Method for the production of a glycosylated immunoglobulin

Herein is reported a method in the field of immunoglobulin production in cells, whereby the glycosylation pattern of the produced immunoglobulin can be modified based on the cultivation conditions.

Background of the Invention

In recent years the production of immunoglobulins has steadily increased and it is likely that immunoglobulins will become the biggest group of therapeutics available for the treatment of various diseases in the near future. The impact of immunoglobulins emerges from their specificity, which comprises their specific target recognition and binding function as well as the activation of specific effects concurrently with or after antigen/Fc-receptor binding.

The specific target recognition and binding is mediated by the variable region of the immunoglobulin. Other parts of the immunoglobulin molecule, from which effects originate, are posttranslational modifications, such as the glycosylation pattern. The posttranslational modifications do have an influence on the efficacy, stability, immunogenic potential, binding etc. of an immunoglobulin. In connection therewith complement-dependent cytotoxicity (CDC), antibody-dependent cellular cytotoxicity (ADCC) and induction of apoptosis have to be addressed.

It has been reported that the glycosylation pattern of immunoglobulins, i.e. the saccharide composition and number of attached glycostructures, has a strong influence on the biological properties (see e.g. Jefferis, R., Biotechnol. Prog. 21 (2005) 11-16). Immunoglobulins produced by mammalian cells contain 2-3 % by mass carbohydrates (Taniguchi, T., et al., Biochem. 24 (1985) 5551-5557). This is equivalent e.g. in an immunoglobulin of class G (IgG) to 2.3 oligosaccharide residues in an IgG of mouse origin (Mizuochi, T., et al., Arch. Biochem. Biophys. 257 (1987) 387-394) and to 2.8 oligosaccharide residues in an IgG of human origin (Parekh, R.B., et al., Nature 316 (1985) 452-457), whereof generally two are located in the Fc-region and the remaining in the variable region (Saba, J.A., et al., Anal. Biochem. 305 (2002) 16-31).

In the Fc-region of an immunoglobulin of class G oligosaccharide residues can be introduced via N-glycosylation at amino acid residue 297, which is an asparagine residue (denoted as Asn^{297}). Youings et al. have shown that a further

N-glycosylation site exists in 15 % to 20 % of polyclonal IgG molecules in the Fab-region (Youings, A., et al., Biochem. J., 314 (1996) 621-630; see e.g. also Endo, T., et al., Mol. Immunol. 32 (1995) 931-940). Due to inhomogeneous, i.e. asymmetric, oligosaccharide processing, multiple isoforms of an immunoglobulin with different glycosylation pattern exist (Patel, T.P., et al., Biochem. J. 285 (1992) 839-845; Ip, C.C., et al., Arch. Biochem. Biophys. 308 (1994) 387-399; Lund, J., et al., Mol. Immunol. 30 (1993) 741-748). Concurrently the structure and distribution of the oligosaccharides is both highly reproducible (i.e. non-random) and site specific (Dwek, R.A., et al., J. Anat. 187 (1995) 279-292).

Some characteristics of an immunoglobulin are directly linked to the glycosylation of the Fc-region (see e.g. Dwek, R.A., et al., J. Anat. 187 (1995) 279-292; Lund, J., et al., J. Immunol. 157 (1996) 4963-4969; Lund, J., FASEB J. 9 (1995) 115-119; Wright, A. and Morrison, S.L., J. Immunol. 160 (1998) 3393-3402), such as for example thermal stability and solubility (West, C.M., Mol. Cell. Biochem. 72 (1986) 3-20), antigenicity (Turco, S.J., Arch. Biochem. Biophys. 205 (1980) 330-339), immunogenicity (Bradshaw, J.P., et al., Biochim. Biophys. Acta 847 (1985) 344-351; Feizi, T. and Childs, R.A., Biochem. J. 245 (1987) 1-11; Schauer, R., Adv. Exp. Med. Biol. 228 (1988) 47-72), clearance rate/circulatory half-life (Ashwell, G. and Harford, J., Ann. Rev. Biochem. 51 (1982) 531-554; McFarlane, I.G., Clin. Sci. 64 (1983) 127-135; Baenziger, J.U., Am. J. Path. 121 (1985) 382-391; Chan, V.T. and Wolf, G., Biochem. J. 247 (1987) 53-62; Wright, A., et al., Glycobiology 10 (2000) 1347-1355; Rifai, A., et al., J. Exp. Med. 191 (2000) 2171-2182; Zukier, L.S., et al., Cancer Res. 58 (1998) 3905-3908), and biological specific activity (Jefferis, R. and Lund, J., in Antibody Engineering, ed. by Capra, J.D., Chem. Immunol. Basel, Karger, 65 (1997) 111-128).

Factors influencing the glycosylation pattern have been investigated, such as for example presence of fetal calf serum in the fermentation medium (Gawlitzek, M., et al., J. Biotechnol. 42(2) (1995) 117-131), buffering conditions (Müthing, J., et al., Biotechnol. Bioeng. 83 (2003) 321-334), dissolved oxygen concentration (Saba, J.A., et al., Anal. Biochem. 305 (2002) 16-31; Kunkel, J.P., et al., J. Biotechnol. 62 (1998) 55-71; Lin, A.A., et al., Biotechnol. Bioeng. 42 (1993) 339-350), position and conformation of the oligosaccharide as well as host cell type and cellular growth state (Hahn, T.J. and Goochee, C.F., J. Biol. Chem. 267 (1992) 23982-23987; Jenkins, N., et al., Nat. Biotechnol. 14 (1996) 975-981), cellular nucleotide-sugar metabolism (Hills, A.E., et al., Biotechnol. Bioeng. 75 (2001) 239-251), nutrient limitations (Gawlitzek, M., et al., Biotechnol. Bioeng. 46 (1995)

536-544; Hayter, P.M., et al., Biotechnol. Bioeng. 39 (1992) 327-335), especially glucose restriction (Tachibana, H., et al., Cytotechnology 16 (1994) 151-157), and extracellular pH (Borys, M.C., et al., Bio/Technology 11 (1993) 720-724).

Increased oligomannose structures as well as truncated oligosaccharide structures have been observed by the recombinant expression of immunoglobulins e.g. in NS0 myeloma cells (Ip, C.C., et al., Arch. Biochem. Biophys. 308 (1994) 387-399; Robinson, D.K., et al., Biotechnol. Bioeng. 44 (1994) 727-735). Under glucose starvation conditions variations in glycosylation, such as attachment of smaller precursor oligosaccharides or complete absence of oligosaccharide moieties, have been observed in CHO cells, Murine 3T3 cells, rat hepatoma cells, rat kidney cells and Murine myeloma cells (Rearick, J.I., et al., J. Biol. Chem. 256 (1981) 6255-6261; Davidson, S.K. and Hunt, L.A., J. Gen. Virol. 66 (1985) 1457-1468; Gershman, H. and Robbins, P.W., J. Biol. Chem. 256 (1981) 7774-7780; Baumann, H. and Jahreis, G.P., J. Biol. Chem. 258 (1983) 3942-3949; Strube, K.-H., et al., J. Biol. Chem. 263 (1988) 3762-3771; Stark, N.J. and Heath, E.C., Arch. Biochem. Biophys. 192 (1979) 599-609). A strategy based on low glutamine/glucose concentrations was reported by Wong, D.C.F., et al., Biotechnol. Bioeng. 89 (2005) 164-177.

