

# Chapter 9

## Tumor-Associated Glycans and Their Functional Roles in the Multistep Process of Human Cancer Progression

Reiji Kannagi, Keiichiro Sakuma, Bi-He Cai, and Shin-Yi Yu

**Abstract** Cancer develops through a multistep process of carcinogenesis. This process accompanies incremental alterations of expression of biologically functional glycans on the surface of cancer cells. A variety of glycans are expressed in nonmalignant epithelial cells, including several normal glycans serving as ligands for siglecs, the immunosuppressive molecules carried by interstitial immune cells. These normal glycans decrease or disappear and are replaced by cancer-associated glycans at the early stages of carcinogenesis. This glycan transition facilitates production by mucosal immune cells of inflammatory mediators that are known to promote cancer progression. Expression of glycans that regulate growth factor receptor functions is also affected at the early stages of cancers. The major mechanism involved in glycan alteration at the early stages is epigenetic silencing through DNA methylation and/or histone deacetylation/methylation of genes responsible for synthesis of normal glycans, leading to their incomplete synthesis. In the locally advanced stages, multiple glycan-related genes are induced transcriptionally and posttranscriptionally by tumor hypoxia and epithelio-mesenchymal transition, thus further culminating in abnormal expression of cancer-associated glycans. Some such glycans serve as specific ligands for selectins, the cell adhesion molecules carried by vascular endothelial cells, and facilitate tumor vascularization and ultimately hematogenous metastasis. Advanced cancer cells which have undergone epithelio-mesenchymal transition share biological characteristics with so-called cancer stem cells, and glycans associated with such cells are currently known to be frequently expressed in human embryonic stem cells as well.

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## 9.1 Introduction

Cancer develops through a multistep process of carcinogenesis. Tumor progression is caused by genetic and epigenetic alterations of a variety of key regulatory molecules, and this process accompanies an incremental alteration of expression of biologically functional glycans on the surface of cancer cells. Here we will review recent findings on the mechanisms through which genetic and epigenetic alterations affect glycan expression in cancer cells and the pathophysiological roles of altered glycan expression during the course of cancer progression.

## 9.2 Epigenetic Silencing of Glycan-Related Genes Causing “Incomplete Synthesis” of Normal Glycans at Early Stages of Cancer

It has long been known that glycans undergo drastic changes upon carcinogenesis. We had classified the cancer-associated changes of glycan expression into two categories almost three decades ago; one had been “incomplete synthesis” of normal glycans and the other “*neosynthesis*” of abnormal glycans (Hakomori and Kannagi 1983).

The concept of “incomplete synthesis” had referred to the accumulation of structurally simpler abnormal glycans due to disturbance of synthetic pathways for normal glycans, which mainly occurs during the course of early carcinogenesis. This concept assumed some suppression to occur in the transcription/translation of genes involved in the synthesis of normal glycans during carcinogenesis. At present, the major suppression mechanism is regarded to be epigenetic silencing. The process of “incomplete synthesis” is known to start working at relatively early stages of carcinogenesis.

