COVER STORY



Expanded Bed Adsorption (EBA) for Purification of Protein Product of Biotechnology

By: Dr Norhafizah binti Abdullah, Universiti Putra Malaysia

large percentage of the products emerging from the rapidly expanding biotechnology industry are proteins. Proteins represent the most useful and diverse class of biopolymers [1]. They are important as foods, food supplements, industrial catalysts, cleaning agents and pharmaceuticals. In the area of pharmaceuticals, their usefulness lies in their properties, such as their enzymatic activity, specific recognition interactions with other molecules or other therapeutic actions. Proteins may be formed in, or obtained from a variety of sources such as fermentation broths of bacterial, yeast or mammalian cells or preparations of naturally occurring tissues or fluid. If one considers the heterogeneity of courses from which these proteins are derived, their intended use and their diversity, the need for a great variety of recovery processes becomes apparent [2]. These recovery processes are usually collectively described by the term 'downstream processing' which in its narrowest definition is the processes involve the recovery, which purification and stabilisation of such products from conditioned media or fermentation broth.

Techniques suitable for the purification of proteins have to meet boundary conditions, which are different from those applied to traditional chemical processing. This is on the one hand due to the sensitivity of the native protein structure and function to factors such as temperature, pressure, proteases and interfacial contact [3]. The other important difference between the purification of proteins and the separation of chemically produced compounds is the medium from which the protein has to be isolated. Protein sources typically contain particulate material which has to be removed prior to further purification. To complicate matters further, the liquid itself contains a wide variety of compounds such as other proteins, released lipids and nucleic acids, all in comparatively low concentrations, the desired protein often being only a minor component in this mixture. schemes often contain multiple unit operations. In the past, cascades of 8–10 purification steps were normally used in the downstream processing flowsheet of protein production (Figure 1). Each step in the recovery process will affect the overall process economy by increasing

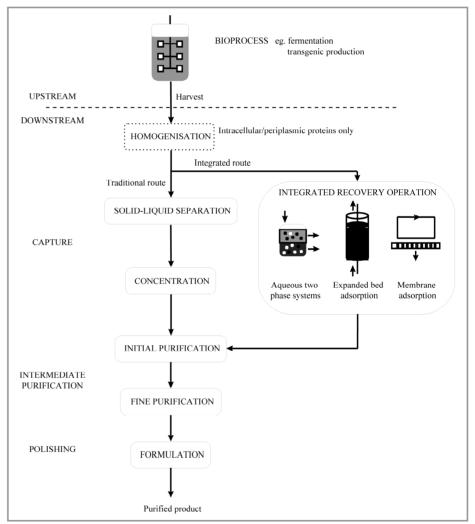


Figure 1: A typical downstream processing flowsheet with a possible site for the inclusion of an integrated unit operation such as expanded bed adsorption.

PROTEIN PURIFICATION FLOWSHEET

Due to the complexity of the separation and the high level of product purity required, the resulting purification operational cost and process time, and also by causing a loss in product yield [4]. Indeed, the purification process itself may contribute up to 80% of total production costs [5]. This highlights the

COVER STORY

need for bioprocess engineers to either achieve very high step yields of 92–98% or to reduce the number of steps for the downstream processing to be economical [6]. The downstream processes that comprises 8–10 unit operations typically exhibiting an average yield of 95% for each step will result in an overall purification yield of 50–80%. This represents 60–80% of the total cost of recombinant protein [7]. Therefore designing in the least possible processing steps offers the most efficient way of attaining high process economy in the overall production process.

A general scheme for the downstream processing flowsheet with a possible site for the inclusion of one or more integrated unit operations is shown in Figure 1. The initial phases of protein capture often involve the processing of feedstock containing particulate matter. In traditional downstream processing, removal of particulate matter from the feedstock is necessary before application to packed chromatography beds [9]. Two of the most widely used techniques for particulate removal are centrifugation and filtration.