The Japanese Patent Application JP 62-258252 reports a perfusion culture of mammalian cells, whereas US 5,443,968 reports a fed-batch culture method for protein secreting cells. In WO 98/41611 a method for cultivating cells is reported effective to adapt the cells to a metabolic state characterized by low lactate production. A method for culturing cells in order to produce substances is reported in WO 2004/048556. Elbein, A.D., Ann. Rev. Biochem. 56 (1987) 497-534, reports that mammalian cells when incubated in the absence of glucose transfer mannose-5 containing structures instead of mannose-9 containing structures to proteins. The dependence of pCO2 influences during glucose limitation on CHO cell growth, metabolism and IgG production is reported by Takuma, S., et al. in Biotechnol. Bioeng. 97 (2007) 1479-1488.

Summary

It has been found that the amount of the mannose-5 glycostructure in the glycosylation pattern of a polypeptide produced by a eukaryotic cell can be modified based on the amount of glucose provided to the cell in the cultivation process. By reducing the amount of glucose available, e.g. by changing the DGL value from 1.0 to smaller values of e.g. 0.8, 0.6, 0.5, 0.4, or 0.2, a modification in

the mannose-5 glycostructure amount in the glycosylation pattern can be obtained. The DGL value or respectively the amount of glucose available per time unit has to be kept constant and at a defined reduced value per time unit.

A first aspect as reported herein is a method for the production of a polypeptide, in one embodiment of an immunoglobulin, in a eukaryotic cell, comprising the following steps

a) providing a eukaryotic cell comprising a nucleic acid encoding the polypeptide,

b) cultivating the cell under conditions wherein the degree of glucose limitation (DGL) is kept constant and wherein the DGL is less than 0.8, and

c) recovering the polypeptide from the culture,

wherein the fraction of the polypeptide with a mannose-5 glycostructure is 10 % or less of the sum comprising the amount of the polypeptide with a mannose-5 glycostructure, the amount of the polypeptide G(0) isoform, the amount of the polypeptide G(1) isoform, and the amount of the polypeptide G(2) isoform.

In one embodiment the DGL is kept constant in the range of from 0.8 to 0.2. In a further embodiment the DGL is kept constant in the range of from 0.6 to 0.4. In another embodiment the fraction of the polypeptide with a mannose-5 glycostructure is 8 % or less of the sum comprising the polypeptide with a mannose-5 glycostructure, the polypeptide G(0) isoform, the polypeptide G(1) isoform, and the polypeptide G(2) isoform. In still another embodiment the polypeptide is an immunoglobulin, in one embodiment an immunoglobulin of class G or E.

Another aspect as reported herein is a method for the production of an immunoglobulin comprising the following steps:

a) providing a mammalian cell comprising a nucleic acid encoding the immunoglobulin,

b) cultivating the cell in a cultivation medium wherein the amount of glucose available in the cultivation medium per time unit is kept constant

and limited to less than 80 % of the amount that could maximally be utilized by the cells in the cultivation medium per time unit, and

c) recovering the immunoglobulin from the cells or the cultivation medium.

In one embodiment the amount of glucose available in the cultivation medium per time unit is kept constant and limited to a value in the range of from 80 % to 20 %. In a further embodiment the range is of from 60 % to 40 %. In another embodiment the cells in the cultivation medium are the viable cells in the cultivation medium.

In one embodiment of the aspects as reported herein the eukaryotic cell is selected from CHO cells, NS0 cells, HEK cells, BHK cells, hybridoma cells, PER.C6® cells, insect cells, or Sp2/0 cells. In one embodiment the eukaryotic cell is a Chinese Hamster Ovary (CHO) cell. In another embodiment of the aspects as reported herein the cultivating is at a pH value in the range of from about pH 7.0 to about pH 7.2.

In still another embodiment of the aspects as reported herein the cultivating is a continuous or a fed-batch cultivating. The methods may comprise in another embodiment a final step of purifying the polypeptide. In still another embodiment the cell is cultivated for six to twenty days or for six to fifteen days. In a further embodiment the cell is cultivated for six to eight days.

Another aspect as reported herein is a composition comprising an immunoglobulin, wherein the composition has been prepared with a method as reported herein.

In one embodiment the immunoglobulin is an anti-IL-6R antibody. In a further embodiment the anti-IL-6R antibody comprises Tocilizumab. In another embodiment the mannose-5 glycostructure attached to the anti-IL-6R antibody is 8 % or less. In still a further embodiment the mannose-5 glycostructure is 6 % or less. In another embodiment the mannose-5 glycostructure is 4 % or less. In a further embodiment the G(0) glycostructure attached to the anti-IL-6R antibody is in the range from 40 % to 46 % and the G(2) glycostructure attached to the anti-IL-6R antibody is in the range from 9 % to 11 %.

Detailed Description

Herein is reported a method for the production of an immunoglobulin comprising the following steps:

a) cultivating a mammalian cell comprising a nucleic acid encoding the immunoglobulin in a cultivation medium at a constant DGL of less than 0.8 (i.e. the amount of glucose available per time unit is constant and 80 % or less of the amount of glucose that can maximally be utilized by the cell per time unit), and

b) recovering the immunoglobulin from the cells or the culture medium.

With the method as reported herein an immunoglobulin can be obtained wherein the amount of the immunoglobulin with a mannose-5 glycostructure depends on the adjusted DGL value, and wherein the amount is the fraction of the sum of the amount of the immunoglobulin with a mannose-5 glycostructure, and of the immunoglobulin G(0) isoform, and of the immunoglobulin G(1) isoform, and of the immunoglobulin G(2) isoform. In one embodiment the DGL is of from 0.8 to 0.2. In this embodiment the fraction is 10 % or less. In another embodiment the DGL is of from 0.6 to 0.4. In this embodiment the fraction is 6 % or less. With the method as reported herein an immunoglobulin can be obtained wherein the fraction of the immunoglobulin having a mannose-5 glycostructure is 10 % or less of the sum comprising the amount of the immunoglobulin with a mannose-5 glycostructure, the amount of the immunoglobulin G(0) isoform, the amount of the immunoglobulin G(1) isoform, and the amount of the immunoglobulin G(2) isoform. In another embodiment the fraction is the area-% fraction determined in a liquid chromatography method. In one embodiment the DGL is maintained in the range of from 0.8 to 0.2. In another embodiment the DGL is maintained in the range of from 0.6 to 0.2. In still another embodiment the DGL is maintained in the range of from 0.6 to 0.4. In one embodiment the amount of glucose that can maximally be utilized by the cell per time unit is the average amount of glucose that is utilized in a cultivation in which all compounds are available in excess, i.e. no compound is limiting the growth of the cell, determined based on at least five cultivations. In one embodiment the fraction is determined on day seven of the cultivation.

Methods and techniques known to a person skilled in the art, which are useful for carrying out the current invention, are described e.g. in Ausubel, F.M. (ed.), Current Protocols in Molecular Biology, Volumes I to III (1997), Wiley and Sons;

Sambrook, J., et al., Molecular Cloning: A Laboratory Manual, Third Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001); Glover, N.D. (ed.), DNA Cloning: A Practical Approach, Volumes I and II (1985); Freshney, R.I. (ed.), Animal Cell Culture (1986); Miller, J.H. and Calos, M.P. (eds.), Gene Transfer Vectors for Mammalian Cells, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1987); Watson, J.D., et al., Recombinant DNA, Second Edition, N.Y., W.H. Freeman and Co (1992); Winnacker, E.L., From Genes to Clones, N.Y., VCH Publishers (1987); Celis, J. (ed.), Cell Biology, Second Edition, Academic Press (1998); Freshney, R.I., Culture of Animal Cells: A Manual of Basic Techniques, Second Edition, Alan R. Liss, Inc., N.Y. (1987).

