DEVELOPMENT OF MULTIPLE PROBE CRYO-CONCENTRATION SYSTEM FOR PROGRESSIVE FREEZE CONCENTRATION OF LYSOZYME AQUEOUS SOLUTION

NORSHAFIKA BINTI YAHYA

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School of Chemical and Energy Engineering Faculty of Engineering Universiti Teknologi Malaysia

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ABSTRACT

A new crystalliser to concentrate lysozyme aqueous solution through freeze concentration was designed in this study to overcome the shortcomings of the currently available methods in concentrating protein. A new compatible, simple, reliable and low maintenance design was developed in this study based on progressive freeze concentration principles called multiple probe cryo-concentration system (MPCC). Progressive freeze concentration process is a process which rejects all impurities or solute by generating ice crystal lattice from the mother liquor, thus the remaining solution is more concentrated. The aim of this research is to observe the possibility of the new design system in producing high concentration lysozyme aqueous solution according to the four-effect parametric condition which includes coolant temperature, stirrer speed, operation time and initial concentration. The complete design of MPCC system consists of a solution tank with outer tubular cooling jacket and insulator, containing the protein solution and the cooled multiple probes immersed in it. The concentration process began when the temperature of the lysozyme aqueous solution dropped until the ice crystal formed on the wall of the probe while assisted by the stirrer. The concentrated protein solution was then separated from the ice crystal layer formed and collected as product. In order to evaluate the capability of the design, effective partition constant (K), solute yield of lysozyme (Y), concentration index (CI) and average ice growth rate (\tilde{v}_{ice}) were analysed using UV-Vis spectrophotometer to determine the solute concentration. The findings revealed that coolant temperature at -12 °C, stirrer speed at 350 rpm, operation time at 40 minutes and initial concentration at 10 mg/ml gave the best result of K, Y and Cl and \tilde{v}_{ice} . Meanwhile, the determination of optimum condition by response surface methodology indicated that coolant temperature is the most significant parameter followed by stirrer speed and operation time but initial concentration was found to be not significant in affecting the process for both responses of K-value and Y. A thermodynamic prediction model was also built and its validity for ice crystal growth rate prediction was found to be adequately accurate compared to the actual experimental result based on the error analysis obtaining R-squared of 0.98 and absolute average relative deviation of 8.08 %. The heat transfer analysis discovered that the overall heat transfer coefficient, U_0 and heat remover, Q are quite similar for stirrer speed and operation time where increased stirrer speed and lower operation time resulted in lower U_o and Q while increased initial concentration would increase the U_o and Q. Despite, U_o and Q are slightly different and contradict with each other when coolant temperature was increased where U_0 would increase but Q was decreased. The results from the analysis and investigation shed light on the theory behind the concentration method of protein using freezing method with the newly designed cryo-concentration device, which has never been investigated, tested and discussed specifically for protein concentration.

