

Sialyltransferases for the production of 6'-sialyllactose

The present invention relates to sialyltransferases and their use in the production of sialylated oligosaccharides.

Background

5 More than 150 structurally distinct human milk oligosaccharides (HMOs) have been identified to date. Although HMOs represent only a minor amount of total human milk nutrients, their beneficial effects on the development of breast-fed infants became evident over the past decades.

10 Among the HMOs, sialylated HMOs (SHMOs) were observed to support the resistance of infants to enteropathogenic bacteria and viruses. Interestingly, recent studies further demonstrated a protective effect of long-chained SHMO against necrotizing enterocolitis, which is one of the most common and lethal diseases in preterm infants. In addition, SHMOs are believed to support an infant's brain development and its cognitive capabilities. Also, sialylated oligosaccharides have
15 been shown to neutralize enterotoxins of various pathogenic microbes including *Escherichia coli*, *Vibrio cholerae* and *Salmonella*. Further, it was found that sialylated oligosaccharides interfere with the colonization of the gut by *Helicobacter pylori* and can thereby prevent or inhibit gastric and duodenal ulcers.

20 Among the sialylated oligosaccharides in human milk, 3'-sialyllactose, 6'-sialyllactose, sialyllacto-*N*-tetraose a, sialyllacto-*N*-tetraose b, sialyllacto-*N*-tetraose c and disialyllacto-*N*-tetraose are the most prevalent members.

Since sialylated oligosaccharides have a complex structure, their chemical or (chemo-)enzymatic syntheses are challenging and associated with extensive difficulties, e.g. control of stereochemistry, formation of specific linkages, availability of
25 feedstocks, etc. As a consequence, commercially available sialylated oligosaccharides have been very expensive due to their low quantity in natural sources.

To overcome lack of commercial availability of SHMOS, efforts in metabolic engineering of microorganisms to produce sialylated oligosaccharides have been made, since this approach appears to be the most promising way for producing HMOs in an industrial scale.

- 5 Microbial fermentation uses genetically modified microorganisms which (over-) express at least one heterologous glycosyltransferase. Upon cultivation of such microorganisms in a medium and under conditions permissive for the microorganisms to express said heterologous glycosyltransferase, an HMO can be produced by said microorganisms and recovered from the culture medium or cell lysate.
- 10 However, glycosyltransferases, including sialyltransferases, typically use a broad spectrum of substrate such that their (over-)expression for the production of a desired oligosaccharide usually leads to undesired by-products. Typically, these by-products are oligosaccharides too, but have to be removed from the desired oligosaccharide preparation for the product's commercial use. However, removing
- 15 such by-products from the desired oligosaccharide might be difficult and cumbersome.

- Several sialyltransferases (SiaTs) from bacterial species have been identified and characterized to date, e. g. from *Neisseria*, *Campylobacter*, *Pasteurella*, *Helicobacter* and *Photobacterium*, as well as from mammals and viruses. Sialyltrans-
- 20 ferases have been generally classified into six glycosyltransferase (GT) families, based on protein sequence similarities. All eukaryotic and viral sialyltransferases are grouped into the GT family 29, whereas bacterial SiaTs are grouped into one the GT4, GT38, GT42, GT52 or GT80 family. Besides, sialyltransferases and polysialyltransferases can be distinguished due to the glycosidic linkages that they
- 25 form, e. g. into α -2,3-, α -2,6- and α -2,8-sialyltransferases. All these sialyltransferases transfer the sialic acid residue from cytidine 5'-monophosphate sialic acid (e. g. CMP-NeuNAc) to a variety of acceptor molecules, usually a galactose (Gal) moiety, an *N*-acetylgalactosamine (GalNAc) moiety or an *N*-acetylglucosamine (GlcNAc) moiety or another sialic acid (Sia) moiety.

Several bacterial α -2,6-sialyltransferases were well characterized in the past and are already proven to be suitable for the production of 6'-sialyllactose (6'-SL). The most commonly used enzymes for microbial 6'-SL production originate from marine bacteria: Pst-6 of *Photobacterium* sp. JT-ISH-224, St0160 of *Photobacterium*
5 *damselfae* JT0160, PlsT6 of *Photobacterium leiognathi* JT-SHIZ-119 and PlsT6 of *Photobacterium leiognathi* JT-SHIZ-145. However, these known bacterial α -2,6-sialyltransferases also produce disialyllactose as undesired by-product.

Drouillard *et al.* (Carbohydrate Research 345 (2010) 1394–1399) discloses the production of 6'-sialyllactose by an engineered *E. coli* cell which encodes for the
10 sialyltransferase gene of the marine bacterium *Photobacterium* sp. JT-ISH-224. Due to the promiscuity of this enzyme (broad acceptor/donor substrate acceptance) by-products such as 6,6'-disialyllactose and KDO-lactose are formed during cultivation. Only by downregulating the expression of the sialyltransferase gene, the
15 accumulation of these carbohydrate by-products can be restricted. However, downregulation of sialyltransferase gene expression is an undesired compromise since this limits the productivity of the production process as well as its industrial applicability.

Mehr and Withers (Glycobiology 26 (2016): 353-359) describe sialidase activity (de-sialylation/hydrolysis of a sialylated carbohydrate) and trans-sialidase activity
20 (transfer of a sialic acid residue from a sialylated carbohydrate to an acceptor substrate) of bacterial sialyltransferases from the glycosyltransferase family 80 using the representative α -2,6-sialyltransferases St0160 of *Photobacterium damselfae* JT0160 and Pst-6 of *Photobacterium* sp. JT-ISH-224. Considering the
25 sialyltransferases' desired application in processes for the production of a distinct sialylated product such as 6'-sialyllactose, enzymatic activities leading to product conversion and/or degradation are obviously counterproductive.

Prior art clearly discloses major limitations for the economic production of sialylated oligosaccharides such as 6'-sialyllactose in industrial scale. In particular, prior art
30 does not teach how to prevent formation of disialyllactose by a 6'-sialyllactose producing bacterial strain in a feasible manner.

It was therefore an object of the present invention to provide an improved method for the production of 6'-sialyllactose by microbial fermentation in an industrial scale, wherein concomitant formation of undesired by-products such as disialyllactose is prevented or at least significantly reduced.

5 Summary

The object is solved by the identification of α -2,6-sialyltransferases which exhibit low or no specificity for a sialyllactose as a substrate for sialylation reactions catalyzed by the enzyme, and the provision of their use in the production of 6'-sialyllactose. Hence, provided herein are, *inter alia*, enzymes, compositions, genetically
10 engineered cells, and methods for the production of 6'-sialyllactose.

According to a first aspect, provided are α -2,6-sialyltransferases for use in the production of 6'-sialyllactose, wherein said α -2,6-sialyltransferases are lactose-accepting α -2,6-sialyltransferases which comprises an amino acid sequence that is at least to 25 % identical over a stretch of at least 100 amino acids to one of the
15 amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2.

According to a second aspect, provided is a genetically engineered cell for the production of 6'-sialyllactose, wherein said cell has been genetically engineered to possess a lactose-accepting α -2,6-sialyltransferase which comprises an amino acid sequence that is at least to 25 % identical over a stretch of at least 100 amino acids
20 to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2.

According to a third aspect, provided is a method for the fermentative production of 6'-sialyllactose, the method comprises providing a genetically engineered cell for the production of 6'-sialyllactose, wherein said cell has been genetically engineered to possess a lactose-accepting α -2,6-sialyltransferase which comprises an amino acid
25 sequence that is at least to 25 % identical over a stretch of at least 100 amino acids to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2; cultivating said cell in a culture medium and under conditions

permissive for the production of 6'-sialyllactose; and optionally recovering said 6'-sialyllactose.

