radial coordinate. Unlike in PF reactor, the flow in PMWR models is not one-dimensional.

Mathematical models for bacteria regrowth proposed in the literature (see, for example, [7]) are usually derived for the case of a single straight long pipe or a system of straight long pipes which are assumed as PF reactors. The objective of this study was to develop model for PMWR reactors. By comparing results from PF and PMWR reactors we intended to test common perception of similar behaviour of bacteria in both type of reactors in long term.

2. EXPERIMENTAL SETUP

Propella® (Xenard, Mechanique de Precision, Seichamps, France) was used as PMWR reactor in this study. This reactor has been widely applied before and it allows simultaneously to control temperature, flow velocity, hydraulic residence time and Reynolds number, as well as the nature of the material being tested. Propella® reactor consisted of a 500 mm long 100 mm diameter water distribution pipe made of high-density polyethylene (HDPE) with an approximate volume of 2.23 L. A propeller inside the inner cylinder establishes and controls the flow between the cylinder and the pipe wall. The retention time was controlled by the inlet flow. Constant temperature in Propella® is maintained by circulation of raw water trough the inner cylinder (height 460 mm, internal diameter 44.0 mm, external diameter 72.5 mm) of reactor. The formation of a biofilm on the pipe wall and the concentration of embedded bacterial cells were studied using 20 PVC coupons (1.7 cm²) that were installed into the inner surface of the pipe wall. Flow velocity along the pipe wall of 0.2 m/s and a residence time of 15 hours. The same typical parameters were used in Propella® reactor experiment by Dailloux et al., [3]. 100 m pipe with diameter of 100 mm was used as PF type of reactor. No recycling of water was occurring in the reactor. Flow velocity along the pipe wall was assumed as 0.2 m/s.

3. MATHEMATICAL MODEL

In this study, we consider growth of biofilm bacteria and free bacteria in both water distribution pipe (PF reactor) and Propella® reactor (PMWR reactor) affected by substrate (biologically degradable organic carbon), chlorine and temperature. We used model developed by Zhang et al. [7] which suggest that the equations governing the concentration of chlorine, substrate and both free and attached bacteria are:

$$\frac{\partial X_b}{\partial t} = -v \frac{\partial X_b}{\partial x} + D_d \frac{\partial^2 X_b}{\partial x^2} + \mu_b X_b + k_{\text{det}} X_a v / R_h - k_d X_b - k_{\text{dep}} X_b \quad (1)$$

$$\frac{\partial X_a}{\partial t} = \mu_a X_a - k_{\text{det}} X_a v - k_d X_a + K_{\text{dep}} X_b R_h \quad (2)$$

$$\frac{\partial S}{\partial t} = -v \frac{\partial S}{\partial x} + D_d \frac{\partial^2 S}{\partial x^2} - \left(\frac{1}{Y_g \beta} \right) \left(\frac{\mu_a X_a}{R_h} + \mu_b X_b \right) \quad (3)$$

$$\frac{\partial Cl_2}{\partial t} = -v \frac{\partial Cl_2}{\partial x} + D_d \frac{\partial^2 Cl_2}{\partial x^2} - k_b Cl_2 - k_w / R_h \quad (4)$$

where Cl_2 is concentration of chlorine in water, D_d is dispersion and diffusion coefficient of the flow, k_b is first-order kinetic constant for chlorine decay in bulk water, k_d is bacterial mortality rate, k_{dep} is first-order kinetic constant for free bacteria to deposit onto pipe wall, k_{det} is first-order kinetic constant for bacteria detachment, k_w is zero-order wall reaction, R_h is hydraulic radius, S is concentration of biodegradable carbonated substrate (nutrient medium) in water, X_a is concentration of attached bacteria in biofilm on inner surface of pipe wall,

X_b is free bacteria in bulk water, Y_g is growth yield coefficient of bacteria, β is equivalent number of bacteria for 1 mg organic carbon in cell biomass, μ_a is specific growth rate of attached bacteria in biofilm, μ_b is specific growth rate of free bacteria in bulk water. Detailed description of all the coefficients used in the model is given in Zhang et al. [7].