The use of recombinant DNA technology enables the production of numerous derivatives of a polypeptide. Such derivatives can, for example, be modified in individual or several amino acid positions by substitution, alteration or exchange. The derivatization can, for example, be carried out by means of site directed mutagenesis. Such variations can easily be carried out by a person skilled in the art (Sambrook, J., et al., Molecular Cloning: A Laboratory Manual, Third Edition, Cold Spring Harbor Laboratory Press, New York, USA (2001); Hames, B.D. and Higgins, S.G., Nucleic acid hybridization - a practical approach (1985) IRL Press, Oxford, England).

The term "nucleic acid" denotes a naturally occurring or partially or fully non-naturally occurring nucleic acid molecule encoding a polypeptide. The nucleic acid can be build up of DNA-fragments which are either isolated or synthesized by chemical means. The nucleic acid can be integrated into another nucleic acid, e.g. in an expression plasmid or the genome/chromosome of a eukaryotic cell. The term “plasmid” includes shuttle and expression plasmids. Typically, the plasmid will also comprise a prokaryotic propagation unit comprising an origin of replication (e.g. the ColE1 origin of replication) and a selectable marker (e.g. ampicillin or tetracycline resistance gene), for replication and selection, respectively, of the plasmid in prokaryotic cells. To a person skilled in the art procedures and methods are well known to convert an amino acid sequence, e.g. of a polypeptide, into a corresponding nucleic acid encoding the respective amino acid sequence. Therefore, a nucleic acid is characterized by its nucleic acid sequence consisting of individual nucleotides and likewise by the amino acid sequence of a polypeptide encoded thereby.

The term “expression cassette” denotes a nucleic acid that contains the elements necessary for expression and optionally for secretion of at least the contained structural gene in/from a cell, such as a promoter, polyadenylation site, and 3’- and 5’-untranslated regions.

The term “gene” denotes e.g. a segment on a chromosome or on a plasmid, which is necessary for the expression of a polypeptide. Beside the coding region a gene comprises other functional elements including a promoter, introns, and one or more transcription terminators. A “structural gene” denotes the coding region of a gene without a signal sequence.

The term "expression" denotes the transcription and translation of a structural gene within a cell. The level of transcription of a structural gene in a cell can be determined on the basis of the amount of corresponding mRNA that is present in the cell. For example, mRNA transcribed from a selected nucleic acid can be quantitated by PCR or by Northern hybridization (see e.g. Sambrook et al. (supra)). A polypeptide encoded by a nucleic acid can be quantitated by various methods, e.g. by ELISA, by determining the biological activity of the polypeptide, or by employing methods that are independent of such activity, such as Western blotting or radioimmunoassay, using antibodies that recognize and bind to the polypeptide (see e.g. Sambrook et al. (supra)).

The term "cell" denotes a cell into which a nucleic acid encoding a polypeptide, in one embodiment a heterologous polypeptide, has been introduced. The term "cell" includes both prokaryotic cells used for propagation of plasmids/vectors as well as eukaryotic cells used for expression of the structural gene. In one embodiment a eukaryotic cell for the expression of an immunoglobulin is a mammalian cell. In another embodiment the mammalian cell is selected from CHO cells, NS0 cells, Sp2/0 cells, COS cells, HEK cells, BHK cells, PER.C6® cells, and hybridoma cells. A eukaryotic cell can be selected in addition from insect cells, such as caterpillar cells (Spodoptera frugiperda, sf cells), fruit fly cells (Drosophila melanogaster), mosquito cells (Aedes aegypti, Aedes albopictus), and silkworm cells (Bombyx Mori), and the like.

The term "polypeptide" denotes a polymer of amino acid residues joined by peptide bonds, whether produced naturally or synthetically. Polypeptides of less than about 20 amino acid residues may be referred to as "peptides". Polypeptides of more than 100 amino acid residues or covalent and non-covalent aggregates comprising more than one polypeptide may be referred to as “proteins”. Polypeptides may comprise

non-amino acid components, such as carbohydrate groups. The non-amino acid components may be added to the polypeptide by the cell in which the polypeptide is produced, and may vary with the type of cell. Polypeptides are defined herein in terms of their amino acid sequence in N- to C-terminal direction. Additions thereto, such as carbohydrate groups, are generally not specified, but may be present nonetheless.

The term "heterologous DNA" or ”heterologous polypeptide” denotes a DNA molecule or a polypeptide, or a population of DNA molecules or a population of polypeptides, which do not exist naturally within a given cell. DNA molecules heterologous to a particular cell may contain DNA derived from the cell’s species (i.e. endogenous DNA) so long as that DNA is combined with non-host DNA (i.e. exogenous DNA). For example, a DNA molecule containing a non-cell’s DNA segment, e.g. encoding a polypeptide, operably linked to a cell’s DNA segment, e.g. comprising a promoter, is considered to be a heterologous DNA molecule. Likewise, a heterologous DNA molecule can comprise an endogenous structural gene operably linked to an exogenous promoter. A polypeptide encoded by a heterologous DNA molecule is a "heterologous" polypeptide.

The term "expression plasmid" denotes a nucleic acid comprising at least one structural gene encoding a polypeptide to be expressed. Typically, an expression plasmid comprises a prokaryotic plasmid propagation unit, including an origin of replication and a selection marker, e.g. for E.coli, an eukaryotic selection marker, and one or more expression cassettes for the expression of the structural gene(s) of interest each in turn comprising a promoter, at least one structural gene, and a transcription terminator including a polyadenylation signal. Gene expression is usually placed under the control of a promoter, and such a structural gene is to be "operably linked to" the promoter. Similarly, a regulatory element and a core promoter are operably linked if the regulatory element modulates the activity of the core promoter.

The term "isolated polypeptide" denotes a polypeptide that is essentially free from associated cellular components, such as carbohydrate, lipid, or other proteinaceous or non-proteinaceous impurities, which are not covalently associated with the polypeptide. Typically, a preparation of an isolated polypeptide contains in certain embodiments the polypeptide in a highly purified form, i.e. at least about 80 % pure, at least about 90 % pure, at least about 95 % pure, greater than 95 % pure, or greater than 99 % pure. One way to show that a particular protein preparation

contains an isolated polypeptide is by the appearance of a single band following sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-page) of the preparation and Coomassie Brilliant Blue staining of the gel. However, the term "isolated" does not exclude the presence of the same polypeptide in alternative physical forms, such as dimers, or alternatively glycosylated or derivatized forms.

Immunoglobulins in general are assigned into five different classes: IgA (immunoglobulin of class A), IgD, IgE, IgG and IgM. Between these classes the immunoglobulins differ in their overall structure and/or amino acid sequence but have the same building blocks. Complete immunoglobulins are built up of two pairs of polypeptide chains, each comprising an immunoglobulin light polypeptide chain (short: light chain) and an immunoglobulin heavy polypeptide chain (short: heavy chain). In turn the chains comprise a variable region and a constant region. In a light chain both regions consist of one domain, whereas in a heavy chain the variable region consists of one domain and the constant region comprises up to five domains (in N- to C-terminal direction): the C_H1-domain, optionally the hinge region domain, the C_H2-domain, the C_H3-domain, and optionally the C_H4-domain. An immunoglobulin can be dissected in a Fab- and an Fc-region. The entire light chain, the heavy chain variable domain and the C_H1 domain are referred to as Fab-region (fragment antigen binding-region). The Fc-region comprises the C_H2-, C_H3-, and optionally the C_H4-domain.