Brief description of the drawings

Fig. 1 shows the structural formula representing 6'-sialyllactose.

5 Fig. 2 shows the result of a thin layer chromatography indicating the carbohydrates detectable after a cultivation of an engineered *E. coli* strain (as described in example 2) encoding the sialyltransferase *pIsT6* (F). S: standard substance.

10 Fig. 3 displays the results of a thin layer chromatography from an exemplary in vitro assay illustrating sialyltransferase activity of various enzymes when providing CMP-NeuNAc as donor substrate and 20 mM lactose as acceptor substrate.

15 Fig. 4 displays the results of a thin layer chromatography from an exemplary in vitro assay illustrating sialyltransferase activity of various enzymes when providing CMP-NeuNAc as donor substrate and 20 mM 6'-SL as acceptor substrate.

20 Fig. 5 displays the results of a thin layer chromatography from an exemplary in vitro assay illustrating sialyltransferase activity of a sialyltransferase from *S. suis* when providing CMP-NeuNAc as donor substrate and 20 mM lactose or 20 mM 6'-SL as acceptor substrate.

Detailed description

According to the first aspect, α -2,6-sialyltransferases for the production of 6'-sialyllactose are provided.

25 The term "6'-sialyllactose" (6'-SL) as used herein refers to a trisaccharide, wherein said trisaccharide consists of the monosaccharide residues glucose (Glc), galactose (Gal) and *N*-acetylneuraminic acid/sialic acid (NeuNAc) to form a

compound possessing the chemical structure NeuNAc(α 2,6)Gal(β 1,4)Glc as shown in Fig. 1.

The term “sialyltransferase” as used herein refers to polypeptides being able to possess sialyltransferase activity. “Sialyltransferase activity” refers to the transfer of an *N*-acetylneuraminic acid (NeuNAc) residue from a donor substrate, typically 5 CMP-NeuNAc, to an acceptor molecule. The term “sialyltransferase” comprises functional fragments of the sialyltransferases described herein, functional variants of the sialyltransferases described herein, and functional fragments of the functional variants. “Functional” in this regard means that the fragments and/or variants 10 possess sialyltransferase activity. Functional fragments of a sialyltransferase encompass truncated versions of a sialyltransferase as encoded by its naturally occurring gene, which truncated version is capable of possessing sialyltransferase activity. Examples of truncated versions are sialyltransferases which do not comprise a so-called leader sequence which typically directs the polypeptide to a 15 specific subcellular localization. Typically, such leader sequence is removed from the polypeptide during its subcellular transport, and is absent in the naturally occurring mature sialyltransferase.

The α -2,6-sialyltransferase of the present disclosure is capable of transferring a *N*-acetylneuraminic acid residue from a donor substrate to an acceptor molecule. The 20 term “capable of” with respect to the heterologous sialyltransferase refers to the sialyltransferase activity of the heterologous sialyltransferase and the provision that suitable reaction conditions are required for the heterologous sialyltransferase to possess its enzymatic activity. In the absence of suitable reaction conditions, the heterologous sialyltransferase does not possess its enzymatic activity, but retains its 25 enzymatic activity and possesses its enzymatic activity when suitable reaction conditions are restored. Suitable reaction conditions include the presence of a suitable donor substrate, the presence of suitable acceptor molecules, the presence of essential cofactors such as – for example – monovalent or divalent ions, a pH value in an appropriate range, a suitable temperature and the like. It is not necessary 30 that the optimum values for each and every factor effecting the enzymatic reaction of the heterologous sialyltransferase is met, but the reaction

- conditions have to be such that the heterologous sialyltransferase performs its enzymatic activity. Accordingly, the term “capable of” excludes any conditions upon which the enzymatic activity of the heterologous sialyltransferase has been irreversibly impaired, and also excluded exposure of the heterologous
- 5 sialyltransferase to any such condition. Instead, “capable of” means that the sialyltransferase is enzymatically active, i.e. possesses its sialyltransferase activity, if permissive reactions conditions (where all requirements being necessary for the sialyltransferase to perform its enzymatic activity) are provided to the sialyltransferase.
- 10 Sialyltransferases can be distinguished on the type of glycosidic linkage they form. As used herein, the terms “ α -2,3-sialyltransferase” and “ α -2,3-sialyltransferase activity” refer to polypeptides and their enzymatic activity which add sialic acid with an alpha-2,3 linkage to galactose or a galactose residue of the acceptor molecule. Likewise, the terms “ α -2,6-sialyltransferase” and “ α -2,6-sialyltransferase activity”
- 15 refer to polypeptides and their enzymatic activity which add sialic acid with an alpha-2,6 linkage to galactose or a galactose residue of the acceptor molecule.

The α -2,6-sialyltransferase of the present disclosure is a lactose-accepting sialyltransferase. Hence, the disaccharide lactose is an acceptor substrate of the α -2,6-sialyltransferase for the transfer of a NeuNAc moiety from the donor substrate

20 CMP-NeuNAc.

The α -2,6-sialyltransferase of the present disclosure does not accept a sialyllactose, i.e. 3'-SL or 6'-SL, as substrate. More specifically, the α -2,6-sialyltransferase of the present disclosure neither accepts a sialyllactose as an acceptor substrate for the transfer of a NeuNAc moiety from CMP-NeuNAc as

25 donor substrate nor as a donor substrate for the transfer of the NeuNAc moiety from said sialyllactose to lactose as acceptor substrate as determined by *in vitro* sialylation reactions as described herein below in example 3. Hence, the α -2,6-sialyltransferase of the present disclosure is not able to catalyze formation of disialyllactose. Furthermore, the α -2,6-sialyltransferase of the present disclosure

30 does not possess trans-sialidase activity.

The α -2,6-sialyltransferase of the present disclosure comprises an amino acid sequence that is at least 25 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 over a stretch of at least 100 amino acids.

- 5 In some embodiments, the α -2,6-sialyltransferase comprises an amino acid sequence that is at least 30 %, at least 35 %, at least 40 %, at least 45 %, at least 50 %, at least 55 %, at least 60 %, at least 65 %, at least 70 %, at least 75 %, at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 98 %, or at least 99 % identical to one of the amino acid sequences as represented by SEQ ID No. 1
10 and SEQ ID No. 2 over a stretch of at least 100 amino acids.

The amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 were revealed from genomic databases that were searched for putative sialyltransferases. The amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 were found to be encoded by putative genes from *Streptococcus suis*.

- 15 In various embodiments, the α -2,6-sialyltransferase comprises a stretch of amino acids consisting of at least 100, at least 150, at least 200, at least 250 or at least 300 amino acids that is at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 98 %, at least 99 %, or 100 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2.
- 20 In an embodiment, the α -2,6-sialyltransferase comprises an amino acid sequence that is at least 98 %, 99 %, 99.1 %, 99.2 %, 99.3 %, 99.4 %, 99.5 %, 99.6 %, 99.7 %, 99.8 %, 99.9 %, or 100 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2.

- In some embodiments, the α -2,6-sialyltransferase comprises an amino acid
25 sequence as represented by SEQ ID No. 1 or SEQ ID No. 2.

The amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 were retrieved from genomic databases that were searched for putative sialyltransferases. The amino acid sequences as represented by SEQ ID No. 1 and SEQ ID

No. 2 were found to be encoded by nucleotide sequences that are present in the genome of the bacterial cells of the genus *Streptococcus suis*. Although said nucleotide sequences were not annotated at the time of their retrieval from the databases, they were annotated as putative sialyltransferases in the meantime.

- 5 However, annotation as putative sialyltransferase occurred without identification or classification of their enzymatic activities.