Problem (1) – (4) was solved by DMOLCH routine included in the IMSL library. For simulation of Propella® reactor the solution is obtained for 0.1 m/s flow of water in a 1 m long pipe (one cycle in a 500-mm Propella® reactor). The selected simulation period is equal to 10 min., this is the time needed for water to make a completed loop. The initial and boundary conditions are:

$$\begin{aligned}
 X_a(0,t) = 0 \text{ cell/cm}^2 \quad \frac{\partial X_a(1,t)}{\partial x} = 0 \quad X_a(x,0) = 0 \\
 X_b(0,t) = 10 \text{ cell/mL} \quad \frac{\partial X_b(1,t)}{\partial x} = 0 \quad X_b(x,0) = 0 \\
 Cl_2(0,t) = 1 \text{ mg/L} \quad \frac{\partial Cl_2(1,t)}{\partial x} = 0 \quad Cl_2(x,0) = 0 \\
 S(0,t) = 0.4 \text{ mg/L} \quad \frac{\partial S(1,t)}{\partial x} = 0 \quad S(x,0) = 0
 \end{aligned} \tag{5}$$

After the simulation of a one single loop was completed, the boundary values on the right side were copied to the left side thus representing a closed cycle. Then a simulation for another 10 min. was performed and data for next cycle were acquired. This process was repeated 7200 times, so 200 hours of water flow in Propella® reactor were simulated. For comparison, data of the last 100 cycles (last 100 meters of flow) were taken. For pipe simulation the solution was obtained for the same flow velocity and pipe diameter for 100 m long pipe. The initial and boundary conditions were the same as in (5).

4. RESULTS AND DISCUSSION

As it has already been stated above, there are differences between flow models in the Propella® reactor and in the pipe. Water in the pipe is continuously replaced and the boundary conditions remain unchanged during the whole simulation period. In the Propella® reactor water is flowing in a closed loop, and is replaced after every 15 h during the whole simulation period, and boundary conditions change at each simulation cycle.

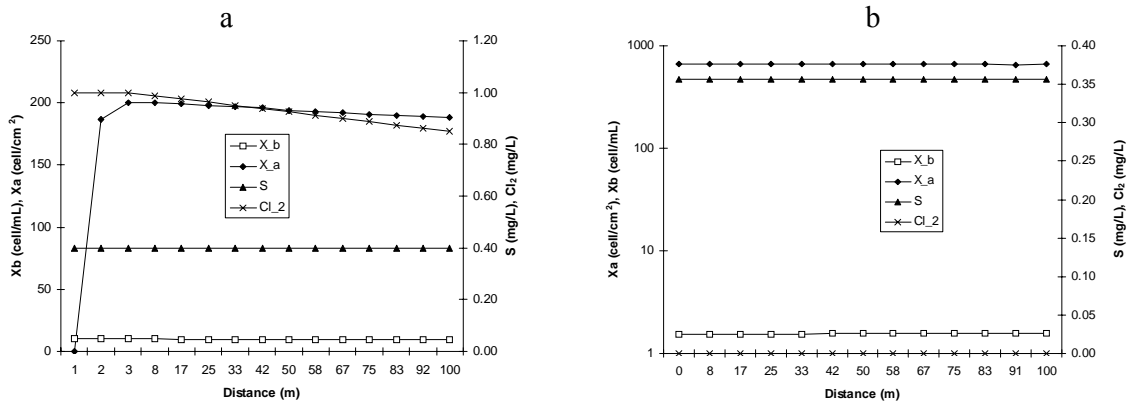


Figure. Results from bacteria regrowth simulation in (a) pipe (as a model of PF type of reactor) and (b) in Propella® (as PMWR type of reactor) (Y-axis in log scale, on X-axis the last 100 m are shown). Notes: X_b - bacterial number in water, X_a - bacterial number in biofilm, S- substrate (biodegradable organic carbon), Cl_2 – residual chlorine concentration.

Figure presents results of 200 h bacteria growth simulation in the 100 meter long pipe (as PF reactor) and in the Propella® reactor (as PMWR reactor). Biofilm bacteria concentration (X_a) goes to zero at the left side of the pipe (Figure, a) according to the boundary value. The constant bacterial number is reached after about 3m in pipe reactor. Further all values are relatively constant except concentration of chlorine. Mathematical models showed that the chlorine concentration decreases gradually from 1 mg/L to about 0.85 after 100 m of water passage in the pipe, whereas in Propella®, the chlorine level dropped below 0.1 mg/L after 2.5 hours during every cycle (data not shown). This can not be observed in Figure (b) as only the last 100 m of water passage through the reactor are shown. It is because water in the Propella® reactor is replaced every 15 hours whereas simulation results are shown for the last minutes of experiment when chlorine is completely consumed. These results agree well with data observed in the full scale studies [4]. The model also shows that bacteria number in biofilm (X_a) in reactor with high concentration of chlorine is lower: in Propella® bacteria number in biofilm was about 5 times higher than in the pipe. This could be explained by the inhibitory effect of chlorine on bacterial growth. In turn, the higher total (biofilm and water phase) bacterial number in Propella® leads to lower concentration of substrate, because; in the reactor with higher bacterial number, more of substrate is consumed by bacteria.

