Research Article

E. coli Inactivation Kinetics Modeling in a Taylor-Couette UV Disinfection Reactor

M. L. Palacios-Contreras,¹ F. Z. Sierra-Espinosa,² K. Juárez,³ S. Silva-Martínez,² A. Alvarez-Gallegos,² and M. L. Alvarez-Benítez¹

¹Posgrado en Ingeniería y Ciencias Aplicadas, Universidad Autónoma del Estado de Morelos, Av. Universidad 1001, Campus Chamilpa, 62209 Cuernavaca, Morelos, Mexico
²Centro de Investigación en Ingeniería y Ciencias Aplicadas, Universidad Autónoma del Estado de Morelos, Av. Universidad 1001, Campus Chamilpa, Cuernavaca, Morelos 62209, Mexico
³Instituto de Biotecnología, UNAM, Av. Universidad 1001, Campus Morelos, 62209, Mexico

Correspondence should be addressed to A. Alvarez-Gallegos; aalvarez@uaem.mx and M. L. Alvarez-Benítez; maria.alvarez@uaem.mx

Received 6 October 2019; Accepted 28 December 2019; Published 3 February 2020

1. Introduction

In recent years, UV light exposure has been recognized as one of the best available options for water treatment [1, 2]. However, the design of a reliable UV disinfection system should take into account several factors [3, 4], such as germicidal effect, sensor, water quality, UV reflection, and divergence. The microbial inactivation prediction is a useful tool because it provides guidance to assess the efficiency of UV disinfection systems. The survival behavior of microorganisms subjected to UV disinfection may obey different kinetic models [4–9]. However, for a long time, it was documented that, under certain experimental conditions, the survival behavior of the microorganisms subjected to UV disinfection may obey a simple exponential curve [10]. Indeed, in the absence of shoulder effects or in the case that they can be ignored, the UV inactivation of microorganisms can be fitted to a first-order decay rate [4, 8, 11]:

\[
\log\left(\frac{N_t}{N}\right) = -k \text{UV}_{\text{dose}},
\]

(1)

where \(N\) is the initial microbial concentration, \(N_t\) is the microbial concentration after contact time \(t\), \(\text{UV}_{\text{dose}}\) is
the fluence (mW·s·cm\(^{-2}\)), and \(k\) is the inactivation rate constant (cm\(^2\)·mW\(^{-1}\)·s\(^{-1}\)). However, if some deviation from the exponential law is noticed, UV inactivation of microorganisms must be interpreted by a more complex inactivation kinetics model [6, 12–14]. Although equation (1) looks simple, the prediction/modeling of a practical microorganism inactivation behavior based in such equation is a challenging task. Indeed, the parameter UV\(_{\text{dose}}\) may be defined as

\[
\text{UV}_{\text{dose}} = \frac{\text{UV}_{\text{flux}} \cdot t}{\text{radiating surface}},
\]

where UV\(_{\text{flux}}\) is the radiant power (W), \(t\) is the exposure time (s), and radiating surface is in cm\(^2\). Although some protocols for determining the UV\(_{\text{dose}}\) were developed for low-pressure mercury vapor lamps (LP UV) [3, 15–17], it is difficult to select a UV\(_{\text{dose}}\) value that can inactivate a given microorganism under different experimental conditions. Indeed, the presence of a set of attenuation/expansion factors affects exposure time and UV\(_{\text{flux}}\); therefore, the UV\(_{\text{dose}}\) is affected [18]. If one of the main attenuation/expansion factors is systematically changed while the rest are kept constant, its contribution to the UV inactivation process can be evaluated by the inactivation rate constant (\(k\)). Indeed, this parameter can be evaluated from experimental data and its interpretation is strongly related to the sensitivity of microorganisms to the UV\(_{\text{dose}}\). The best set of experimental conditions during UV disinfection can be identified taking into account the numerical value of \(k\). Surely, a high \(k\) value is always associated to one or more good combinations of the components of equation (2). This criterion can be illustrated by a couple of examples: Firstly, the inactivation profiles of four different microbial species were obtained at the same wavelength as a function of the UV-LED exposure time. It was found that E. coli was the more sensitive species because its \(k\) was the highest obtained value [19]. Secondly, it was found that \(k\) (evaluated from fluence inactivation response of B. subtilis spores) is not altered by the flow rate (10.8 to 7.8 mL·min\(^{-1}\)). However, the \(k\) value increased when the disinfection experiment was repeated in a static test [20].