According to a second aspect, provided is a genetically engineered cell for the production of 6'-sialyllactose in the cell, wherein said cell possesses a lactose-accepting α -2,6-sialyltransferase as described herein before. In various embodiments, the cell has been genetically engineered to possess said lactose-accepting α -2,6-sialyltransferase.

- The term "genetically engineered" as used herein refers to the modification of the cell's genetic make-up using molecular biological methods. The modification of the cell's genetic make-up may include the transfer of genes within and/or across species boundaries, inserting, deleting, replacing and/or modifying nucleotides, triplets, genes, open reading frames, promoters, enhancers, terminators and other nucleotide sequences mediating and/or controlling gene expression. The modification of the cell's genetic make-up aims to generate a genetically modified organism possessing particular, desired properties. Genetically engineered cells can contain one or more genes that are not present in the native (not genetically engineered) form of the cell. Techniques for introducing exogenous nucleic acid molecules and/or inserting exogenous nucleic acid molecules (recombinant, heterologous) into a cell's hereditary information for inserting, deleting or altering the nucleotide sequence of a cell's genetic information are known to the skilled artisan.
- 25 Genetically engineered cells can contain one or more genes that are present in the native form of the cell, wherein said genes are modified and re-introduced into the cell by artificial means. The term "genetically engineered" also encompasses cells that contain a nucleic acid molecule being endogenous to the cell, and that has been modified without removing the nucleic acid molecule from the cell. Such
- 30 modifications include those obtained by gene replacement, site-specific mutations, and related techniques.

In some embodiments, the lactose-accepting α -2,6-sialyltransferase is a heterologous α -2,6-sialyltransferase.

The term "heterologous" as used herein refers to a polypeptide, amino acid sequence, nucleic acid molecule or nucleotide sequence that is foreign to a cell or organism, i.e. to a polypeptide, amino acid sequence, nucleic acid molecule or nucleotide sequence that does not naturally occurs in said cell or organism. A "heterologous sequence" or a "heterologous nucleic acid" or "heterologous polypeptide", as used herein, is one that originates from a source foreign to the particular host cell (e.g. from a different species), or, if from the same source, is modified from its original form. Thus, a heterologous nucleic acid operably linked to a promoter is from a source different from that from which the promoter was derived, or, if from the same source, is modified from its original form. The heterologous sequence may be stably introduced, e.g. by transfection, transformation, conjugation or transduction, into the genome of the host microbial host cell, thus representing a genetically modified host cell. Techniques may be applied which will depend on the host cell the sequence is to be introduced. Various techniques are known to a person skilled in the art and are, e.g., disclosed in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). Accordingly, a "heterologous polypeptide" is a polypeptide that does not naturally occur in the cell, and a "heterologous sialyltransferase" is a sialyltransferase that does not naturally occur in the cell.

The genetically engineered cell is a prokaryotic cell or a eukaryotic cell. Preferably, the genetically engineered cell is a microbial cell. Appropriate microbial cells include yeast cells, bacterial cells, archaeobacterial cells, algae cells, and fungal cells.

In an additional and/or alternative embodiment, the microbial cell is a prokaryotic cell, preferably a bacterial cell, more preferably a bacterial cell selected from the group consisting of *Bacillus*, *Lactobacillus*, *Lactococcus*, *Enterococcus*, *Bifidobacterium*, *Sporolactobacillus* spp., *Micromonospora* spp., *Micrococcus* spp., *Rhodococcus* spp., and *Pseudomonas*. Suitable bacterial species are *Bacillus subtilis*,

- Bacillus licheniformis*, *Bacillus coagulans*, *Bacillus thermophilus*, *Bacillus laterosporus*, *Bacillus megaterium*, *Bacillus mycoides*, *Bacillus pumilus*, *Bacillus lentus*, *Bacillus cereus*, *Bacillus circulans*, *Bifidobacterium longum*, *Bifidobacterium infantis*, *Bifidobacterium bifidum*, *Citrobacter freundii*, *Clostridium cellulolyticum*,
- 5 *Clostridium ljungdahlii*, *Clostridium autoethanogenum*, *Clostridium acetobutylicum*, *Corynebacterium glutamicum*, *Enterococcus faecium*, *Enterococcus thermophiles*, *Escherichia coli*, *Erwinia herbicola* (*Pantoea agglomerans*), *Lactobacillus acidophilus*, *Lactobacillus salivarius*, *Lactobacillus plantarum*, *Lactobacillus helveticus*, *Lactobacillus delbrueckii*, *Lactobacillus rhamnosus*, *Lactobacillus*
- 10 *bulgaricus*, *Lactobacillus crispatus*, *Lactobacillus gasseri*, *Lactobacillus casei*, *Lactobacillus reuteri*, *Lactobacillus jensenii*, *Lactococcus lactis*, *Pantoea citrea*, *Pectobacterium carotovorum*, *Propionibacterium freudenreichii*, *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Streptococcus thermophiles* and *Xanthomonas campestris*.
- 15 In an alternative embodiment, the eukaryotic cell is a yeast cell, an insect cell, a plant cell or a mammalian cell. The yeast cell is preferably selected from the group consisting of *Saccharomyces sp.*, in particular *Saccharomyces cerevisiae*, *Saccharomycopsis sp.*, *Pichia sp.*, in particular *Pichia pastoris*, *Hansenula sp.*, *Kluyveromyces sp.*, *Yarrowia sp.*, *Rhodotorula sp.*, and *Schizosaccharomyces sp.*
- 20 In an additional and/or alternative embodiment, the genetically engineered cell has been transformed to contain and express a nucleic acid molecule which comprises a nucleotide sequence which encodes lactose-accepting α -2,6-sialyltransferase as described herein before. In some embodiments, the nucleotide sequence is selected from the group consisting of
- 25 a) nucleotide sequences encoding a lactose accepting α -2,6-sialyltransferase which comprises an amino acid sequence that is at least 25 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 over a stretch of least 100 amino acids;
- b) nucleotide sequences encoding a polypeptide as represented by any one of
- 30 SEQ ID No's: 1 and 2;
- c) nucleotide sequences as represented by SEQ ID No. 3 and SEQ ID No. 4;

- d) nucleotide sequences which are complementary to any one of the nucleotide sequences set forth in a) to c); and
 - e) nucleotide sequences that hybridize to any one of the nucleotide sequences set forth in a) to d).
- 5 The term "hybridizing" as it is used herein means hybridizing under conventional conditions, as they are described in Sambrook et al. (Molecular Cloning. A laboratory manual, Cold Spring Harbor Laboratory Press, 2nd edition, 1989), preferably under stringent conditions. Stringent hybridization conditions are for example: hybridizing in 4 X SSC at 65 °C and subsequent multiple washing in 0.1 X
- 10 SSC at 65 °C for a total of 1 hour. Less stringent hybridization conditions are for example: hybridizing in 4 X SSC at 37 °C and subsequent multiple washing in 1 X SSC at room temperature. The term "stringent hybridization conditions" as used herein can also mean: hybridizing at 68 °C in 0.25 M sodium phosphate, pH 7.2, 7 % SDS, 1 mM EDTA and 1 % BSA for 16 hours and subsequent washing twice
- 15 with 2 X SSC and 0.1 % SDS at 68 °C.

In the genetically engineered cell, the nucleotide sequence that encodes the lactose-accepting α -2,6-sialyltransferase is operably linked to expression control sequences effecting transcription and/or translation of said nucleotide sequence encoding the lactose-accepting α -2,6-sialyltransferase in the genetically engineered

20 cell.