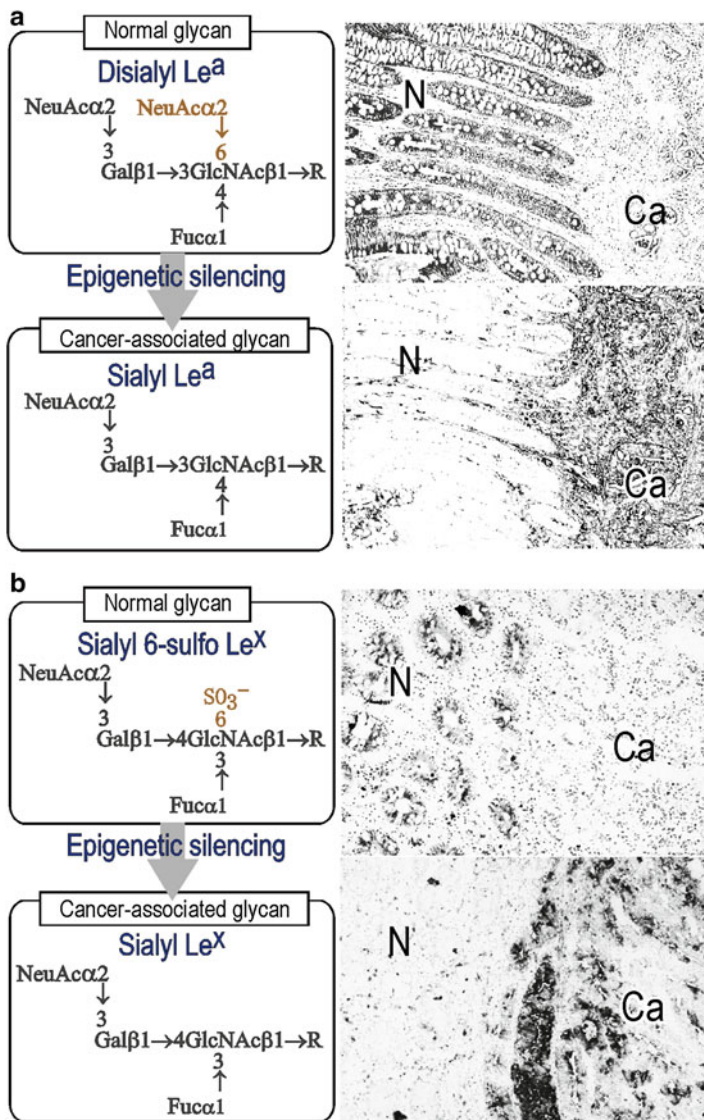
On the other hand, the concept of “*neosynthesis*” had referred to the appearance of abnormal glycans in cancers, which are not present, or present only in a negligible amount, in normal cells. This had been assumed to be due to transcriptional induction of genes involved in the synthesis of abnormal glycans along with progression of cancers. Nowadays, acceleration of transcription/translation of genes involved in the synthesis of these abnormal glycans is known to occur frequently along with the multistep progression of cancers at advanced stages.

### 9.3 Examples of Key Glycan-Related Genes Exhibiting Epigenetic Silencing at Early Stages of Cancer

A variety of glycans are expressed in normal epithelial cells, expression of some of which is conventional in that they are also constitutively expressed in cancers. In contrast, some other glycans exhibit preferential expression in nonmalignant epithelial cells and tend to decrease or disappear and be replaced by cancer-associated glycans upon malignant transformation. These glycans are aptly named “normal” glycans, although in a narrow definition of the word (Fig. 9.1).

Such normal glycans include disialyl Lewis A, which was found to be preferentially expressed in nonmalignant epithelial cells of the digestive organs (Kannagi et al. 1988; Itai et al. 1990, 1991), and clinical evaluation of it in patients’ sera was proposed to be useful for making differential diagnoses of benign and malignant diseases, especially when routine serum determination of sialyl Lewis A, a well-known cancer-associated glycan, gave false-positive results (Kannagi 2007). Soon it was found that the disialyl Lewis A glycan is a normal counterpart of the cancer-associated glycan, sialyl Lewis A, and that epigenetic silencing of *ST6GalNAc6*, a gene for  $\alpha$ 2,6sialyltransferase, is the key for diminishing expression of disialyl Lewis A and inducing sialyl Lewis A in cancers (Miyazaki et al. 2004). Downregulation of *ST6GalNAc6* was observed at the early stages of colon carcinogenesis in the normal-adenoma-carcinoma sequence (Bowden et al. 2007). This interconversion of glycans seems to be applicable to a wider range of cancers than initially expected. In addition to the cancers of digestive organs, preferential loss of disialyl Lewis A expression is also noted in prostate cancers (Young et al. 1988), and cancer-associated decrease of the *ST6GalNAc6* mRNA level is noted in breast (Potapenko et al. 2010) and renal (Senda et al. 2007) cancers, as well as glioblastoma (Kroes et al. 2007).

