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Estimation and Simulation in Batch Fermentation of Baker's Yeast Production

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Abstract

Baker's Yeast is an important additive among the substances, which improves bred quality, thus, a consideration has been made to study the conditions and parameters that affecting the production of the yeast in a batch fermenter experimentally and theoretically. Experimental runs were implemented in a 12-liter pilot-scale fermenter to predict the rate of growth and other parameters such as amount of additive consumed and the amount of heat generated. The process is modeled and performed using a computer programming prepped for this purpose, the model gave a good agreement comparing to the experimental work specially in the log phase.

Keywords: fermentation, simulation, yeast.

Introduction

The understanding and study of any process requires a mathematical representation or model of the process. The model is usually based on the prior physical or subjective knowledge about the process itself, and the engineering laws. Mathematical models for fermentation processes that have been developed in recent years[1] shows some complication. The growth and metabolism of sacchromyces cervisia (baker's yeast) have been investigated by many workers, some of the more significant of these include studies of varying glucose concentration[2] oxygen availability[2,3], type of sugar fermented[4] microbuble dispersion to increase oxygen transfer[5] and using date syrup as a substrate[6].

This paper reports the development and experimental confirmation of a mathematical model describing the growth of yeast organism. As this model is based on a proposed, relation between heat generation pH and growth rate.

Mathematical modeling

Batch fermentation refer to a partially closed system in which most of the materials required are loaded onto the fermenter, decontaminated before the process start and then removed at the end. Conditions are continuously changing with time, and the fermenter is an unsteady-state system, although in a well-mixed reactor, conditions are supposed to be uniform throughout the reactor at any instant of time.

Mathematical model of batch fermentation process can be written based on a dynamic model as follows[7]:

$$\frac{dx}{dt} = \left(\frac{\mu_{max}.s}{km+s} - K_d\right).x \quad (1)$$

$$\frac{ds}{dt} = -\frac{\mu_{max}.s}{Y_{xs}.(km+s)}\,x \quad (2)$$

$$\frac{dp}{dt} = \frac{\mu_{max}.s}{km+s}.x.Y_{px} \quad (3)$$

$$\frac{dH^+}{dt} = \frac{kn.\mu_{max}.s}{km+s}x \quad (4)$$

$$\frac{dT}{dt} = \frac{\mu_{max}\,s.x}{(km+s).m.C_P.Y_d} - \frac{h.A.T}{m.C_P} + \frac{1}{m.C_P}\left[P_m + h.A.T_{sur} - M_v.\Delta h_v\right] \quad (5)$$

Those five equations represent the biomass concentration, substrate concentration, product concentration, pH and temperature behavioure in the reactor (fermenter). The kinetics of most biological reaction are reasonably well represented by the Monod-model[8&9]:

$$\mu = \frac{\mu_{\max} s}{K_m + s} \quad (6)$$

where: μ is the specific growth rate, μmax is the maximum specific growth rate, s is the substrate concentration and Km is the Monod growth rate constant.

Programming simulation

Integration of the differential equation (1-6) are carried out on a computer programming, prepared to this form of equations, by using a fourth-order Runge-kutta solution. The program in Q-Basic language used to plotted directly biomass x, substrate s, product p, hydrogen ions H+ and temperature T agents the time. The program is prepared to read the initial value to calculate the first metabolic phase and then estimate the specific growth and product rate to calculate the second metabolic phase.

Experimental Work

Equipment description

The scale-up fermenter was run in a 12-liter pilot-scale fermenter (BIOSTAT® U50, B. Braun Company, Germany).

The temperature and the pH of the vessel was controlled. Heating or cooling water was supplied via the integrated jacket heat exchanger. Two-resistance thermocouples type-j were equipped into the input and output streams of the jacket in order to estimate the amount of energy Q consumed or generated by the fermenter. Air was injected into the vessel bottom (throughout the jacket from the top) via a sparger having 2.5-mm diameter orifice below the impeller. The turbulence of the broth was increased by four baffles, which were attached to the inner wall of the vessel. The pH value of the culture solution was measured by means of a sterilizable combination electrode (InFit 746-50®, Ingold Company). The stirrer drive variable speed system is designed as a top drive and is equipped with three 6-flat-blade disk-turbine impellers. The actual stirrer speed is measured by a precision DC tachogenerator integrated into the motor.

Experiment description

Fermentations were carried out in a 12-liter pilot-scale stirred tank fermenter. Yeast started culture S. cerevisiae was prepared in proportion to the scale-up volume. The fermentation was started after chalking the initial condition of the medium. Calculating the initial concentration of broth xo, sucrose so and other initial medium materials. Table 1 shows the variable according to experimental system data, with variable biomass and substrate initial concentration at constant other parameter.

Table (1) experimental system data, with variable biomass and substrate initial concentration at constant other parameter.

Run No.	*Initial Biomass Concentration* x_o gm/l	Initial Substrate Concentration s_o *gm/l*	μ_{max} hr^{-1}	Y_{xs} g_{bio}/g_{sub}
1	*0.15*	*12*	*0.271*	*0.55*
2	*0.5*	*12*	*0.269*	*0.4783*
3	*1.5*	*12*	*0.23*	*0.4992*
4	*0.15*	*18*	*0.247*	*0.5225*
5	*0. 5*	*18*	*0.241*	*0.5347*
6	*1.5*	*18*	*0.29*	*0.5167*
7	*0.15*	*25*	*0.228*	*0.458*
8	*0. 5*	*25*	*0.258*	*0.4842*
9	*1.5*	*25*	*0.361*	*0.4867*

Results and Discussion

A mathematical model of the bakers' yeast batch fermentation process has been reviewed in the previous chapter. The kinetic model from chapter three (equations 1 to 5) has been chosen to be part of simulation to compare with the actual data. Actual data were obtained from main experimental study at laboratory scale fermenter. The mathematical model is consisting of many kinetic parameters some of them have been evaluated and the other was taken from other workers. The five mathematical model and experimental data are presented in the following Figures (1-5) listed below.

