5th International Chemical Engineering Congress and Exhibition
Kish Island, 2 - 5 January 2008

Modeling of temperature gradients in packed-bed solid-state bioreactors

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Abstract

Normal operation of packed-bed bioreactors used for solid-state fermentation involves a static bed aerated from the bottom throughout the fermentation. Due to the rapid heat generating dynamics, temperature limitation remains a problem. This leads to axial temperature profiles with the highest temperature, sometimes over 10°C higher than the optimum temperature, occurring at the top of the bed. We present a model for the kinetics of microbial growth that incorporates the influence of the temperature variations that typically occur during solid-state fermentation in large-scale bioreactors. In this model, despite the fact that the growth rate depends on the current temperature of bioreactor through the specific growth rate constant that was expressed as a function of the temperature, it also depends on the time–temperature treatment that the organism has previously undergone through the rate of change in the level of the physiological factor, since the past temperatures affect the current value of physiological factor. Model predictions were compared to literature data for the growth of *Aspergillus niger* on wheat bran and agreed reasonably with experimental results. This approach to modeling has good potential for application in models of solid-state bioreactors. Also in this study, to investigate the temperature gradients in packed-bed bioreactors, two dynamic heat transfer models were considered and compared: (1) lumped dynamic heat transfer model, and (2) distributed dynamic heat transfer model. The predictions of distributed model have remarkably good agreement with experimental data rather than lumped model.

Keywords: Solid-state fermentation; Packed-bed bioreactor; Growth kinetics; Heat transfer model;

1. Introduction

Solid-state fermentation (SSF) is defined as the fermentation involving solids in absence (or near absence) of free water. However, substrate must possess enough moisture to support growth and metabolism of microorganism. SSF has been conventionally more applicable for filamentous fungi, which grow on the surface of the particle and penetrate through the inter particle spaces into the depth of the bed [1]. These processes are particularly attractive to industrial applications, offering higher production yields (measured in terms of product per volume) and different expression of microbial metabolites compared with submerged fermentations (SmF) [2]. SSF offers lower energy requirements, lower operating costs and investment outlays, less downstream processing, and produce lesser wastewater than SmF, and are environmental-friendly as they resolve the problem of solid wastes disposal. In spite of these promising features, a large amount of heat is generated during SSF, which is directly proportional to the metabolic activities of the microorganism. Sometimes heat accumulation is high, which denatures the product formed and accumulated in the bed. Lack of free water and low conductivity of solid particles can lead to heat gradients in SSF [1-3]. Consequently, SSF systems are more complex than most SmF systems. Unfortunately, compared to the extensive literature for SmF, little is known about how to design and operate large-scale bioreactors for

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SSF. This lack of knowledge limits the successful development of commercial scale SSF processes.

Although mixing can significantly improve heat removal via the reactor wall, it isn't used in all solid-state reactors, because not all fungi and solid substrates can tolerate the shear and collision forces that result from mixing [3]. Therefore, the current work focuses on those SSF processes in which mixing is deleterious to bioreactor performance. As a result, the substrate bed must be maintained static during the fermentation. Two bioreactor types are available that provide static, or largely static, operation: tray bioreactors and packed-bed bioreactors. In tray bioreactors, in which air is not blown forcefully through the tray, heat removal is limited to the tray surfaces. Consequently, bed heights within trays are limited to a few centimeters. Therefore, such reactors are restrictive in the amount of substrate that can be fermented. In packed-beds these problems are partially overcome by forced aeration, but high temperatures can still be reached near the air outlet. Larger bed heights are possible with packed-bed bioreactors, in which air is forced through the bed [4-6]. Consequently, in these bioreactors oxygen supply is not limiting, unlike tray bioreactors. Thus packed-bed bioreactors would be very efficient for SSF processes and therefore, in this current work, we consider packed-bed bioreactors.

In packed-bed bioreactors, it is impossible to maintain the bed temperature at the optimum value for growth, and therefore, the microorganism will suffer variations in temperature during the process. For example, during times of peak heat production, the temperature can rise to values 10 °C or more above the optimum temperature [6]. The kinetic model should be capable of describing the effects of these temperature variations on growth.

The approach taken in formulating the model is different from that which has previously been used in models that describe growth in SSF processes. In the majority of cases, the growth rate has been expressed solely as a function of the current temperature according to experimental results collected by the approach that is so-called "isothermal approach" [7]. This approach is explained in section 4. For example, in applying this approach, Saucedo-Castaneda et al. [8] expressed the specific growth rate constant (μ) as a function of the current temperature. The bed temperatures predicted by their model were significantly lower than the measured values and they were only able to predict the temperatures measured experimentally when the growth rate was assumed to remain constant as the temperature increased. In the work of Dalsenter et al. [9] the growth rate expressed as a function of the temperature regime suffered beforehand by the organism. In their model, μ did not depend on temperature, and the sole effect of temperature on growth rate was expressed by the effect of temperature on an essential component within the biomass, and therefore, they were not properly able to describe the effect of present value of temperature on growth. In our model, despite the fact that the growth rate depends on the current temperature of bioreactor through the parameter μ that was expressed as a function of the temperature, it also depends on the time–temperature treatment that the organism has previously undergone through the rate of change in the level of the physiological factor, since the past temperatures affect the current value of physiological factor. The value of this factor was expressed as a function of the temperature and μ within the growth kinetic equation was multiplied by this factor. The model developed is suitable for incorporation into mathematical models describing SSF bioreactor operation.