As used herein, the term "immunoglobulin" denotes a protein consisting of one or more polypeptides. The encoding immunoglobulin genes include the different constant region genes as well as the myriad immunoglobulin variable region genes. The term “immunoglobulin” comprise in one embodiment monoclonal antibodies and fragments thereof, such as an isolated heavy chain, or a heavy chain constant region, as well as fusion polypeptides comprising at least an immunoglobulin heavy chain C_H2-domain. In one embodiment of the method as reported herein the immunoglobulin is a complete immunoglobulin, in another embodiment the immunoglobulin is an Fc-region of a complete immunoglobulin. In another embodiment the immunoglobulin is an immunoglobulin, or an immunoglobulin fragment, or an immunoglobulin conjugate.

The term “immunoglobulin fragment” denotes a polypeptide comprising at least the C_H2-domain of an immunoglobulin delta, epsilon, or alpha heavy chain, and/or the C_H3-domain of an immunoglobulin epsilon or delta heavy chain. Encompassed

are also derivatives and variants thereof wherein the N-glycosylation motif Asn-Xaa-Ser/Thr in the C_H2- or C_H3-domain is not changed.

The term "immunoglobulin conjugate" denotes a polypeptide comprising at least the C_H2-domain of an immunoglobulin delta, epsilon, or alpha heavy chain, and/or the C_H3-domain of an immunoglobulin epsilon or delta heavy chain fused to a non-immunoglobulin polypeptide. Therein the N-glycosylation motif Asn-Xaa-Ser/Thr in the C_H2- or C_H3-domain is not changed.

The oligosaccharides attached to Asn^{297} (IgG, IgE) or Asn^{263} (IgA) of a C_H2-domain and/or to Asn^{394}, Asn^{445}, or Asn^{496} (IgE, IgD) of a C_H3-domain of an immunoglobulin heavy chain have a biantennary structure (Mizuochi, T., et al., Arch. Biochem. Biophys. 257 (1987) 387-394), i.e. they consist of a core structure of

Man(α1-4)GlcNAc(β1-4)GlcNAc→Asn

with an optional Fuc(α1-6) linkage at the terminal GlcNAc residue. Two outer-arms are connected to the terminal mannose of the core structure having the formula

Gal(β1-4)GlcNAc(β1-2)Man(α1-6)→Man, and

Gal(β1-4)GlcNAc(β1-2)Man(α1-3)→Man,

wherein the terminal galactose residues are optional (Man = mannose, GlcNAc = N-acetyl glucose, Gal = galactose; Fuc = fucose).

Table 1: Glycosylation sites of immunoglobulins.

immunoglobulin class	residue to which a glycostructure can be attached
IgG	Asn 297
IgE	Asn 255, Asn 297, Asn 361, Asn 371, Asn 394
IgA	Asn 263, Asn 459
IgD	Asn 445, Asn 496
IgM	Asn 395

The term "the amount of the immunoglobulin G(0) isoform, the amount of the immunoglobulin G(1) isoform, and the amount of the immunoglobulin G(2) isoform" denotes the sum of the amounts of the different, heterogeneous, biantennary oligosaccharides N-linked to an asparagine (Asn) of an immunoglobulin. The G(2) isoform has a terminal galactose residue on each of the outer-arms of the oligosaccharide structure, the G(1) isoform bears only a galactose

residue on either the (α1-6) or (α1-3) linked outer-arm, and the G(0) isoform bears no galactose residue on both outer-arms.

The term "mannose-5 glycostructure" denotes an oligomannose-structure linked to an Asn residue of a polypeptide comprising or consisting of five mannose residues and two N-acetyl glucose core residues, forming a triantennary structure.

One aspect as reported herein is a method for the production of an immunoglobulin comprising the following steps:

a) cultivating a eukaryotic cell, preferably a mammalian cell, comprising one or more nucleic acid(s) encoding the immunoglobulin in a cultivation medium wherein the amount of glucose available in the cultivation medium per time unit is kept constant and limited to a value of less than 80 % of the amount that could maximally be utilized by the eukaryotic cells in the cultivating per time unit, and

b) recovering the immunoglobulin from the cell or the culture medium and thereby producing an immunoglobulin.

With this method an immunoglobulin is obtained comprising at most 10 % of an immunoglobulin with a mannose-5 glycostructure. The 10 % are calculated based on the sum of the amount of the immunoglobulin with a mannose-5 glycostructure, the amount of the immunoglobulin G(0) isoform, the amount of the immunoglobulin G(1) isoform, and the amount of the immunoglobulin G(2) isoform.

The terms "degree of glucose limitation" and its abbreviation "DGL", which can be used interchangeably herein, denote the ratio of the current specific glucose consumption rate of a single cell in a cultivation to the maximum known specific glucose consumption rate of the single cell or a single cell of the same kind. The degree of glucose limitation is defined as

$$DGL = \frac{qGlc}{qGlc_{max}}$$

with qGlc = current specific glucose consumption rate of a single cell;
$qGlc_{max}$ = maximum known specific glucose consumption rate for this single cell or a single cell of the same kind.

The DGL can vary between $DGL_{maintenance}$ and 1 whereby $DGL_{maintenance}$ (< 1 and > 0) denotes complete growth limitation and 1 denotes no limitation or complete glucose excess.

The introduction of glycostructures to polypeptides, e.g. immunoglobulins, is a post-translational modification. Due to incompleteness of the glycosylation procedure of the respective cell every expressed polypeptide is obtained with a glycosylation pattern comprising different glycostructures. Thus, a polypeptide is obtained from a cell expressing it in form of a composition comprising differently glycosylated forms of the same polypeptide, i.e. with the same amino acid sequence. The sum of the individual glycostructures is denoted as glycosylation pattern, comprising e.g. polypeptides with completely missing glycostructures, differently processed glycostructures, and/or differently composed glycostructures.

One glycostructure is the mannose-5 glycostructure (also denoted as high-mannose, Man5, M5, or oligo-mannose). It has been reported, that the fraction of recombinantly produced polypeptides with the mannose-5 glycostructure is increased with prolonged cultivation time or under glucose starvation conditions (Robinson, D.K., et al., Biotechnol. Bioeng. 44 (1994) 727-735; Elbein, A.D., Ann. Rev. Biochem. 56 (1987) 497-534).

It has been found that the amount of the mannose-5 glycostructure in the glycosylation pattern of a polypeptide produced by a eukaryotic cell can be modified based on the amount of glucose provided to the cell in the cultivation process. It has been found that by reducing the amount of glucose, i.e. by changing the DGL value from 1.0 to smaller values of e.g. 0.8, 0.6, 0.5, 0.4, or 0.2, a modification in the mannose-5 glycostructure amount in the glycosylation pattern can be achieved. In one embodiment the DGL value is kept constant at a value within a range, such as from 0.8 to 0.2, or from 0.6 to 0.4. That is, the production of a polypeptide, in one embodiment of an immunoglobulin, can be performed under conditions wherein a restricted amount of glucose is available to the cultivated cell in order to obtain the polypeptide with a defined amount of the mannose-5 glycostructure in the glycosylation pattern. It has been found that a cultivation with an amount of glucose available per time unit of 80 % or less of the amount of glucose that can maximally be utilized by the cells per time unit, in one embodiment by exponentially growing cells, i.e with a DGL of 0.8 or less, yields a polypeptide with a glycosylation pattern in which the amount of the mannose-5 glycostructure is changed compared to a cultivation with a DGL of 1.0. In one

embodiment the cell density is the viable cell density. Additionally the obtained polypeptide yield is increased.