Another example of a “normal” glycan is sialyl 6-sulfo Lewis X, which was found to be preferentially expressed in nonmalignant epithelial cells of the colon and to disappear in colonic cancer cells (Izawa et al. 2000). This finding was in line with the classical histochemical finding on colon cancer glycans that the amount of sulfomucin is decreased in cancers compared to nonmalignant colonic tissues (Shamsuddin et al. 1981). Sialyl 6-sulfo Lewis X glycan is a normal counterpart of the well-known cancer-associated glycan, sialyl Lewis X, and epigenetic silencing of *SLC26A2*, a gene for sulfate transporter DTDST, was found to be a key mechanism responsible for diminished expression of sialyl 6-sulfo Lewis X and appearance of sialyl Lewis X in cancers (Yusa et al. 2010). Downregulation of *SLC26A2* was also observed at the early stages of colon carcinogenesis (Lee et al. 2006). It is notable that not only the genes for glycosyltransferases, which are directly involved in glycan synthesis, but also those for some transporters or enzymes in the intermediate carbohydrate metabolism are capable of playing a key role in the cancer-associated glycan alteration.



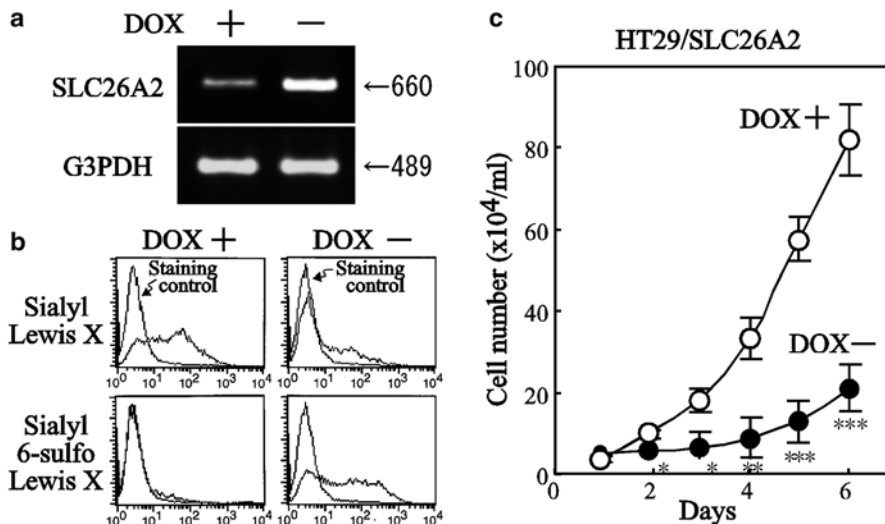
**Fig. 9.1** Examples of interconversion of normal glycans into cancer-associated glycans. *Panel a*, transition of normal glycan, disialyl Lewis A, to cancer-associated glycan, sialyl Lewis A, upon malignant transformation. *Panel b*, conversion of normal glycan, sialyl 6-sulfo Lewis X, to a cancer-associated glycan, sialyl Lewis X glycan, upon malignant transformation. Typical distribution patterns shown were obtained by immunohistochemical staining using specific anti-glycan antibodies of consecutive sections prepared from colon cancer tissues. *Ca* cancer cells, *N* nonmalignant epithelial cells (Adopted from references Izawa et al. 2000; Miyazaki et al. 2004; Lim et al. 2008)