In the absence of shoulder effects, the kinetics of microbial inactivation is a function of UV\(_{\text{dose}}\) and it might be described by equation (1). However, due to the set of attenuation/expansion factors, such equation fails to describe the experimental inactivation of microorganisms during UV irradiation. Such phenomenon has been noticed for a long time. As an example, it can be mentioned that a commercial UV water purifier was used to inactivate E. coli (obeying an apparent first-order decay rate) at different flow rates [21]. The highest percent kill was achieved at the lowest flow rate (0.03 mL·min\(^{-1}\)). However, if the fluid pattern is modified to force all water closer to the UV lamp, the percent kill at the fastest flow rate (1.92 mL·min\(^{-1}\)) was raised. Since then, it was understood that the flow field and reactor geometry are linked to the UV disinfection systems [20, 22]. Depending on the reactor design, batch/flow-through reactors may develop flow conditions, at low or high flow rates, leading to water volumes of lower UV radiation. Additionally, the spatial distribution of microorganism concentration is also linked to the fluid pattern. A proper simulation/prediction of the UV\(_{\text{dose}}\) implies the combination/integration of several models that describe the fluence rate, flow pattern, and kinetics of microbial inactivation.

During the past decades, several models have been developed to predict UV disinfection systems, and such models evolved from a fairly limited approach to models that globally include complex UV systems. In the first case, a model was used to predict the radiation intensity field [23] and another model was focused on the inactivation behavior of microorganisms [24] in UV reactors; similarly, using computational fluid dynamics (CFD), a radiation model was developed to improve the fluence rate distribution in an annular UV reactor [25]. In the second case, two or more models were combined to simulate a more complex UV microbial inactivation. Under this approach, experimental radiation profile data were used to derive a radiation distribution model. This model was then combined with the CFD software to predict the fluence rate distribution within the reactor [26]. In fact, when the prediction of UV microbial inactivation includes the hydrodynamics of the UV reactor, CFD is a powerful tool for describing the fluid pattern. The simulation of UV disinfection in an open channel configuration [27] was performed using a combination of four mathematical models (hydrodynamic pattern, intensity field, dose distribution, and inactivation kinetics) fed with several experimental data sets (collimated beam, Doppler laser velocimetry, UV transmittance, and UV output power). The design of the UV reactor (including the water inlet/outlet) and the position and distribution of the UV lamps located inside the reactor modify the fluid pattern and can be described by CFD [28, 29]. Therefore, the UV\(_{\text{dose}}\) within a reactor depends largely on the accuracy to numerically describe the turbulent structures developed based on the geometry of the UV reactor [30–33]. With the growing technique of LP UV disinfection for water treatment, the interest of modeling and after predicting the inactivation behavior of microorganisms is justified.

The aim of this work is to improve and predict the kinetics of microbial inactivation by the LP UV disinfection technique. The survival behavior of the microorganisms subjected to UV disinfection in a Taylor-Couette reactor is systematically studied according to the fluid pattern. The set of experimental results obtained are used to develop a simple model (using a minimum number of parameters) that combines the kinetics of microbial inactivation (equation (1)) with the numerical description of the fluid pattern to predict the experimental inactivation kinetics of E. coli in a Taylor-Couette UV disinfection reactor. However, the microbial inactivation kinetics model and the numerical description of the fluid pattern model are carried out separately, which provides a simple model to predict UV disinfection. This approach offers greater flexibility for discussions of results and interpretations. The simulated UV response kinetics in E. coli based on its concentration and the hydrodynamic pattern when a Taylor-Couette vortex was absent and then formed, are included in this work. In both cases (Taylor
vortex is present/absent), the simulation of UV disinfection showed good agreement with the experimental results.