The term "operably linked" as used herein, refers to a functional linkage between the nucleotide sequence encoding the lactose-accepting α -2,6-sialyltransferase and a second nucleotide sequence, the nucleic acid expression control sequence (such as promoter, operator, enhancer, regulator, array of transcription factor binding sites,

25 transcriptional terminator, ribosome binding site), wherein the expression control sequence affects transcription and/or translation of the nucleic acid corresponding to the nucleotide sequence encoding the lactose-accepting α -2,6-sialyltransferase. Accordingly, the term "promoter" designates DNA sequences which usually "precede" a gene in a DNA polymer and provide a site for initiation of the

30 transcription into mRNA. "Regulator" DNA sequences, also usually "upstream" of (i.e., preceding) a gene in a given DNA polymer, bind proteins that determine the

frequency (or rate) of transcriptional initiation. Collectively referred to as "promoter/ regulator" or "control" DNA sequence, these sequences which precede a selected gene (or series of genes) in a functional DNA polymer cooperate to determine whether the transcription (and eventual expression) of a gene will occur. DNA sequences which "follow" a gene in a DNA polymer and provide a signal for termination of the transcription into mRNA are referred to as transcription "terminator" sequences.

In some embodiments, the genetically engineered cell possesses an increased production of one or more nucleotide-activated sugars selected from the group consisting of CMP-*N*-acetylneuraminic acid, UDP-*N*-acetylglucosamine, UDP-galactose and GDP-fucose. Preferably, the at least one genetically engineered cell has been genetically engineered to possess an increased production of one or more of said nucleotide-activated sugars. The production of the at least one of said nucleotide activated sugars is increased in the genetically engineered cell as compared to the production of the same nucleotide-activated sugar(s) in the cell prior to be genetically engineered to possess an increased production of at least one of said nucleotide-activated sugars.

In an additional and/or alternative embodiment, the cell has been genetically engineered to overexpress, as compared to the cell prior to be genetically engineered, one or more genes encoding for a polypeptide being capable of possessing an enzymatic activity selected from the group consisting of L-glutamine:D-fructose-6-phosphate aminotransferase, *N*-acetylglucosamine-1-phosphate uridylyltransferase, glucosamine-1-phosphate acetyl transferase, phosphoglucosamine mutase, glucosamine-6-phosphate-*N*-acetyltransferase, *N*-acetylglucosamine-2-epimerase, UDP-*N*-acetylglucosamine-2-epimerase, sialic acid synthase, phosphoenolpyruvate synthase, CMP-sialic acid synthase, UDP-galactose-4-epimerase, galactose-1-phosphate uridylyltransferase, phosphoglucomutase, glucose-1-phosphate uridylyltransferase, phosphomannomutase, mannose-1-phosphate guanosyltransferase, GDP-mannose-4,6-dehydratase, GDP-L-fucose synthase and fucosekinase/L-fucose-1-phosphate-guanylyltransferase.

Overexpression of one or more of said genes increases the amount of the corresponding enzyme(s) in the genetically engineered cell, and hence increases the corresponding enzymatic activity in the cell to enhance intracellular production of at least one of said nucleotide-activated sugars.

- 5 Preferably, said nucleotide sequences are operably linked to at least one nucleic acid expression control sequence effecting transcription and/or translation of said nucleotide sequences in the genetically engineered cell.

In an additional and/or alternative embodiment, the genetically engineered cell possesses a glutamine:fructose-6-phosphate aminotransferase (GlmS), preferably a
10 heterologous glutamine:fructose-6-phosphate aminotransferase, more preferably a glutamine:fructose-6-phosphate aminotransferase which is derived from *E. coli* (acc. no. NP_418185), or a functional variant of the *E. coli* GlmS. Most preferably, the functional variant is a version of the *E. coli* GlmS which shows significantly reduced sensitivity to glucosamine-6-phosphate inhibition as the wild-type enzyme does, as
15 example as encoded by the mutant *glmS* gene (Deng *et al.*, Metab Eng. 7 (2005): 201-214.).

The enzyme glutamine:fructose-6-phosphate aminotransferase (EC 2.6.1.16) catalyzes the conversion of fructose-6-phosphate to glucosamine-6-phosphate using glutamine. This enzymatic reaction is typically considered to be the first step in the
20 hexosamine biosynthesis pathway. Alternative names of the glutamine:fructose-6-phosphate aminotransferase are D-fructose-6-phosphate amidotransferase, GFAT, glucosamine-6-phosphate synthase, hexosephosphate aminotransferase, and L-glutamine–D-fructose-6-phosphate amidotransferase.

In an additional and/or alternative embodiment, the genetically engineered cell
25 comprises a glucosamine-6-phosphate *N*-acetyltransferase (Gna1), preferably a heterologous glucosamine-6-phosphate *N*-acetyltransferase, more preferably a glucosamine-6-phosphate *N*-acetyltransferase which is derived from *S. cerevisiae* (acc. no. NP_116637), or a functional variant of the *S. cerevisiae* Gna1. However, glucosamine-6-phosphate *N*-acetyltransferases, their deduced
30 amino acid sequences and the nucleotides sequences encoding these glucosa-

mine-6-phosphate *N*-acetyltransferases are known from a variety of different species, and may also be used as suitable glucosamine-6-phosphate *N*-acetyltransferases.

In an additional and/or alternative embodiment, the genetically engineered cell
5 expresses a *N*-acetylglucosamine-6-phosphate phosphatase, preferably a sugar
phosphatase of the HAD-like superfamily which catalyzes the conversion of *N*-
acetylglucosamine-6-phosphate (GlcNAc6P) to *N*-acetylglucosamine (GlcNAc). The
HAD-like superfamily is named after the bacterial enzyme haloacid dehydrogenase
and includes phosphatases. A suitable phosphatase of the HAD-like superfamily
10 catalyzing the conversion of GlcNAc6P to GlcNAc may be selected from the group
consisting of fructose-1-phosphate phosphatase (YqaB, acc. no. NP_417175) and
alpha-D-glucose 1-phosphate phosphatase (YihX, acc. no. NP_418321). The *E. coli*
YqaB and *E. coli* YihX enzymes are considered to also act on GlcNAc6P (Lee, S.-
W. and Oh, M.-K. (2015) *Metabolic Engineering* 28: 143-150). In an embodiment,
15 the sugar phosphatase of the HAD-like superfamily catalyzing the conversion of
GlcNAc-6-phosphate to GlcNAc is a heterologous enzyme in the genetically
engineered cell. In an additional and/or alternative embodiment, the sugar
phosphatase of the HAD-like superfamily catalyzing the conversion of GlcNAc6P to
GlcNAc is selected from the group consisting of *E. coli* YqaB, *E. coli* YihX, and
20 functional variants thereof.

In an additional and/or alternative embodiment, the genetically engineered cell
contains a nucleic acid molecule which comprises a nucleotide sequence encoding
a sugar phosphatase of the HAD-like superfamily catalyzing the conversion of
GlcNAc6P to GlcNAc. In an additional and/or alternative embodiment, the nucleotide
25 sequence encoding the sugar phosphatase of the HAD-like superfamily catalyzing
the conversion of GlcNAc6P to GlcNAc is a heterologous nucleotide sequence. In
an additional and/or alternative embodiment, the nucleotide sequence encoding the
sugar phosphatase of the HAD-like superfamily catalyzing the conversion of
GlcNAc6P to GlcNAc encodes the *E. coli* fructose-1-phosphate phosphatase or the
30 *E. coli* alpha-D-glucose 1-phosphate phosphatase or a functional fragment of one of
these two enzymes.

In an additional and/or alternative embodiment, the non-naturally-occurring cell has been genetically engineered to contain a nucleic acid molecule comprising a nucleotide sequence encoding a sugar phosphatase of the HAD-like superfamily catalyzing the conversion of GlcNAc6P to GlcNAc or a functional fragment of said
5 HAD phosphatase and/or to comprise a sugar phosphatase of the HAD-like superfamily catalyzing the conversion of GlcNAc6P to GlcNAc or functional variant thereof.