## 9.4 Biological Functions of Normal Glycans

The hallmark of early carcinogenesis is the acquisition of a highly proliferative activity and/or suppression of apoptosis by the transforming cells. Several glycans are known to affect cell proliferation. GM3 and other monosialogangliosides have long been known to suppress EGF receptor signaling by their direct interaction with the receptor molecule (Bremer and Hakomori 1982; Hakomori 2010). Likewise, GM2 is known to suppress c-Met kinase pathway (Todeschini et al. 2008). On the other hand, disialogangliosides, such as GD3 and GD2, are reported to enhance cell proliferation through activation of FAK and Lyn kinases (Furukawa et al. 2012). N-glycans and related genes including *MGAT5* are also known to affect growth factor receptor signaling (Matsumoto et al. 2008; Park et al. 2012; also reviewed in Lau and Dennis 2008). The glycan-related genes involved in O-glycan synthesis such as *GALNT14*, *GALNT2*, and *CIGALT1* on death receptors, and growth factor receptors such as c-Met and EGFR have recently been suggested to affect cancer cell apoptosis and proliferation (Wagner et al. 2007; Wu et al. 2011, 2013). Altered expression of these glycans may well play significant roles during the course of carcinogenesis.

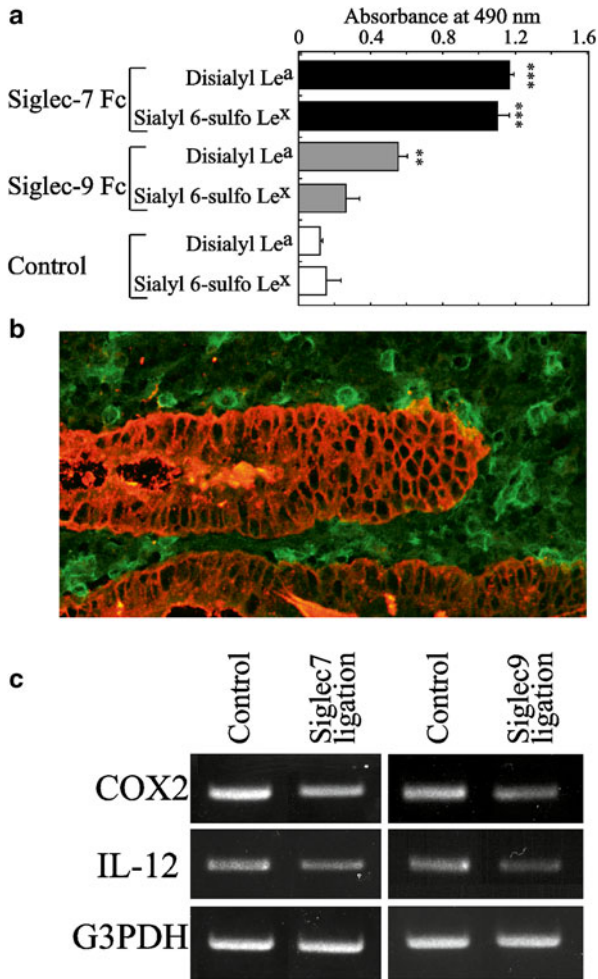
There are other indications for a more indirect association of cell proliferation status with glycan expression. For instance, the decreased transcription of *SLC26A2* in cancers mediates the loss of normal glycan sialyl 6-sulfo Lewis X and induction of cancer-associated glycan sialyl Lewis X and at the same time strongly induces cell proliferation (Yusa et al. 2010). The growth suppressive effect of the *SLC26A2* gene was clearly reproduced in experiments using a Tet-off expression vector for *SLC26A2* (Yusa et al. 2010) (Fig. 9.2). It is not clear whether or not the growth suppression conferred by this gene is due to its effects on glycan sulfation, because *SLC26A2* is a sulfate transporter gene which can affect not only glycan sulfation but also sulfation of other molecules such as proteins and lipids. Still, it can at least be proposed that this is another example indicating the close link between change in glycan expression and cell proliferation status.

