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Hong Xin
The University of Auckland

Xiao Dong Chen
The University of Auckland

Necati Özkan
The University of Auckland

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Hong Xin, Xiao Dong Chen* and Necati Özkan

Department of Chemical and Materials Engineering, The University of Auckland, Private Bag 92019, Auckland, New Zealand * Corresponding author; E-mail: d.chen@auckland.ac.nz

ABSTRACT

Based on a polymer dissolution controlled chemical cleaning mechanism, a mathematical model has been developed to describe the different stages of the removal of milk protein fouling from a hard surface. Various processes, such as reptation, disengagement, mass transfer through the boundary layer and surface area changes during the decay cleaning stage have been taken into account in the modelling process. The successful prediction of the cleaning process under various conditions indicates that the model has proposed a rational mechanism accounting for the removal of milk protein fouling.

INTRODUCTION

Milk fouling on heat transfer surfaces is a serious problem in dairy processing plants, where frequent cleaning is required in order to meet the strict hygienic standards and to maintain the normal production capability. Cleaning is a multistage process comprising various steps that may be controlled by mechanical action, chemical reactions, and mass transfer.

Mathematical modeling plays a significant role in understanding the cleaning process and can be used to optimise the cleaning process. A chemical dissolution based mass transfer controlled cleaning mechanism has already been suggested by several researchers (Schlussler 1970). In the study of the cleaning procedure of milk fouling, Gallot-Lavallée and Lalande (1985) have provided a pseudo-physical cleaning model. Although this model has been widely recognized as one of the best models for describing the removal of porous deposits obtained from the thermal treatment of milk fluid. The definition of the surface concentration has been criticized by various authors for their lack of theoretical or experimental basis (Leclercq-Perlat, 1991; Bird 1993). The analytical and numerical modelling curve provided by Bird (1993) gave a reasonable fit of experimental cleaning data. However, the assumption of the time to reach the maximum cleaning rate depending on the time required to convert all the deposits to a removable form is doubtful (Xin 2003).

The basic structure of milk protein deposits is made of aggregated milk protein molecules and voids. Milk protein molecules have long molecular chains like polymers. The swelling of the protein deposit and the final removal of this swollen layer are analogous to the dissolution process of polymers when they are treated with suitable solvents. Therefore, the polymer dissolution concept can be applied to reveal the cleaning mechanism of the protein deposits. In a recent study (Xin, 2002a), based on mass transfer theory and the polymer dissolution concept, the constant cleaning rates in the uniform stage have been predicted. The successful prediction of the constant cleaning rate under various conditions indicates that the model has proposed a rational mechanism accounting for the removal of milk protein fouling. In this study, based on the polymer dissolution controlled chemical cleaning mechanism, a mathematical model that can be used to describe the different stages of the cleaning process will be further developed.

MECHANISMS AND MATHEMATICAL MODELS

Polymer Dissolution Based Cleaning Mechanisms

Adopting the polymer dissolution concept, the essential physical features of the cleaning of milk protein deposit are depicted in Figure 1. First, the cleaning solution is transported from bulk solution to the surface of the deposit through a fluid boundary layer. Then the contact of the cleaning solution with the deposit will trigger a series of reactions, generating some intermediate reaction products (certain protein molecules). Further penetration of the cleaning solution into the deposit will build up a “reaction zone” and form a swollen gel layer. A disengagement process is needed before the intermediate reaction products can be transferred across the boundary layer into the bulk cleaning solution.

The disengagement process of the protein molecules from the gel-solution interface is very complicated. In the swollen region, the cleaning solution concentration is high and the protein molecules have a high mobility;the movement of the protein molecules essentially starts from this region. After a short reptation time, the protein molecular chains on the gel side of the gel-solution interface tend to disengage from the interface and move into the solution. The long and mutually entangled protein chains are inhibited from entering the liquid phase due to the friction between themselves. The disengagement rate of

protein molecules is one of the factors controlling the dissolution process.

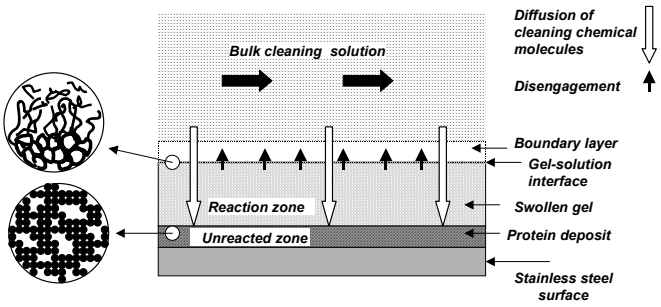

Fig. 1 A schematic diagram of the whey protein concentrate (WPC) gel film dissolution process.

