

CHO cells in biotechnology for production of recombinant proteins: current state and further potential

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Abstract Recombinant Chinese hamster ovary cells (rCHO) cells have been the most commonly used mammalian host for large-scale commercial production of therapeutic proteins. Recent advances in cell culture technology for rCHO cells have achieved significant improvement in protein production leading to titer of more than 10 g/L to meet the huge demand from market needs. This achievement is associated with progression in the establishment of high and stable producer and the optimization of culture process including media development. In this review article, we focus on current strategies and achievements in cell line development, mainly in vector engineering and cell engineering, for high and stable protein production in rCHO cells. The approaches that manipulate various DNA elements for gene targeting by site-specific integration and *cis*-acting elements to augment and stabilize gene expression are reviewed here. The genetic modulation strategy by “direct” cell engineering with growth-promoting and/or productivity-enhancing factors and omics-based approaches involved in transcriptomics, proteomics, and metabolomics to pursue cell engineering are also presented.

Keywords CHO cells · Cell line development · Vector engineering · Cell engineering · Omics-based approaches

Introduction

The approval of human tissue plasminogen activator (Genentech, USA) as the first therapeutic protein from recombinant mammalian cells in 1986 triggered the emergence of mammalian cell culture as the industry’s workhorses for biopharmaceutical production. Although a variety of alternative expression systems exists, such as microbial, insect, transgenic animal and plants, mammalian cells are the principle hosts for the commercial production of therapeutic proteins. Among the 58 biopharmaceuticals approved from 2006 to 2010, 32 are produced from mammalian cells (Walsh 2010). Despite the availability of a number of other mammalian cell lines, such as baby hamster kidney, mouse myeloma-derived NS0, human embryonic kidney (HEK)-293, and the human retina-derived PerC6, nearly 70% of all recombinant therapeutic proteins produced today are made in Chinese hamster ovary (CHO) cells (Jayapal et al. 2007).

The popularity of CHO cells can be attributed to the following reasons. Firstly, since CHO cells have been demonstrated as safe hosts for the past two decades, it may be easier to obtain approval to market the therapeutic proteins from regulatory agencies like the FDA. Secondly, low specific productivity (*q*), which is one of the disadvantages of using mammalian cells for protein production, can be overcome by gene amplification in CHO cells. For CHO cells, powerful gene amplification systems, such as dihydrofolate reductase (DHFR)-mediated or glutamine synthetase (GS)-mediated gene amplification, are available. Thirdly, CHO cells have the capacity for efficient post-translational modification, and they produce recombinant proteins with glycoforms that are both compatible with and bioactive in humans. Finally, CHO cells can be easily adapted to growth in the regulatory-friendly serum-free (SF) suspension

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conditions, a characteristic preferred for large-scale culture in bioreactors. Currently, stirred tank bioreactors over 10,000 L scale are readily used for SF suspension cultures of recombinant CHO (rCHO) cells producing therapeutic antibody.

With an increasing biopharmaceutical market showing an average yearly growth of 35% since 2001, the popularity of CHO cells as the host for commercial production of therapeutic proteins is likely to persist, at least in the near future. Over the past two decades, a more than 100-fold yield improvement of titers in rCHO cell culture has been observed, and this improved product yield has been largely attributed to the development of serum-free medium as well as the optimization of feeding strategies (Hacker et al. 2009). Nevertheless, the demands of the ever-increasing highly competitive market still require cells to be more highly productive and to be grown in bioreactors at higher cell densities under rigorous optimization schemes. In this review, we summarize the current strategy of rCHO cell line development and discuss current achievements in vector engineering and cell engineering that make rCHO cell lines highly productive and robust for large-scale commercial production of therapeutic proteins.

Current strategy for rCHO cell line development

In many cases, a cell line is established based on clones exhibiting high productivity, and process development for manufacturing is performed using that cell line. However, every CHO clone reacts differently to different media and culture conditions, and significant effort is repeatedly required from process development teams whenever new clones are used to produce new therapeutic proteins. Accordingly, to carry out a specific cell culture process, clones suitable for that process should be selected because of clonal variability. For example, clones suitable for SF suspension fed-batch culture are selected for large-scale commercial production of therapeutic antibody. In the same context, many biotech companies have their own therapeutic protein production platform, and clones suitable for that platform are selected to facilitate and speed up the process development of new therapeutic proteins.

Figure 1 shows a representative schematic diagram of the steps involved in cell line development for therapeutic antibody production. Since development of a production cell line requires a considerable investment of time and resources, the gene of interest is first transiently expressed in HEK or CHO cells to test its efficacy and manufacturability. Once proven, the gene of interest is introduced into CHO host cell lines such as DHFR-deficient CHO (DXB11 and DG44) and CHO-K1 mostly by lipofection. The CHO host cell lines have been adapted for growth in SF suspension to save the

time and effort of adapting the resulting rCHO production cell line to grow in SF suspension culture.

Once the DNA enters the host cell nucleus, it integrates into the chromosome at a random location. If necessary, high producing parental clones are subjected to gene amplification for further enhancement of q .

Increased heterogeneity, resulting from the random integration of a transfected foreign gene into the chromosome and the altered position of the integrated gene by a gene amplification system, contributes to a wide variety of individual clones regarding q . Since the isolation of clones with a high expression level clearly depends on the number of clones that have been screened, screening procedures such as the limiting dilution method are time-consuming and labor-intensive. As a result, there has been increasing use of efficient high-throughput cell screening systems, such as fluorescence-activated cell sorting (FACS), the ClonePix™ system (Genetix), the LEAP™ system (Cytellect), and the CellCelector™ system (Aviso).

Clones are selected on the basis of their high expression levels, and their performance is further tested in SF suspension fed-batch culture, which is most widely used for large-scale commercial production of therapeutic antibody. Clones showing the best performance in SF suspension fed-batch culture in lab-scale bioreactors with pre-developed feeding cocktails are usually selected as production cell lines.