Axial temperature gradients, which can sometimes be steep, are impossible to avoid within packed-bed bioreactors due to the end-to-end aeration, and the use of convective cooling with unidirectional flow of air [10,11]. Experimental work shows that temperature gradients have a great potential to limit bioreactor performance [6]. To this reason, two kinds of dynamic heat transfer models namely, lumped and distributed dynamic heat transfer models, are considered in this paper to investigate the temperature gradients in packed-bed bioreactors and then these models are compared.

2. Mathematical model

Modeling is a useful tool in guiding experimental programs for the design, scale-up and control of bioreactors for solid-state fermentation, since it can be used to identify promising strategies and eliminate unfruitful strategies.

2.1. Kinetic model

The growth of biomass occurs according to the logistic equation. The logistic equation is an unstructured model that is largely descriptive, empirical and based on experimental observations [3,12]. In spite of mathematical simplicity, the logistic equation can almost give an adequate approximation of the whole growth curve in a single equation, including the lag, exponential growth and stationary phases, but it cannot provide a complete representation that includes the death phase [13,14]. Therefore, we modified the logistic equation as follows:

$$\frac{dX}{dt} = \mu\phi X\left(1-\frac{X}{X_m}\right) \tag{1}$$

Where X, X_m and ϕ are the biomass concentration, the maximum possible biomass concentration and the level of a physiological factor, respectively. In fact, the physiological factor represents a dimensionless quantity related to the physiological state of the cells that not only plays a key role in the growth process, but also is responsible for its own synthesis. Thermal denaturation of this factor is expressed as a first-order process, and the rate of auto-synthesis of the factor is expressed according to the power-law version of the logistic equation as follows:

$$\frac{d\phi}{dt} = \gamma_S\phi\left(1-\phi^{\alpha}\right)-\gamma_D\phi \tag{2}$$

Where α is the exponent in the power-law version of the logistic equation, and γ_S and γ_D are the rate coefficients of the synthesis and denaturation reactions, respectively. These rate coefficients are expressed as functions of temperature according to the Arrhenius equation:

$$\gamma_S = \gamma_{S_0}\exp\left(\frac{-E_S}{R(T+273)}\right) \tag{3}$$

$$\gamma_D = \gamma_{D_0}\exp\left(\frac{-E_D}{R(T+273)}\right) \tag{4}$$

Where γ_{S_0} and γ_{D_0} are the frequency factors for the synthesis and denaturation reactions, E_S and E_D are the activation energies for the synthesis and denaturation reactions, and T is the bed temperature, respectively. The specific growth rate constant is expressed empirically as a function of temperature [15]:

$$\mu = \left(\frac{s+(T_{\max}-T_{opt}}{(T_{\max}-T_{opt})}\right)\left(\frac{\mu_{opt}(T_{\max}-T)}{s+(T_{\max}-T)}\right) \tag{5}$$

Where μ_{opt} is the specific growth rate constant at the optimal temperature for growth (T_{opt}) and T_{max} is the maximum temperature at which growth can occur. The parameter s describes the sensitivity of the specific growth rate to increases in temperature.

The parameter values used in the kinetic model are given in Table 1 [3,6,15-17]. The determination of these parameters is described in Section 3.

Table 1. Parameter values used in the simulations with the kinetic model

Symbol	Value	Source
E_D	294516 J mol^{-1}	Fitting of Figs. 2 and 4
E_S	68138 J mol^{-1}	Fitting of Figs. 2 and 4
R	8.314 J mol^{-1} °C	[16]
s	6.275 (dimensionless)	[15]
t	t_o= 0 hr	Independent variable
T_{opt}	35 °C	[17]
T_{max}	52 °C	[6]
X	X_o=0.0071 kg-biomass kg-substrate-1	[3]
X_m	0.22 kg-biomass kg-substrate^{-1}	[3]
α	11 (dimensionless)	Fitting of Figs. 2 and 4
ϕ	ϕ_o=1 (dimensionless)	Calculated by Eq. (2)
γ_s	hr^{-1}	Calculated by Eq. (3)
γ_{s_0}	9.761×108 hr^{-1}	Fitting of Figs. 2 and 4
γ_D	hr^{-1}	Calculated by Eq. (4)
γ_{D_0}	8.74×1045 hr^{-1}	Fitting of Figs. 2 and 4
μ	hr^{-1}	Calculated by Eq. (5)
μ_{opt}	0.173 hr^{-1}	Fitting of data, see text