In addition to the disengagement, a mass transfer resistance also exists at the surface. If the disengagement rate is relatively small, the mass transfer resistance through the external boundary layer may be ignored. However, if they occur at comparable rates, then the dissolution process can be both disengagement and diffusion limited (Ranade, 1995). With increasing cleaning time, the disengaged polymer chains will begin to accumulate on the gel-solution interface until a maximum volume fraction is reached. Then, the rate of disengagement from the interface would be constrained by the rate of mass transfer to the bulk solution. A concentration gradient between the interface of the swollen gel and the bulk cleaning solution provides a driving force for the movement of the disengaged protein molecules. The dissolution rate then reaches the highest value.

Mathematical Model of Cleaning

Polymer dissolution models involving some complicated moving boundary layer problems have been established (Peppas, 1994; Parker, 2000). Although these models have provided insights for the development of a cleaning model, they are generally complex. In this study, we have attempted to capture the key mechanisms by using a simple mathematical model.

The diffusion of cleaning solution and the chemical reactions take place very rapidly. After contact with the cleaning solution, a gel layer on the surface of the deposit can be observed very quickly. The mass transfer of cleaning solution to the deposit is normally quicker than the mass transfer back the dissolved protein chains due to the smaller size. In this study, it is assumed that the disengagement of protein molecules from the swollen gel-solution interface and the transfer of these disengaged protein molecules into the bulk cleaning solution are the rate limiting steps for the cleaning process. During the swelling and uniform stage, the cleaning rate may be calculated in terms of the mass transfer coefficient and the concentration gradient of the disengaged protein molecules in the boundary layer. In the decay stage, an effective surface area may be used to correlate the cleaning rate. For simplicity, the accumulation of the disengaged protein molecular chains in the boundary layer is neglected. The moving boundary layer problem and the different protein volume fractions within the swollen gel are not considered.

Swelling and uniform stage Based on the conventional concept of mass transfer, the cleaning rate (or mass flux) of the WPC gel molecules from the gel-solution interface may be written as:

$$R = \frac{dm}{Adt} = k_\phi \left(\phi - \phi_b\right) \tag{1}$$

where m is the mass removed, R is the cleaning rate, k_ϕ is the mass transfer coefficient, A is the surface area, ϕ is the volume fraction of the disengaged protein molecules at gel-solution interface, ϕ_b is the volume fraction of the disengaged protein molecules in the bulk cleaning solution. When ϕ_b is very small, Eq. (1) becomes

$$R = \frac{dm}{Adt} = k_\phi \phi \tag{2}$$

The volume fraction of disengaged protein molecular chains accumulated on the interface between the gel and the cleaning solution at any time has been assumed to change according to a first-order reaction mechanism:

$$\frac{d\phi}{dt} = k_d \phi \tag{3}$$

where k_d is the disengagement rate constant. The physics of the disengagement process has been elaborated by Devotta et al (1993). The disengagement rate is recognized to be directly proportional to the mobility of polymer molecules, whereas the mobility of the polymer molecules will depend on its volume fraction. It has been assumed that the variation of the mobility of polymer chains is a product of a kinetic constant and the extent of the departure from the maximum mobility (Devotta, 1995). Based on this assumption, it is assumed that the disengagement rate constant of the molecule chains, k_d, reduces with increasing ϕ, and approaches to zero when the maximum value (ϕ_m) is reached. As a first estimation, k_d takes the following form:

$$k_d = \xi\left(1 - \frac{\phi}{\phi_m}\right) \tag{4}$$

where ξ is a kinetic constant, ϕ_m is the maximum volume fraction taken up by the disengaged protein molecules. The change of the volume fraction of the disengaged protein molecules in the boundary layer is then expressed by the following equation.

$$\frac{d\phi}{dt} = \xi(1-\frac{\phi}{\phi_m})\phi \tag{5}$$

Since a polymer chain requires a finite induction time to disengage from the gel-solution interface, the disengagement rate is initially zero. This minimum induction time required for the 'first few' chains to disengage is equivalent to the reptation time (t_r). Thus, it is assumed that the following initial condition exists at the gel-solution interface.