Biomass concentration behavior

A concentration compression between the actual data and the simulation of the behavior of the biomass (ie equation 1); with variable initial biomass and substrate concentration are shown in Figures 1. The Figure 1 shows the biomass response and the behavior of the actual biomass compared with that of the simulation for run No.1 in Table 1. This Figure that the simulation response nearly agrees with the actual responses under different conditions of run for case of lag phase (the exponential growth).

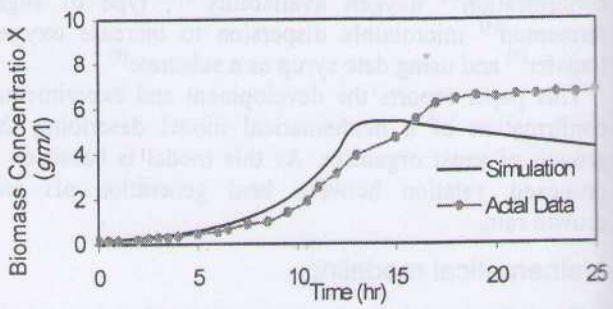

Figure 1 comparison of biomass concentration between actual data and simulation (0.15 *gm/l* biomass 12 *gm/l* substrate initial concentration) Run No.1

Substrate concentration behavior

The simulation of the substrate model (ie equation 2) reviews the behavior of the substrate (glucose) concentration as shown in figure 2.

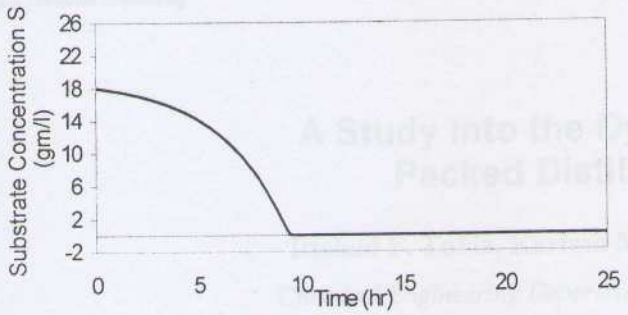

Figure 2 substrate concentration profile simulation curve with initial substrate concentration is12 *gm/l* (Run No. 1).

Product concentration behavior

The Figure 3 shows the simulation of equation 3 for the product (ethanol) formation during the main batch growth. It can be seen that the maximum value of the product is too low and the concentration is dilution, this indication means that the process goes to growth-associated product formation direction not to non growth-associated product formation.

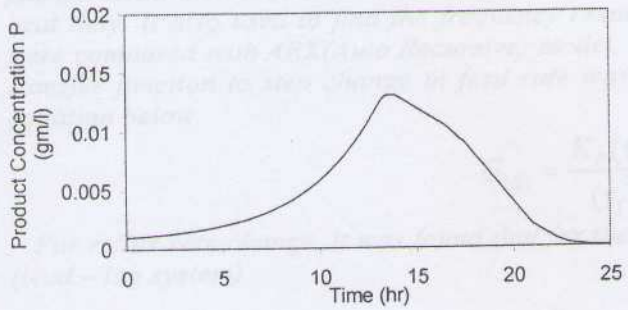

Figure 3 the product concentration simulation curve during the main batch growth, (Run No. 1).

The acidity (pH) behavior

Growth of microorganism requires a limited range of acidity, for bakery's yeast the range between 4-7. In reality, the pH must maintained at constant value (set point), but in this work, the dynamic behavior is shown without any control device in order to study and record the acidity behavior of the batch fermenter. A comparison between actual data and simulation are illustrated in the Figure 4 as examples, which show an acceptable agreement between actual and simulated results.

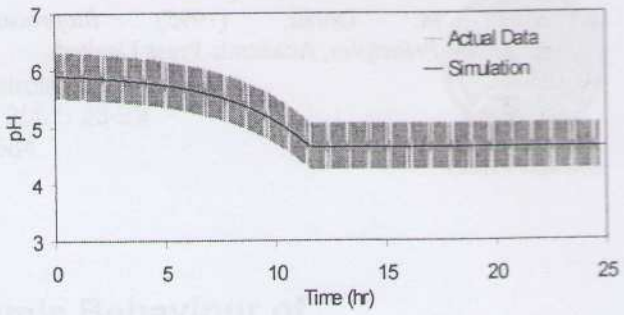

Figure 4 comparison of pH between actual data and simulation (Run No. 1)

The temperature behavior

The dynamics behaviors of the fermentation temperature are presented in the Figures 5. This Figure show a comparison between the actual and simulated responses, a closed fit was obtained.

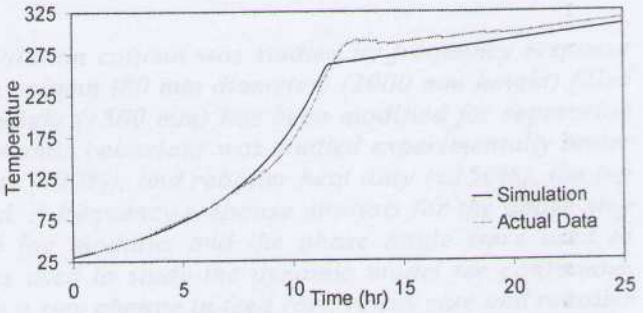

Figure 5 comparison temperature between actual data and simulation

Conclusions

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