2.2. Dynamic heat transfer models

The packed-bed bioreactor modeled is cylindrical, and it consists of a bed of substrate supported on a perforated base plate through which saturated air with water vapor is blown (Fig. 1). The moist wheat bran is inoculated with *Aspergillus niger* and placed in the bioreactor at time zero. Models concentrate on the heat transfer phenomena. Due to the increase in temperature as the air flows through the bed, heat removal phenomena are considered in the axial direction, and in the absence of internal heat transfer plates, radial conduction removes as little as 8% of the metabolic waste heat [11]. Therefore, heat removal through the walls of the bioreactor is ignored in this modeling work. Also the air and the moist solid at any particular location within the bed are assumed to be in thermal equilibrium.

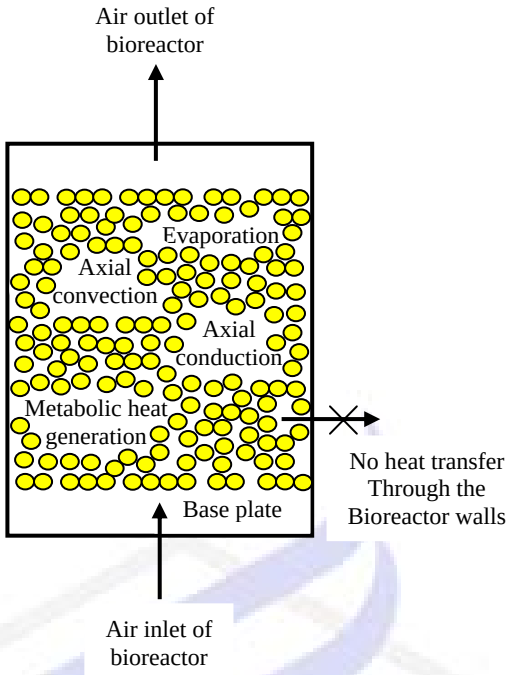

Fig. 1. Schematic of a packed-bed bioreactor as modeled in this work, showing the various heat transfer processes occurring. Axial conduction is ignored in the lumped Dynamic heat transfer model.

2.2.1. Lumped dynamic heat transfer model

Lumped dynamic heat transfer model includes terms for the generation of heat from microbial growth, convective and evaporative heat removal as below:

$$\rho_b C_{pb}\left(\frac{\partial T}{\partial t}\right) = \rho_s (1-\varepsilon) Y_Q \frac{dX}{dt} + \rho_a C_{pa} \frac{V_z}{Z}(T_a - T) + \rho_a f\lambda \frac{V_z}{Z}(T_a - T) \qquad (6)$$

Where $C_{pb}, C_{pa}, \rho_b, \rho_a, \rho_s, Y_Q, V_z, \varepsilon, Z, T_a, f$ and λ are heat capacity of the bed, heat capacity of the moist air, bed density, moist air density, substrate density, metabolic heat yield coefficient, superficial velocity of the moist air, void fraction, bed height, temperature of inlet air, water carrying capacity of air, and latent heat of evaporation of water, respectively. In above equation each term has the units of J hr^{-1} m^{-3}. Air moves only in the axial direction, with a constant velocity profile across the bed.

2.2.2. Distributed dynamic heat transfer model

Sangsurasak and Mitchell [15] described the development of a model which was identical with our distributed dynamic heat transfer model except that it described heat transfer in both the vertical and horizontal directions. Despite the existing terms in lumped model, axial conduction term has been also taken into account in distributed model:

$$\rho_b C_{pb}\left(\frac{\partial T}{\partial t}\right) = \rho_s (1-\varepsilon) Y_Q \frac{dX}{dt} - \rho_a C p_a V_z \left(\frac{\partial T}{\partial z}\right) - \rho_a f\lambda V_z \left(\frac{\partial T}{\partial z}\right) + k_b \left(\frac{\partial^2 T}{\partial z^2}\right) \qquad (7)$$

Where, k_b is the thermal conductivity of the bed. In Eqs. (6) and (7), values for density, thermal conductivity and heat capacity of the bed were calculated as weighted averages of the properties of the air and substrate within the bed as below:

$$\rho_b = \varepsilon\rho_a + (1-\varepsilon)\rho_s \tag{8}$$

$$k_b = \varepsilon k_a + (1-\varepsilon)k_s \tag{9}$$

$$C_{pb} = [\varepsilon\rho_a(C_{pa} + f\lambda) + (1-\varepsilon)\rho_s C_{ps}]/\rho_b \tag{10}$$

Where k_a and k_s are the thermal conductivity of moist air and substrate, respectively, and C_{ps} is the heat capacity of substrate.