ABSTRAK

Satu pengkristal baharu untuk memekatkan larutan berair lysozyme melalui pemekatan beku direka dalam kajian ini untuk mengatasi kekurangan kaedah yang ada sekarang dalam pemekatan protein. Reka bentuk yang serasi, mudah, boleh dipercayai dan berpenyelenggaraan rendah yang baharu telah dibangunkan dalam kajian ini berdasarkan prinsip-prinsip kepekatan pembekuan progresif yang dipanggil pemekat krio berbilang kuar (MPCC). Proses pemekatan beku progresif adalah proses yang menolak semua bendasing atau bahan larut dengan menghasilkan kekisi kristal ais daripada larutan utama, akhirnya meninggalkan larutan yang lebih pekat. Tujuan penyelidikan ini adalah untuk melihat kemungkinan sistem reka bentuk baharu dalam menghasilkan larutan berair lysozyme yang berkepekatan tinggi mengikut empat parameter termasuk suhu penyejuk, kelajuan pengaduk, masa operasi dan kepekatan awal. Reka bentuk lengkap sistem MPCC ini terdiri daripada tangki larutan dengan jaket menyejuk tiub luar dan penebat yang mengandungi larutan protein dan kuar yang disejukkan terendam di dalamnya. Proses pemekatan bermula apabila suhu larutan berair lysozyme turun sehingga kristal ais terbentuk pada dinding kuar sambil dibantu oleh pengaduk. Larutan protein pekat kemudian dipisahkan dari lapisan kristal ais yang terbentuk dan dikumpulkan sebagai produk. Untuk menilai keupayaan reka bentuk, pemalar pemisahan berkesan (K), hasil larutan lysozyme (Y), indeks kepekatan (CI) dan purata kadar pertumbuhan ais (vice) dianalisis dengan menggunakan spektrofotometer UV-Vis untuk menentukan kepekatan larutan. Penemuan menunjukkan bahawa suhu penyejuk pada -12 °C, kelajuan pengadukan pada 350 rpm, masa operasi pada 40 minit dan kepekatan awal pada 10 mg/ml memberikan hasil terbaik K, Y, Cl dan \tilde{v}_{ice} . Sementara itu, penentuan keadaan optimum oleh kaedah tindakbalas permukaan menunjukkan bahawa suhu penyejuk adalah parameter yang paling penting diikuti oleh kelajuan pengaduk dan masa operasi tetapi kepekatan awal didapati tidak penting dalam mempengaruhi proses bagi kedua-dua K dan Y. Model ramalan termodinamik juga dibina dan kesahannya untuk ramalan kadar pertumbuhan ais kristal didapati cukup tepat berbanding dengan keputusan eksperimen sebenar berdasarkan analisis ralat yang memperoleh R-kuadrat 0.98 dan sisihan relatif purata mutlak 8.08 %. Analisis pemindahan haba mendapati bahawa pekali pemindahan haba keseluruhan, U_o, dan kehilangan haba, Q, adalah hampir sama untuk kelajuan pengaduk dan masa operasi di mana kelajuan pengaduk yang semakin meningkat dan masa operasi yang lebih rendah memberikan Uo dan Q yang rendah manakala peningkatan kepekatan awal akan meningkatkan U_o dan Q. Walaubagaimanapun, U_o dan Q sedikit berbeza dan bercanggah antara satu sama lain apabila suhu penyejuk dinaikkan di mana U_o akan meningkat tetapi Q berkurangan. Keputusan dari analisis dan penyiasatan menggambarkan teori di sebalik kaedah pemekatan protein menggunakan kaedah pembekuan dengan alat pemekatan krio yang baharu yang direka, yang tidak pernah diselidiki, diuji dan dibincangkan khusus untuk kepekatan protein..

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LIST OF ABBREVIATIONS

PFC	-	Progressive freeze concentration
SFC	-	Suspension freeze concentration
MPCC	-	Multiple probe cryo-concentrator
RSM	-	Response surface methodology
UV-vis	-	Ultraviolet-visible spectrophotometry
FC	-	Freeze concentration
BSA	-	Bovine serum albumin
rpm	-	Rotation per minute
CCD	-	Central composite design
ANOVA	-	Analysis of variance
DOE	-	Design of experimental
CTemp	-	Coolant temperature
OpTime	-	Operation time
StSp	-	Stirrer speed
InCon	-	Initial concentration
SST	-	Total sum of square
SSres	-	Residual/error
MS	-	Mass square
Cl	-	Concentration Index

LIST OF SYMBOLS

Κ	-	Effective partition constant
\dot{Q}_{LC}	-	Energy demand
Uo	-	Overall heat transfer coefficient
β	-	Beta
Y	-	Yield
C_L	-	Concentration of liquid
Cs	-	Concentration of solid
V_L	-	Volume of liquid
Т	-	Time
ρ_{ice}	-	Density of ice
ρ _{liq}	-	Density of liquid
А	-	Area (cm)
%	-	Percentage
U	-	Rate of crystal front
μ	-	Rate of advance of crystal front
'n	-	Mass flow rate
C _{Fs}	-	Final solute concentration
Cs	-	Concentration of solute
C _{H2O}	-	Concentration of water
C_1	-	Initial solute concentration
Μ	-	Mass
\mathbf{v}_1	-	Initial volume
W	-	Watt
α	-	Alfa
°C	-	Degree celsius
Θ	-	Entropy production per unit
Q	-	Total heat transfer