Although the improved capacity of the centrifugation process has allowed larger volumes of process liquid to be processed at industrial scales [10], the efficiency of continuous centrifuges for clearing smaller particles remains poor. This is due to the lower centrifugal forces and the shorter residence times than those achieved by batch-operated centrifuges. Centrifugation is also damaging - the process may shear sensitive cells such as mammalian cells. The generation of a fine mist during centrifugation may also be unacceptable in certain cases, particularly for processes involving genetically-modified organisms [11, 12]

Filtration is an alternative method for the clarification of the process liquid. The shear force in a filtration unit is gentler than centrifugation and is therefore more suitable for shear sensitive organisms. However, filtration rates are limited by filter fouling, in particular when smaller particles ranging in size between 0.1–1 m are to be filtered. Limitations arising from a dramatic decrease in the flux per unit area of membrane during operation

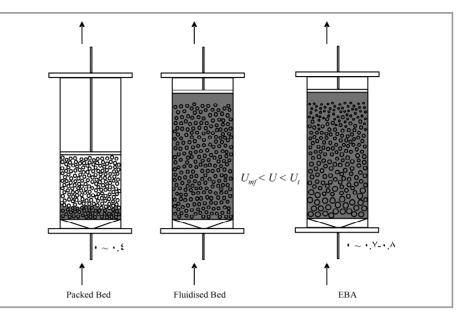


Figure 2: Comparison between packed bed, conventional fluidised bed and EBA. U is the adsorbent velocity, U_{mt} is the minimum adsorbent velocity, U_i is the terminal settling velocity and e is the bed voidage.

often result in a subsequent requirement for large membrane areas [13]. They often result in long processing times and the use of large units is often necessary [14].

In a simplified downstream processing flowsheet, the initial phase of protein recovery is integrated into a single step. This integrative recovery route (Figure 1) not only simplifies solid and liquid separation, but also combines originally independent steps to form new unit operations. This enables substantial improvements to downstream processing. Integrative protein recovery operations should be able to tolerate particles containing biological suspensions and deliver a clarified protein concentrate. Ideally a degree of purification of the target protein should also be achieved, thus combining clarification. concentration and purification in a single step. In a simplified integrated downstream processing flowsheet, the initial phase of protein recovery is integrated into a single step. This is of great significance since any reduction in the number of stages required in the flow sheets has always been of industrial interest. In fact, it is regarded as a tool for improving process performance and productivity. An integrated capture step is a challenging operation particularly when large quantities of contaminants and large volume of liquids are involved [15].

There are many different ways of achieving this integration of previously independent processes. Considering an adsorption solution to the integration problem, the conventional operating formats for the recovery of proteins are the packed bed, the stirred tank, the fluidised bed and the membrane. Packed beds cannot be challenged with particulate containing feedstreams as they act as depth filters, the voids of the bed rapidly blocking resulting in the pressure drop across the bed increasing until pump or pipe failure occurs. There are no occlusion problems with the stirred tank method, but the tank operates as just one equilibrium stage at best, resulting in inefficient capture at all but the highest partition coefficients. Problems can also arise with adsorbent handling and solid/liquid separation; however several benchscale batch and continuous applications have been developed [16, 17, 18, 19]. By fluidising the adsorbent, the average interparticle distance is increased such that any particles in the feedstock may pass freely through the interstitial voidage of the bed. Although there are a number of methods of achieving a stable fluidised bed [20, 21, 22, 23] it is evident that the basic structure of a fluidised bed might allow separation of proteins from unclarified feeds. Membrane-based chromatography has the advantage over

COVER STORY

conventional chromatography on columns of porous particles due to the absence of pore diffusion [24]. Operation in crossflow mode can allow the adsorption of proteins to the inner surface of the through pores, whilst cellular debris is rejected [25, 26]. The only disadvantages of this method are the low surface area for adsorption and the dependence on the transmembrane flux, which can fail due to fouling with particulates.

Aqueous two phase adsorption is also capable of handling particulates; however the degree of purification attainable is usually lower than with chromatographic separations. Fluidised bed (FBA) adsorption would seem to have greater potential for efficient protein capture than stirred tanks, aqueous two phase extraction or crossflow microfiltration approaches.