$$\frac{d\phi}{dt} = 0\,, t < t_r \tag{6}$$

After the reptation process, from $t = t_r$ to $t > t_r$, the volume fraction of the disengaged protein molecules in the boundary layer can be calculated by integrating Eq. (5):

$$\phi = \frac{\phi_m e^{\xi(t-t_r)}}{\frac{\phi_m}{\phi_0} - 1 + e^{\xi(t-t_r)}} \tag{7}$$

where ϕ_0 is the volume fraction of the tangling protein chains at the solution side of gel-solution interface at the time $t = t_r$ ($\phi_0 \neq 0$). We now define a dimensionless parameter ψ as

$$\psi = \frac{\phi_m}{\phi_0} - 1 \tag{8}$$

Combining Eq. (2) and (7), the cleaning rate can be rewritten as follows:

$$R = \frac{dm}{Adt} = \frac{R_m e^{\xi(t-t_r)}}{\psi + e^{\xi(t-t_r)}} \tag{9}$$

where R_m (the constant cleaning rate during the uniform cleaning stage) is defined as

$$R_m = -k_\phi \phi_m \tag{10}$$

The amount of mass removed (under a certain constant cleaning condition with a known temperature, velocity, and concentration of cleaning solution, etc) from the deposit as a function of time can then be calculated by integrating Eq. (9) from time $t \geq t_r$ to $t \leq t_{su}$ (t_{su} is the total cleaning time during the swelling and uniform stages).

$$m = \frac{AR_m}{\xi}\left(Ln\frac{\left(\psi + e^{\xi(t-t_r)}\right)}{\left(\psi+1\right)} \right) \tag{11}$$

Decay stage At the end of the uniform stage, the continuous film of WPC deposit is broken up and only the patches of the deposit film are left on the stainless steel surface. In the study of the removal of organic films in the decay stage, the change of the surface area of the remaining film has been modelled as a first order process (Beaudoin, 1995). Adopting this approach, the protein gel removal in the decay stage is given as:

$$\frac{dA_L}{dt} = -k_A A_L \tag{12}$$

where A_L is the surface area covered by the protein film in the decay stage, k_A is the first order rate constant for the surface area reduction. This rate constant is expected to be dependent on temperature, mechanical properties of deposit, cleaning solution concentration, and flow velocity. The initial condition for Eq. (12) is:

$$A_L = A_{L,0} \text{ when } t = t_{su}$$

where $A_{L,0}$ is the total surface area covered by the protein film. Integrating Eq.(12) from $t \geq t_{su}$ to $t \leq t_t$ (the total cleaning time):

$$\frac{A_L}{A_{L,0}} = e^{(-k_A(t-t_{su}))} \tag{13}$$

Assuming that the cleaning rate during the decay stage depends on the remaining protein film area A_L, the cleaning rate during this stage can be expressed as:

$$R = R_m \frac{A_L}{A_{L,0}} \tag{14}$$

Combining Eq. (13) and (14), gives

$$R = R_m e^{(-k_A(t-t_{su}))} \tag{15}$$

In order to calculate t_{su} and the total cleaning time t_t, a critical protein mass remaining (m_c) at the start of the decay stage is defined as:

$$m_c = m_0 - m_{su} \tag{16}$$

where m_0 is the original mass of the deposit, m_{su} is total mass removed during the swelling and the uniform stage. m_{su} can be calculated from Eq. (11) with the boundary

condition at $t = t_{su}$. Combining Eq. (11) and (16), the mass removed during the decay stage can be determined as:

$$m_c = m_0 - \frac{AR_m}{\xi} Ln \frac{\left(\psi + e^{\xi(t_{su}-t_r)}\right)}{(\psi+1)} \tag{17}$$

Rearranging Eq. (17), t_{su} is given by the following equation:

$$t_{su} = \frac{1}{\xi} Ln\left((\psi+1) e^{\frac{(m_0-m_c)\xi}{R_m A}} - \psi \right) + t_r \tag{18}$$

The mass loss of the deposit during the decay stage can also be expressed as:

$$\frac{dm}{A_L dt} = \frac{dm}{Ae^{(-k_A(t-t_{su}))}dt} = R_m \tag{19}$$

Integration with the boundary conditions:

$$m = 0 \text{ and } A_L = A_{L,0}, \text{ when } t = t_{su} \tag{19a}$$

$$m = m_c \text{ and } A_L = 0, \text{ when } t = t_t \tag{19b}$$

Then, m_c can be expressed as:

$$m_c = \frac{R_m A}{k_A}\left(1 - e^{(-k_A(t_t - t_{su}))}\right) \tag{20}$$

Rearranging the above equation, t_t is given by the following equation:

$$t_t = -\frac{1}{k_A} Ln\left(1 - \frac{m_c k_A}{R_m A}\right) + t_{su} \tag{21}$$