The initial values of X, ϕ and T are assumed constant over the whole height of the bed as X_0, ϕ_0 and T_0. The boundary conditions of the bed temperature are assumed as below:

$$\begin{cases} 1)\ at\ z = 0, \quad T = T_a \\ 2)\ at\ z = Z, \quad \dfrac{\partial T}{\partial z} = 0 \end{cases} \tag{11}$$

The parameter values for the lumped and distributed dynamic heat transfer models are given in Table 2 [6,8,16,18-20].

Table 2. Parameter values used in the simulations with lumped and distributed heat transfer models

Symbol	Value	Source
C_{pa}	1180 J kg^{-1} °C^{-1}	[16]
C_{pb}	J kg^{-1} °C^{-1}	Calculated by Eq. (10)
C_{ps}	2500 J kg^{-1} °C^{-1}	[18]
f	0.00246 kg-water kg-air^{-1} °C^{-1}	[19]
k_a	74.16 J hr^{-1} m^{-1} °C^{-1}	[19]
k_b	J hr^{-1} m^{-1} °C^{-1}	Calculated by Eq. (9)
k_s	1080 J hr^{-1} m^{-1} °C^{-1}	[18]
T	T_o=30 °C	[6]
T_a	30 °C	[6]
V_z	51m hr^{-1}	[6]
Y_Q	8.366×10^6 J kg-biomass^{-1}	[8]
Z	0.17m	see text
ε	0.35 (dimensionless)	[20]
λ	2414300 J kg-water^{-1}	[16]
ρ_a	1.14 kg m^{-3}	[16]
ρ_b	kg m^{-3}	Calculated by Eq. (8)
ρ_s	700 kgm^{-3}	[8]

2.3. Numerical solution of the models

Ordinary differential equations (ODEs) in the kinetic and lumped dynamic heat transfer models were solved using the fourth-order Runge-Kutta method with variable step size defined by the function *ode45* in MATLAB® (version 7.0).

To solve the distributed heat transfer model, the partial derivatives were approximated by finite difference method using n equal space grids (including the two end grids) [21]. Using central difference approximation, Eq. (7) was discretized and a non-linear ordinary differential equation was obtained for each grid. The resulting set of non-linear ODEs are:

$$\frac{dT_i}{dt} = \frac{\rho_s(1-\varepsilon)Y_Q}{\rho_b C_{pb}}\frac{dX}{dt} - \frac{1}{2h}\frac{\rho_a C_{pa} V_z}{\rho_b C_{pb}}(T_{i+1} - T_{i-1}) - \frac{1}{2h}\frac{\rho_a f\lambda V_z}{\rho_b C_{pb}}(T_{i+1} - T_{i-1}) + \frac{1}{h^2}\frac{k_b}{\rho_b C_{pb}}(T_{i+1} - 2T_i + T_{i-1}) \quad for\ i = 2,3,...,n \tag{12}$$

Where h is the height step size. For simultaneous solving of the above set of ODEs, the fourth-order Runge-Kutta method was used with variable time step size defined by the function *ode45* in MATLAB®. The method cited above is so-called "line method" that in fact, it is a explicit method with variable time step size.

3. Results

The optimum temperature for the growth of *Aspergillus niger* is 35°C [17]. The optimum value of specific growth rate constant (μ_{opt}) for the growth of *Aspergillus niger* on wheat bran was obtained at 35°C and moisture content of 60% by non-linear regression of the logistic equation based on experimental data of Hamidi-Esfahani et al. [3]. This value is used in all simulations. Note that, non-linear regression was done by the function *nlinfit* in MATLAB®.

To verify the validity of the proposed kinetic model, the experimental data of Hamidi-Esfahani et al. [3] at two temperatures (35 and 40 °C) and moisture content of 60% are used. The results are shown in Fig. 2. As can be seen from the results, the model predictions agreed reasonably well with the experimental data.

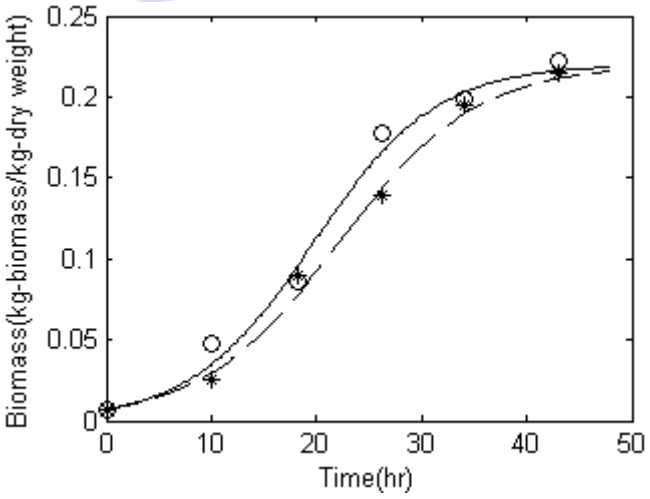

Fig. 2. Comparison between the predictions of the model and the experimental data of Hamidi-Esfahani et al. [2] for the growth of *Aspergillus niger* on wheat bran. (o) experimental data and (—) model predictions at 35°C; (✳) experimental data and (– – –) model predictions at 40°C;