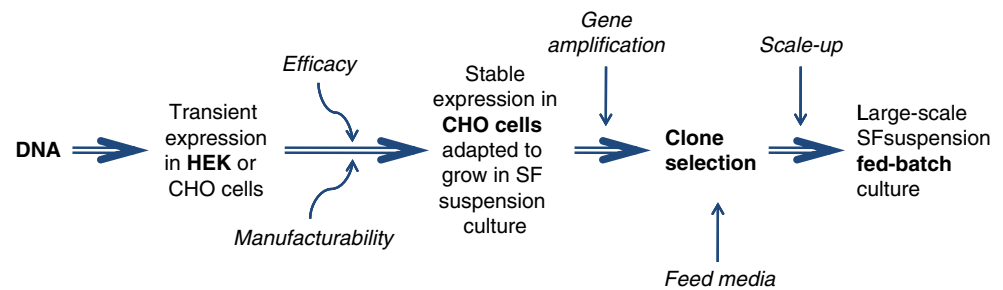
Vector engineering in cell line development

As described earlier, the establishment of a high-producing, stable rCHO cell line by gene amplification followed by an extensive screening is time-consuming and labor-intensive. Vector engineering which modulates transcriptional activity facilitates rCHO cell line development. High q can be achieved by modulating transcriptional activity via insertion of various DNA elements into a vector. In addition, the instability of q , which often occurs during long-term culture, may also be overcome by vector engineering. Although the mechanism responsible for reduced q is not fully understood, it is likely to be due to loss of gene copies, silencing of a gene by chromosomal rearrangement, and/or transcriptional inactivation by methylation (Barnes et al. 2003). In this section, the current vector engineering, which includes gene targeting by site-specific integration and a *cis*-acting element to augment gene expression, is discussed as an efficient and reliable method to establish a high-producing, stable rCHO cell line.

Gene targeting by site-specific integration

Site-specific integration of transgenes leads to predictable expression properties and circumvents extensive

Fig. 1 Schematic diagram of steps involved in cell line development for therapeutic antibody production in rCHO cells



screening. This technique, however, requires information on the chromosomal loci at which a transgene is stably and highly expressed, a so-called hot-spot. After screening the hot-spot, a new desired transgene is introduced into this pre-defined position by vector-based site-specific integration. Successful integration of the desired transgene into the hot-spot may guarantee the fast and efficient selection of high-producing stable clones. For effective recombination and exclusion of unnecessary vector sequences of prokaryotic origin, site-specific integration is conducted using recombinase-mediated cassette exchange strategy. Among various recombinases, Cre and Flp, which respectively recognize *loxP* and *FRT* sequences, are most widely used. Until now, genome engineering by site-specific modification has been applied in various fields of biotechnology.

Kito et al. (2002) first reported the use of gene targeting based on the Cre/*loxP* system for human monoclonal antibody production in rCHO cells. Fluorescence in situ hybridization analysis of rCHO cells constructed using a *loxP* and *FRT* strategy revealed that the antibody genes were all located in the original *FRT*-tagged locus in the gene-targeted and gene-amplified cells (Huang et al. 2007).

Because the *loxP* and *FRT* sequence affects the recombination efficiency of Cre and Flp recombinase, the mutant forms of these sequences, such as *lox2272* and *m2* in the Cre/*loxP* system, *F3* and *F5* in the Flp/*FRT* system should be evaluated. To this end, a simple and accurate analysis system was developed to estimate recombination efficiency using FACS to compare the efficiency of recombination related to various spacer mutants (Kim et al. 2007, 2008; Kim and Lee 2008). Recently, Kameyama et al. (2010) developed an accumulative site-specific gene integration system using a series of Cre-mediated integration reaction with mutated *loxPs* sequences, allowing the repeated insertion of multiple genes into one target site.

Besides the Cre/Flp-based gene targeting, various endonucleases for genome engineering have been also applied. The endonucleases include chemical nucleases, Zinc-finger nucleases, meganucleases, and transcription activators like effectors (TALE-nucleases) (Silva et al. 2011). Because homologous gene targeting is inefficient in mammalian cells, meganucleases are applied to make DNA double-

strand break (Cabaniols et al. 2010). Another recent gene targeting system is the DNA recombinase-based mammalian artificial chromosome engineering system (ACE system), which offers a clear advantage of large cloning capacity compared to other systems. An antibody-producing clone with high and stable expression was generated by utilizing this ACE system (Kennard et al. 2009).

cis-acting element for augmenting gene expression

Genetic elements may remodel chromatin to maintain the transgene in an active configuration. Generally, two components of transcription, *trans*-acting factors (transcription factor) and *cis*-acting elements (enhancer sequence and stable element for messenger RNA (mRNA)), are used to augment gene expression. Until now, a number of *cis*-acting elements have been applied to rCHO cells to enhance the expression and stability of protein production.

The most popular *cis*-acting element in rCHO cell culture is a scaffold/matrix attachment region (S/MAR), which maintains the chromatin structure in an “active” configuration through the creation of chromatin loops. This element can increase the expression of a transgene by its boundary effect, although the detailed mechanism is currently unknown. A variety of S/MARs such as chicken lysozyme MAR, human β -globin MAR, and β -interferon SAR have been tested to evaluate their use to augment expression in rCHO cells (Girod et al. 2005; Kim et al. 2004, 2005; Zahn-Zabal et al. 2001). Interestingly, Girod et al. (2005) reported that chicken lysozyme MAR acts as a *cis*-acting element on the transgene expression vector and *trans*-acting factors transfected with a separate plasmid. Furthermore, transgene expression was maximized when the chicken lysozyme MAR was simultaneously introduced with the *cis*-acting element and *trans*-acting factors.