2. Materials and Methods

2.1. Specifications of the UV Disinfection Reactor. A schematic configuration of the Taylor-Couette UV disinfection reactor is depicted in Figure 1. Both cylinders were made of Pyrex glass with the same length (17 cm). The inner radius of the outer cylinder was 2.75 cm, while the external radius of the inner cylinder was 1.75 cm. The inner cylinder was driven through a belt by a stepping motor (Siemens, 0.373 kW, 60 Hz, 220/440 V, and 1.80/0.90 A). The cylinder-rotation rates, measured with a frequency counter, were stable and accurate up to the maximum value used, 2500 revolutions per minute. The reactor sample point/inlet was located at the top of the external cylinder. The low-pressure mercury lamp (G15T8, Tecnolite, 254 nm, 15 W, 40 cm length) was located inside the diameter of the inner cylinder.

2.2. Cultivation and Enumeration of Bacteria. *E. coli* (XL-1 Blue) was chosen as the microorganism model, and its culture was carried out in a Luria-Bertani medium under anaerobic conditions at 37 °C and 200 revolutions per minute (rpm) using an incubator. Bacterial growth was followed by spectrophotometry (model DU® 730, Beckman Coulter®) at 600 nm and stopped when the optical density reached 0.2–0.3. Subsequently, a volumetric sample (67–45 mL) was taken and centrifuged (model Sorvall ST 16R, Thermo Fisher Scientific) at 4000 rpm for 8 min at 20 °C. The pellet was washed (using sterilized water, pH 7) and then suspended in 190 mL of sterilized water and vigorously mixed to obtain \(10^8\) colony-forming units mL\(^{-1}\). Except for the UV test, all samples were kept in the dark. Appropriated dilutions were made when necessary. For the quantification of bacteria, the samples were properly diluted and then spread on LB agar plates before the incubation at 37 °C for 24 h. Subsequently, the colonies were counted.

2.3. Fluid Dynamics Modelling. The numerical description of the fluid pattern inside the Taylor-Couette UV disinfection reactor was performed by a commercial CFD package (Fluent, Ansys version 15) based on a finite volume method. The fluid flow can be described considering the conservation of mass, momentum, and energy. However, considering some practical restrictions, the fluid pattern can be described simply by simultaneously solving mass and momentum conservation equations, as described in more detail elsewhere [34]. The stagnant fluid contained between two coaxial cylinders generates a set of counterrotating vortices in the annular gap when the inner cylinder rotates. The effects of this turbulence can be further described by turbulence models that can be solved alongside the set of mass and momentum conservation equations. Nowadays, CFD packages include a set of turbulent models to better describe a turbulent fluid flow. The selection of the best turbulence model depends on the nature of the hydrodynamic problem to be solved, the level of accuracy required, and user expertise [30]. In this work, the normalization-group model (RNG) was selected to describe the development of the fluid pattern as a function of the rotating speed of the internal cylinder. The accuracy of the numerical solution depends on the cell number (thin or rough grid) of the computational domain (the reactor annular gap). Several simulations were performed to find out the grid dependency of the results. A set of four different cell numbers \((2.5 \times 10^5, \ 5 \times 10^5, \ 1.0 \times 10^6, \text{and} \ 1.5 \times 10^6)\) were investigated. Finally, the computational domain is discretized in 505,164 hexahedral cells (the convergence index of the grid was 0.205%) in whose center the equations are solved. Once the boundary conditions for a particular cell center are established, the solution is applied to the cell boundaries by interpolation. The information obtained is used to advance stepwise to the neighboring cell until the entire domain is covered. The boundary conditions were defined as inlet conditions according to the inner cylinder rotating velocity (0, 300, 600, 1200, and 2000 rpm) and the physical properties of the fluid (density: 998.2 kg m\(^{-3}\); kinematic viscosity: \(1.01 \times 10^{-6}\) m\(^2\) s\(^{-1}\); dynamic viscosity: 0.001 kg m\(^{-1}\) s\(^{-1}\); and temperature: 25 °C).