Combining Eq. (18) and (21), then the total cleaning time t_t can be determined as:

$$t_t = \frac{1}{\xi} Ln\left((\psi+1) e^{\frac{(m_0-m_c)\xi}{R_m A}} - \psi \right) - \frac{1}{k_A} Ln\left(1 - \frac{m_c k_A}{R_m A}\right) + t_r \tag{22}$$

EXPERIMENTAL PROCEDURES

The cleaning system designed to determine the cleaning kinetics of WPC gel deposits from a stainless steel tube is illustrated schematically in Figure 2. The stainless steel tube (ID=16mm and Length=150mm), were pre-coated with a WPC gel film using a rotation rig. In the once-through cleaning loop, the cleaning solution (0.5 wt% NaOH), containing the removed deposits was continuously transported to the UV spectrophotometer by a sample pump. The UV absorption data were recorded at ten-second intervals to monitor the whole cleaning process. The detailed information about the UV assay and preparation of WPC gel films are discussed elsewhere (Xin, 2002a; Xin, 2002b).

RESULTS AND DISCUSSION

The cleaning experiments were carried out under various experimental conditions with flow velocities ranging from 0.07 (Re =2400) to 0.62 m/s (Re =21000) and temperatures ranging from 35 to 85 ^{o}C using 0.5 wt.% NaOH cleaning solutions. The amount of whey protein concentrate (WPC) gel layer on the stainless steel surface ranges from 205 to 747 g/m^2. A typical cleaning rate against time curve with the descriptions for the three cleaning stages, the reptation time (t_r), the cleaning time during the swelling and the uniform stage (t_{su}), the constant cleaning rate (R_m), and the critical mass remaining (m_c) are shown in Figure 3. the m_c represents the deposit mass removed during the decay cleaning stage. The slight decrease of the cleaning rate in the uniform stage might be due to the faster removal of the inlet region of the gel layer caused by the hydrodynamic disturbance. A repeatability study of the experiments was conducted and no significant differences were observed from the cleaning rate curves.

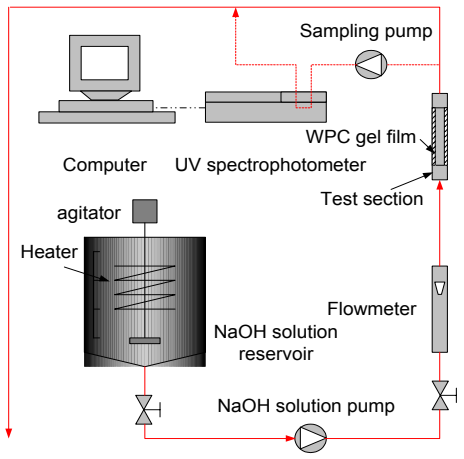

Fig. 2 A schematic illustration of the cleaning apparatus.

Identification of Model Parameters

Four parameters ($R_{m,}$ ξ , t_r *and* k_A) are used to characterize the cleaning process.

The constant cleaning rate R_m was determined from the experimental results using the following equation:

$$R_m = \frac{m_u}{t_u} \tag{24}$$

where, m_u and t_u are the mass removed and the cleaning time during the uniform stage, respectively

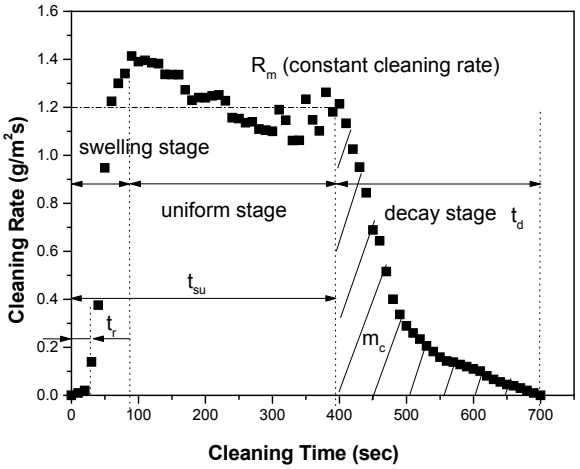

Fig. 3 A typical cleaning rate against cleaning time curve.