Cancer microenvironments also play crucial roles during the course of carcinogenesis. In the mouse model of colon carcinogenesis, mutation in the APC gene induces proliferation of epithelial cells leading to multiple benign polyp formation. Meanwhile, Taketo's group found that the malignant transformation of adenoma cells was observed selectively at the locus where interstitial cells in colonic mucosal membranes produce COX2, which is a pro-inflammatory molecule known to promote cancer progression (Oshima et al. 1996). This finding became the theoretical basis for developing COX2 inhibitors for the chemoprevention of colon carcinogenesis. Although difficulty was encountered during the development of specific COX2 inhibitors because they have intrinsic toxic cardiac effects, it is still true that inflammatory signaling pathways are activated in various cancers including colon cancer linking chronic inflammation to oncogenesis. Alternative modalities are now awaited for the chemoprevention of colon carcinogenesis.



**Fig. 9.2** Possible link between glycan expression change and cancer cell growth. Results of RT-PCR (*panel a*), flow-cytometry (*panel b*), and cell proliferation assays (*panel c*) are shown on colon cancer cell line HT29 that was transfected with Tet-off inducible expression vector for *SLA26A2*. When cultured without doxycycline, the *SLA26A2* gene is actively transcribed, resembling nonmalignant epithelial cells, and the normal glycan, sialyl 6-sulfo Lewis X, is strongly expressed on the cell surface. This is associated with suppression of cell proliferation. In contrast, when cultured with doxycycline, transcription of *SLA26A2* is repressed and resembles cancer cells, leading to the extinction of normal glycan expression and induction of the cancer-associated glycan, sialyl Lewis X, which is coupled with enhanced cell proliferation. The difference was statistically significant at \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; and \*\*\*,  $p < 0.001$  (Adopted from reference Yusa et al. 2010)

In this context, it is noteworthy that the normal glycans in colonic epithelial cells such as disialyl Lewis A and sialyl 6-sulfo Lewis X were both shown to serve as ligands for siglecs, which are glycan-recognition molecules having immunosuppressive ITIM motifs in their cytoplasmic domains and are expressed by a variety of immune cells. The sialyl 6-sulfo Lewis X glycan was shown to be the ligand for siglec-7, and disialyl Lewis A was found to serve as a ligand for both siglec-7 and siglec-9 (Miyazaki et al. 2004, 2012) (Fig. 9.3). A significant number of tissue macrophage-like cells expressing siglec-7 or siglec-9 were present in normal colonic mucosal membranes, and ligation of either siglec had suppressive effects on the production of COX2 and IL-12 by macrophage-like cells (Miyazaki et al. 2012) (Fig. 9.3). Based on these results, it was proposed that normal glycans may play a role in maintaining immunological homeostasis and preventing cancer progression. The loss of these normal glycans due to epigenetic silencing of the key genes upon malignant transformation is expected to further facilitate carcinogenesis.



**Fig. 9.3** Normal glycans serve as ligands for siglecs. *Panel a*, normal glycans such as disialyl Lewis A and sialyl 6-sulfo Lewis X, but not cancer-associated glycans, serve as specific ligands for siglecs, which are immunosuppressive receptors carried by immune cells in mucosal membranes. *Panel b*, a human colon tissue stained with anti-siglec and anti-glycan MoAbs, suggesting possible interaction between tissue macrophage-like cells expressing siglec-7 (green) and colonic epithelial cells expressing its ligand disialyl Lewis A (red). *Panel c*, suppression of LPS-induced COX2 and IL-12 in cultured macrophage-like cells by ligation of siglec-7/-9. TPA-treated U937 cells transfected with siglec-7 or siglec-9 were stimulated with LPS with or without a F(ab')<sub>2</sub> fragment of an anti-siglec-7 or anti-siglec-9 antibody (Adopted from references Miyazaki et al. 2004, 2012)