2.4. Modeling of Survival Curves. In our approach, microorganisms were considered as soluble species reacting; therefore, they are transported in the UV reactor throughout a spatial distribution described by the fluid velocity profile (Eulerian approach) [35, 36]. The parameters that were not directly evaluated in this work are UV intensity, UV fluence rate, UV fluence received by particles, and reflective and diffuse fraction of the Pyrex glass walls. All of them were taken as unknown constant values. However, their important contribution to the UV microbial inactivation kinetics was experimentally evaluated by the inactivation rate constant. Except in the first 100 minutes, the microbial inactivation kinetics follows an apparent first-order kinetic equation and
can be adjusted to equation (1). In this model, \( N \) is a constant but does not represent the initial microbial concentration (such constant has no physical meaning in the studied experiment). However, the rest of the parameters in equation (1) kept the same meaning described before. All the experiments were repeated three times and then averaged. For a given bacteria concentration, four microbial inactivation curves (log (\( N_i/N_f \)) vs. exposure time) were obtained in the Taylor-Couette UV disinfection reactor, as a function of the Taylor number (Ta). From each microbial inactivation curve, a pair of \( N \) and \( k \) values were obtained. For a given bacteria concentration, \( k \) values can be correlated to the Ta number (the hydrodynamic pattern describing the Taylor-Couette vortex) expressed as a polynomial equation. Inside of the experimental conditions studied, a \( k \) value can be obtained for an unknown Ta number by the polynomial equation. Therefore, a microbial inactivation simulation curve can be obtained when time starts to increase in equation (1). Similar correlations were used to develop simple chemical models for predicting wastewater treatment [37–39].

3. Results and Discussion

3.1. Numerical Description of Taylor-Couette Vortex. The fluid contained in the annular gap of two coaxial cylinders presents instability when the inner cylinder rotates. Instability produces a series of counterrotating vortices throughout the annular gap. The vortices move the flow of the fluid into and out of the best-lit region of the reactor, creating a highly effective radial mixing within the Taylor-Couette vortex. Between vortices, the hydraulic boundaries form a mass transfer barrier that minimizes the exchange of fluid elements between them [40] and improves the kinetics of microbial inactivation, which is one of the objectives of this work.

The residence time of the bacteria near the UV lamp is, therefore, a function of both, the vortex size and its angular velocity (mainly, axial linear velocities, \( y \)-direction and radial linear velocities, and \( x \)-direction). Without axial flow, the fluid pattern is a function of the Ta number defined as follows [40–42]:

\[
\text{Ta} = \frac{r_i \omega_i d}{v} \left[ \frac{d}{r_i} \right]^{1/2},
\]

where \( r_i \) is the inner cylinder radius (cm), \( d \) is the gap width between two concentric cylinders (cm), \( \omega_i \) is the angular velocity of the inner cylinder (s\(^{-1}\)), and \( v \) is the kinematic viscosity (cm\(^2\)s\(^{-1}\)).

When the Ta number exceeds a critical value, \( \text{Ta}_C \) (this numerical value depends on \( d/r_i \)), the counterrotating toroidal vortices along the cylinder axis develop, describing five modes of flow along the annular gap [41, 42]:

1. Laminar flow \( \text{Ta} < \text{Ta}_C \)
2. Laminar vortex (individually periodic) flow \( \text{Ta}_C < \text{Ta} < 800 \)
3. Transition (double-periodic) flow \( 800 < \text{Ta} < 2000 \)
4. Turbulent vortex flow \( 2000 < \text{Ta} < 10,000-15,000 \)
5. Turbulent flow \( \text{Ta} > 15,000 \)

The numerical description of the fluid instability was performed at 8 different Ta numbers (131, 132, 191, 1309, 4116, 8231, 16462, and 27437) to visualize the formation/development of the counterrotating toroidal vortices within the annular space, for the same reactor configuration used in the experimental study. Figures 2, 3, 4, 5, and 6 show the evolution of the vortices. At the lowest angular velocity (9.55 rpm, \( \text{Ta} = 131 \)), the fluid is already unstable, but only a pair of rotating toroidal vortices formed at both ends of the reactor length, in the annular space. The maximum averaged linear velocity was evaluated as \( 1.17 \times 10^{-3} \) m s\(^{-1}\). When the angular velocity increases slightly (9.65 rpm, \( \text{Ta} = 132 \)), 8 counterrotating toroidal vortices formed well at each end (top and bottom) of the reactor length, in the annular gap. In the center of the reactor, a weak formation of 4 more vortices developed. (Image 1)

The maximum averaged linear velocity was evaluated as \( 2.31 \times 10^{-3} \) m s\(^{-1}\) (Figure 3). As the angular velocity gradually increases, the resulting toroidal vortices increase in both size and linear velocity. As \( \text{Ta} \) increases, a smaller number of counterrotating toroidal vortices formed along the length of the reactor, in the annular gap. For the angular velocity of 95.5 rpm (\( \text{Ta} = 1309 \)), 18 vortices were well formed with...
Following the same trend, for 300 rpm, a maximum average linear velocity of $2.85 \times 10^{-2}$ m s$^{-1}$ (Figure 3). Following the same trend, for 300 rpm (Ta = 4116) and 600 rpm (Ta = 8231), 16 and 14 vortices were formed, respectively.