The term "the amount of glucose that can maximally be utilized by the cell per time unit" denotes the amount of glucose that is maximally consumed or utilized or metabolized per time unit by a single cell under optimum growth conditions in the exponential growth phase in a cultivation without any nutrient limitation. Thus, the amount of glucose that can maximally be utilized by the cell per time unit can be determined by determining the amount of glucose that is metabolized per time unit by a cell under optimum growth conditions in the exponential growth phase in a cultivation without any nutrient limitation. A further increase of the available amount of glucose will not further increase, i.e. change, the amount of glucose that can maximally be utilized by the cell per time unit. This amount defines the maximum level of glucose consumption of a single cell. This does not denote that a genetically modified version of the cell might not have an even higher maximum level of glucose consumption. Alternatively the amount of glucose that can be maximally be utilized by the cell per time unit can be determined based on previous cultivations and the monitored data.

The process as reported herein is particularly simple to carry out, associated with a minimum effort for measuring and control, and particularly economic.

Without restrictions, e.g. insufficient nutrient supply, cultivated cells grow and consume nutrients at maximum rates in an uneconomic manner. One of the consumed culture medium nutrients is glucose, which is metabolized by the cultivated cells in order to produce energy and building blocks for the cell's metabolism. In the presence of excess glucose the cell's metabolism is running at the maximum turnover rate for glucose. The amount of glucose that can maximally be utilized by the cell per time unit can for example be determined from the glucose consumption of exponentially growing cells in the presence of excess glucose cultivated with or under the same cultivation conditions that will also be used in the cultivation with restricted glucose, i.e. with an amount of glucose available per time unit that is smaller than that which can be utilized by the cell. This maximum amount can be calculated easily by determining the cell density and glucose concentration at the beginning and end of a fixed time range. The value is normally in a range of from 0.006 to 190 mmol/hour/10^9 cells (Baker, K.N., et al., Biotechnol. Bioeng. 73 (2001) 188-202; WO 98/41611; Müthing, J., et al., Biotechnol. Bioeng. 83 (2003) 321-334; WO 2004/048556). In one embodiment

the $qGlc_{max}$ is about 0.142 mmol/hour/10^9 cells under standard process conditions at pH 7.0.

The method as reported herein is performed in one embodiment under conditions wherein the amount of glucose available per time unit is kept constant and at 80 % or less of the amount of glucose that can maximally be utilized by the cell per time unit ($0.8 \geq DGL > 0$), in one embodiment the amount of glucose available is kept constant and at 60 % or less ($0.6 \geq DGL > 0$), in another embodiment at 50 % or less ($0.5 \geq DGL > 0$), and in still another embodiment at about 40 %. The term "about" as used within this application denotes that the value is no exact value it is merely the central point of a range wherein the value can vary up to 10 %, i.e. the term "about 40 %" denotes a range of from 44 % to 36 % (DGL = 0.44 - 0.36).

In one embodiment the cultivating is with an amount of glucose available per time unit that is kept constant in a range between 80 % and 10 % of the amount of glucose that can maximally be utilized by the cell per time unit ($0.8 \geq DGL \geq 0.1$). In another embodiment the amount of glucose available is kept constant in a range between 60 % and 10 % ($0.6 \geq DGL \geq 0.1$). In a further embodiment the amount of glucose available is kept constant in a range between 50 % and 10 % ($0.5 \geq DGL \geq 0.1$). In another embodiment the amount of glucose available is kept constant in a range between 45 % and 20 % ($0.45 \geq DGL \geq 0.2$). In also an embodiment the amount of glucose available is kept between 80 % and 60 % ($0.8 \geq DGL \geq 0.6$).

In one embodiment the method comprises the step of cultivating the cell under conditions wherein the DGL is kept constant and at a value of about 0.4, whereby the cultivating comprises starting with a DGL between 1.0 and 0.5, lowering the DGL to a value of about 0.4, and keeping the DGL constant thereafter. In one embodiment the lowering of the DGL is within a time period of 100 hours. The term "keeping the DGL constant" and grammatical equivalents thereof denote that the DGL value is maintained during a time period, i.e. the variation of the DGL value is within 10 % of the value (see e.g. Figure 2).

The immunoglobulin is recovered after production, either directly or after disintegration of the cell. The recovered immunoglobulin is in one embodiment purified with a method known to a person skilled in the art. Different methods are well established and widespread used for protein purification, such as affinity chromatography with microbial proteins (e.g. protein A or protein G affinity chromatography), ion exchange chromatography (e.g. cation exchange (carboxymethyl resins), anion exchange (amino ethyl resins) and mixed-mode

exchange), thiophilic adsorption (e.g. with beta-mercaptoethanol and other SH ligands), hydrophobic interaction or aromatic adsorption chromatography (e.g. with phenyl-sepharose, aza-arenophilic resins, or m-aminophenylboronic acid), metal chelate affinity chromatography (e.g. with Ni(II)- and Cu(II)-affinity material), size exclusion chromatography, and electrophoretical methods (such as gel electrophoresis, capillary electrophoresis) (Vijayalakshmi, M.A., Appl. Biochem. Biotech. 75 (1998) 93-102).

For example, a purification process for immunoglobulins in general comprises a multistep chromatographic part. In the first step non-immunoglobulin polypeptides are separated from the immunoglobulin fraction by an affinity chromatography, e.g. with protein A or G. Afterwards, e.g., ion exchange chromatography can be performed to disunite the individual immunoglobulin classes and to remove traces of protein A, which has been coeluted from the first column. Finally a chromatographic step is employed to separate immunoglobulin monomers from multimers and fragments of the same class.

General chromatographic methods and their use are known to a person skilled in the art. See for example, Heftmann, E. (ed.), Chromatography, 5th edition, Part A: Fundamentals and Techniques, Elsevier Science Publishing Company, New York, (1992); Deyl, Z. (ed.), Advanced Chromatographic and Electromigration Methods in Biosciences, Elsevier Science BV, Amsterdam, The Netherlands, (1998); Poole, C. F. and Poole, S. K., Chromatography Today, Elsevier Science Publishing Company, New York (1991); Scopes, R.K., Protein Purification: Principles and Practice (1982); Sambrook, J., et al. (eds.), Molecular Cloning: A Laboratory Manual, Third Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001); or Ausubel, F. M., et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, Inc., New York (1990).

In one embodiment the recovered immunoglobulin is characterized by the amount of the immunoglobulin having a mannose-5 glycostructure with respect to the amount of a population, which is the sum of the amount of the immunoglobulin with a mannose-5 glycostructure, the immunoglobulin G(0) isoform, the immunoglobulin G(1) isoform, and the immunoglobulin G(2) isoform. With the method as reported herein the amount of the immunoglobulin with a mannose-5 glycostructure is in one embodiment 10 % or less of the population, in another embodiment 8 % or less of the population, and in a further embodiment 6 % or less of the population.