Stuart et al. [22] obtained temperatures as high as 48 °C during cultivations in a rotating drum bioreactor, whereas, in experiments done in agar plates according to the isothermal approach, significant growth was not observed at temperatures above 40 °C [23]. Our model can explain growth at temperatures higher than those at which growth is noted in isothermal experiments. Fig. 3 shows the model predictions at 35, 40 °C and higher temperatures. Unfortunately, experimental data does not exist at temperatures above 40 °C to compare with predictions. It is clear from Fig. 3 that the biomass grows at a lower rate when the temperature is above T_{opt} , and almost no growth observe at 52 °C, which corresponds with the results obtained by Ghildyal et al. [6].

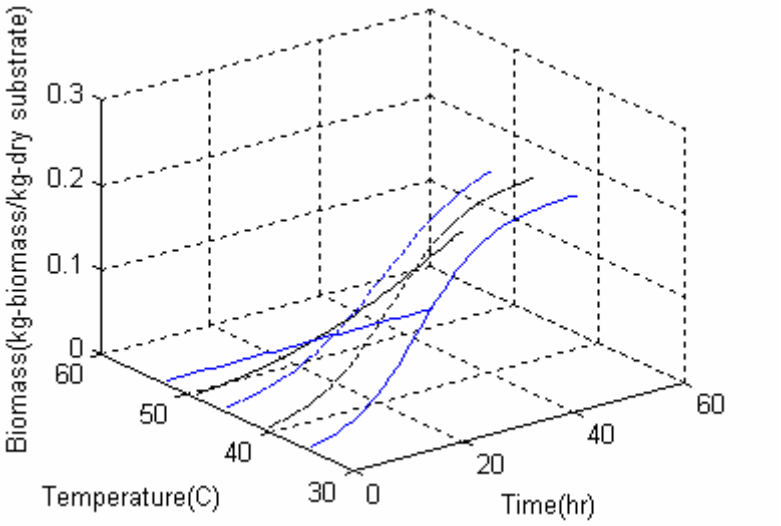

Fig. 3. Model predictions at 35, 40 °C and higher temperatures.

In the present work it is assumed that the effect of moisture content on growth is negligible, since in the majority of SSF processes it is assumed that the substrate bed is always maintained at the optimum water activity for growth, supposedly by dripping water into the bed at many points. Although in the absence of mixing, the best strategy is to choose a substrate which can undergo large changes in moisture content with only relatively small changes in water activity [24]. Smits et al. [25] showed that the water activity of wheat bran remains close to one at low moisture contents, which is in conformity with the assumption that was made in our work.

The experimental data used in this investigation to assess the heat transfer models in a SSF process, were taken from Ghildyal et al. [6]. The bioreactor used in their work was a stainless-steel packed column, 34.5 cm high and 15 cm in diameter and was aerated from the bottom. They measured temperatures at various different heights (3.3, 17, 28 cm) during the growth of *Aspergillus niger* on wheat bran for production of *amyloglucosidase*, but they reported temperature profiles only at 17 cm height and therefore, this same height was used as a bioreactor height in the simulations to enable us to evaluate models predictions with their experimental data. They also applied various different superficial air velocities (17, 34, 51, 68, 85 m hr^{-1}) and we used the value of 51 m hr^{-1} in the simulations, because at superficial air velocities lower than this value, bed temperature increases into deleterious values, whereas at superficial air velocities higher than this value, pressure drops increase, which are undesirable from both technical and economical points of view [4], and also evaporation rate increases which causes drying out of the bed. For instance, Ghildyal et al. [6] reported that at 17 m hr^{-1}, bed temperature reaches to 52°C, which is deleterious for *Aspergillus niger* and at 85 m hr^{-1}, the moisture content of the bed decreases to 22% in which this value limits the growth. Fig. 4 shows the predictions of lumped and distributed dynamic heat transfer models with the

experimental results obtained by Ghildyal et al. [6]. The results show that the predictions of distributed model are remarkably in good agreement with experimental data rather than lumped model.

