Journal of Industrial and Engineering Chemistry xxx (2017) xxx–xxx

Contents lists available at ScienceDirect

Journal of Industrial and Engineering Chemistry

journal homepage: www.elsevier.com/locate/jiec

Development of an efficient process for recovery of fucose in a multi-component mixture of monosugars stemming from defatted microalgal biomass

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ARTICLE INFO

Article history:
Received 7 June 2017
Received in revised form 14 July 2017
Accepted 15 July 2017
Available online xxx

Keywords:
Simulated moving bed
Fucose
Continuous separation
Optimal design
Microalgae

ABSTRACT

One of highly promising ways for fucose production is to utilize the defatted residue of microalgae as the fucose source. A prerequisite for such fucose-production strategy is a robust separation process that can perform an efficient recovery of fucose in a monosugar mixture coming from the hydrolysis of the defatted microalgal biomass. To develop such process, we first selected a prospective large-scale adsorbent that had a sufficiently high selectivity between fucose and other monosugar components. The selected adsorbent was then experimented in accordance with the principle of multiple frontal analysis in order to obtain the intrinsic parameters of the relevant monosugar components. Using the resultant parameters, the optimal design of the fucose-separation process of interest was carried out on the basis of a simulated moving bed (SMB) technology. The validity of the designed process was investigated first with detailed model simulation, and then with a continuous fucose-separation experiment based on the self-assembled SMB equipment. The results of the SMB experiment demonstrated that the developed process was highly effective in continuous separation of fucose with the purity of 97.1% while maintaining its loss as low as 0%. It is thus expected that the results in this study can contribute to a meaningful improvement in the economical efficiencies of both a microalgae based biodiesel-production process and a fucose-production process.

Introduction

Fucose has been recognized as one of rare sugars that has a great potential for high-value applications in various industries [1–9]. It was widely accepted that fucose could play a key role in the manufacture of anti-aging cosmetics, anti-cancer drugs, and anti-allergic drugs [1,4–9]. It is also known to be associated with the improvement of long-term memory capability [2,3]. Furthermore, it was revealed from recent studies that fucose can be utilized as a precursor for preparing fucosyllactose, which is the main constituent for human milk oligosaccharides [9,10].

Several methods for the production of fucose were reported previously. One of the methods is to use a chemical synthesis, in which other monosugars serve as starting materials for generating fucose [11–13]. In addition to such a chemical synthesis, a microbial or an enzymatic synthesis can also become a route for fucose production [14,15]. The other methods involving no synthesis step are mostly based on the concept of recovering fucose from the hydrolyzate of a polysaccharide-containing biomass, which is available from hardwood, softwood, grain straw, corn husks, corn fibers, and seaweeds [8,9].

According to the literature, the use of the aforementioned methods as a means of developing a large-scale process for fucose production could often have some difficulties due to the following reasons [8,9]. First, in case of the methods based on fucose synthesis, the use of an expensive reagent and a multi-step process is inevitable, and further a highly efficient process for separating

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http://dx.doi.org/10.1016/j.jiec.2017.07.011
1226-086X/

fucose from the output of fermentation or enzymatic reaction should be established. Secondly, in case of the methods based on fucose recovery from the biomasses of natural origin, one should pay attention to the cost associated with securing biomass resources and the issue of establishing a highly-efficient recovery process.

From the above-mentioned points, it can be inferred that the first requirement for guaranteeing high economical efficiency in fucose production is to minimize the cost associated with securing the source for fucose-containing biomass. In regard to this issue, it is worth paying particular attention to recent studies on the usability of microalgal biomass, which reported that the residue remaining after the extraction of lipid from microalgae contained several monosugars including fucose [16]. In such processing, the extracted lipid has been a main interest because of its usefulness in biodiesel production. By contrast, the defatted residue of microalgae has been regarded as a by-product or waste that was of less significance than the lipid component [16]. For this reason, it is quite worth considering the use of the by-product from microalgae processing (i.e., defatted microalgal biomass) as the source for fucose production, which will obviously be of benefit to both a microalgae based biodiesel-production process and a fucose-production process.

To make the aforementioned fucose-production strategy industrially viable, it is important to secure a highly efficient separation process for recovery of fucose from the hydrolyzate of defatted microalgal biomass. Since the hydrolysis of defatted microalgal biomass generates a monosugar mixture containing fucose, rhamnose, ribose, xylose, mannose, glucose, and galactose [16], the target process should be tailored to the task of a separation between fucose and the other monosugars. When it comes to the separation for the system containing sugars, several studies have been accomplished previously [17–21]. However, the separation of fucose from a multi-component monosugar mixture has not been attempted so far.