In general, the results from model simulation are in agreement with a common understanding of behaviour of bacteria in drinking water distribution networks. The tendency of bacterial growth was similar in both types of reactors; however the absolute values were different.

5. CONCLUSIONS

The mathematical model for bacterial regrowth in PMWR reactor Propella® with water recycling was developed in this study. The results of model simulation for the PMWR reactor and for the PF reactor were obtained. Similar trends in development of biofilm and variation of water phase bacteria concentration have been observed in both reactors; however, absolute values were different. The model predicted behaviour of bacteria regrowth agreed with the observation in water distribution networks.

The results confirmed that PMWR reactor such as the Propella® may be used for mathematical model validation and that the results can be used in prediction of bacterial regrowth in real water distribution networks.

REFERENCES

1. Bois, F. Y., Fahmy, T., Block, J. C., & Gatel, D. 1997. Dynamic modelling of bacteria in a pilot drinking-water distribution system, *Water Res.* 31(12): 3146–3156.
2. Camper, A. K. 1996. Factors limiting microbial growth in distribution systems: Laboratory and pilot-scale experiments, *Rep. No. 90708*, American Water Works Research Foundation.
3. Dailloux, M., Albert, M., Laurain, C., Andolfatto, S., Lozniewski, A., Hartemann, P., & Mathieu, L., 2003. *Mycobacterium xenopi* and Drinking Water Biofilms, *Applied and Environmental Microbiology*. Nov. 2003:6946 – 6948.
4. Zhang, W and DiGiano F.A. 2002. Comparison of bacterial regrowth in distribution systems using free chlorine and chloramine: a statistical study of causative factors, *Water. Res.*, 36: 1469-1482.
5. Dukan, S., Levi, Y., Piriou, P., Guyon, F., & Villon, P. 1996. Dynamic modelling of bacterial growth in drinking water networks, *Water Res.*, 30(9):1991–2002.
6. Servais, P., Laurent, P., Gatel, D., & Prevost, M. 1994. Modelling bacterial dynamics in distribution systems, *AWWA WQTC Conf. Proc.*, San Francisco.
7. Zhang, W., Miller C. T., & DiGiano, F. A. 2004. Bacterial Regrowth Model for Water Distribution Systems Incorporating Alternating Split-Operator Solution Technique, *J. Environmental Eng.*, Sep. 2004:932-941.

T. Juhna, A. Kolyshkin, I. Lukyanets, S. Nazarovs, J. Rubulis, A. Spalvins. Comparison of Bacteria Growth Simulation Results for Water Recycling and Plug Flow Type Reactor

Simulation of bacteria growth in water and biofilm affected by nutrient medium and chlorine has been performed. Simulation results were obtained for both Propella® reactor and a pipe. It has been found that changes in concentration of nutrient, chlorine and bacteria follow the same trends both for the Propella® reactor and the pipe.

T. Juhna, A. Koliškina, I. Lukjaņeca, S. Nazarovs, J. Rubulis, A. Spalviņš. Baktēriju attīstības modelēšanas salīdzinājums ūdens recirkulācijas reaktoram un ūdensvada caurulei

Darbā aprakstīta baktēriju attīstības modelēšana ūdensvada caurulē un Propella® reaktorā. Ņemta vērā temperatūras, barības vielu koncentrācijas un hlora koncentrācijas ietekme. Rezultātu salīdzinājums norādīja, ka matemātiskā modeļa aprakstītās hlora, barības vielu koncentrācijas izmaiņas ir līdzīgas gan Propella® reaktorā, gan ūdensvada caurulē.

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Сравнение результатов моделирования роста бактерий в реакторе с рециркуляцией воды и в трубе водоснабжения.

Сравнение результатов моделирования роста бактерий в полностью смешанном реакторе и в реакторе проточного типа.

В статье приведено сравнение результатов моделирования роста бактерий в трубе водоснабжения и в реакторе типа «Пропелла»®. Моделирование было произведено с учетом влияния концентрации хлора и питательных веществ на рост бактерий. Полученные результаты указывают на то, что изменение концентрации бактерий, хлора и питательных веществ имеет похожие тенденции как в случае трубы водоснабжения, так и в случае реактора типа «Пропелла»®.