Ubiquitous chromatin opening elements (UCOE) are another well-known type of *cis*-acting element. Benton et al. (2002) evaluated the augmentation effect of UCOEs on viral human cytomegalovirus (hCMV) promoter-derived gene expression. A dramatic increase in the antibody production of rCHO cells was achieved because of the beneficial effect of maintaining chromatin in an “open” configuration by UCOEs.

Cell engineering in cell line development

To improve the characteristics of rCHO cells in regard to cell growth and foreign protein production, numerous cell engineering strategies have been attempted. Cell engineering has been targeted mainly to increase the time integral of viable cell concentration (IVCC) and/or q .

Figure 2 schematically depicts the effect of cell engineering for improved culture characteristics, resulting in enhanced lifespan and production. ICVV can be increased by enhanced culture longevity, improved specific growth rate (μ), and increased maximum viable cell density. This strategy targets to the reduction of cell death at the end of culture and the induction of cell proliferation at the initial stage. For the aim of enhancing q , the components in regulation of the cell cycle, folding, transport, and secretion are chosen to be key regulators. Reconstruction of the metabolic pathway also improves protein production.

Anti-apoptosis engineering

Cell death is considered an important issue to be dealt with because it affects the viable cell concentration as well as the product quantity and quality (Arden and Betenbaugh 2004). During rCHO cell culture, cell death is triggered by a variety of stresses including nutrient depletion, accumulation of toxic by-products, elevated osmolarity, and shear stress.

Cell death occurs in two forms—necrosis or two types of programmed cell death (PCD), namely, apoptosis and autophagy. While necrosis is a sudden and passive form, PCD is an active, genetically controlled process. Many researchers have recognized PCD as a target to overcome

the problem mentioned above. Apoptosis has gained importance in mammalian cell culture, including that of rCHO cells for therapeutic protein production over the last two decades. The prevention of apoptosis by establishing apoptosis-resistant rCHO cells appears to be beneficial.

The apoptotic process is regulated by either activation or suppression of members of the Bcl-2 family proteins which includes three groups: anti-apoptotic Bcl-2-like proteins (Bcl-2, Bcl-xL, Bcl-w, and Mcl-1), pro-apoptotic Bax-like proteins (Bax, Bak, and Bok), and pro-apoptotic BH3-only proteins (Bim, Bad, Bid, PUMA, and Noxa) (Adams and Cory 2001). Considering their function as key regulators in apoptosis, the activation of anti-apoptotic Bcl-2-like proteins and suppression of pro-apoptotic factors is of particular interest in delaying the onset of apoptosis.

Figure 3 illustrates the genetic engineering strategies employed to overcome apoptosis in rCHO cells. Previously, it was found that apoptosis in rCHO cells was alleviated by the overexpression of anti-apoptotic proteins that include Bcl-2, Bcl-xL, and Mcl-1, or down-regulation of pro-apoptotic proteins such as Bak and Bax, resulting in increased protein production (Chiang and Sisk 2005; Cost et al. 2010; Kim and Lee 2001; Majors et al. 2009; Meents et al. 2002a; Tey et al. 2000).

Apoptotic signal is mediated by a caspase-cascade system, which is a series of proteolytic cascade in caspase by other activated cleaved caspases. Because the caspases play an essential role in apoptosis regulation including induction, transduction, and amplification of signals, the suppression of caspase activation is a promising strategy. Caspases can be divided functionally into two groups: initiator caspase and effector caspase. Inhibition of caspase-8/caspase-9,

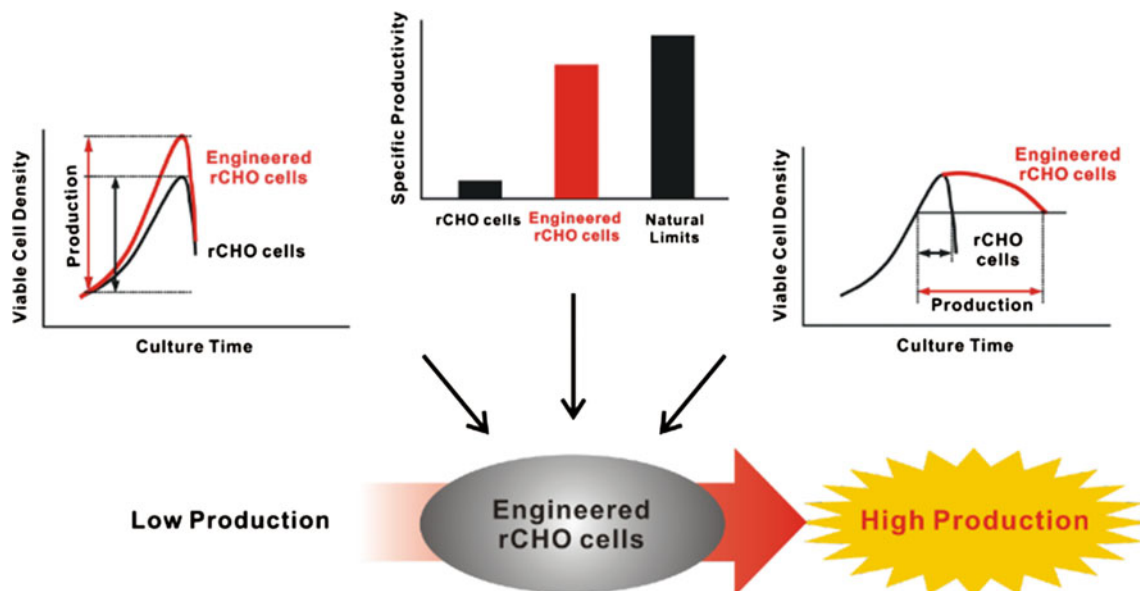


Fig. 2 Schematic depiction of the effect of cell engineering on improved culture characteristics. Cell engineering leads to enhancement of cell growth and q , which reflects on the product titer