Nucleotide sequences encoding a suitable sugar phosphatase of the HAD-like superfamily catalyzing the conversion of GlcNAc6P to GlcNAc may be selected from
10 the group of nucleotide sequences encoding *E. coli* YqaB, *E. coli* YihX and functional variants thereof.

In an additional and/or alternative embodiment, the genetically engineered cell possesses a *N*-acetylglucosamine 2-epimerase, preferably the heterologous *N*-acetylglucosamine 2-epimerase Slr1975 of *Synechocystis* sp. PCC 6803 (acc. no.
15 BAL35720).

N-acetylglucosamine 2-epimerase (EC 5.1.3.8) is an enzyme that catalyzes the conversion of *N*-acetylglucosamine (GlcNAc) to *N*-acetylmannosamine (ManNAc). The enzyme is a racemase acting on carbohydrates and their derivatives. The systematic name of this enzyme class is *N*-acyl-D-glucosamine 2-epimerase. This
20 enzyme participates in amino-sugar metabolism and nucleotide-sugar metabolism.

In an additional and/or alternative embodiment, the genetically engineered cell comprises a sialic acid synthase or a functional variant thereof, preferably the heterologous sialic acid synthase NeuB of *Campylobacter jejuni* (acc. no. AF305571).

25 Sialic acid synthase or *N*-acetylneuraminate synthase or *N*-acetylneuraminic acid synthase (EC 2.5.1.56) is an enzyme that catalyzes the conversion of *N*-acetylmannosamine to *N*-acetylneuraminic acid using phosphoenolpyruvate (PEP). The *N*-acetylneuraminic acid synthase (NeuB) is encoded by the *neuB* gene.

In an additional and/or alternative embodiment, the genetically engineered cell synthesizes more PEP than the wildtype of the cell. In an additional and/or alternative embodiment, the genetically engineered cell has been genetically engineered to possess an enhanced PEP biosynthesis pathway. Preferably, the genetically engineered cell has been genetically engineered to possess an increased phosphoenolpyruvate synthase activity, for example in that the *ppsA* gene encoding the phosphoenolpyruvate synthase (acc. no. ACT43527) is overexpressed and/or in that the genetically engineered cell contains at least one additional copy of a nucleotide sequence allowing the expression of a phosphoenolpyruvate synthase or a functional variant thereof. Overexpression of *ppsA* enhances intracellular PEP synthesis such that more PEP is available for the production of sialic acid. For example, a suitable phosphoenolpyruvate synthase is PpsA of *E. coli*.

In an additional and/or alternative embodiment, the genetically engineered cell comprises a CMP-sialic acid synthetase or a functional variant thereof, preferably the heterologous CMP-sialic acid synthetase NeuA of *Campylobacter jejuni* (acc. no. AF305571).

Said CMP-sialic acid synthetase being overexpressed in the cell is capable of transferring a CMP residue onto sialic acid for generating CMP-activated sialic acid (CMP-Neu5Ac).

In an additional and/or alternative embodiment, the at least one genetically engineered cell lacks or possesses a decreased activity of one or more enzymatic activities selected from the group consisting of β -galactosidase activity, glucosamine-6-phosphate deaminase, *N*-acetylglucosamine-6-phosphate deacetylase, *N*-acetylmannosamine kinase, *N*-acetylmannosamine-6-phosphate epimerase and *N*-acetylneuraminic acid aldolase as compared to the cell prior to be genetically engineered.

In an additional and/or alternative embodiment, one or more of the genes encoding a β -galactosidase, a glucosamine-6-phosphate deaminase, a *N*-acetylglucosamine-6-phosphate deacetylase, a *N*-acetylmannosamine kinase, a *N*-acetylmanno-

samine-6-phosphate epimerase and a *N*-acetylneuraminic acid aldolase has/have been deleted from the genome of the genetically engineered cell or the expression of one or more of the genes encoding a β -galactosidase, a glucosamine-6-phosphate deaminase, a *N*-acetylglucosamine-6-phosphate deacetylase, a *N*-acetylmannosamine kinase, a *N*-acetylmannosamine-6-phosphate epimerase and a *N*-acetylneuraminic acid aldolase has/have been inactivated in the genetically engineered cell.

In an additional and/or alternative embodiment, the at least one genetically engineered cell comprises at least one polypeptide selected from the group consisting of a functional lactose permease, a functional fucose permease and a functional sialic acid transporter (importer), preferably comprises and expresses at least one nucleotide sequence encoding one selected from the group consisting of a functional lactose permease, a functional fucose permease and a functional sialic acid transporter (importer).

In an additional and/or alternative embodiment, the genetically engineered cell possesses activity of at least one glycosyltransferase selected from the group consisting of a β -1,3-*N*-acetylglucosaminyltransferase, a β -1,3-galactosyltransferase, a β -1,4-galactosyltransferase, a α -2,3-sialyltransferase and a α -2,6-sialyltransferase.

According to a third aspect, provided is a method for the production of 6'-sialyllactose in a cell, wherein the method comprises

- providing a genetically engineered cell for the production of 6'-sialyllactose, wherein said cell has been genetically engineered to possess a lactose-accepting α -2,6-sialyltransferase as described herein before, i.e. a lactose-accepting α -2,6-sialyltransferase which comprises an amino acid sequence that is at least to 25 % identical over a stretch of at least 100 amino acids to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2;
- cultivating said cell in a culture medium and under conditions permissive for the production of 6'-sialyllactose; and
- optionally recovering said 6'-sialyllactose

For the production of 6'-sialyllactose, the at least one genetically engineered cell is cultivated in a culture medium and under conditions that is/are permissive for the production of 6'-sialyllactose in said cell.

The culture medium contains at least one carbon source for the genetically engineered cells. The at least one carbon source is preferably selected from the group consisting of glucose, fructose, sucrose, glycerol, and combinations thereof.

In an additional and/or alternative embodiment, the culture medium contains at least one selected from the group consisting of galactose, lactose and sialic acid.

The method comprises the step of recovering 6'-sialyllactose that has been produced in/by the at least one genetically engineered cell during its cultivation in the culture medium. The 6'-sialyllactose can be recovered from the fermentation broth after the genetically engineered cell(s) has/have been removed, for example by centrifugation, and/or can be recovered from the cells, for example in that the cells are harvested from the fermentation broth by centrifugation, and are subjected to a cell lysis step. Subsequently, 6'-SL can be further purified from culture medium and/or cell lysates by suitable techniques known to the skilled artisan. Suitable techniques include microfiltration, ultrafiltration, diafiltration, simulated moving bed type chromatograph, electrodialysis, reverse osmosis, gel filtration, anion exchange chromatography, cation exchange chromatography, and the like.

The present invention will be described with respect to particular embodiments and with reference to drawings, but the invention is not limited thereto but only by the claims. Furthermore, the terms first, second and the like in the description and in the claims, are used for distinguishing between similar elements and not necessarily for describing a sequence, either temporally, spatially, in ranking or in any other manner. It is to be understood that the terms so used are interchangeable under appropriate circumstances and that the embodiments of the invention described herein are capable of operation in other sequences than described or illustrated herein.

It is to be noticed that the term “comprising”, used in the claims, should not be interpreted as being restricted to the means listed thereafter; it does not exclude other elements or steps. It is thus to be interpreted as specifying the presence of the stated features, integers, steps or components as referred to, but does not preclude
5 the presence or addition of one or more other features, integers, steps or components, or groups thereof. Thus, the scope of the expression “a device comprising means A and B” should not be limited to devices consisting only of components A and B. It means that with respect to the present invention, the only relevant components of the device are A and B.