The method as reported herein can be performed in certain embodiments as continuous cultivation, as fed-batch cultivation, or as combination thereof, e.g. starting as fed-batch cultivation with subsequent crossover to a continuous cultivation. Additionally, the method as reported herein can be performed in different ways. For example, in one embodiment prior to the cultivating under conditions with a DGL value below 1.0, i.e. for example under conditions wherein the available amount of glucose is 80 % or less of the amount of glucose that can maximally be utilized by the cell in the culture per time unit, the cultivating is with an excess of glucose, i.e. a DGL value of 1.0. In another embodiment the cultivating is started with an amount of glucose as contained in standard culture media, e.g. between 1 and 10 g/l culture medium, e.g. in order to obtain a predefined cell density, e.g. in one embodiment of 10^5 cell/ml. In a further embodiment the starting of the cultivating is in the presence of an excess amount of glucose, i.e. a DGL of 1.0, and adding an amount of glucose per time unit, which is 80 % or less of the amount of glucose that can maximally be utilized per time unit by the cells in the cultivation. In another embodiment the feeding is started once the amount of glucose present in the culture medium has dropped to or below a preset value in the cultivation. In the last two cases the amount of glucose available in the culture is reduced by the metabolism of the cells in the cultivation.

In one embodiment the amount of glucose, which is available or added per time unit and which is less than the amount of glucose that can maximally be utilized, is kept at the same value, i.e. constant, in the method as reported herein. For example, if an amount of 50 % of the amount of glucose that can maximally be utilized per time unit is available, this amount is available in all time units of the method in which a restricted glucose feeding is performed. It has to be pointed out that this value is a relative value. Though, as the viable cell density changes during the cultivation (i.e. it increases in the beginning, reaches a maximum, and drops thereafter again) the absolute amount of available glucose changes accordingly as it is a relative value depending on the absolute viable cell density. As the relative value is kept constant (i.e. at e.g. 80 %) but the absolute reference value changes (i.e. e.g. increasing viable cell density) also the relative absolute value changes (i.e. 80 % of an increasing value are also increasing).

The term “per time unit” denotes a fixed time range, such as 1 minute, 1 hour, 6 hours, 12 hours, or 24 hours. In one embodiment the time unit is 12 hours or 24 hours. The term “amount of glucose available per time unit” as used within this application denotes the sum of 1) the amount of glucose contained in the

cultivation medium of a cultivation at the beginning of a fixed time range and 2) the amount of glucose added, i.e. fed, during the time unit. Thus, an amount of glucose is added to the cell cultivation medium, e.g. to the cultivation vessel, which increases the amount of glucose in the cultivation medium at the beginning of the fixed time range to the predetermined amount. This amount of glucose can be added, e.g., as solid, dissolved in water, dissolved in a buffer, or dissolved in a nutrient medium, whereby water and buffer shall not contain glucose. The amount of glucose to be added corresponds to the amount of glucose to be available reduced by the amount of glucose present in the medium in the cultivation vessel. The process of adding the amount of glucose can be performed either as single addition, as multiple addition of small, equal fractions, or as continuous addition during a time unit as described above.

The method as reported herein is suitable for any kind of cultivation and any cultivation scale. For example, in one embodiment the method is used for continuous or fed-batch processes; in another embodiment the cultivation volume is of from 100 ml up to 50,000 l, in another embodiment of from 100 l to 10,000 l. The method as reported herein is useful for the production of immunoglobulins with 10 % or less, or 8 % or less, or 6 % or less of the immunoglobulin having a mannose-5 glycostructure. In one embodiment the immunoglobulin is an immunoglobulin G or E. The method as reported herein comprises a eukaryotic cell, wherein the cell in turn comprises a nucleic acid encoding the heavy chain of an immunoglobulin or a fragment thereof and a nucleic acid encoding the light chain of an immunoglobulin or a fragment thereof. The eukaryotic cell is in one embodiment selected from CHO cells, NS0 cells, BHK cells, hybridoma cells, PER.C6® cells, Sp2/0 cells, HEK cells, and insect cells.

A person skilled in that art is familiar with medium compositions and components as well as nutrient concentrations required by different cells for optimal growth in addition to the amount of glucose and will choose an appropriate medium for the cultivation of the cell (see e.g. Mather, J.P., et al., in Encyclopedia of Bioprocess Technology: Fermentation, Biocatalysis, and Bioseparation, Vol. 2 (1999) 777-785).

In one embodiment the amount of glucose that has to be available to the cells in a cultivation according to the method as reported herein is calculated by multiplying the viable cell density, which can be achieved normally in the culture vessel at a certain point of time of the cultivation, with the volume of the culture vessel and

the amount of glucose that can maximally be utilized by the exponentially growing cells per time unit and by the intended DGL. In more detail, from the course of the glucose concentration in the cultivation and the course of the cell density in the cultivation prior to the actual point of time the future course of the glucose concentration and the cell density are predicted. With this prediction the amount of glucose that has to be added to the cultivation to achieve the intended DGL is calculated with the following formula:

(glucose to be added [pg glucose/ml/h]) =
(current cell density [cells/ml]) x
(maximum glucose consumption rate of the cell [pg glucose/cell/h]) x (DGL value) –
amount of glucose present in the medium in the cultivation vessel.

In one embodiment the pH value of the cultivation is between pH 6.5 and pH 7.8. In another embodiment the pH value is between pH 6.9 and pH 7.3. In a further embodiment the pH value is between pH 7.0 and 7.2. It has been found as outlined in Example 1 that in combination with a restricted glucose feeding with a pH value of 7.0 in the constant feeding method the M5 content can efficiently be regulated to defined values, i.e. below 8 %, compared to a pH value of 7.2. In the cultivations in the fed-batch method at pH values of 7.0 or 7.2, respectively, it was found that with the DGL control method the M5 content could be regulated to be less than 5.5 %. It has been found that with a reduction of the pH value of the cultivation an increase of the M5 amount due to the lowering of the DGL value can be traversed.

The cultivation is in one embodiment performed at a temperature between 27 °C and 39 °C, in another embodiment between 35 °C and 37.5 °C.

With the method as reported herein any polypeptide containing a glycostructure can be produced, such as immunoglobulins, interferons, cytokines, growth factors, hormones, plasminogen activator, erythropoietin and the like.

The cultivating in the method as reported herein can be performed using any stirred or shaken culture devices for mammalian cell cultivation, for example, a fermenter type tank cultivation device, an air lift type cultivation device, a culture flask type cultivation device, a spinner flask type cultivation device, a microcarrier type cultivation device, a fluidized bed type cultivation device, a hollow fiber type cultivation device, a roller bottle type cultivation device, or a packed bed type cultivation device.

The method as reported herein is performed in one embodiment for up to 15 days. In another embodiment the cultivating is for 6 to 15 days. In one embodiment the immunoglobulin is an anti-IL-6R antibody.

The method as reported herein is exemplified with an antibody to human interleukin-6 receptor as reported e.g. in EP 0 409 607, EP 0 628 639, US 5,670,373, or US 5,795,965 (herewith incorporated by reference in their entirety) as this antibody and the cell line expressing it were available at sufficient quantity in our laboratory at the time of the invention. This is not intended to restrict the scope of the invention.

The following examples and figures are available to aid the understanding of the present invention, the true scope of which is set forth in the appended claims. It is understood that modifications can be made in the procedures set forth without departing from the spirit of the invention.

Description of the Figures

Figure 1 Viable cell density (a) and cell viability profiles (b) in the fed-batch mode using the DGL control; open circle: initial cell density of 8×10^5 cells/ml; filled triangle: initial cell density of 10×10^5 cells/ml; open square: initial cell density of 12×10^5 cells/ml.

Figure 2 Time courses of DGL in the fed-batch mode in immunoglobulin production; circle: initial cell density of 8×10^5 cells/ml; triangle: initial cell density of 10×10^5 cells/ml; square: initial cell density of 12×10^5 cells/ml.