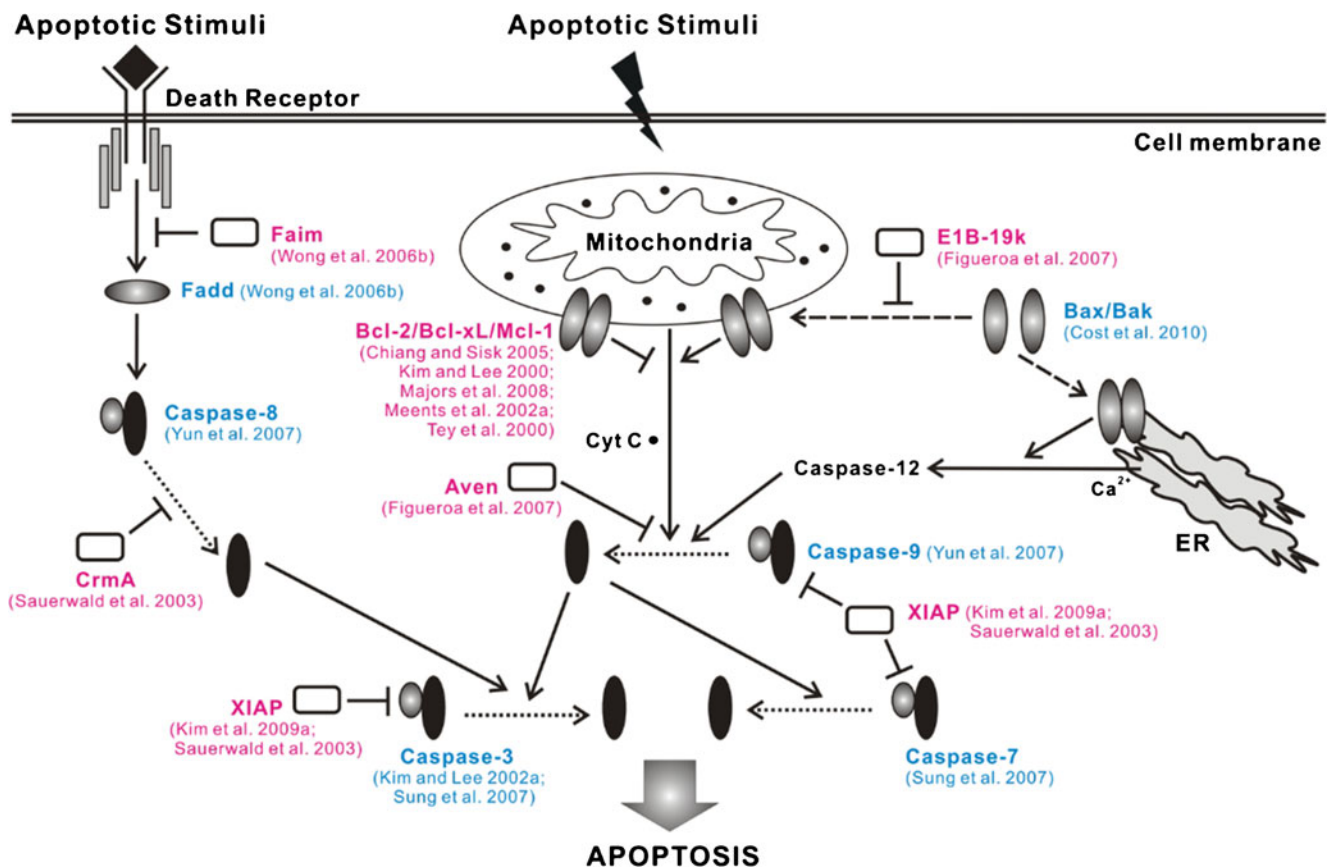


Fig. 3 Schematic diagram illustrating the genetic engineering strategies employed to overcome apoptosis in rCHO cells

initiator caspases, by overexpression of dominant negative mutants and caspase-3/caspase-7, effector caspases, by introduction of antisense RNA or small interfering RNA showed a positive effect on cell growth (Kim and Lee 2002a; Sung et al. 2007; Yun et al. 2007). Another strategy for suppressing caspases is the overexpression of intracellular caspase inhibitors, such as X-linked mammalian inhibitor of apoptosis, an inhibitor of caspase-3/caspase-7/caspase-9, and protein cytokine response modifier A, a strong inhibitor of caspase-1/caspase-8 and a weak inhibitor of caspase-3/caspase-6 (Sauerwald et al. 2002, 2003).

In addition to CHO cell engineering based on Bcl-2 family proteins and caspases, various other factors have also been applied to inhibiting apoptosis. Overexpression of adenovirus-derived anti-apoptotic E1B-19K, 30Kc6 isolated from silkworm hemolymph, and Aven, the inhibitor of apoptosome activation via interacting Apaf-1, successfully blocked apoptosis progression (Choi et al. 2006; Figueroa et al. 2007). In addition, murine double mutant-2, the inhibitor for the p53 tumor suppressor protein, was used to confer apoptosis resistance (Arden et al. 2007). Human telomerase reverse transcriptase-overexpressing rCHO cells induced the proliferation and promotion of the resistance to apoptosis (Crea et al. 2006).

Interestingly, the reports dealing with two heat shock proteins (HSPs) and taurine transporter proposed that the factors not directly involved in the apoptotic pathway can be good candidates to delay apoptosis with enhanced *q* (Lee et al. 2009; Tabuchi et al. 2010).

The beneficial effect of the overexpression of anti-apoptotic Bcl-2-like proteins on rCHO culture longevity is common. In contrast, there are conflicting reports on its effectiveness on *q* (Chiang and Sisk 2005; Lee and Lee 2003; Meents et al. 2002a; Tey et al. 2000). Some found a positive effect on *q*, while others found no effect on *q*. These conflicting results may be due to clonal variability which usually occurs in the rCHO cell line development. Inducible overexpression of Bcl-xL, which allows comparison of identical cell populations under different conditions, did not affect *q* of rCHO cells producing erythropoietin (Kim and Lee 2009). Nevertheless, overexpression of Bcl-2-like proteins does not have a negative effect on *q*.