J_q	-	Flux of heat
J _{H2O}	-	Mass flux of water
J _s	-	Mass flux of solute
V _{ice}	-	Molar volume of ice
V _{H2O}	-	Molar volume of water
A _m	-	Logarithmic mean area
Ai	-	Inner surface area
Ao	-	Outer surface area
Ci	-	Concentration interface between ice and solution
ki	-	Kinetic coefficient
Kc	-	Mass transfer coefficient
R	-	Resistance
ω_{s}	-	Solute mass fraction
δ	-	Film thickness
Δ_fH	-	Enthalpy of freezing
υ_{ice}	-	Velocity of ice growth
ΰ _{ice}	-	Average ice growth rate
q	-	Factor
Κ	-	Run

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CHAPTER 1

INTRODUCTION

1.1 Research Background

Chemical engineering separation technologies have always demanded for process efficiency, predictability, economic and simplicity aspect, same goes to technology of protein concentration and purification methods. The key is to develop technologies that are transforming and improving the way of innovation due to shortcomings of the existing protein separation methods or techniques. The separation methods of these types of protein for example egg white have been developed since early 1900 but preparation methods of these protein for commercial application are still under research and development. Those sequential preparation techniques of separation for these multiple protein are very important criteria involving simplicity, scalability and use of nontoxic chemicals for further commercial production and application (Abeyrathne *et al.*, 2013a). Freeze concentration is believed to be an applicable method to separate protein due to its simplicity which does not involve toxic chemical despite of its shortcoming, low productivity and low increment of protein separation compared to other methods used in previous research.

In protein purification, one of the steps is to remove water from the protein aqueous solution. It is familiar that protein in aqueous solution is surrounded by water which has different properties from bulk water. The water called hydration water is more difficult to remove from the protein due to low activity (Rickard *et al.*, 2010). Water hydration also has fewer degrees of freedom and a long residence time (Rickard *et al.*, 2010). Other than that, protein destabilization /stabilization also depends on the initial hydration level of protein and the water content in acetonitrile (Sirotkin and Kuchierskaya, 2017).

In order to complete the study about the protein separation of water from protein aqueous solution, hen egg-white lysozyme was used as a model protein in this research due to its high availability in the market, cheapest compared to the other proteins and most importantly, it is applied and studied in biophysical and biotechnological investigation. Lysozyme is well known as an effective immunological agent and an antimicrobial peptide with a high enzymatic activity (Ercan and Demirci, 2016). Large amounts of lysozyme can be found in egg white and several in secretion including tears, saliva, human milk and mucus. Lysozyme is also one of the protein enzymes which have a lot of benefits including bladder health support, healthy inflammation management, infection management, also support for wound repair and has many applications in both food and dietary supplements. Water content surrounding lysozyme can be interpreted in Figure 1. 1. The connected red and white coloured atoms represent molecules of water content, light blue colour represents other substance, meanwhile striped blue colour represents the structure of lysozyme.

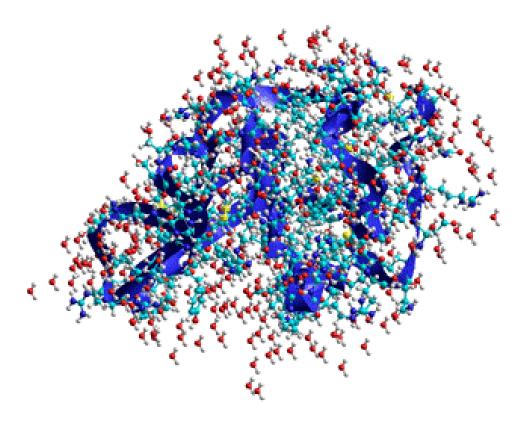


Figure 1.1 Schematic of human lysozyme with water content (Chaplin, 2019).

The process of removing water and concentrating lysozyme aqueous solution is very important in order to make sure the desired concentration is achieved for further application. Major challenges to concentrate the protein are to achieve high end product concentration, better quality with preserved or retained original biological structure of protein and to reduce operation time intended for subcutaneous administration. Most of the methods can achieve approximately in the range of 30 to 40 mg/ml of lysozyme concentration but they are lacking in the maintenance methods (ultrafiltration and dialysis) and they utilize longer time which is more than an hour. Thus, the biochemical companies and especially the researchers are always looking for the best technique or method to achieve a good result of concentration process for further applicable analysis, reaction and administration procedure.