10 Reference throughout this specification to “one embodiment” or “an embodiment” means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, appearances of the phrases “in one embodiment” or “in an
15 embodiment” in various places throughout this specification are not necessarily all referring to the same embodiment, but may. Furthermore, the particular features, structures or characteristics may be combined in any suitable manner, as would be apparent to one of ordinary skill in the art from this disclosure, in one or more embodiments.

Similarly, it should be appreciated that in the description of exemplary embodiments
20 of the invention, various features of the invention are sometimes grouped together in a single embodiment, figure, or description thereof for the purpose of streamlining the disclosure and aiding in the understanding of one or more of the various inventive aspects. This method of disclosure, however, is not to be interpreted as reflecting an intention that the claimed invention requires more features than are
25 expressly recited in each claim. Rather, as the following claims reflect, inventive aspects lie in less than all features of a single foregoing disclosed embodiment. Thus, the claims following the detailed description are hereby expressly incorporated into this detailed description, with each claim standing on its own as a separate embodiment of this invention.

30 Furthermore, while some embodiments described herein include some but not other features included in other embodiments, combinations of features of different embodiments are meant to be within the scope of the invention, and form different

embodiments, as would be understood by those in the art. For example, in the following claims, any of the claimed embodiments can be used in any combination.

Furthermore, some of the embodiments are described herein as a method or combination of elements of a method that can be implemented by a processor of a computer system or by other means of carrying out the function. Thus, a processor
5 with the necessary instructions for carrying out such a method or element of a method forms a means for carrying out the method or element of a method. Furthermore, an element described herein of an apparatus embodiment is an example of a means for carrying out the function performed by the element for the
10 purpose of carrying out the invention.

In the description and drawings provided herein, numerous specific details are set forth. However, it is understood that embodiments of the invention may be practiced without these specific details. In other instances, well-known methods, structures and techniques have not been shown in detail in order not to obscure an
15 understanding of this description.

The invention will now be described by a detailed description of several embodiments of the invention. It is clear that other embodiments of the invention can be configured according to the knowledge of persons skilled in the art without departing from the true spirit or technical teaching of the invention, the invention being limited
20 only by the terms of the appended claims.

Example 1: Identification of α -2,6-sialyltransferases

Gene sequences of characterized or putative sialyltransferases were received from the literature and public databases. In addition, sequence similarity searches were conducted by using the amino acid sequences of known sialyltransferases as
25 template sequences. Protein coding nucleotide sequences were synthesized by GenScript cooperation either, as annotated, in a full-length form or, when a signal peptide is predicted, as a truncated variant lacking the N-terminal signal peptide.

Proper software tools enabling the identification of putative signal peptides are known to the skilled artisan.

The sialyltransferases were either subcloned as an operon with *neuA* into pDEST14 by SLIC using gene specific primers, yielding plasmids of the general kind:

- 5 pDEST14-*siaT-neuA*, or were directly subcloned by GenScript cooperation into plasmid pET11a using restriction sites *NdeI* and *BamHI*. Both expression systems allow the IPTG-inducible gene expression. For *in vivo* activity screenings, the plasmids were transformed into *E. coli* strains, either capable of *de novo* synthesis of sialic acid or in a strain encoding for a sialic acid importer (e.g. *E. coli nanT*) as
10 well as a CMP-sialic acid synthetase (e.g. *C. jejuni neuA*). For *in vitro* assays an *E. coli* BL21(DE3) wild type or a *lacZ*-lacking variant thereof was used.

The activities of the screened enzymes were determined by product identification using thin layer chromatography and/or mass spectrometry analysis.

- Samples analysed by thin layer chromatography (TLC) were applied on Silica Gel
15 60 F₂₅₄ (Merck KGaA, Darmstadt, Germany). A mixture of butanol:acetone:acetic acid:H₂O (35/35/7/23 (v/v/v/v)) was used as mobile phase. For detection of the separated substances, the TLC plate was soaked with thymol reagent (0.5 g thymol solved in 95 ml ethanol, 5 ml sulfuric acid added) and heated.

- Mass spectrometry analysis was performed by MRM (multiple reaction monitoring)
20 using a LC Triple-Quadrupole MS detection system. Precursor ions are selected and analyzed in quadrupole 1, fragmentation takes place in the collision cell using argon as CID gas, selection of fragment ions is performed in quadrupole 3.

- Chromatographic separation of carbohydrates was performed on a XBridge Amide HPLC column (3.5 µm, 2.1 x 50 mm (Waters, USA) with a XBridge Amide guard
25 cartridge (3.5 µm, 2.1 x 10 mm) (Waters, USA). Column oven temperature of the HPLC system was 50°C. The mobile phase was composed of acetonitrile:H₂O with 10 mM ammonium acetate. A 1 µl sample was injected into the instrument; the run was performed for 3.60 min with a flow rate of 400 µl/min. Carbohydrates were analyzed by MRM in ESI positive ionization mode. Lactose forms an ion of m/z

341.00 [M-H]. The precursor ion of lactose was further fragmented in the collision cell into the fragment ions m/z 179.15, m/z 161.15 and m/z 101.05.

Organism	Acc. No.	GT family
<i>Photobacterium</i> sp.	BAF92026	GT80
<i>Photobacterium damsela</i>	BAA25316	GT80
<i>Photobacterium leiognathi</i>	BAI49484	GT80
<i>Photobacterium leiognathi</i>	BAF91416	GT80
<i>Streptococcus suis</i>	AGL48117	GT52
<i>Streptococcus suis</i>	EEF64774	GT52
<i>Photobacterium phosphoreum</i>	CDN97322	GT80
<i>Alistipes timonensis</i>	WP_026020701	GT80
<i>Haemophilus parasuis</i>	KEZ22922	GT52
<i>Acinetobacter pittii</i>	EOQ74854	GT52
<i>Porphyromonas</i> sp.	KGO00880	GT52
<i>Photobacterium damsela</i>	WP_005298232	GT80
<i>Pasteurella multocida</i>	EGP04633	GT80
<i>Actinobacillus ureae</i>	WP_005624339	GT52
<i>Actinobacillus equuli</i>	WP_039196193	GT52
<i>Acinetobacter calcoaceticus</i>	WP_017391462	GT52
<i>Acinetobacter baumannii</i>	WP_032039596	GT52
<i>Acinetobacter oleivorans</i>	WP_042898369	GT52
<i>Acinetobacter baumannii</i>	ELX04805	GT52
<i>Acinetobacter gyllenbergii</i>	WP_032865812	GT52
<i>Shigella boydii</i>	ACD37071	GT52
<i>Kingella kingae</i>	WP_026036248	GT52
<i>Alysiella crassa</i>	WP_034294366	GT52
<i>Alistipes</i> sp.	EFR56292	GT80
<i>Streptococcus suis</i>	WP_024397787	GT52
<i>Fusobacterium mortiferum</i>	EEO36694	GT52
<i>Porphyromonas catoniae</i>	WP_005467220	GT52

Table 1: Enzymes with proven α -2,6-sialyltransferase activity (GT: glycosyltransferase; AA: amino acid; NA: nucleic acid)

Sialyllactose forms an ion of m/z 656.2 $[M+Na]$. The precursor ion of sialyllactose was further fragmented in the collision cell into the fragment ions m/z 612.15, m/z 365.15 and m/z 314.15. Disialyllactose forms an ion of m/z 942.4 $[M+H+NH_3]$. The precursor ion of disialyllactose was further fragmented in the collision cell into the
 5 fragment ions m/z 292.30, m/z 274.30 and m/z 634.05. Collision energy, Q1 and Q3 Pre Bias were optimized for each analyte individually.