The beneficial effect of overexpression of anti-apoptotic Bcl-2-like proteins is highlighted with *q*-enhancing factors, because the single use of some *q*-enhancing factors, such as sodium butyrate (NaBu) and hyperosmolality, has a detrimental effect on cell growth. The combined use of anti-apoptosis engineering with *q*-enhancing factors, e.g., NaBu

or hyperosmolality results in a dramatic increase in foreign protein production in rCHO cell culture (Kim and Lee 2001, 2002b; Kim et al. 2009a; Sung et al. 2007). We found that the maintenance of mitochondria is crucial in inhibiting apoptosis by overexpressing an anti-apoptotic protein from these studies (Sung et al. 2007).

Anti-autophagy engineering

Autophagy, also known as type II PCD, is a catabolic process that takes place through a caspase-independent lysosomal-mediated degradation pathway, which is distinguished from apoptosis, type I PCD (Levine and Klionsky 2004). Inhibition of apoptosis does not guarantee the blocking of autophagy-mediated cell death due to the independency between the two processes. Until now, only apoptosis has been the focus of studies on the alleviation of cell death in rCHO cell culture. Recently, the occurrence of autophagy at the end of batch culture of rCHO cells was observed when the nutrients were exhausted (Hwang and Lee 2008). Inversely, supplementation of nutrients could reduce cell death mediated by both apoptosis and autophagy (Han et al. 2011). In addition, the hyperosmotic condition introduced by feeding media and pH control during fed-batch culture could induce apoptosis and autophagy in rCHO cell culture (Han et al. 2010). Engineered CHO cells with overexpressed Bcl-xL or a constitutively active form of Akt could delay the autophagic cell death induced by nutrient depletion (Hwang and Lee 2009; Kim et al. 2009b).

Proliferation engineering

Successfully engineered rCHO cells with proliferation-related proteins showed an increased growth parameter, μ , and/or maximum viable cell concentration. Although μ can influence the maximum viable cell concentration, the extent of increase in one factor does not correlate with that of the other.

The rCHO cell engineering conducted with cell cycle progression by cyclin-dependent kinase like 3, cyclin E, and E2F-1 cell cycle transcription factor improved μ and/or the maximum viable cell concentration (Jaluria et al. 2007; Majors et al. 2008; Renner et al. 1995). A typical oncogenic protein, c-myc, which also has a role in cell cycle progression, was successfully applied to generate highly proliferative rCHO cells with high μ and maximum viable cell concentration (Kuystermans and Al-Rubeai 2009). Recently, mammalian target of rapamycin, which is known to have various roles in translation, vesicle traffic, cell survival, and cell proliferation, was successfully introduced to rCHO cells to improve key bioprocess-relevant characteristics of rCHO cells, including proliferation and q (Dreesen

and Fussenegger 2011). The effectiveness of targets on cell proliferation discovered via omics-based approaches, such as valosin-containing protein (VCP), requiem, Alg-2, and malate dehydrogenase II, have been evaluated (Chong et al. 2010; Doolan et al. 2010; Wong et al. 2006b). The details of omics-based CHO cell engineering will be discussed in a later section.

Cell cycle engineering

A common feature of q -enhanced conditions, including physical (low temperature and hyperosmolality) and chemical (NaBu) perturbations, is cell cycle arrest (Sunley and Butler 2010). Based on this consensus, p27^{KIP1} and p21^{CIP1}, cell cycle-regulating factors, have been used in rCHO cell engineering to obtain a similar effect. Fussenegger et al. (1997) achieved the q enhancement by transiently introducing p27^{KIP1} and p21^{CIP1} into secreted alkaline phosphatase (SEAP)-producing CHO cells. The use of cell cycle-arrested rCHO cells by stably overexpressing p27^{KIP1} showed beneficial q -enhancing effects on the production of SEAP and soluble intracellular adhesion molecule-1 (Mazur et al. 1998; Meents et al. 2002b). Although this enhancing mechanism is not fully understood, the expanded metabolic consumption concomitant with increased consumption rates of oxygen/glutamine/glucose and an intracellular pool of AMP/ADP/ATP may partly be affected (Carvalho et al. 2003). Similarly, p21^{CIP1} overexpression can arrest the cell cycle and growth, leading to improved q accompanied by increased cell volume and biogenesis of mitochondria and ribosomes (Bi et al. 2004). The combinatorial strategy with growth-enhancing factor, Bcl-xL, and its stabilizer, C/EBP α (CCAAT/enhancer binding protein α), resulted in a further enhancement of cell growth (Astley and Al-Rubeai 2008; Fussenegger et al. 1998).

Chaperone engineering

The bottleneck in enhancing q is believed to be a post-translational step evidenced by the irrelevance of secreted protein level with increased gene copy number or mRNA level (Mohan et al. 2008). The endoplasmic reticulum (ER)-resident proteins have the major role in protein folding, so these proteins, mainly chaperone, were thought to be a good resource for enhancing q . Numerous reports dealing with chaperone engineering have revealed mixed results, depending on the overexpressed chaperones, target therapeutic protein, and expression system (Mohan et al. 2008). Engineered rCHO cells with overexpression of Erp57 and co-overexpression of calnexin/calreticulin exhibited q -enhancing effect on thrombopoietin (TPO) production (Chung et al. 2004; Hwang et al. 2003). Overexpression of PDI, the most studied chaperone for rCHO cell engineering,

could enhance q depending on the target protein. It appears to positively affect the antibody-producing rCHO cells, but not the rCHO cells producing TPO, interleukin-15, or a tumor necrosis factor receptor:Fc fusion protein (Borth et al. 2005; Davis et al. 2000; Mohan et al. 2007). However, in the recent report by Hayes et al. (2010), the transient expression of PDI family proteins, PDI, ERp72, or pancreatic PDI (PDIp), did not result in any improvement in the antibody productivity of rCHO cells, although this was not confirmed with stable rCHO cells. The PDI effectiveness may also depend on the q values of the rCHO cells used. The extent to which q_{Ab} was enhanced by the application of low temperature decreased as q of the antibody-producing rCHO cells used increased (Yoon et al. 2004).