Figure 3 Feeding profiles based on DGL by the fed-batch mode in immunoglobulin production; circles: initial cell density of 8×10^5 cells/ml; triangle: initial cell density of 10×10^5 cells/ml; square: initial cell density of 12×10^5 cells/ml.

Figure 4 Immunoglobulin production profiles by the fed-batch mode in the DGL control; open circles: initial cell density of 8×10^5 cells/ml; filled triangle: initial cell density of 10×10^5 cells/ml; open square: initial cell density of 12×10^5 cells/ml; filled small circle: constant feeding method: FR = 0.02 g glucose/h (control)

Figure 5 Time curse of DGL during a fed-batch cultivation of a cell: diamond: single feed daily feeding, square: dual feed daily

feeding; triangle: single feed profile feeding; X: dual feed profile feeding.

Examples

Materials and Methods

Cell line:

An exemplary CHO cell line in which the amount of the mannose-5 glycostructure of a recombinantly produced immunoglobulin can be modified is a CHO cell line comprising a nucleic acid encoding an anti-IL-6 receptor antibody according to EP 0 409 607 and US 5,795,965. For the cultivation of the recombinant CHO cell any culture medium can be used as long a glucose supplementation according to the method of the invention can be performed. Exemplary culture media are IMDM, DMEM or Ham's F12 medium or combinations thereof, which have been adapted to the method as reported herein in as much as the mass ratios of the culture medium components to glucose are adopted. It is likewise possible to exclude glucose from the cultivation medium and add it to the cultivation separately.

Cultivation:

CHO cells expressing an anti-IL-6R antibody were cultivated in a 1 l or 2 l fermentation vessel. The feeding medium contained 15 to 40 g/l glucose. Glucose could be fed with a separate concentrated solution containing of e.g. 400 g/l glucose. The cultivation was performed at a pH value of in the range of from pH 7.0 to pH 7.2.

Determination of the glycostructure:

For the analysis of IgG glycosylation pattern a method according to Kondo et al. (Kondo, A., et al., Agric. Biol. Chem. 54 (1990) 2169-2170) was used. The IgG was purified from the centrifuged supernatant of the cultivation medium using a small scale protein A column. The oligosaccharide of the purified IgG was released using N-glycosidase F (Roche Diagnostics GmbH, Mannheim, Germany) and labeled with 2-amino pyridine at the reducing terminus. The labeled oligosaccharide was analyzed by reverse-phase chromatography (HPLC). Each peak was assigned by both mass spectrometry and standards for the oligosaccharides.

Glucose determination:
The glucose concentration was determined using an YSI 2700 SELECT™ analyzer (YSI, Yellow Springs, OH, USA) with a method according to the manufacturer's manual.

Viable cell density determination:
Viable Cell density was determined using an automatic image processing and analysis system (CEDEX®; Innovatis, Germany) and the trypan blue dye-exclusion method.

Example 1

Effects of the DGL control and pH on antibody production and mannose-5 glycostructure (M5) content

A test was conducted using a CHO cell strain producing humanized anti-human IL-6 receptor antibody (Tocilizumab, RoACTEMRA®), which was prepared in accordance with the method described in Referential Example 2 of Japanese Unexamined Patent Publication No. 99902/1996 by use of human elongation factor Iα promotor as reported in Example 10 of International Patent Application Publication No. WO 92/19759 (corresponding to US 5,795,965, US 5,817,790, and US 7,479,543).

In the constant absolute amount feeding method, effects of pH control on immunoglobulin production were observed. Table 2 shows the effects of pH control on antibody oligosaccharides production and M5 content in constant feeding mode.

Table 2: Effects of pH control in constant absolute amount feeding mode.

No.	Sample on [day]	pH set-point	DGL	Relative antibody concentration [%]	M5 content [%]
1	7	7.0	0.80-0.45	90.1	3.6
2	7	7.0	0.49-0.21	100	5.4
3	7	7.2	0.73-0.35	135.1	11.7
4	7	7.2	0.69-0.30	120	10.8
5	7	7.2	0.35-0.29	127	25.2
6	7	7.2	0.64-0.25	122.5	8.7

At pH 7.0 the amount of the mannose-5 glycostructure (M5) was regulated to less than 5.5 %. The DGL value declined from 0.80 to 0.21 due to the change of cell

density. On the other hand, at pH 7.2, the M5 amount fluctuated between 8.7 % and 25.2 % and was higher than that at pH 7.0. The DGL value at pH 7.2 varied from 0.73 to 0.25. Moreover, in this case, immunoglobulin production at pH 7.2 was more than 120 % (relative value compared to pH 7.0). Higher immunoglobulin production in the constant absolute amount feeding method induces a higher M5 content of more than 8 %. Therefore, with a pH 7.0 control in the constant absolute amount feeding method the M5 content could efficiently be regulated to lower values, i.e. below 8 %, compared to pH 7.2 control method.

The DGL control method (= constant relative amount feeding method) was also used for the immunoglobulin production by fed-batch mode at various pH values, and the M5 content was analyzed. Table 3 shows the effects of DGL control after the start of feeding at day 2-3 and pH on immunoglobulin production and M5 content.

Table 3: Effects of DGL and pH control in fed-batch mode.

No.	Sample on [day]	pH set-point	DGL	Relative antibody concentration [%]	M5 content [%]
1	7	7.0	0.8	102.7	2.9
2	7	7.0	0.6	96.2	2.7
3	7	7.0	0.4	100.0	3.3
4	7	7.0	0.3	91.1	3.9
5	7	7.0	0.2	83.0	4.0
6	7	7.2	0.6	100.9	4.4
7	7	7.2	0.4	90.1	5.3

At pH 7.0 the DGL control method was applied in the range of a DGL of from 0.2 to 0.8. As a result, the M5 content was regulated to be equal or less than 4.0 %. On the other hand, at pH 7.2, the DGL value was operated in the range of from 0.4 to 0.6. Here the M5 content could be controlled to be less than 5.5 %.

Example 2

Cultivating with different DGL values

The cultivating of a CHO cell comprising a nucleic acid encoding an anti-IL-6R antibody was performed with different DGL values. The results are summarized in the following Table 4.

Table 4: Effects of DGL control value on immunoglobulin production and M5 content.

No.	Sample on [day]	DGL	Relative antibody concentration [%]	M5 content [%]	G(0) content [%]	G(1) content [%]	G(2) content [%]
1	7	0.6-0.5	107.3	3.5	38.4	46.7	11.4
2	7	0.4	111.0	3.5	38.8	46.9	10.8
3	7	0.2	111.5	4.5	40.1	45.2	10.1
4	8	const. feeding	100.0	5.9	43.8	42.0	8.3

Compared to a constant feeding shows the controlled DGL strategy with a DGL value of 0.4 to 0.6 a reduced mannose-5 content.

Example 3

Cultivating with different feeding strategies

The cultivating of a CHO cell comprising a nucleic acid encoding an anti-IL-6R antibody was performed with one DGL value but with different feeding strategies. The results are summarized in the following Table 5.

Table 5: Effects of feed strategy on viability and viable cell density.

No.	Sample after [h]	DGL	feeding	adjustment	viability [%]	viable cell density [x10^6 cells/ml]
1	112	0.4	single	daily	71	5.1
2	115	0.4	dual	daily	75	5.8
3	115	0.4	single	profile	73	4.9
4	115	0.4	dual	profile	70	5.1

In the single feed experiments a single feed was used containing all nutrients and glucose. In the dual feed experiments two feeds were used: the first feed contains all nutrients and glucose at a low concentration of 15 g/l and the second feed contains a high concentration of glucose. These different feed experiments were performed in one set with a daily adjustment of the feeding rate and in another set following a predetermined profile based on the viable cell density development recorder in earlier cultivations. As can be seen from Table 5 viability and viable cell density are comparable independently of the employed feeding strategy.