During the swelling stage, after the cleaning solution contacts with the deposit, a certain delay time, referred to as 'the reptation time', exists before a finite amount of dissolved WPC protein become measurable in the cleaning solution. A delay before the start of the cleaning process has been observed in previous cleaning studies (Gallot-Lavallée and Lalande, 1985; Bird 1993). A theoretical basis of the reptation time as a function of flow velocity and temperature is not available. However, at low temperature and low flow velocity, the reptation time can be observed directly from the experimental results.

For a given polymer-solution pair and polymer molecular weight, it is reasonable to assume a unique value of interfacial polymer volume fraction at the gel-solution interface (Papanu, 1989). A recent study showed that the interfacial polymer concentration did not vary significantly with time during the dissolution process (Devotta, 1995). During the fouling and cleaning process, the molecular weights of the disengaged proteins are difficult to estimate due to the complicated chemical reactions. For simplicity, it is assumed that the dimensionless value ψ is a constant. Rearranging Eq. (9), a relationship between ψ and the reptation time can be expressed by the following equation:

$$\ln\left(\frac{\psi R}{R_m - R}\right) = \xi\left(t - t_r\right) \tag{25}$$

Using the measured reptation times at various low temperatures, a simple regression method was used to identify the value of ψ. A plot of $\ln\left(\frac{\psi R}{R_m - R}\right)$ against time should give a nearly straight line passing through the point where $t = t_r$ when $\ln\left(\frac{\psi R}{R_m - R}\right) = 0$, providing an appropriate value for ψ was selected (see Figure 5.6). The minimised sum of the square deviations was obtained when an average ψ value of 25±5 was chosen. The value of ψ is independent of ξ, and subsequently is used in all the other calculations. After obtaining the value of ψ, it is also possible to determine ξ and t_r from the same plot, especially when t_r is too small to be directly observed from the experimental results.

The time at which the decay stage commences is given by Eq. (18) and the cleaning rate during this stage is given by Eq. (15). Another two parameters m_c and k_A have been used to model the cleaning progress during the decay cleaning stage. The mass of the gel layer left at the start of the decay stage is referred to as the critical mass (m_c), and can be used to determine the swelling-uniform cleaning time t_{su}. The critical mass value can be calculated by the area integration of the cleaning rate curve in the decay stage as shown in Figure 3. k_A is the rate constant for the surface area reduction in the decay stage. Rearranging Eq. (15), the following equation is obtained:

$$Ln\left(\frac{R}{R_m}\right) = k_A\left(t - t_{su}\right) \tag{26}$$

The value of k_A can be determined from the slope of the plot of $ln\left(\frac{R}{R_m}\right)$ against $\left(t - t_{su}\right)$.

Effects of Temperature and Velocity on Cleaning

The effect of temperature on the cleaning rate has been studied at a constant Reynolds number at temperatures ranging from 35 to 75 ^{o}C. The experimental results are illustrated in Figure 4. The effect of flow velocity (0.09-0.46 m/s) on the cleaning rate at 65 ^{o}C is shown in Figure 5.

In the analysis of the model parameters, it was found that the critical mass (m_c) was not much dependent on temperature and flow velocity, as a result, the critical mass (m_c) may be taken as a characteristic constant for a given fouling and cleaning system. An average critical mass value of 100 g/m^2 was determined from the experimental data for the WPC gel deposits used in this study.

Figures 4 and 5 show that with increase of the temperature and flow velocity of the cleaning solution, the cleaning rate during the swelling and uniform stages is increased and the cleaning time in the decay stage is reduced. As a result, the whole cleaning time is reduced.

These observations are consistent with the changes of the model parameters.

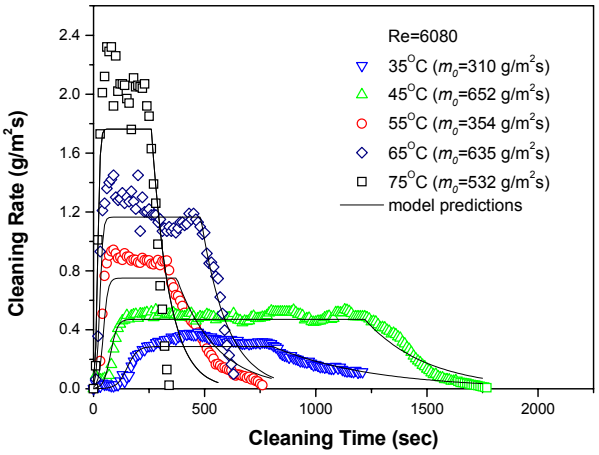

Fig. 4 The comparison of the experimental and predicted cleaning results at different temperatures at a constant Reynolds number (Re = 6080).