Unfolded protein response-based engineering

The ER has a major role in protein processing and the transmission of signals, including signal transduction pathway for unfolded protein response (UPR) to maintain cellular homeostasis (Ron and Walter 2007). A common feature of UPR signaling pathway is elevated gene transcription encoding various ER-resident chaperones. The regulation of components in the UPR signaling pathway has drawn attention in rCHO cell engineering, considering the important roles of chaperones as described in the earlier section.

X-box binding protein 1 (XBP-1) is a protein which has been widely explored in UPR signaling pathway. Tigges and Fussenegger (2006) revealed that XBP-1s (a spliced form of XBP-1) overexpression can increase q of various therapeutic proteins, which q is not increased by XBP-1u (an unspliced form of XBP-1) in transient and stable expression studies. Similarly, it could be applied to fed-batch culture, resulting in enhanced q and titer of antibody with physicochemical properties similar to those of non-engineered cells (Becker et al. 2008). Furthermore, recent reports suggested that this strategy is specifically effective when it is applied to rCHO cells experiencing secretion bottleneck (Ku et al. 2008).

Another possible strategy is to restore the attenuation of translation in response to ER stress. Activating transcription factor (ATF4), one of the key regulators in UPR system, can return the signal of translational attenuation by phosphorylation of eukaryotic initiation factor-2 α via induction of growth arrest and DNA damage inducible protein 34 (GADD34). In two reports with ATF4 and GADD34, the engineered rCHO cells with these proteins showed the enhanced q of antithrombin III (AT-III) (Ohya et al. 2008; Omasa et al. 2008). Interestingly, overexpression of XBP-1 failed to enhance production in AT-III.

Secretion engineering

In vesicle trafficking, soluble *N*-ethylmaleimide-sensitive factor attachment protein receptors (SNAREs) have a central role in membrane fusion between transport vesicles and the target membrane (Toonen and Verhage 2003). The interaction of Sec1/Munc18 (SM) proteins with SNAREs is essential for regulating the SNARE-mediated fusion event. In an effort to increase q by relieving the bottleneck in secretion, components related to the secretory pathway have been introduced for rCHO cells. SNAREs (SNAP-23 and VAMP8) and SM protein (Sly1 and Munc18c)-based secretory engineering showed similar results (Peng et al. 2011; Peng and Fussenegger 2009).

The engineered rCHO cells by these proteins could increase the antibody titer and specific antibody productivity (q_{Ab}) by boosting the secretion, although cell growth was negatively affected. The secretion engineering strategy with ceramide-transfer protein (CERT), which efficiently transfers ceramide from the ER to the Golgi, resulted in an increase in q . Mutant CERT with increased transfer activity showed better enhancement of q than that achieved with wild-type CERT (Florin et al. 2009).

Metabolic engineering

Accumulation of ammonia and lactate during rCHO cell culture is a major concern because they adversely affect cell growth and product quality (Lao and Toth 1997; Yang and Butler 2000). These two toxic waste products are generated from energy sources, such as glutamine and glucose.

The rCHO cells genetically modified with relevant metabolic proteins have been developed for efficient utilization of metabolites. To reduce the ammonia produced from glutamine, a less ammoniagenic substrate, glutamate, was used. As a result, rCHO cells expressing GS, which catalyzes glutamate with ammonia to yield glutamine, was generated. They showed less ammonia production in the glutamate-based culture (Zhang et al. 2006). For a similar purpose, carbamoyl phosphate synthetase I and ornithine transcarbamoylase involved in urea cycle were introduced to rCHO cells, resulting in decreased ammonia accumulation (Park et al. 2000).

Wlaschin and Hu (2007) evaluated the efficiency of the fructose-specific transporter (GLUT5)-transfected rCHO cells for utilizing fructose as an alternative to glucose and its effectiveness on lactate production. Although all GLUT5-overexpressed individual clones could utilize fructose as a carbon source, only the clone with an appropriate expression level exhibited reduced lactate production. Several kinds of genetic modulation strategies to change metabolic pathways related with pyruvate, such as introducing pyruvate

carboxylase or disrupting lactate dehydrogenase A/pyruvate dehydrogenase kinases, have been investigated (Kim and Lee 2007a, b; Zhou et al. 2011).

Omics-based approach in cell line development

Omics-based approaches, such as transcriptomics, proteomics, and metabolomics, have been used in the whole process of developing rCHO cell-based production in both upstream and downstream processes. They range from clone selection, cell engineering, culture media, and culture environments in the upstream process, to protein purification and characterization in the downstream process (Gupta and Lee 2007).

A potential gene of interest has been discovered from basic research, so-called direct cell engineering. However, with the recent advances in omics tools, the detailed detection of global changes in DNA/RNA, protein, and metabolites is possible. In this section, we will review the omics-based approaches for CHO cell engineering.

Transcriptomics

Transcriptomics is the global analysis of genomic information at the transcription level by chasing mRNA expression. Among various tools for genomic analysis, DNA microarray is probably the most efficient tool for the cell culture processes, considering its massiveness and cost.

Initially, due to insufficient Chinese hamster sequence information available for probe design, non-CHO-derived DNA arrays including mouse or rat-derived DNA array were used and assessed regarding their feasibility for CHO cells (Baik et al. 2006; De Leon Gatti et al. 2007). Genomic resources have been mined through the bacterial artificial chromosome-based library and expressed sequence tag-based library (Kantardjieff et al. 2009; Omasa et al. 2009). As the use of defined sequences in proprietary and non-proprietary CHO-derived microarray has been increasing, transcriptomic analysis has become popular in rCHO cell culture. The recent public availability of the genome sequence of CHO will expedite transcriptomic study (Xu et al. 2011).