For all enzymes listed in Table 1, the formation of 6'-SL could be verified when expressed and/or assayed in the presence of lactose.

Example 2: Fermentative production of 6'-SL using an engineered *E. coli* strain encoding for the α -2,6-sialyltransferase *plsT6* of *Photobacterium leiognathi*
 10

A 6'-sialyllactose fed-batch fermentation was conducted employing a recombinant 6'-sialyllactose synthesizing *E. coli* strain (*E. coli* BL21(DE3) $\Delta lacZ$), containing a genomic integration of a α -2,6-sialyltransferase gene from *Photobacterium leiognathi* (acc. No. BA149484). To enable/enhance the biosynthesis of CMP-sialic acid,
 15 genes encoding the glucosamine-6-phosphate synthase GlnS from *E. coli*, the *N*-acetylglucosamine-2-epimerase Slr1975 from *Synechocystis sp.*, the glucosamine 6-phosphat *N*-acetyltransferase Gna1 from *Saccharomyces cerevisiae*, the phosphoenolpyruvat synthase PpsA from *E. coli*, the *N*-acetylneuraminate synthase
 20 NeuB and the CMP-sialic acid synthetase NeuA, the latter both from *Campylobacter jejuni*, were chromosomally integrated into the *E. coli* BL21(DE3) host. Furthermore, the gene encoding the lactose permease LacY from *E. coli*, and the genes *cscB* (sucrose permease), *cscK* (fructokinase), *cscA* (sucrose hydrolase), and *cscR* (transcriptional regulator) from *E. coli* W were integrated into the BL21 genome.
 25 Transcription of integrated genes is initiated from constitutive promoters, either the tetracycline promotor Ptet or the PT5 promotor. A functional *gal*-operon, consisting of the genes *galE* (UDP-glucose-4-epimerase), *galT* (galactose-1-phosphate uridylyltransferase), *galK* (galactokinase), and *galM*

(galactose-1-epimerase) was transferred from *E. coli* K12 to the genome of the BL21 strain.

To prevent degradation of *N*-acetylglucosamine 6-phosphate genes coding for the *N*-acetylglucosamine-6-phosphate deacetylase (NagA), the glucosamine-6-phosphate deaminase (NagB), and the *N*-acetylglucosamine specific PTS protein IIABC (NagE) were deleted from the chromosome. Additionally, the operon *manXYZ*, encoding a sugar transporter of the *E. coli* PTS system for mannose, glucose, glucosamine and *N*-acetylglucosamine was deleted, as well as the genes *nanA*, *nanK*, *nanE*, and *nanT*, encoding the *N*-acetylneuraminate lyase, the *N*-acetylmannosamine kinase, the *N*-acetylmannosamine-6-phosphate epimerase, and the sialic acid transporter, respectively. The gene encoding the *N*-acetylgalactosamine-6-phosphate deacetylase (AgaA) was also deleted.

For the fermentative production of 6'-sialyllactose, the strain was grown in a defined mineral salts medium, comprising 7 g l⁻¹ NH₄H₂PO₄, 7 g l⁻¹ K₂HPO₄, 2 g l⁻¹ KOH, 0.3g l⁻¹ citric acid, 5 g l⁻¹ NH₄Cl, 1 ml l⁻¹ antifoam (Struktol J673, Schill + Seilacher), 0.1 mM CaCl₂, 8 mM MgSO₄, trace-elements (0.101 g l⁻¹ nitrilotriacetic acid, pH 6.5, 0.056 g l⁻¹ ammonium ferric citrate, 0.01 g l⁻¹ MnCl₂ x 4 H₂O, 0.002 g l⁻¹ CoCl₂ x 6 H₂O, 0.001g l⁻¹ CuCl₂ x 2 H₂O, 0.002 g l⁻¹ boric acid, 0.009 g l⁻¹ ZnSO₄ x 7 H₂O, 0.001 g l⁻¹ Na₂MoO₄ x 2 H₂O, 0.002 g l⁻¹ Na₂SeO₃, 0.002 g l⁻¹ NiSO₄ x 6 H₂O) and 2 % sucrose as carbon source.

The sucrose feed (500 g l⁻¹) was supplemented with 8 mM MgSO₄, 0.1 mM CaCl₂, trace elements, and 5 g l⁻¹ NH₄Cl. For 6'-sialyllactose formation, a lactose feed of 216 g l⁻¹ was employed. The pH was controlled by using ammonia solution (25 % v/v). Fed batch fermentation was conducted at 30 °C under constant aeration and agitation for 72 hours by applying a sucrose feeding rate of 5.5 - 7 mL L⁻¹ h⁻¹, referring to the starting volume. Lactose that was not converted into 6'-sialyllactose at the end of the production process was degraded by addition of β-galactosidase and monosaccharides from hydrolysis of lactose were metabolized by the production strain. Substantial amounts of 6'-SL were excreted by the bacterial cells into the culture supernatant. However, in addition, a disialyllactose was formed (Figure 2), which could be verified by mass spectrometry analysis as well as thin layer

chromatography. The ratio of 6'-Di-SL to 6'-SL in the culture broth, determined by HPLC, was approximately 8 %.

High-performance liquid chromatography (HPLC) analysis, using a refractive index detector (RID-10A) (Shimadzu, Germany) and a Waters XBridge Amide Column 3.5µm (250 x 4.6mm) (Eschborn, Germany) connected to an HPLC system (Shimadzu, Germany), was conducted to estimate the ratio of 6'-disialyllactose to 6'-sialyllactose within the fermentation broth. Elution was performed isocratically with 71 % (v/v) ACN in ddH₂O (adjusted to pH 4.2 with acetic acid) at 35 °C and at a flow rate of 1.4 ml·min⁻¹. HPLC samples were sterile filtered (0.22 µm pore size) and heated to 80 °C for 5 minutes prior to injection. 10 µl of the samples were applied to the column. The retention times of 6'-SL and 6'-Di-SL were determined by applying purified standards. The ratio of 6'-Di-SL to 6'-SL can be determined by building the quotient of the AUC (area under the curve) of the corresponding peaks in the chromatogram.

Example 3: Novel α -2,6-sialyltransferases for the production of 6'-sialyllactose

Sialyltransferases originating from *Streptococcus suis* demonstrated a good sialyltransferase activity when using galactosides (e.g. galactose or lactose) as acceptor substrates, thus, revealing an alternative to α -2,6-sialyltransferases originating from marine bacteria. No annotated/putative *S. suis* sialyltransferase has ever before been characterized as a lactose accepting enzyme, thus, no *S. suis* sialyltransferase has been applied for 6'-SL production so far.

For an in-depth characterization, *in vitro* enzyme assays were conducted. Therefore, *Escherichia coli* BL21(DE3) harbouring plasmids encoding the sialyltransferases were grown at 30 °C in 100 ml shake flasks filled with 20 ml of 2YT medium supplemented with ampicillin 100 µg ml⁻¹. When the cultures reached an OD₆₀₀ of 0.1 to 0.3, gene expression was induced by addition of 0.3 mM IPTG and the incubation was continued for 12 to 16 hours. Cells were harvested by centrifugation and mechanically disrupted in a defined volume of 50 mM Tris-HCl pH7.5 using glass beads. The protein extract was kept on ice until the assay started.