Following the same order, the maximum average linear velocities were evaluated as $9.3 \times 10^{-2}$ m s$^{-1}$ and $1.64 \times 10^{-1}$ m s$^{-1}$, respectively (Figure 4). Finally, for the last two higher angular velocities at 1200 rpm (Ta = 16,462) and 2000 rpm (Ta = 27,437), the rotating toroidal vortex number further decreased to 13 and 10, respectively, while their maximum average linear velocities increased to $3.1 \times 10^{-1}$ m s$^{-1}$ and $5.7 \times 10^{-1}$ m s$^{-1}$, respectively. In addition, for the highest angular velocity studied, at the ends of the reactor length, the vortex size increased dramatically in the annular gap, while at the center of the reactor length, the toroidal shape of the vortex begins to gradually be lost in the annular gap (Figure 5). This last phenomenon can negatively impact the kinetics of microbial inactivation.

Figure 6 shows the axial velocities, evaluated in the middle of a toroidal vortex height as a function of the annular gap distance (x-direction, from 0 to 0.01 m).
the Taylor-Couette UV disinfection reactor used in this work. At higher $T_{ac}$ values, the removal of bacterial efficacy is improved.

The UV microbial inactivation kinetics was experimentally evaluated for three different concentrations of bacteria. For the first bacterial concentration of 35,000 PFU mL$^{-1}$, four microbial inactivation curves were obtained in the Taylor-Couette UV disinfection reactor based on the following angular velocities: 0, 300, 600, and 2000 rpm (Figure 8). Except for the first 100 minutes, the microbial inactivation kinetic follows an apparent first-order kinetic equation and the following set of $k$ values of each microbial inactivation curve ($\log (N_t/N)$ vs. time) was obtained: 0 rpm ($k = -4.42 \times 10^{-4}$ s$^{-1}$; $R^2 = 0.9671$), 300 rpm ($k = -4.91 \times 10^{-4}$ s$^{-1}$; $R^2 = 0.9833$), 600 rpm ($k = -7.34 \times 10^{-4}$ s$^{-1}$; $R^2 = 0.9795$), and 2000 rpm ($k = -8.02 \times 10^{-4}$ s$^{-1}$; $R^2 = 0.9804$), as depicted in Figure 9. Taking as reference the constant value of the inactivation rate obtained at 0 rpm, the angular velocity increases improve the kinetics of microbial inactivation.

The $k$ value gradually improves by 11%, 66%, and 82% when the angular velocity increases by 300, 600, and 2000 rpm, respectively. Starting from 0 rpm and following the same angular velocity sequence, the removal of bacterial efficiency ($\% = (N - N_t/N) \times 100$) in 900 s was 63%, 67%, 79%, and 83%, as shown in Figure 9.

For this bacterial concentration, the inactivation rate constant was correlated with $\omega$ (angular velocity, measured in rpm), including the stationary fluid, by the following polynomial equation:

$$k = -1.911(10)^{-10}(\omega)^2 + 5.795(10)^{-7}(\omega) + 4.096(10)^{-4},$$

$$R^2 = 0.9073.$$
For any arbitrary angular velocity, within the experimental conditions studied, a $k$ value can be obtained using equation (4). Therefore, a simulation curve of microbial inactivation can be obtained using equation (1). Figure 10 shows (dashed lines) the first 900 s of simulation of the survival behavior of microorganisms subjected to a UV irradiation process in the Taylor-Couette reactor at different angular velocities ($\omega$) 0 rpm, (●) 600 rpm, and (×) 2000 rpm. The corresponding experimental data are shown in the same figure.