Comparative transcriptome analysis using DNA microarray in rCHO cells has been done under *q*-enhancing culture conditions, including low culture temperature (Baik et al. 2006; Yee et al. 2009), high osmotic condition (Shen et al. 2010), and NaBu treatment (Yee et al. 2008). In addition, similar approaches have been performed with different rCHO cell lines with high μ (Doolan et al. 2010) or high *q* (Nissom et al. 2006) and recombinant human bone morphogenetic protein-2 (rhBMP-2)-producing rCHO cells with PACEsol overexpression (Doolan et al. 2008). Furthermore,

comparative transcriptomic analysis has been performed to find key factors regulating the apoptosis which occurs at the later stages of batch and fed-batch cultures. Four apoptosis-related genes, Fadd, Faim, Alg-2, and Requiem, were identified as a result (Wong et al. 2006a). These identified proteins were applied to anti-apoptotic CHO cell engineering by their overexpression or knockdown (Wong et al. 2006b). Nowadays, a transcriptomic result is often combined with proteome changes to consider transcriptional changes and post-transcriptional alteration (Baik et al. 2006; Doolan et al. 2010; Kantardjieff et al. 2010; Nissom et al. 2006; Yee et al. 2008).

Another fascinating resource in transcriptomics is microRNA (miRNA), which is single-stranded, non-coding RNA (18–25 nucleotides in length) and complementary to the mRNA. It can regulate global gene expression at the post-transcriptional level by mRNA cleavage or translational repression, or both. The miRNA is an attractive alternative in CHO cell engineering due to regulation of multiple targets, easy introduction into cells, and reduction in metabolic burden (Müller et al. 2008).

Gammell et al. (2007) have identified miR-21, a growth inhibitory miRNA, as being up-regulated during stationary phase growth induced either by temperature shift to low temperature or during normal batch culture. Similarly, introduction of miR-16 and let-7b, miRNAs considered as significant change in batch culture of HEK293 cells using miRNA microarray, could control the cell cycle via down-regulating of cell cycle-related proteins (Koh et al. 2009). Furthermore, miR-7 was found to be down-regulated at low culture temperature, and its overexpression could significantly increase *q* in CHO cells at 37°C (Barron et al. 2011). With advances in miRNA profiling technology, the study of miRNA to identify cellular targets for CHO cell engineering will increase.

Proteomics

Two-dimensional gel electrophoresis (2-DE) combined with mass spectrometric analysis is a widely used proteomic tool for identifying proteins changed under specific conditions in rCHO cells, as summarized in Table 1.

To enhance *q*, several strategies have been attempted in rCHO cell culture through physical or chemical manipulation of environmental perturbations (O'Callaghan and James 2008). Temperature and osmolarity are the key factors in the cell culture process. It is well-known that rCHO cells under hypothermia and hyperosmolarity show enhanced *q*. To understand the intracellular events, proteomic studies have been investigated under these conditions (Baik et al. 2006; Kantardjieff et al. 2010; Kaufmann et al. 1999; Kumar et al. 2008; Lee et al. 2003). Similarly, the effects of various chemical components, such as NaBu, DMSO, zinc sulfate,

Table 1 Comparative proteomics under specific conditions in rCHO cells

Comparison	Product	Culture condition	Reference
Temperature shift (30°C)	SEAP	Serum/adherent/T-flask/batch	Kaufmann et al. (1999)
Temperature shift (33°C)	EPO	Serum/adherent/T-flask/batch	Baik et al. (2006)
Temperature shift (31°C)	–	Serum/suspension/spinner flask/batch	Kumar et al. (2008)
Temperature shift (33°C) 2 mM Butyrate	Antibody	SFM/suspension/shaking flask/batch	Kantardjieff et al. (2010)
Hyperosmotic (450 mOsm/kg)	Antibody	Serum/adherent/T-flask/batch	Lee et al. (2003)
0.5 mM Butyrate 80 μ M Zinc sulfate 1.5 μ g/mL Tunicamycin	hGH	SFM/adherent/T-flask/batch	Van Dyk et al. (2003)
3 mM Butyrate	hTPO	SFM/suspension/shaker flask/batch	Baik et al. (2008)
1 mM Butyrate	IFN- γ	Serum/adherent/T-flask/batch	Yee et al. (2008)
1.5% DMSO	HBsAg	Serum/adherent/T-flask/batch	Li et al. (2006)
Cytochalasin D	SEAP	Serum/adherent/T-flask/batch	Hayduk and Lee (2005)
Insulin or bFGF	–	Serum/adherent/T-flask/batch	Lee et al. (1996a)
Hydrolysate	Antibody	SFM/suspension/shaking flask/batch	Kim et al. (2011)
3 mM Butyrate Bcl-xL overexpression	EPO	SFM/suspension/bioreactor/batch	Baik and Lee (2010)
Bcl-xL overexpression	–	SFM/suspension/bioreactor/fed-batch	Carlage et al. (2009)
E2F-1 overexpression	–	Serum/adherent/T-flask/batch	Lee et al. (1996b)
PACEsol overexpression	rhBMP-2	CDM/suspension/shaking flask/batch	Meleady et al. (2008)
c-myc overexpression	–	Serum/adherent/T-flask/batch	Kuystermans et al. (2010)
With different metabolic profiles	Antibody	SFM/suspension/bioreactor/fed-batch	Pascoe et al. (2007)
With different growth rates	Antibody	CDM/suspension/shaking flask/batch	Doolan et al. (2010)
With different media compositions	EPO	SFM/suspension/shaker flask/batch	Baik et al. (2011)

tunicamycin, cytochalasin D, and growth factors, which increase μ and/or q , on the changes of rCHO proteome also have also been studied (Baik et al. 2008; Hayduk and Lee 2005; Kantardjieff et al. 2010; Lee et al. 1996a; Li et al. 2006; Van Dyk et al. 2003; Yee et al. 2008). Recently, differently expressed proteins of rCHO cells cultivated in SF medium supplemented with optimized hydrolysates mixtures, yielding the highest μ or the highest q_{Ab} , were identified by comparative proteomics (Kim et al. 2011).