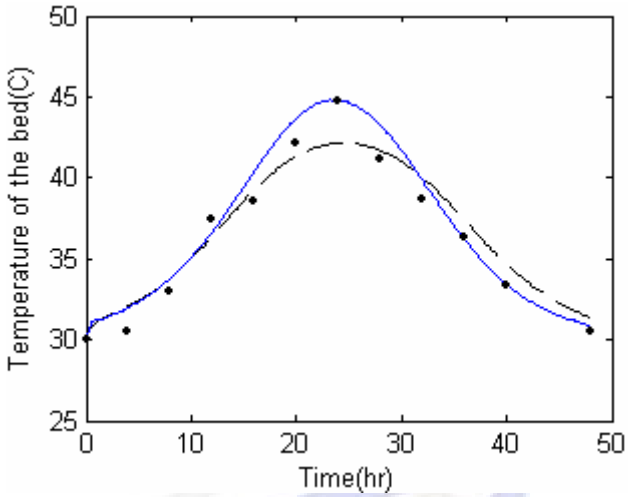

Fig. 4. Comparison of the predictions of lumped and distributed heat transfer models with the experimental data of Ghildyal et al. [4]. (•) experimental data; (– – –) lumped model predictions; (—) distributed model predictions.

Note that, the lumped model can just predict the temporal temperature profiles; in contrast, the distributed model provides detailed predictions, being able to make predictions about the temperature at any time and position within the bed. Fig. 5 shows the time-temperature profile at various different bed heights as predicted by distributed model.

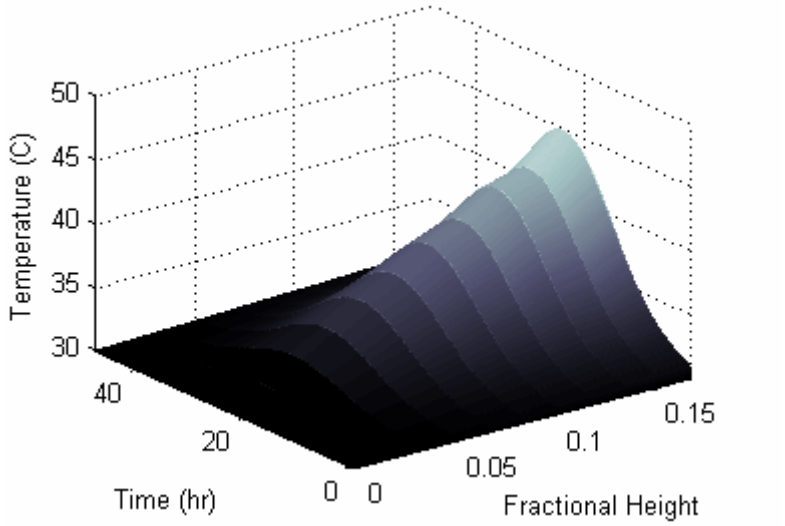

Fig. 5. time-temperature profile at various different bed heights as predicted by distributed model.

Reaching to a temperature 5°C above T_{opt} is undesirable for any part of the bioreactor. This temperature will be referred to as the critical temperature. Therefore, the critical temperature for *Aspergillus niger* is 40°C. The temperature higher than critical temperature could trigger sporulation, or could have adverse effects on growth and product formation. In fact, these temperatures impose a limit on growth. As Fig. 5 shows, in the region near the air inlet, the temperature is near the optimum for growth, the growth rate is high, and heat removal from the bioreactor is unable to remove all the metabolic heat, so the temperature increases with height, and as been clear from Fig. 5, some temperature limitations on growth are observed

during the fermentation. For example, these limitations, especially in the upper regions of the bed, are observable between 17-32 hr after the beginning of the fermentation.

4. Discussion

The logistic equation includes a limitation on growth and based on the concept that SSF is a contact process limited by available surface area [3,12]. This empirical approach to describing growth kinetics has allowed reasonable predictions of bioreactor performance. Further, its parameters can be theoretically linked to parameters associated with microscale events such as hyphal elongation and branching [11,14]. The logistic growth equation has limitations for building reliable models, since it cannot provide a complete representation during the death phase. Therefore, death or inactivation kinetic rates have been sometimes included in the models [14]. Our model in the present work would give similar results if all the viable biomass were considered to be fully healthy and ϕ were used to denote the fraction of the total biomass that was viable, with X denoting the total biomass, both dead and viable.

To date most models of SSF bioreactors have used isothermal approach to describing the effect of a varying temperature on growth. In this approach a range of cultures are incubated at a range of different temperatures, but with each culture being subjected to a constant temperature throughout the whole fermentation. The kinetic profile obtained for each culture is then analyzed by non-linear regression in order to extract the values of the kinetic model parameters. The growth parameters generated at each temperature are then plotted against the temperature and an empirical equation is then fitted by non-linear regression to express each parameter as a function of temperature [7,13]. Growth models developed using the isothermal approach do not accurately represent the situation in SSF bioreactors, where growth typically starts at the optimum temperature for growth, but then high temperatures occur in the substrate bed [11]. The model presented in the present work predicts that the growth rate at a particular instant not only depends on the temperature at that instant, but also depends on temperatures that the organism has experienced in the past. Although the analyses have been done for a particular microorganism and substrate, but this modeling approach can be used for other microorganisms and substrates if the appropriate parameters are available for them.