Protein name	Organism	Acc. No.	Identity with Pst-6 [%]	Sialyltransferase activity on different acceptor substrates		
				Lactose	6'-SL	3'-SL
Pst-6	<i>Photobacterium sp.</i>	BAF92026	-	+++	+	+
St0160	<i>Photobacterium damsela</i>	BAA25316	39,6	+++	+	+
PlsT6	<i>Photobacterium leiognathi</i>	BAI49484	54,2	+++	+	+
PlsT6	<i>Photobacterium leiognathi</i>	BAF91416	52,3	+++	+	+
Cpa16Q	<i>Streptococcus suis</i>	AGL48117	12,2	++	-	-
Cps1O	<i>Streptococcus suis</i>	EEF64774	13,5	++	-	-

Table 2: Summary of candidate α -2,6-sialyltransferases tested for their ability to accept different carbohydrates for sialylation during *in vivo* and/or *in vitro* assays. The activity of each sialyltransferase was semi-quantitatively compared, separately for each acceptor substrate, to Pst-6.

For determining their sialyltransferase properties, the *in vitro* assays were carried out in a total volume of 25 μ l including 50 mM Tris-HCl pH7.5, 5 mM MgCl₂, 10 mM CMP-Neu5Ac and varying concentrations of acceptor substrates such as lactose, 3'-SL or 6'-SL. The assay started with the addition of 3 μ l protein extract and continued for up to 16 hours. Product formation was determined by thin layer chromatography and was verified by mass spectrometry. Exemplary results of these *in vitro* assays are depicted in FIG. 3, 4 and 5. Whereas *Photobacterium* α -2,6-sialyltransferases are capable to convert lactose as well as 6'-SL to 6'-SL and Di-SL, respectively, the *Streptococcus suis* enzyme solely demonstrates detectable α -2,6-sialyltransferase activity when lactose is provided as acceptor substrate. The summarized results can be found in Table 2. Surprisingly, neither of the *S. suis* sialyltransferases was capable of disialyllactose formation.

For the determination of a sialidase/trans-sialidase activity, the *in vitro* assays were carried out in a total volume of 25 μ l including 50 mM Tris-HCl pH7.5, 5 mM MgCl₂

- and varying concentrations of 3'-SL or 6'-SL. The assay started with the addition of 3 μ l protein extract and continued for up to 16 hours. Lactose and/or disialyllactose formation was determined by thin layer chromatography and/or mass spectrometry. In contrast to the sialyltransferases originating from marine bacteria, neither of the
- 5 *S. suis* sialyltransferases was capable of converting 3'-SL and/or 6'-SL to lactose and/or disialyllactose (Table 3).

Protein name	Organism	Acc. No.	Sialidase/Trans-sialidase activity
Pst-6	<i>Photobacterium sp.</i>	BAF92026	+
St0160	<i>Photobacterium damsela</i>	BAA25316	+
PlsT6	<i>Photobacterium leiognathi</i>	BAI49484	+
PlsT6	<i>Photobacterium leiognathi</i>	BAF91416	+
Cps16Q	<i>Streptococcus suis</i>	AGL48117	-
Cps1O	<i>Streptococcus suis</i>	EEF64774	-

Table 3: Summary of candidate α -2,6-sialyltransferases tested for their sialidase/trans-sialidase activity during *in vitro* assays. The activity of each enzyme was semi-quantitatively compared to Pst-6.

10 **Example 4: Fermentative production of 6'-SL using an engineered *E. coli* strain encoding for the α -2,6-sialyltransferase *cps16Q* of *Streptococcus suis***

- An *E. coli* strain, metabolically engineered as described in example 2 but containing a genomic integration of the α -2,6-sialyltransferase gene from *Streptococcus suis*
- 15 (acc. No. AGL48117), was applied to a fed-batch fermentation. The cultivation conditions are described in example 2. After discontinuation of the cultivation, substantial amounts of 6'-SL, comparable to the process described in example 2, were detectable in the culture supernatant but no disialyllactose.

CLAIMS

1. A α -2,6-sialyltransferase for use in the production of 6'-sialyllactose, wherein said α -2,6-sialyltransferase is a lactose-accepting α -2,6-sialyltransferase which comprises an amino acid sequence that is at least to 25 % identical
5 over a stretch of at least 100 amino acids to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2.
2. The α -2,6-sialyltransferases according to claim 1, wherein the α -2,6-sialyltransferases comprises an amino acid sequence that is at least 30 %, at least 35 %, at least 40 %, at least 45 %, at least 50 %, at least 55 %, at least 60 %, 10 at least 65 %, at least 70 %, at least 75 %, at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 98 %, or at least 99 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 over a stretch of least 100, least 150, at least 200, at least 250 or at least 300 amino acids.
- 15 3. The α -2,6-sialyltransferases according to claim 1 or, wherein the α -2,6-sialyltransferase comprises an amino acid sequence as represented by SEQ ID No. 1 or SEQ ID No. 2.
4. A genetically engineered cell for the production of 6'-sialyllactose, wherein said cell has been genetically engineered to possess a lactose-accepting α -
20 2,6-sialyltransferase which comprises an amino acid sequence that is at least to 25 % identical over a stretch of at least 100 amino acids to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2.
5. The genetically engineered cell according to claim 4, wherein the cell is selected from the group consisting of prokaryotic cells and eukaryotic cells,
25 preferably from the group consisting of yeast cells, bacterial cells, archaeobacterial cells, algae cells, and fungal cells.
6. The genetically engineered cell according to claim 4 or 5, wherein the α -2,6-sialyltransferases comprises an amino acid sequence that is at least 30 %, at least 35 %, at least 40 %, at least 45 %, at least 50 %, at least 55 %, at least

- 60 %, at least 65 %, at least 70 %, at least 75 %, at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 98 %, or at least 99 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 over a stretch of least 100, least 150, at least 200, at least 250 or at least 300 amino acids.
- 5
7. The genetically engineered cell according to any one of claims 4 to 6, wherein the α -2,6-sialyltransferase comprises an amino acid sequence as represented by SEQ ID No. 1 or SEQ ID No. 2.
8. The genetically engineered cell according to any one of claims 4 to 7, wherein the cell contains a nucleic acid molecule which comprises a nucleotide sequence which encodes lactose-accepting α -2,6-sialyltransferase as describe herein before. In some embodiments, the nucleotide sequence is selected from the group consisting of
- 10
- a) nucleotide sequences encoding a lactose accepting α -2,6-sialyltransferase which comprises an amino acid sequence that is at least 25 % identical to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2 over a stretch of least 100 amino acids;
- 15
- b) nucleotide sequences encoding a polypeptide as represented by any one of SEQ ID No's: 1 and 2;
- 20
- c) nucleotide sequences as represented by SEQ ID No. 3 and SEQ ID No. 4;
- d) nucleotide sequences which are complementary to any one of the nucleotide sequences set forth in a) to c); and
- 25
- e) nucleotide sequences that hybridize to any one of the nucleotide sequences set forth in a) to d) under stringent conditions.
9. A method for producing 6'-sialyllactose in a cell, the method comprises
- providing a genetically engineered cell for the production of 6'-sialyllactose, wherein said cell has been genetically engineered to possess a lactose-accepting α -2,6-sialyltransferase which comprises an amino acid sequence that is at least to 25 % identical over a stretch of at least 100
- 30

amino acids to one of the amino acid sequences as represented by SEQ ID No. 1 and SEQ ID No. 2;

- cultivating said cell in a culture medium and under conditions permissive for the production of 6'-sialyllactose; and
 - 5 - optionally recovering said 6'-sialyllactose.
10. The method according to claim 9, wherein the culture medium contains at least one carbon source selected from the group consisting of glucose, fructose, sucrose, and glycerol.
11. The method according to claim 9 or 10, wherein the culture medium contains
10 at least one compound selected from the group consisting of lactose, galactose and sialic acid.
12. The method according to any one of claims 9 to 11, wherein the 6'-sialyllactose is recovered from the culture medium and/or the bacterial cell.