INTEGRATIVE EXPANDED BED ADSORPTION (EBA)

A distinction should be made at this point between a packed, fluidised and an expanded bed (Figure 2). Liquid solid fluidised beds, with small density differences between phases, show particulate fluidisation behaviour, rather than the aggregative behaviour shown by gas solid systems. The mixing in particulate systems is less severe, however in many situations, particularly where there is uneven distribution of liquid across the cross section of the bed, there is still a significant and undesirable amount of mixing. This mixing leads to inferior adsorption performance within the fluidised bed as compared to the packed bed, where plug flow of liquid maximises the number of theoretical equilibrium stages (or plates). By introducing a distribution of both size and density into the solid phase, a classification occurs upon fluidisation eventually giving a stratified bed with the higher buoyant weight particles at the base and the lower buoyant weight particles at the top [4]. The reduction in solid and associated liquid dispersion results adsorption in performance similar to the packed bed. The term 'expanded bed' has been used extensively in the literature and by manufacturers to describe fluidised beds which have been stabilised by careful adsorbent and equipment design to give limited axial dispersion and higher plate numbers, and to distinguish them from well-mixed alternatives. A number of recent reviews of EBA have been published, covering operational and design aspects and more theoretical considerations [4, 14, 8].

OPERATIONAL PROCEDURE FOR EBA

EBA was introduced to meet the challenge of an increasing demand for fewer purification steps and shorter processing times. It integrates clarification, concentration and enables initial purification of the target proteins directly from unclarified feedstock in a single step [4, 14, 8]. In principle, expanded bed processes are operated in a similar fashion to packed bed processes, the main difference being the direction of liquid flow. The standard sequence of frontal chromatography is generally followed as in Figure 3, which are column equilibration, renatured inclusion bodies [9, 36, 37] and milk preparations [38]. EBA has also been proven to be successful for the separation of E.coli and yeast cells [39], monocytes from human peripheral blood [40], nano-particles, such as plasmid DNA from E.coli cell lysates [41, 42] and calf thymus DNA [43]. Pilot-and production-scale processes have also been reported, including the purification of annexin V from E. coli homogenates using ion-exchange adsorbents [9], exotoxin A capture from E. coli BL21 (IDE3) homogenate using an anion exchanger adsorbent [15], IgG1 isolation from mouse hybridoma cells [35, 11] and the recovery of recombinant human serum albumin (rHSA) from Pichia pastoris suspension [44]. The same purity of monoclonal antibody from CHO cell culture is reported via a three-phase purification strategy in which Protein A adsorbent was used in an expanded bed capture step, as achieved by conventional processing routes [45]. These wide ranges of applications of EBA reported in the literature demonstrate

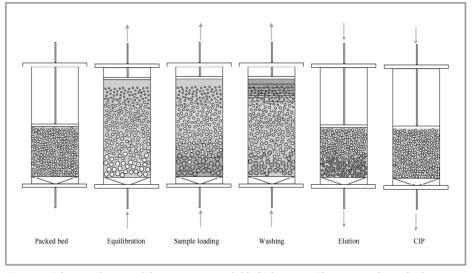


Figure 3: Schematic diagram of the stages in expanded bed adsorption. The arrows indicate the direction of liquid flow through the column (either upwards or downward).

sample application, washing, elution and clean in place.

APPLICATION OF EBA

There have been many successful applications of EBA for the purification of proteins and other biomolecules from crude (solid-containing) fermentation broth. Proteins have been captured from a wide range of particulate containing feedstock such as bacterial [9, 27, 28], yeast homogenates [29, 30, 31], mammalian cell cultures [32, 33, 34, 35], solutions of others

this technology to be robust and economical for the early recovery of proteins directly from crude feedstock [2, 14, 46].