## 9.5 Mechanisms for Epigenetic Silencing of Glycan-Related Genes During the Course of Carcinogenesis

Aberrant promoter CpG island hypermethylation is one of the most common and well-established epigenetic abnormalities in cancer. In earlier studies, DNA methylation of A- and B-enzymes was shown to cause a decrease of normal A- and B-blood type glycans in cancers (Kominato et al. 1999; Chihara et al. 2005). Likewise, loss of the Sd<sup>a</sup> blood group substance in colon cancer was shown to be due to DNA methylation of the *B4GALNT2* gene promoter (Kawamura et al. 2008). The decrease in all these glycan epitopes attached to the lactosamine or polylactosamine backbone structures is proposed to facilitate expression of cancer-associated glycan epitopes such as sialyl Lewis A and sialyl Lewis X, synthesized from common precursors, by leaving the surplus substrates for the enzymes responsible for synthesis of the latter two cancer-associated glycans (Kannagi et al. 2008).

Table 9.1 summarizes hitherto known glycan-related genes in cancers which represent epigenetic silencing. There are many examples of genes involved in glycan synthesis which are regulated by DNA methylation. *HS3ST2* (*3OST2*) is a typical example of genes known to be strongly hypermethylated in a variety of cancers (Miyamoto et al. 2003) and is sometimes utilized even as a positive control in DNA methylation analyses. The biological significance of this gene was not known until the heparan sulfate 3-O-sulfotransferase encoded by this gene was recently reported to suppress cell proliferation and migration (Hwang et al. 2013). The exact mechanisms behind these observed phenomena await further investigation, but this is an indication of another link between glycan expression and cancer cell proliferation. The roles of extracellular heparan sulfates as extracellular coreceptors for growth factors have been well documented (Fuster and Esko 2005).

Histone modification is also intimately involved in cancer-associated epigenetic silencing of glycan-related genes. Transcription of *ST6GalNAc6* was initially reported to be recovered either by treatment with histone deacetylation inhibitor (butyrate) or DNA methylation inhibitor (5-aza-2'-deoxycytidine) (Miyazaki et al. 2004), but the effect of the DNA methylation inhibitor was later found to be dependent on the cell lines used in experiments, and histone deacetylation turned out to be the major mechanism for silencing this gene. Histone modification was also proposed to be the major mechanism for epigenetic silencing of the sulfate transporter gene *SLC26A2*, and in the case of this gene, significant participation of histone trimethylation at H3K27 was suspected in addition to histone deacetylation (Yusa et al. 2010) (Fig. 9.4). Accordingly, addition of not only HDAC inhibitors, but histone methyltransferase inhibitor DZNep, was shown to stoichiometrically induce *SLC26A2* transcription (Fig. 9.4). Participation of DNA methylation in cancer-associated suppression of this gene was recently reported for papillary thyroid cancer (Zhang et al. 2012).

Epigenetic drugs are not yet actively utilized for therapy of cancers, but several reports suggest them to be beneficial for chemoprevention of cancers (Ravillah et al. 2014; Timp and Feinberg 2013). Assessment of normal glycan expression may be useful for monitoring therapeutic effects in such regimens.