The proteome in rCHO cells engineered by overexpressing and/or down-regulating an effector protein may be altered. Proteomic approaches to chase global protein changes by Bcl-xL overexpression have been performed to determine the key components (Baik and Lee 2010; Carlage et al. 2009). Influences on rCHO proteome by overexpression of E2F-1, which has a positive function in the cell proliferation, have been evaluated (Lee et al. 1996b). In addition, influences on rCHO proteome by the overexpression of soluble paired

basic amino acid cleaving enzyme (PACEsol), which affects q of rhBMP-2, have also been evaluated (Meleady et al. 2008). Recently, the differentially expressed intracellular proteins by overexpressing c-myc, known to be a typical oncogenic protein and enhanced integral viable cell density, were investigated (Kuystermans et al. 2010).

Proteomic results have been successfully applied to rCHO cell engineering. Pascoe et al. (2007) analyzed the protein changes by comparing two different antibody-producing rCHO cells with different lactate profiles in the same fed-batch culture condition. Similarly, the proteome of rCHO cells with high μ was compared with that of cells with low μ . The proteomic result along with the transcriptomic result could provide a potential candidate for the enhancement of cell growth (Doolan et al. 2010). The overexpression of the identified protein, VCP, could improve cell concentration without affecting cell viability, although the effectiveness depended on the clone. Recently, Baik et al. (2011) evaluated the intracellular

responses in rCHO cells adapted to grow in serum-free suspension culture. The overexpression of the identified protein, heat shock protein 70 kDa and/or 60 kDa (HSC70, HSP60), showed 10% to 15% enhanced cell concentration during serum-free adaptation and 15% to 33% reduction of adaptation time. In conventional 2-DE, a quantitative comparison of the proteins on different gels is challenging due to the high degree of gel-to-gel variations, arising from the heterogeneity of polyacrylamide gel in preparation and fluctuations due to changes in electrical current, pH, and temperature during the procedure.

In addition, staining methods, especially silver staining, also contribute to this variation. To overcome the gel-to-gel variation in conventional 2-DE, two-dimensional differential in-gel electrophoresis (2-D DIGE) was developed (Timms and Cramer 2008). Generally, the most widely used labeling reagents in the 2-D DIGE are synthetic *N*-hydroxysuccinimidyl (NHS) ester derivatives of cyanine dyes, Cy2, Cy3, and Cy5 (NHS-Cy2, NHS-Cy3, and NHS-Cy5). The mixture of Cy3 and Cy5-labeled test samples and Cy2-labeled internal standard are resolved on a single 2-D gel and three images of the gel are compared. The 2-D DIGE technique has recently been applied to rCHO cells to evaluate the altered protein expression level under various culture conditions (Baik and Lee 2010; Doolan et al. 2010; Kumar et al. 2008; Meleady et al. 2008).

Metabolomics

Another omics-based approach attracting attention in rCHO cell culture is metabolomics, which is coupled with nuclear magnetic resonance (NMR) or mass spectrometry (MS) to chase low molecular endogenous metabolites. In general, the extent of changes in metabolite is significant compared with the extent of changes in DNA, RNA, and protein. However, unlike the DNA/RNA and protein, the qualitative analysis system for metabolite has not been fully established yet.

Easy amplification of a sample for DNA/RNA and the existence of specific probe, antibody, for protein are benefits for qualitative analysis. In contrast, there is a limitation to analysis of metabolites due to non-amplifiable characteristics and the lack of public probes for them. Despite the technical difficulty, there are reports to identify crucial extracellular metabolites or to chase intracellular metabolite flux for media development and apoptosis reduction using liquid chromatography–MS-based or NMR spectroscopy-based metabolomics in rCHO cell culture (Bradley et al. 2010; Chong et al. 2009, 2010, 2011; Goudar et al. 2010). Among them, Chong et al. (2010) demonstrated the typical metabolomics-based CHO cell engineering. They found that malate accumulation was most significant in the medium of rCHO fed-batch culture. Subsequent cell engineering to overexpress malate dehydrogenase II resulted in significant growth improvement in IVCC.

Concluding remarks

Significant improvement in therapeutic protein production of rCHO cells has been achieved with the development of cell line and culture processes involving media development. In particular, the establishment of a highly and stably producing cell line is of utmost importance considering the heterogeneity and different responses to the various environments of rCHO cells. This review focuses on current achievements in vector engineering and cell engineering in cell line development.

The combinatorial cell engineering strategy with regulation of multiple targets is becoming popular. In the same context, the use of miRNA in cell engineering will increase in the future because miRNA can regulate the global gene expression and can easily be introduced into cells. In addition, combinatorial analysis of transcriptomics with proteomics will enter into general use to compensate the transcriptional changes as well as post-transcriptional alteration.

Although the application of vector engineering and cell engineering to rCHO cell culture has various benefits, the limited success, to date, in its application may be due to the insufficient genomic information of rCHO cells. In this regard, a recent report dealing with CHO-K1 genomic sequence can lead to the greatest progression in the current strategy of cell line development (Xu et al. 2011). The finding of hot-spots and better understanding of its neighboring sequence may help to generate high producers, as described in the previous bioinformatics analysis for identifying it in the human genome using a computational method (Girod et al. 2007). In addition, the complete genomic information of CHO cells will be helpful in the identification step in omics-based approaches.

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