CONCLUDING REMARKS

With many successful demonstrations and applications, EBA is becoming recognised as a realistic alternative to existing procedures for protein recovery. Indeed, examples of full scale industrial processes are beginning to appear. This may be attributed to the increasing number and diversity of successful applications at bench scale, the 008•010•012-013•EBA 28/12/06 3:35 PM Page 13

COVER STORY

development of purpose-designed adsorbents [2] and equipment and increasingly tighter process control and understanding. Such processes are proving to be efficient and compliant with the tough requirements of regulatory bodies such as the Food and Drug Administration (FDA). Validation considerations have been

REFERENCES

- Becker, T., Ogez, J. R., Builder, S. E. Downstream Processing of Proteins, (1983), *Biotech Advs.*, 1, 247-261
- [2] Abdullah, N. (2004). Strategies for Expanded Bed Purification of Recombinant Protein, *PhD. Thesis, Cambridge University*, United Kingdom
- [3] Kaufmann, M.(1997). Unstable Proteins: How to Subject Them to Chromatographic Separations for Purification Procedures. J. Chromatogr. A, 699, 347-369.
- Chase, H. A.(1994). Purification of Proteins by Adsorption Chromatography in Expanded Beds, *TIBTECH*, 12, 296-303.
- [5] Gupta, N. M. and Mattiasson, B. (1994). Novel Technologies in Downstream Processing, *Chemistry* and Industry, 17, 673-675.
- [6] Fish, N. M. and Lilly, M. D. (1984). The Interactions Between Fermentation and Protein Recovery, *Biotechnology*, 623-627
- [7] Walter, J. K. (1998). Strategies and Considerations for Advanced Economy in Downstream Processing of Biopharmaceutical Proteins, <u>Bioseparation and</u> <u>Bioprocessing</u> (Ed. Subramaniam, G.), 447-460, Wiley-VCH, Wienheim, Germany
- [8] Thömmes, J. (1997). Fluidised Bed Adsorption as a Primary Recovery Step in Protein Purification, Adv. Biochem. Eng. Biotech., 58, 185-230.
- [9] Barnfield-Frej, A.-K., Hjorth, R. and Hammarstrom, A. (1994). Pilot Scale Recovery of Recombinant Annexin V from Unclarified *Escherichia Coli* Homogenate Using Expanded Bed Adsorption, *Biotechnology and Bioengineering*, 44, 922-929.
- [10] Datar, R. V. and Rosen, C.-G. (1996). Cell and Cell Debris Removal: Centrifugation and Cross Flow Filtration, *Bioprocessing*, (Ed. Stephanopoulos, G.), VCH. Weinheim, 472.
- [11] Amerskamp, N., Priesner, F., Lehman, J. and Lütkemeyer, D. (1999). Pilot Plant Recovery of Monoclonal Antibodies by Expanded Bed Ion Exchange Adsorption, *Bioseparation*, 8, 169-188.
- [12] Hjorth, R., Leijon, P., Barnfield Frej, A.K. and Jägersten, C. (1998). Expanded Bed Adsorption Chromatography. <u>Bioseparation and</u> <u>Bioprocessing</u> (Ed. Subramaniam, G.), Volume 2, 199-225, Wiley-VCH, Weinheim, Germany.
- [13] Fane, A. G. and Radovich, J. M. (1990). In <u>Separation Processes in Biotechnology</u>, (Ed. Asenjo, A.), Marcel Dekker, 209-262.
- [14] Hjorth, R. (1997). Expanded Bed Adsorption In Industrial Bioprocessing: Recent Developments, *TIBTECH*, 15, 230-235.
- [15] Johansson, H.J., Jagersten, C. and Shiloach, J. (1996). Large Scale Recovery and Purification of Periplasmic Recombinant Protein From E.coli Using Expanded Bed Adsorption Chromatography Followed by New Ion Exchange Media J. Biotechnology, 48, 9-14.
- [16] Gordon, N. F. and Cooney, C. L. (1990). In: Protein purification: From Molecular Mechanisms to Large Scale Processes, ACS Symposium Series 240, (Eds. Ladisch, M. R., Wilson, R. C., Painton, C.-D. C. and Builder, S. E.), Washington DC, USA.
- [17] McCreath, G. E., Chase, H. A., Purvis, D. R. and Lowe, C. R. (1993). Novel Affinity Separations Based

on Perfluorocarbon Affinity Emulsions. Use of a Perfluorocarbon Affinity Emulsion for the Direct Extraction of G6PDH from Homogenised Bakers' Yeast, *J. Chromatogr.*, **629**, 201-213.