**Table 9.1** Examples of glycan-related genes in cancers which are known to represent epigenetic silencing

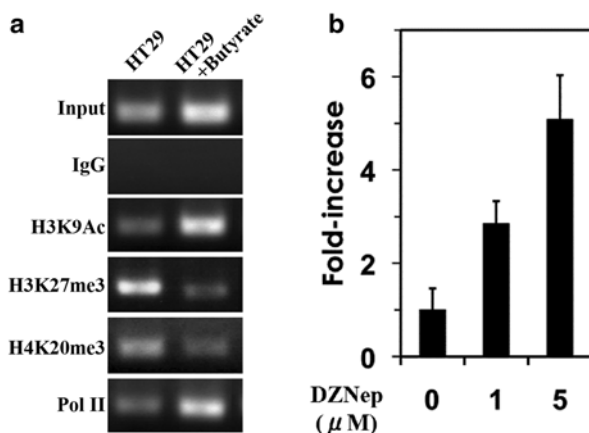
Genes	Glycans involved	Mechanisms	References
<i>ABO</i>	ABO(H) blood group substance	DNA methylation	Kominato et al. (1999)
<i>HS3ST2 (3OST2)</i>	Heparan sulfate (3S)	DNA methylation	Miyamoto et al. (2003)
<i>GNE</i>	CMP-sialic acid	DNA methylation	Oetke et al. (2003)
<i>ST6GALNAC6</i>	Sialyl Lewis A/disialyl Lewis A	Histone acetylation, DNA methylation	Miyazaki et al. (2004)
<i>EXT1</i>	Heparan sulfate	DNA methylation	Ropero et al. (2004)
<i>EXTL3</i>	Heparan sulfate	DNA methylation	Karibe et al. (2008)
<i>FUT3</i>	Lewis A	DNA methylation	Serpa et al. (2006)
<i>MGAT5</i>	<i>N</i> -glycan branching	DNA methylation	Chakraborty et al. (2006)
<i>MGAT4A</i>	<i>N</i> -glycan branching	DNA methylation, histone acetylation	Ide et al. (2006)
<i>SULF1</i>	Heparan sulfate (6S)	DNA methylation, histone acetylation	Staub et al. (2007)
<i>B4GALNT2, ST3GAL6</i>	Sd <sup>a</sup> /sialyl Lewis A	DNA methylation	Kawamura et al. (2008)
<i>B4GALNT2</i>	Sd <sup>a</sup>	DNA methylation	Wang et al. (2008)
<i>SLC26A2 (DTDST, sulfate transporter)</i>	Sialyl Lewis X/sialyl 6-sulfo Lewis X	Histone methylation, histone acetylation	Yusa et al. (2010)
<i>FX, SLC35C1 (GDP-fucose transporter), FUT4</i>	Fucose in TRAIL signaling	DNA methylation	Moriwaki et al. (2010)
<i>HS3ST1, HS3ST2, HS3ST3A1 (3-OST1, 3-OST2, 3-OST3A)</i>	Heparan sulfate (3S)	DNA methylation	Bui et al. (2010)
<i>C4ST1, DSE</i>	Chondroitin/dermatan sulfate	DNA methylation	Kalathas et al. (2010)
<i>GMDS, FX, MGAT4A, MGAT5</i>	Core fucose/ <i>N</i> -glycan branching	DNA methylation	Saldova et al. (2011)
<i>ST3GAL6</i>	Sialyl Lewis X	DNA methylation	Chachadi et al. (2011)
<i>HS3ST3B1 (3-OST-3B1)</i>	Heparan sulfate (3S)	DNA methylation, histone acetylation	Song et al. (2011)
<i>B4GALNT1, ST8SIA1</i>	Gangliosides	histone acetylation	Suzuki et al. (2011)

(continued)

**Table 9.1** (continued)

Genes	Glycans involved	Mechanisms	References
<i>MGAT5B</i>	N-glycan branching	DNA methylation, histone acetylation, histone methylation	Kizuka et al. (2011)
<i>B3GALT5</i>	Sialyl Lewis A	DNA methylation, histone acetylation, histone methylation	Caretti et al. (2012)
<i>Cosmc</i>	Mucin core 1	DNA methylation	Mi et al. (2012)
<i>B3GALT1</i>	Sialyl Lewis A	Histone acetylation	Chachadi et al. (2013)
<i>B3GNT7</i>	Sialyl Lewis A/X	DNA methylation	Lu et al. (2014)

Candidate glycans which are expected to be affected by these alterations are also included



**Fig. 9.4** Epigenetic silencing of *SLC26A2* gene in colon cancer cells. *Panel a*, results of ChIP assays in human colon cancer HT29 cells cultured with or without an HDAC inhibitor, butyrate. *Panel b*, effect of histone methyltransferase inhibitor DZNep on the transcription level of the *SLC26A2* gene (Adopted from reference Yusa et al. 2010)