For the second bacterial concentration equal to 400,000 PFU mL$^{-1}$, five microbial inactivation curves were obtained in the Taylor-Couette UV disinfection reactor as a function of the angular velocity (Figure 11). The following set of $k$ values of each microbial inactivation curve was obtained: 0 rpm ($k = -4.23 \times 10^{-4} \text{s}^{-1}$; $R^2 = 0.995$), 300 rpm ($k = -4.84 \times 10^{-4} \text{s}^{-1}$; $R^2 = 0.988$), 600 rpm ($k = -5.72 \times 10^{-4} \text{s}^{-1}$; $R^2 = 0.998$), 1200 rpm ($k = -7.19 \times 10^{-4} \text{s}^{-1}$; $R^2 = 0.958$), and 2000 rpm ($k = -7.34 \times 10^{-4} \text{s}^{-1}$; $R^2 = 0.987$). Also, in this case, the microbial inactivation kinetics is a function of angular velocity.

Taking as a reference the constant value of the inactivation rate obtained at 0 rpm, the constant of inactivation rate gradually improves by 14%, 35%, 70%, and 73% when the angular velocity increases to 300 rpm (●), 600 rpm (○), 1200 (×), and 2000 rpm (♦), respectively. In the same order, the bacteria efficiency removal was 67%, 79%, and 83%.

For 35,000 PFU mL$^{-1}$, at 0 rpm the inactivation rate constant value is $k = -4.42 \times 10^{-4} \text{s}^{-1}$ and the bacteria efficiency removal was 63% (○). The $k$ value improves gradually by 11%, 66%, and 82% when the angular velocity increases to 300 rpm (●), 600 rpm (○), and 2000 rpm (×), respectively. In the same order, the bacteria efficiency removal was 67%, 79%, and 83%.

For 400,000 PFU mL$^{-1}$, at 0 rpm the inactivation rate constant value is $k = -4.23 \times 10^{-4} \text{s}^{-1}$ and the bacteria efficiency removal was 66% (○). The $k$ value improves gradually by 14%, 35%, 70%, and 73% when the angular velocity increases to 300 rpm (●), 600 rpm (○), 1200 (×), and 2000 rpm (♦), respectively. In the same order, the bacteria efficiency removal was 73%, 78%, 80%, and 83%.
function of the angular velocity. The next set of \( k \) values was obtained from each of the following microbial inactivation curves: 0 rpm \( (k = 4.05 \times 10^{-4} \text{ s}^{-1}; \ R^2 = 0.9933) \), 300 rpm \( (k = 6.73 \times 10^{-4} \text{ s}^{-1}; \ R^2 = 0.9756) \), and 600 rpm \( (k = 7.68 \times 10^{-4} \text{ s}^{-1}; \ R^2 = 0.9870) \). It was found that, for both angular velocities of 600 and 1200 rpm, the microbial inactivation curves were very similar and only one of them is represented in Figure 13.

In addition, for 2000 rpm, the microbial inactivation kinetics does not follow an apparent first-order kinetic equation and was not included in Figure 13. The bacteria exposure time near the UV lamp is a function of the flow pattern (angular velocity) and a random bacteria association to form a clump (getting more important at higher bacteria concentration). Although the cause of the observed deviation is not clear, it is accepted that at short exposure time or subsequent exposure of microorganisms, damage by UV rays to higher fluences can alter the kinetic breakdown of the microorganism [8, 20]. Therefore, it is likely that at higher angular velocities and a higher bacteria concentration, the bacteria exposure time near the UV lamp was not enough to cause an irreparable damage in the bacteria DNA/RNA. A partial DNA/RNA damage could be repaired. This may be attributed to the observed deviation from the apparent first-order UV disinfection kinetics. Taking as a reference the constant value of the inactivation rate obtained at 0 rpm, the inactivation rate constant improves rapidly from 66% to 89% when the angular velocity increases by 300 and 600 rpm, respectively. From 0 rpm and following the sequence of 300 and 600 rpm, the removal of bacterial efficiency in 2700 s was 90%, 98%, and 100% (Figure 13). For this concentration of bacteria, the inactivation rate constant was correlated with \( \omega \) (including the stationary fluid) by the following polynomial equation:

\[
k = -9.572 \times 10^{-10} \omega^2 + 1.179 \times 10^{-6} (\omega) + 4.054 \times 10^{-4}
\]