The level of ϕ varies between 0 and 1, where a value of 1 represents the normal level of the physiological factor within a fully healthy cell. It is worth to mention that it can increase in the absence of growth: when X equal to X_m there is no growth, but if ϕ is less than one it can increase. The effect of ϕ is to delay responses to shifts in temperature. As the temperature rises, it takes time for the physiological factor ϕ to denature. On the other hand, when the temperature falls from deleterious values to values at which the organism is capable of growing in perfect health, it takes time for the normal levels of the physiological factor ϕ to be reestablished. Physiological factor could be intracellular enzymes or ribosomes that play a key role in determining the velocity of growth, and the deleterious effects of high temperature may in part be due to denaturation of these components [27].

According to the Arrhenius equation, the rate of chemical reactions increases with temperature, and therefore, it might be expected that the maximum specific growth rate that the organism is capable of would increase with temperature. In fact, this is probably the dominant effect below the optimum temperature for growth. However, growth is not a simple chemical reaction, but rather requires the coordination of many chemical reactions. Possibly this coordination is adversely affected at temperatures above the optimum temperature for growth. These metabolic processes are so complex that any model attempting to describe them mechanistically would be too complex to be useful within a mathematical model of

growth in SSF bioreactors. The model proposed in the current work aims to capture this effect while maintaining simplicity.

The assumption of thermal and moisture equilibrium between the solid particles and the inter-particle gases will be approach to reality if saturated air is used to aerate the bed. It allows the bed to be treated as a single "pseudohomogeneous" phase, which has the mass weighted average properties of the air and the substrate [24]. von Meien and Mitchell [24] employed a two-phase models, namely model that explicitly treats the gas and solids phase as separate subsystems for describing heat and mass transfer. Simulations with this model indicated that, under the aeration conditions typically used for packed beds, equilibrium is nearly established between the solids and gas phases, which correspond with the assumption that was made in present study.

In fact, f is the slope of the curve of the humidity of saturated air plotted as a function of temperature. This curve was regarded as a straight line over the narrow temperature range of interest, of approximately 20°C. Ideally, the humidity of the air should be described by the Antoine equation but the linear approximation that is used in the model equations is reasonable over temperature ranges mentioned above. For example, linear regression of the humidity curve between 27 and 47°C gives a correlation coefficient of 0.989. The combination $f\lambda$ arises from the assumption that the air remains saturated as it flows through the bed: the evaporation of water to maintain saturation gives the air a higher apparent heat capacity [10]. The model confirmed that evaporation has the major potential to remove heat from the system. Even with saturated air at the inlet, evaporation contributes about two-thirds of the heat removal.

Inlet air temperature can be set several degrees below the optimum temperature for growth, but there are practical limits on how low T_a can be. It must be sufficiently high to support reasonable growth rates, since the region near the base of the column will be maintained near T_a by the incoming air. To this point the current work has assumed a T_a of 30°C, 5°C below T_{opt}. If T_a is set at T_{opt}, which has commonly been done with packed beds, the bed temperature in upper regions would much increase that would be undesirable effect on bioreactor performance.

5. Conclusions

Modeling could be a good tool for design, scale-up and control studies but such results need to be validated by experimental findings. We have presented a kinetic model that describes the influence of past and current temperatures on growth. This approach to kinetic modeling has good potential for application in models of solid-state bioreactors. This study also provides the useful tools for investigating the heat transfer dynamics of packed bed bioreactors under different operating conditions, since all heat transfer mechanisms are considered in modeling. In description of temperature gradients, distributed model is more successful than lumped model.

References

1. Pandey, A., "Solid-state fermentation," *Biochem. Eng. J.*, 13, 81 (2003).
2. Lekanda, J.S., Pérez-Correa, J.R., "Energy and water balances using kinetic modeling in a pilot-scale SSF bioreactor," *Process Biochem.*, 39, 1793 (2004).
3. Hamidi-esfahani, Z., Shojaosadati, S.A., Rinzema, A., "Modelling of simultaneous effect of moisture and temperature on *A. niger* growth in solid-state fermentation," *Biochem. Eng. J.*, 21, 265 (2004).
4. Khanahmadi, M., Roostaazad, R., Mitchell, D.A., Miranzadeh, M., Bozorgmehri, R., Safekordi, A., "Bed moisture estimation by monitoring of air stream temperature rise in packed-bed solid-state fermentation," *Chem. Eng. Sci.*, 61, 5354 (2006).