- [18] Nigram, S. C., Sakoda, A. and Wang, H. Y. (1988). Bioseparation Recovery From Unclarified Broths and Homogenates Using Immobilised Adsorbents, *Biotech. Prog.*, 4, 166-172.
- [19] Sakoda, A. and Wang, H. Y. (1989). A New Isolation and Purification Method for Staphylococcal Protein a Using Membrane Encapsulated Rabbit Igg-Agarose, *Biotech. Bioeng.*, 34, 1098-1103.
- [20] Buijs, A, and Wesselingh, J. A. (1980). Batch Fluidised Ion-Exchange Column for Streams Containing Suspended Particles, J. Chromatography, 201, 319-327
- [21] Van der Wiel, J. P. and Wesselingh, J. A. 1989. In: <u>Adsorption: Science and Technology</u>, (Eds. Rodriguez, M. D., LeVan, M. D. and Tondeur, D.), Kluwer Academic Publishers, Netherlands.
- [22] Burns, M. A. and Graves, D. J. (1985). Continuous Affinity Chromatography Using a Magnetically Stabilised Fluidised Bed, *Biotech. Prog.*, 1, 95-103.
- [23] Chetty, A. S. and Burns, M. A. (1991). Continuous Protein Separation in a Magnetically Stabilised Fluidised Bed Using Nonmagnetic Supports, *Biotech. Bioeng.*, 38, 963-971.
- [24] Thommes, J. and Kula, M.-R. (1995). Membrane Chromatography - An Integrative Concept in the Downstream Processing of Proteins, *Biotech. Prog.*, 11, 357-367.
- [25] Finger, U. B., Thommes, J., Kinzelt, D. and Kula, M.-R. (1995). Application of Thiophilic Membranes for the Purification of Monoclonal Antibodies From Cell Culture Media, *J. Chromatogr. A*, 664, 69-78.
- [26] Kroner, K. H., Krause, S. and Deckwer, M. D. (1992). BIO forum, 12/92, 455-458.
- [27] Abdullah, N. and Chase, H.A, (2005). Removal of Poly-Histidine Fusion Tags from Recombinant Proteins Purified from Expanded Bed Adsorption, *Biotech. Bioeng.*, 92 (4):501-13
- [28] Clemmitt, R. H. and Chase, H. A. (2000). Facilitated downstream processing of a histidine-tagged protein from unclarified *Ecoli* homogenates using immobilised metal affinity expanded-bed adsorption, *Biotech. Bioeng.*, **67**(2), 206-216.
- [29] McCreath, G. E., Chase, H. A. and Owen, R. O. (1995). Expanded Bed Affinity Chromatography of Dehydrogenases From Baker's Yeast Using Dye-Ligand Perfluoropolymer Supports, *Biotech. Bioeng.*, 48, 341-354.
- [30] Chang, Y. K. and Chase, H. A. (1996). Ion exchange Purification of G6PDH from Unclarified Yeast Cell Homogenates using Expanded Bed Adsorption, *Biotech. Bioeng.*, 49, 204-216.
- [31] Owen, R. O. (1997). Continuous Counter-Current Contacting for the Direct Extraction of Proteins, *PhD Thesis, University of Cambridge*, UK.
- [32] Thömmes, J., Badar, A., Halfar, M, Karau, A. and Kula, M. -R. (1996). Isolation of Monoclonal Antibodies from Cell Containing Hybridoma Broth using a Protein A Coated Adsorbent in Expanded Beds, J. Chromatogr. A, 752, 111-222.

reviewed with regard to EBA applications and the first fully commissioned processes are beginning to appear [47].