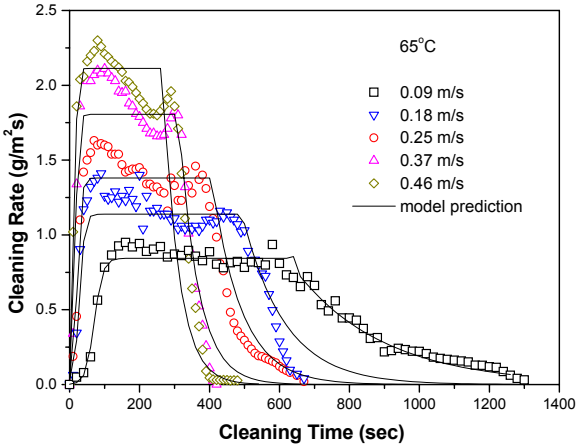

Fig. 5 The comparison of the experimental and predicted cleaning results at different flow velocities at 65 °C.

Previous study has shown that the reptation time gets shorter with increasing temperature (Peppas, 1994). It is expected that the values of ξ increase with increasing temperature since the protein chains have higher mobility and larger disengagement rates at higher temperatures. Both the increased maximum volume fraction of disengaged protein molecules and the increased mass transfer coefficient should contribute to a larger R_m at higher temperatures. The changes of k_A with temperature are possibly due to the changes in the microstructure and the mechanical properties of the fouling layer with temperature.

The enhancement of the cleaning with increasing flow velocity would be mainly due to the increasing external mass transfer coefficient. As a result, the transport of the disengaged protein molecules back into the bulk cleaning solution would be more efficient at higher flow velocities, thus giving higher R_m and k_A.

The disengagement rate would be influenced by the action of the hydrodynamic forces on the polymer chains dangling into the liquid, so it is expected that ξ increases with increasing flow velocity as well. The faster disengagement of polymer chains could contribute a shorter reptation time.

To evaluate the role of temperature in each cleaning stage, the temperature dependent cleaning model parameters ($R_{m,}$ $\xi,$ k_A, and $\frac{1}{t_r}$) can be described using the Arrhenius relationship.

Although the effects of Reynolds number (or flow velocity) on the model parameters could be very complex, it was possible to describe the influence of Reynolds number on the model parameters with a simple equation using the analysis results obtained from Figures 4 and 5. Since the effects of Reynolds number on the apparent activation energies are not significant during cleaning processes (Gillham, 1999). It is assumed in this study that the apparent activation energy is independent of Reynolds number. Thus, the dependence of the model parameters on temperature and Reynolds number can be represented by using the following semi-empirical equation:

$$Y = f(\mathrm{Re})\exp\left(-\frac{E_a}{R_g T}\right) \tag{27}$$

where Y represents the model parameters: $R_{m,}$ $\xi,$ k_A, and $1/t_r$, E_a is the apparent activation energy (J/mol), R_g is the molar gas constant, and *f(Re)* is a linear function between Reynolds number and y, which is independent of temperature and defined as:

$$f(\mathrm{Re}) = \alpha + \beta\,\mathrm{Re} \tag{28}$$

where α and β are the constants. The values of α and β can be obtained from the intercept and slope of the $y/\exp\left(-\frac{E_a}{R_g T}\right)$ against *Re* plots, respectively (see Figure 6).

The comparison between experimental results and model predictions are provided in Figure 4 and 5. The parameters used in the model predictions were given in Table 1. In order to confirm the validity of the model provided here, a set of new cleaning experiments were performed at different temperatures ranging from 45 to 85

^{o}C at a constant flow velocity of 0.25 m/s. Using the same parameters provided in Table 1, the cleaning rates are predicted and compared with the experimental results in Figure 7, a good agreement was observed.

Fig 6 $y \cdot \exp\left(\frac{E_a}{RT}\right)$ versus Reynolds number plots at 65 ^{o}C for (a) $y=R_m$, (b) $y=\xi$, (c) $y= k_A$, *and* (d) $y=1/t_r$.