\( R^2 = 1.0000. \) (6)

Figure 14 shows the first 4500 s of simulation of the survival behavior of microorganisms subjected to a UV irradiation process in the Taylor-Couette reactor at different angular velocities (0, 300, and 600 rpm). The bacterial efficiency removal, subjected to the experimental conditions studied here, was expected to be better at higher concentrations (>\( 10^6 \) PFU mL\(^{-1}\)) than at lower concentrations (>\( 10^4 \) PFU mL\(^{-1}\)). In fact, the number of microorganisms

---

**Figure 12:** For 400,000 PFU mL\(^{-1}\), experimental data represent the UV microbial inactivation kinetics. The dashed lines represent the first 1200 s of survival behavior simulation of microorganisms subjected to the UV irradiation process in the Taylor-Couette reactor at different angular velocities: (○) 0 rpm, (■) 600 rpm, and (×) 2000 rpm.

**Figure 13:** Experimental data are represented by symbols. Lines represent a tendency. For 30,000,000 PFU mL\(^{-1}\), at 0 rpm, \( k = -4.05 \times 10^{-4} \text{ s}^{-1} \) and the bacteria efficiency removal was 90% (○). The \( k \) value improves gradually by 66% and 89% when the angular velocity increases by 300 rpm (●) and 600 rpm (◊), respectively. In the same order, the bacteria efficiency removal was 98% and 100%.

**Figure 14:** For 400,000 PFU mL\(^{-1}\), experimental data represent the UV microbial inactivation kinetics. The dashed lines represent the first 4500 s of survival behavior simulation of microorganisms subjected to the UV irradiation process in the Taylor-Couette reactor at different angular velocities. The corresponding experimental points are displayed: (○) 0 rpm, (●) 300 rpm, and (×) 600 rpm.
(or a group of them, considered as soluble reacting species) present in the solution is finite. Therefore, the probability that a single microorganism is irreparably damaged by UV irradiation decreases constantly as the treatment progresses. As time passes, there are fewer microorganisms available. Additionally, the bacterial efficiency removal improves as a function of the angular velocity. Table 1 summarizes the effect of the most important parameters (angular velocity and bacteria concentration) on the inactivation rate constant ($k$).

High $k$ values are always associated to the best experimental conditions. Although under the approach presented in this work, it is not possible to evaluate/predict directly important parameters (such as UV intensity, UV fluence rate, UV fluence received by particles, reflective and diffuse fraction of Pyrex glass walls, and the hydrodynamic pattern) that can accelerate/delay the kinetics of UV microbial inactivation, all these parameters are collected in the inactivation rate constant.

This procedure is less complicated than other approaches [25–27]. In addition, the simulation of the survival behavior of the microorganisms subjected to a UV irradiation process in the Taylor-Couette reactor coincided well with the experimental results.

### 4. Conclusions

It was observed that *E. coli* is not resistant to UV irradiation in discontinuous experiments performed in the reactor in the absence/presence of a Taylor-Couette vortex. Although the formation of counterrotating toroidal vortices within the annular space formed well at ~14 rpm, they have no notable impact on the kinetics of microbial inactivation. The improvement in the bacterial efficiency removal starts from 200 rpm. The removal of bacterial efficiency is improved depending on both of the following parameters: the angular velocity applied and bacteria concentration. The constant value of the inactivation rate increases between 70% and 90% when angular velocity (600 rpm–1200 rpm) is applied to the Taylor-Couette reactor. Beyond 2000 rpm, such improvement begins to decrease. The experimental results (hydrodynamic and kinetic pattern of microbial inactivation) can be correlated with a simple mathematical model to predict the simulation of the survival behavior of *E. coli* subjected to a UV irradiation process in the Taylor-Couette reactor in a wide range of concentrations of bacteria ($10^6–10^8$ PFU mL$^{-1}$) and different angular velocities. This approach would be attractive to biological water treatment designers, since it requires few experiments and minimal physical parameters to define a representative experimental domain of a target water biological treatment.

### Data Availability

The data used to support the findings of this study are included within the article.

### Conflicts of Interest

The authors declare that they have no conflicts of interest.

### References