Freeze concentration is a process of concentrating a solution by freezing out the water content into ice crystals. By comparing to evaporation and membrane technology, freeze concentration has given some benefits compared to the others in producing a concentrate with high quality product because the process occurs at low temperature where no vapour or liquid interface exist resulting minimal loss of volatiles (Jusoh *et al.*, 2013). Recently, a new freeze concentration system has been introduced in the configuration of a one-step system, which is progressive freeze concentration (PFC) that is simpler than the conventional suspension freeze concentration (SFC).

Progressive freeze concentration method was applied in this research because the concept of this method can reduce the water content at almost 90% (Miyawaki *et al.*, 2012) and avoid protein denaturation contributed by vigorous heat. Progressive freeze concentration forms a single block of ice compared to the suspension freeze concentration, where small ice crystals are formed suspended in the mother liquor. Hence the final separation of ice and the concentrate becomes easier. Besides, according to Yahya et al. (2017), the advantage of this feature with the large surface area is that the operation becomes easier because the ice lining process can be neglected. Other than that, supercooling can also be avoided, thus preventing operation at super low temperature to accommodate ice nucleation. This will improve its productivity and reduce operation cost (Yahya *et al.*, 2017a).

1.2 Problem Statement

Protein or lysozyme concentration and purification technology is demanding for simplicity, predictability, efficiency, economic and higher increment of concentration process equipment to overcome the shortcomings of the current and previous methods. Although many methods have been used in this particular process, they still do not achieve all the criteria demanded by the industries and community. Thus, this project is really important to study the improvement that will occur during the process using a newly built innovation of technologies.

There are several methods that are commonly available in carrying out protein concentration process namely, lyophilisation, dialysis, cellulose membrane concentrators, precipitation or salting out, chromatography, ultrafiltration and freeze concentration or cryo-concentration, the method has not yet been investigated. The most common method or technique to concentrate protein in small scale that is usually applied is dialysis technique, meanwhile biotech companies which use large scale frequently rely on membrane filtration and evaporation. Literally, the technique of concentrating protein nowadays has many problems and disadvantages including the high cost required in obtaining the osmotic pressure needed and also for membrane replacement attributable from clogging occurrence, the needs for high energy, the fact that the biological structure could also be destroyed due to high temperature applied, high ammonium sulphate concentration may disrupt the biological activity of the protein and may not return on resolubilization, the proteins may interact with the membrane, less productivity and increment of protein concentration. All the problems and disadvantages may cause reduction of protein quality and sometimes highly concentrated protein could not be adequately produced.

In order to solve the mentioned problems, other techniques or methods are needed to provide better alternative and the best choice is using freeze concentration or cryo-concentration method based on other previous researches which provide good results in reducing the number of unit operations with less time consumption. This is also supported by Miyawaki et al. (2016) where cryo-concentration method is the best method among other methods in concentrating liquid food and biochemical solution due to several advantages: ease of separation of concentrated solution due to simple equipment, low energy requirement, relative component-distribution is kept unchanged, the process temperature is low thus preventing undesirable biochemical and chemical changes, also minimal loss of flavour and aromas (Cisse *et al.*, 2011; Gunathilake *et al.*, 2014a; Gunathilake *et al.*, 2014b; Miyawaki *et al.*, 2016a; Miyawaki *et al.*, 2012). Cryo-concentration is a technique by which pure water can be removed from the feed solution and formed into ice, which leaves behind solution with higher concentration.

Although a recent work by Yu et al., 2014 had used the same material and methods called Solvent Freeze-out Technology (SFOT) from the concept of cryoconcentration technique, they had not achieved high quality separation with low productivity which resulted in yield of only 51.8% and collected 0.29 g of lysozyme using more than an hour to complete the process (Yu *et al.*, 2014). Meanwhile, if compared with other designs like Miyawaki et al. (2016), Samsuri et al. (2015) and Amran et al. (2018), those designs are not suitable and have several disadvantages when it deals with the lysozyme aqueous solution concentration process. This is because, the sequence of lysozyme concentration process will firstly go through the process of isolation in which water salt will be mixed with the impure lysozyme as an attempt to purify the lysozyme by precipitating the lysozyme. Hence, a more suitable design is needed as an agitated unit in place of ice freezing to resist from the gravity in order to avoid the precipitated lysozyme from being entrapped in the ice.