5. Robinson, T., Nigam, P., "Bioreactor design for protein enrichment of agricultural residues by solid state fermentation," *Biochem. Eng. J.*, 13, 197 (2003).
6. Ghildyal, N.P., Gowthaman, M.K., Raghava Rao, K.S.M.S., Karanth, N.G., "Interaction between transport resistances with biochemical reaction in packed bed solid-state fermenters: effect of temperature gradients," *Enzyme Microb. Technol.*, 16, 253 (1994).
7. Mitchell, D.A., Berovic, M., Krieger, N., "Biochemical engineering aspects of solid state bioprocessing," *Adv. Biochem. Eng./Biotechnol*., 68, 61 (2000).
8. Saucedo-Casteneda, G., Gutierrez-Rojas, M., Bacquet, G., Raimbault, M., Viniegra-Gonzalez, G., "Heat transfer simulation in solid substrate fermentation," *Biotechnol. Bioeng*., 35, 802 (1990).
9. Dalsenter, F.D.H., Viccini, G., Barga, M.C., Mitchell, D.A., Krieger, N., "A mathematical model describing the effect of temperature variations on the kinetics of microbial growth in solid-state culture," *Process Biochem.*, 40, 801 (2005).
10. Mitchell, D.A., von Meien, O.F., Krieger, N., "Recent developments in modeling of solid-state fermentation: heat and mass transfer in bioreactors," *Biochem. Eng. J.*, 13, 137 (2003).
11. Mitchell, D.A., Krieger, N., Stuart, D.M., Pandey, A., "New developments in solid-state fermentation II. Rational approaches to the design, operation and scale-up of bioreactors," *Process Biochem.*, 35, 1211 (2000).
12. van de Lagemaat, J., Pyle, D.L., "Modeling the uptake and growth kinetics of *Penicillium glabrum* in a tannic acid containing solid state fermentation for tannase production," *Process Biochem* 40, 1773 (2005).
13. Mitchell, D.A., von Meien, O.F., Krieger, N., Dalsenter, F.D.H., "A review of recent developments in modeling of microbial growth kinetics and intraparticle phenomena in solid-state fermentation," *Biochem. Eng. J.*, 17, 15 (2004).
14. Lareo, C., Sposito, A.F., Bossio, A.L., Volpe, D.C., "Characterization of growth and sporulation of *Mucor bacilliformis* in solid state fermentation on an inert support," *Enzyme Microb. Technol.*, 38, 391 (2006).
15. Sangsurasak, P., Mitchell, D.A., "Validation of a model describing 2-dimensional heat transfer during solid-state fermentation in packed bed bioreactors," *Biotechnol. Bioeng*., 60, 739 (1998).
16. Himmelblau, D.M., Basic Principles and Calculations in Chemical Engineering, 5th ed., Prentice-Hall, Englewood Cliffs, NJ, (1982).
17. Szewczyk, K.W., Myszka, L., "The effect of temperature on the growth of A. Niger in solid state fermentation," *Bioprocess Eng.*, 10, 123 (1994).
18. Sweat, V.E., "Thermal properties of foods," in: Rao, M.A., Rizvi (Eds.), S.S., Engineering Properties of Foods, Marcel Dekker, New York, pp. 49-132 (1986).
19. Perry, R.H., Green, D.W., Maloney, J.O., Perry's Chemical Engineer's Handbook, 6th ed., McGraw-Hill, New York, (1984).
20. Terzic, M.S., Todorovic, M.S., "The experimental investigation of isothermal and nonisothermal fluid flow and heat transfer through porous media," in: Quintard, M., Todorovic (Eds.), M., Heat and Mass Transfer in Porous Media, *Elsevier*, Amsterdam, pp. 585-600 (1992).
21. Gerald, C.F., Wheatley, P.O., Applied numerical analysis, 6th ed., Pearson , (1999).
22. Stuart, D.M., Mitchell, D.A., Johns, M.R., Litster, J.D., "Solid-state fermentation in rotating drum bioreactors: operating variables affect performance through their effects on transport phenomena," *Biotechnol. Bioeng.*, 63, 383 (1999).
23. Mitchell, D.A., "Development of a model system and a mathematical model for solid-state fermentation," Ph.D. thesis, Brisbane, Australia: The University of Queensland, (1989).
24. Von Meien, O., Mitchell, D.A., "A two-phase model for water and heat transfer within an intermittently-mixed solid-state fermentation bioreactor with forced aeration," *Biotech. Bioeng.*, 79, 416 (2002).
25. Smits, J.P., van Sonsbeek, H.M., Tramper, J., Knol, W., Geelhoed, W., Peeters, M., Rinzema, A., "Modelling fungal solid-state fermentation: the role of inactivation kinetics," *Bioprocess Eng.*, 20, 391(1999).
26. McMeekin, T.A., Olley, J., Ratkowsky, D.A., Ross, T., "Predictive microbiology: towards the interface and beyond," *Int. J. Food Microbiol.*, 73, 395 (2002).