The target process for the aforementioned fucose separation should also follow a continuous-separation mode in order to facilitate an industrial-scale separation of fucose. For this issue, it is worth mentioning that one of the trustworthy ways for realizing a continuous-separation mode with high productivity and high purity is to adopt a simulated moving bed (SMB) technology, whose performance has been validated in a variety of large-scale separation tasks in the literature [22–24]. However, there have been no previous studies concerning the task of an SMB separation for the system of a monosugar mixture coming from defatted microalgal biomass.

The goal of this study is to develop an SMB process that can support the feasibility of the aforementioned fucose-production strategy. As a first step for this work, we selected the adsorbent that was suitable for separation of fucose from the considered system and also applicable to a preparative-scale or a large-scale separation process. The selected adsorbent was then packed into a single column, which was experimented in accordance with the principle of multiple frontal analysis in order to determine the intrinsic parameters of the relevant monosugars comprising the system of interest. Using the determined parameters, we carried out the optimal design of an SMB process for a highly efficient recovery of fucose from the considered monosugar mixture, which stems from the hydrolyzate of defatted microalgal biomass as mentioned above. The designed SMB process was then validated through a detailed model simulation and a continuous fucose-separation experiment based on the self-assembled SMB equipment, both of which confirmed the fulfillment of continuous fucose-separation while ensuring high purity and almost no loss for fucose product.

Theory

Simulation model for SMB design

The development of a targeted SMB process in this study was carried out by following a model-based design approach [25,26], which has been recognized to be effective in minimizing trials-and-errors and reducing the number of experiments to be needed for completing a given task. The core principle of this approach is to design an SMB process by utilizing the following three factors; (i) the intrinsic parameters of feed components, (ii) a process simulation, and (iii) a process optimization. Among them, the intrinsic parameters, which are usually determined first through a well-organized experiment, severed as input data for activating the tools for process simulation and optimization. Since such tools can allow us to predict the migrating behavior of each feed component in an adsorbent column and to clarify the operating conditions for optimal SMB separation, they, in fact, correspond to the essential prerequisites for ensuring a successful implementation of the model-based design approach.

As for the column model for a simulation tool, there are several ones available in the literature [22–30]. In consideration of both computational efficiency and accuracy, a lumped mass-transfer model [25–30] was adopted as a means of SMB simulations in this study. This model accounts for the phenomena of convection and dispersion in an interstitial liquid region, and also for the phenomena of film mass-transfer, intra-particle diffusion, and adsorption in a pore liquid region and a solid phase. Its mathematical expressions are available in the literature [25,27,28,30], and their solutions were obtained with the help of Aspen Chromatography simulator, which was based on a biased upwind differencing scheme (BUDS) with 60 nodes per column and Gear integration method.

Optimization tool for SMB design

Following the above-mentioned simulation tool, the use of a convenient optimization tool is also known to conduce to the successful development of an SMB process. To ensure high reliability for an SMB optimization tool, it should be prepared to reflect the following two factors; (i) all possible mass-transfer effects occurring in a column and (ii) a periodic port-switching pattern in an SMB process [26–28,31]. This inevitably requires the use of a highly efficient optimization algorithm, which should then be connected with an SMB column model. One of well-known optimization algorithms for such purpose is a genetic algorithm (GA), whose usefulness in various SMB optimization tasks have been confirmed in many of previous studies [29–32]. Several GA versions have been developed so far by means of adding some operators that were effective in improving convergence speed. Among the GA versions, the latest one is a NSGA-II-JG (elitist nondominated sorting genetic algorithm with jumping genes) [32,33], which is reputed to be highly efficient and robust in searching for the optimal condition of a multi-column process.

In this study, the optimization tool for the considered SMB was prepared using the aforementioned NSGA-II-JG algorithm, whose relevant codes were created in an Excel VBA (visual basic application) software. These codes were configured to implement a series of NSGA-II-JG operations (initialization, reproduction, crossover, mutation, jumping gene, and elitism), and also to run the model simulations for evaluation of SMB performances. In order to start the execution of the optimization tool, the parameters associated with the environment of the NSGA-II-JG operation should be specified beforehand. These parameters are commonly called “NSGA-II-JG parameters” [32,33]. Table 1 presents the values of the NSGA-II-JG parameters that were adopted in the

Please cite this article in press as: S.-B. Hong, et al., Development of an efficient process for recovery of fucose in a multi-component mixture of monosugars stemming from defatted microalgal biomass, J. Ind. Eng. Chem. (2017), http://dx.doi.org/10.1016/j.jiec.2017.07.011