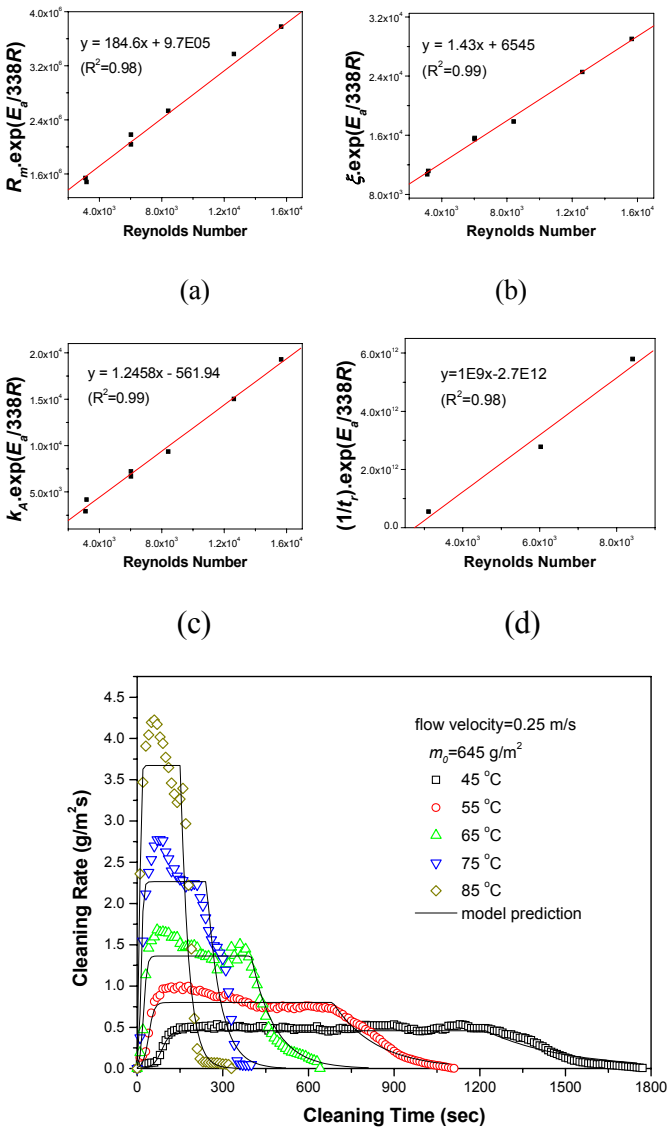

Fig. 7 The comparison of the experimental and predicted cleaning results at various temperatures at a flow velocity of 0.25 m/s.

Literature Cleaning Results

The cleaning model proposed here is obtained from the investigation of a model system based on WPC gel films. Comparing this model system with more realistic experimental systems investigated previously by other researchers would not only confirm the validity of the cleaning model proposed in this study, but also make it possible to apply this cleaning model to realistic protein deposits.

Table 1. The model parameters used in the model predictions for the removal of WPC gel fouling deposits

Stage	Parameters	α	β	E_a (KJ/mol)
Reptation	$1/t_r$ (s^{-1})	-2.7E+12	1.0E+09	85
Swelling	ξ(s^{-1})	6.5E+03	1.4E+00	33
Uniform	R_m (g/m^{2}s)	1.0E+06	1.8E+02	41
Decay	k_A (s^{-1})	-5.6E+02	1.2E+00	38

There are a few systemic studies on the cleaning kinetics using whole milk fouling (Gallot-Lavallée and Lalande), and whey protein fouling (Gillham et al,1999). Using the current model, the data obtained from those previous studies were first analysed, and then the influence of temperature and Reynolds number on model parameters were estimated using Eq. (27) and (28).

Although the real fouling and cleaning systems are quite different from the gel system, it was found that the apparent activation energies obtained from this study are still valid for the protein deposits. The effects of Reynolds number on model parameters were then calculated according to the results obtained from the analyses of the experimental curves. The average critical masses of 34 g/m^2 and 160 g/m^2 were estimated for the experimental results of Gillham and Gallot-Lavallée, respectively. Due to the shortage of the data at the beginning period of the cleaning process, the reptation time was taken as zero for all the following predictions. The literature experimental results and model predictions are compared in Figure 8 and Figure 9. The parameters used for the model predictions are summarised in Table 2.

Table 2. The parameters used in model prediction for the literature cleaning results provided in Figures 8 and 9.

Author	Gallot-Lavallee		Gillham et. al.	
Constant	α	β	α	β
ξ(s^{-1})	-1.5E+05	5.6E+00	7.7E+02	2.3E+00
R_m (g/m^{2}s)	1.0E+06	1.9E+02	7.0E+05	3.4E+00
k_A (s^{-1})	-1.5E+04	8.8E-01	6.5E+03	1.1E+00

note: the same apparent activation energies as that of WPC gels have been used.