Example 4

Degree of glucose limitation (DGL) control for immunoglobulin production by the fed-batch mode

CHO cells (8.0 – 12 x 10^5 cells/ml) were inoculated in serum free culture media as described above. The cells were grown at 37 °C, 98 % relative humidity, and 10 % CO_2 atmosphere. In the fed-batch cultivation the feeding medium containing glucose was started to be fed to the main fermenter on the 2nd or 3rd day from the beginning of the cultivation. The feeding strategy followed the method to control the degree of glucose limitation (DGL) according to U.S. Patent Application Publication No. US 2006/0127975 A1. The DGL can be defined as the ratio of the observed specific glucose consumption rate to the maximum known specific glucose consumption rate when glucose is freely available for these cells (DGL = $Q(glc)/Q(glc)_{max}$,where Q(glc) = currently observed specific glucose consumption rate; $Q(glc)_{max}$ = maximum known specific glucose consumption rate for these cells).

Figure 1 shows the viable cell density and cell viability profiles of the cultivation. The DGL was controlled to be at a value of 0.4 - 0.5 in various cell densities as shown in Figure 2. The feeding rates were changed once or twice a day depending on the cell density at that time. Figure 3 shows the feeding profiles based on DGL by the fed-batch mode. The feeding rate was changed between 0.8 and 1.6 ml/h depending on the cell density. With this feeding strategy applied, an immunoglobulin production profile was obtained as shown in Figure 4. Using the inoculation size of 10 x 10^5 cells/ml and 12 x 10^5 cells/ml, the immunoglobulin production was almost the same and more than 120 % of the immunoglobulin production in constant feeding method at day seven as shown in Table 6 (feeding rate of 0.02 g glucose/h). In spite of the 20 % difference in the initial cell densities, it was possible with the DGL control method to obtain approximately equivalent immunoglobulin titer. Moreover, when the inoculation size was set at 8.0 x 10^5 cells/ml, despite the 20 hour delay of the feeding start point, the immunoglobulin obtained was more than 110 % (relative value) at day seven. In these results, the DGL control method could achieve a stable immunoglobulin production at various inoculation sizes.

Example 5

The effects of the DGL control on the mannose-5 glycostructure and galactosylation of oligosaccharides

Of the immunoglobulin produced by fed-batch cultivation using the DGL control the glycosylation pattern was analyzed. Table 6 shows the result of the oligosaccharide analysis for the immunoglobulin obtained from the DGL controlled fed-batch cultivation in comparison with the constant feeding method (feeding rate: 0.02 g of glucose/h). At the inoculation size of 8.0 x 10^5 cells/ml, the content of mannose-5 glycostructure (M5) was 2.8 %. At the inoculation size of 10 x 10^5 cells/ml and 12 x 10^5 cells/ml, the M5 content was 4.1 % and 3.8 %, respectively. At all cultivation conditions, the DGL control method was able to regulate the M5 content to less than 5.0 %.

Meanwhile, in each condition, immunoglobulin G(0) isoform and immunoglobulin G(2) isoform were controlled at the range from 40 % to 46 % and from 9.0 % to 11 %, respectively.

Table 6: Effects of DGL control value on immunoglobulin production and glycosylation pattern.

No	Sample on [day]	DGL	inoculation cell density [x10^5 cells/ml]	relative antibody concen-tration [%]	M5 content [%]	G(0) content [%]	G(1) content [%]	G(2) content [%]
1	7	constant feeding	10	100.0	3.5	45.7	41.5	9.2
2	7	0.4	8	112.5	2.8	41.7	44.7	10.8
3	7	0.4	10	122.6	4.1	42.9	43.1	9.8
4	7	0.4	12	127.1	3.8	45.5	41.5	9.1

Patent Claims

1. Method for the production of an immunoglobulin comprising

   a) cultivating a eukaryotic cell comprising a nucleic acid encoding the immunoglobulin in a cultivation medium wherein the ratio of the current specific glucose consumption rate of a single cell in a cultivation medium to the maximum known specific glucose consumption rate of the kind of cell is kept constant, and
   b) recovering the immunoglobulin from the culture.

2. Method according to claim 1, characterized in that the ratio is of from 0.8 to 0.2.

3. Method according to claim 2, characterized in that the ratio is of from 0.6 to 0.4.

4. Method for the production of an immunoglobulin comprising

   a) cultivating a eukaryotic cell comprising a nucleic acid encoding the immunoglobulin in a cultivation medium wherein the amount of glucose available in the cultivation medium per time unit is kept constant and limited to a constant value of less than 80 % of the amount that could maximally be utilized by the cells in the cultivation medium per time unit, and
   b) recovering the immunoglobulin from the culture.

5. Method according to claim 4, characterized in that the constant value is less than 80 % and more than 20 %.

6. Method according to any one of the preceding claims, characterized in that the cultivating is a fed-batch cultivating.

7. Method according to claim 6, characterized in that the cultivating is a fed-batch cultivating wherein the feeding is started at day 2 or day 3 of the cultivating.

8. Method according to any one of the preceding claims, characterized in that the cultivating is at a pH value of from pH 6.5 to 7.5.

9. Method according to claim 8, characterized in that the cultivating is at a pH value of from pH 6.9 to 7.3.

10. Method according to claim 9, characterized in that the cultivating is at a pH value of from pH 6.95 to pH 7.05 or at a pH value of from pH 7.15 to pH 7.25.

11. Method according to any one of the preceding claims, characterized in that the immunoglobulin is an immunoglobulin of class G or class E.

12. Method according to any one of the preceding claims, characterized in that the eukaryotic host cell is selected from the group comprising CHO cells, NS0 cells, HEK cells, BHK cells, hybridoma cells, PER.C6® cells, insect cells, and Sp2/0 cells.

13. Method according to claim 12, characterized in that the eukaryotic cell is a Chinese Hamster Ovary (CHO) cell.

14. Method according to any one of the preceding claims, characterized in that cultivating the host cell is performed for six to twenty days.

15. Method according to any one of the preceding claims, characterized in that the immunoglobulin is an anti-IL-6R antibody.

16. Use of a method according to any one of claims 1 to 15 for decreasing the amount of an immunoglobulin with a mannose-5 glycostructure in an immunoglobulin preparation.

17. Composition comprising an immunoglobulin, characterized in that the composition has been prepared with a method according to any one of claims 1 to 15.

18. The composition according to claim 17, characterized in that the immunoglobulin is an anti-IL-6R antibody.

19. The composition according to claim 17, characterized in that the anti-IL-6R antibody comprises Tocilizumab.

20. The composition according to any one of claims 17 to 19, characterized in that the mannose-5 glycostructure attached to the anti-IL-6R antibody is 8 % or less.

21. The composition according to claim 20, characterized in that the mannose-5 glycostructure is 6 % or less.

22. The composition according to claim 21, characterized in that the mannose-5 glycostructure is 4 % or less.

23. The composition according to any one of claims 18 to 22, characterized in that the G(0) glycostructure attached to the anti-IL-6R antibody is in the range from 40 % to 46 % and the G(2) glycostructure attached to the anti-IL-6R antibody is in the range from 9 % to 11 %.