Nevertheless, the progressive cryo-concentration still has many advantages and is proposed to be a method to replace and upgrade the previous methods in removing water and concentrating protein solution. Progressive cryo-concentration is a process where ice crystals are formed as a single block of ice on the surface where cooling is supplied to overcome the drawbacks of the existing process to concentrate the protein. The application of the process could make possible concentration of protein because theoretically, the formation of ice crystal lattice rejects all impurities and should then result in high purity of ice, leaving behind highly concentrated protein solution. Another point to be highlighted is the melting point and freezing point of protein is 25° C (Gorania *et al.*, 2010) and -7^{\circ}C (Wang *et al.*, 2013), respectively. In addition, the

progressive cryo-concentration is not affected by the molecular size. This process has never been widely investigated or used in protein concentration before. Thus, it is important to study the concentration effect toward protein solution in order to offer a new technique of producing desirable concentration of antibody protein.

A new design of ice crystalliser for a PFC process called multiple probe cryoconcentrator (MPCC) has been designed and improved with several additional adjustments in this research to figure out the efficiency of the freezing system towards water removal from the lysozyme solution. The new prototype of separation design (MPCC) is believed can increase the concentration of lysozyme and resolved the problems involved in protein separation.

1.3 Objective of the Study

The aim of this research is to provide a new alternative method of lysozyme protein concentration. The objectives of this research include: -

- 1) To design and fabricate a new crystallizer which is called a multiple probe cryo-concentrator (MPCC) to be applied for lysozyme concentration.
- To investigate the effect of process condition including coolant temperature, operation time, stirrer speed and initial concentration towards the effective partition constant (K), solute yield (Y), concentration index (Cl) and average ice growth (v_{ice}) of lysozyme aqueous solution.
- To determine the optimum operating parameters in concentration for lysozyme aqueous solution for two responses (K and Y) via MPCC system using Response Surface Methodology (RSM).
- 4) To analyse the heat and mass transfer for ice formation and perform a thermodynamic modelling of the solution concentration process, considering thermal conductivity of the concentration system.

1.4 Scope of Research

The design of the new crystalliser (MPCC) was considered the element of surface area for heat transfer and freezing process through the introduction of the probe structure, as well as the design of cooling jacket and stirrer for adequate cooling. Meanwhile the geometrical feature of the MPCC was evaluated based on friction profile and comparison on ice productivity and protein concentration.

Probe temperature, operation time, agitation speed and lysozyme aqueous solution concentration was conducted in the range -6 to -12 °C, 20 to 60 minutes, 200-400 rpm, and 6 to 14 mg/ml of concentration, respectively.

Lysozyme aqueous solution concentration was analysed by UV-vis spectrophotometer and observed at length in region 280 nm.

Thermodynamic modelling was performed by calculating the rate of heat transfer exchanged in the process and simulated using the parameters.

1.5 Theoretical Framework

The operationalization of the research construct considers two (2) major elements that contribute to the effect of the resulting protein concentration as depicted in Figure 1.2.

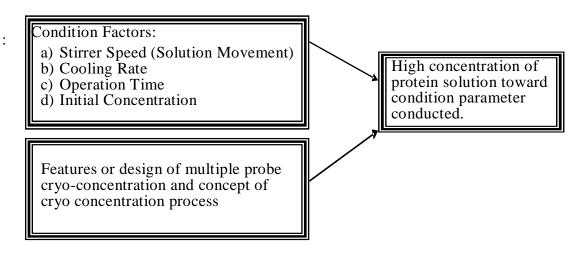


Figure 1.2 Theoretical framework of the study

1.6 Significance of Research

The potential to concentrate a solution at high concentration has always been a priority to apply in small-scale or large-scale. In case of protein solution, the current methods used always create problems that might contribute to low concentration of protein, high cost and maintenance, long process time and affecting the quality of protein concentrate.

However, cryo-concentration can be seen as a way forward or as another alternative method for protein concentration due to the principle of cryo-concentration in which an aqueous solution is concentrated by water freezing and expelling all the impurities. This method has some advantages that contradict the previous existing method. Thus, cryo-concentration method is believed to have potential as a method to concentrate protein solution by using a new crystallizer design from the same concept of cryo-concentration.

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