Similar to the WPC gel removal, all the cleaning results from previous studies on the whey protein fouling and the whole milk fouling showed a typical cleaning rate curve with well-defined three stages. The influence of temperature and flow velocity upon the model parameters show a similar

trend as that of WPC gel, confirming the cleaning mechanism developed to be valid in more complex and realistic proteinaceous fouling and cleaning systems. The same value of the critical mass identified from each fouling and cleaning system suggests that the critical mass may be taken as a system constant.

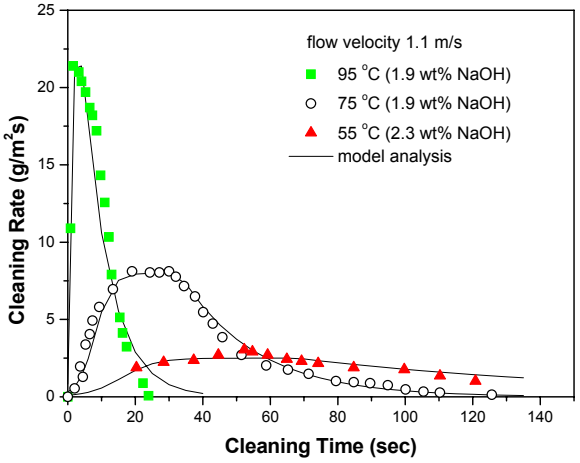

Fig. 8 The model predictions together with the experimental results reported by Gallot-Lavallée and Lalande (1985).

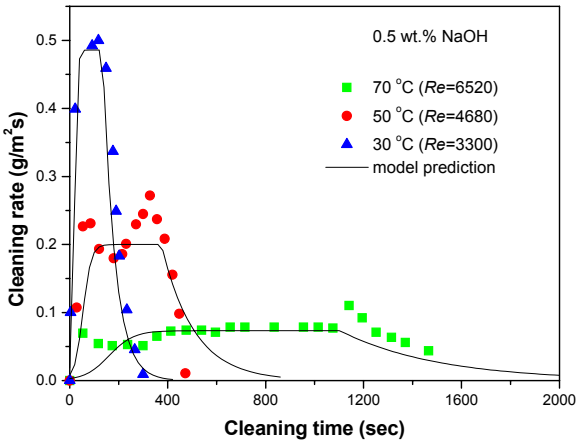

Fig. 9 The model predictions together with the experimental results reported by Gillham et al. (1999).

CONCLUSIONS

Based on the polymer dissolution theory and fundamental mass transfer concept, a cleaning model was developed for estimating the cleaning rate and cleaning time for proteinaceous fouling. Various processes, such as reptation, disengagement, mass transfer through the boundary layer and surface area changes have been taken into account in the modelling process. The experimental results and model predictions support the modelling concepts employed. The successful use of this model in literature cleaning results shows that this new mathematical model can be applied in a real fouling and cleaning process. The current dissolution model does not take account of the role of shear force in the removal of large pieces of deposits. However, the model provides a good foundation for further studies on the cleaning mechanisms of protein-based milk fouling.

ACKNOWLEDGMENTS

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NOMENCLATURE

A surface area of deposits, m^2
A_L deposit surface area left in decay stage, m^2
$A_{L,0}$ total surface area covered by the protein film, m^2
E_a the apparent activation energy, J/mol
$f(R_e)$ a linear function between Reynolds number and model parameters (Eq.28)
k a reaction rate .
k_A a rate constant for the surface area reduction, s^{-1} (Eq.12)
k_d disengagement rate, s^{-1} (Eq.3)
k_ϕ a mass transfer coefficient, g/m^2s (Eq.1)
m mass removed, g/m^2
m_c critical mass, g/m^2
m_u mass removed during uniform stage, g/m^2
m_{su} mass removed during swelling and uniform stage, g/m^2
R_g ideal gas constant, J/molK
Re Reynolds number
R_m constant cleaning rate, g/m^2s
T absolute temperature, K
t_d cleaning time in decay stage, s
t_r reptation time, s
t_{su} sums of cleaning times in swelling and uniform stage, s
t_t total cleaning time, s
t_u reptation time in uniform stage, s
y symbol of model parameters (Eq.27)

Greek letters

α a constant (Eq.28)
β a constant (Eq.28)
ϕ the volume fraction of the disengaged protein molecules at gel-solution interface (Eq.1)
ϕ_m maximum volume fraction of the disengaged protein molecules (Eq.4)
ϕ_0 volume fraction of the tangling protein chains at the solution side of gel-solution interface at the time $t = t_r$.
ξ kinetic constant, s^{-1} (Eq. 4)
ψ dimensionless parameter (Eq.8)

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