- [33] Batt, B. C., Yabannavar, V. M. and Singh, V. (1995). Expanded Bed Adsorption Process for Protein Recovery from Whole Mammalian Cell Culture Broth, *Bioseparation*, 5, 41-52
- [34] Born, C., Thömmes, J., Biselli, M., Wandrey, C. and Kula, M.-R. (1996). An Approach to Integrated Antibody Production: Coupling of Fluidised Bed Cultivation and Fluidised Bed Adsorption, *Bioprocess Engineering*, 15, 21-29
- [35] Lutkemeyer, D., Ameskamp, N., Tebbe, H., Wittler, J. and Lehmann, J. (1999). Estimation of Cell Damage in bench- and Pilot Scale Affinity Expanded-Bed Chromatography for the Purification of Monoclonal Antibodies, *Biotech. Bioeng.*, 65, 114-119.
- [36] Cho, T. H., Ahn, S. J. and Lee, E. K. (2002). Refolding of Protein Inclusion Bodies Directly from *Ecoli* homogenate using Expanded Bed Adsorption Chromatography, *Bioseparation*, **10**, 189-196.
- [37] Choe, W. S., Clemmitt, R. H., Rito-Palomares, M., Chase, H. A. and Middleberg, APJ (2002). Bioprocess Intensification: A radical new process for recovering inclusion body protein, *Trans IChemE*, **80**, 45-50.
- [38] Noppe, W., Hassens, I., Larsen, F., Nygren, P. A. Uhlen, M. and Lundeberg, J. (1996). Simple Two-Step Procedure for the Preparation of Highly Active Pure Equine Milk Lysozyme, J. Chromatogr. A., 719, 327-331.
- [39] Ujam, L. B., Clemmitt, R. H. and Chase, H. A. (2000). Cell separation by expanded bed adsorption: use of ion exchange chromatography for the separation of *Ecoli* and S.cerevisiae, *Bioprocess Eng.*, 23, 245-250.
- [40] Ujam, L. B., Clemmitt, R. H., Clarke, S. A., Brooks, R. A., Rushton, N. and Chase, H. A. (2003). Isolation of Monocytes from Human Peripheral Blood Using Immuno-Affinity Expanded-Bed Adsorption, *Biotech. Bioeng.*, 83, 554-566.
- [41] Varley, D. L., Hitchcock, A. G., Weiss, A. M. E., Horler, W. A., Cowell, R., Peddie, L. Sharpe, G. S., Thatcher, D. R. and Hanak, J. A. J. (1999). Production of plasmid DNA for human gene therapy using modified alkaline cell lysis and expanded bed anion exchange chromatography, *Bioseparation*, 8, 209-217.
- [42] Ferreira, G.N.M., Cabral, J.M.S., and Prazeres, D.M.F. (2000). Anion Exchange Purification of Plasmid DNA Using Expanded Bed Adsorption, *Bioseparation*, 9, 1-6.
- [43] Theodossiou, I. and Thomas, O. R. T. (2002). DNA-Induced Inter-Particle Cross-Linking During Expanded Bed Adsorption Chromatography Impact on Future Support Design, J. Chromatogr. A, 971, 73-86.
- [44] Noda, M., Sumi, A., Ohmura, T and Yokoyama, K.(1996). European Patent Application EP 069 968 7A2.
- [45] Blank, G. S., Zapata, G., Fahrner, R., Milton, M., Yedinak, C., Knudsen, H. and Schmelzer, C. (2001). Expanded Bed Adsorption in the Purification of monoclonal Antibodies: a Comparison of Process Alternative, *Bioseparation*, **10**, 65-71.
- [46] Clemmitt. R.H. (1999). Metal affinity Purification Strategies for Expanded Bed Adsorption, *PhD Thesis, Cambridge University*, United Kingdom.
- [47] Sofer, G. K. and Hagel, L. (1997). <u>Handbook of</u> <u>Process Chromatography: A Guide to Optimisation.</u> <u>Scale-up, and Validation</u> 1st Ed., Academic Press, London, UK.