## 9.6 Acquisition of Resistance to Hypoxia by Cancer Cells in Advanced Stage of Cancers

At the locally advanced stages, cancer cells must cope with hypoxic environments to survive and proliferate, and some cancer cell clones having hypoxia-resistant characteristics appear through accumulation of genetic anomalies. Such hypoxia-resistant cancer cells usually exhibit a higher proliferating rate, enhanced cell

mobility, greater angiogenic activity, and stronger multidrug resistance, thus having multiple advantages over other cancer cell clones, and will eventually occupy all cancer cell nests. The transcription factor HIF-1 $\alpha$  plays a central role for cancer cells in acquiring hypoxia-resistant characteristics.

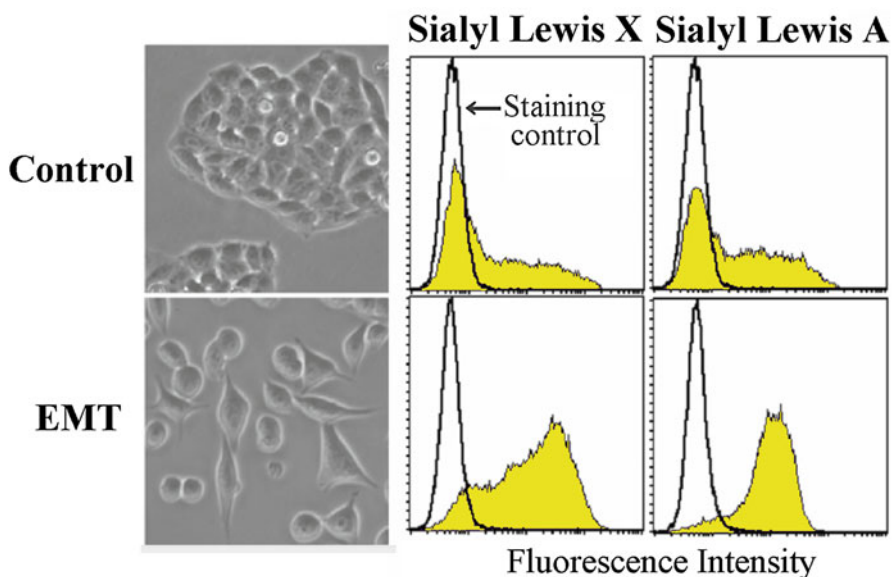
Intense changes of glycan expression are observed in advanced-stage cancers, and this is partly because HIF-1 $\alpha$  induces the transcription of a variety of genes involved in the synthesis of glycans (Kannagi 2004, 2010). For instance, tumor hypoxia induces, through the action of HIF-1 $\alpha$ , transcription of genes for sialyltransferase, fucosyltransferase, and UDP-galactose transporter, which are involved in the synthesis of sialyl Lewis A and sialyl Lewis X (Koike et al. 2004). Tumor hypoxia thus enhances expression of sialyl Lewis A and sialyl Lewis X in cancer cells, which further help cancer cells in coping with hypoxic environments, since these glycans serve as ligands for vascular E-selectin and mediate adhesion of cancer cells to endothelial cells. Interaction between E-selectins on endothelial cells and its ligands on cancer cells is known to facilitate tumor vascularization (Tei et al. 2002). HIF-1 $\alpha$  also induces transcription of genes for several enzymes in the synthetic pathway of the lipid moiety of glycolipids, and this is expected to affect their localization in cell membrane microdomains (Yin et al. 2010).

The gene for sialin, *SLS17A5*, is also induced by HIF-1 $\alpha$  (Yin et al. 2006). Normal cells synthesize sialic acid, usually from the de novo synthetic pathway starting from UDP-GlcNAc. Cancer cells seem to enhance the de novo synthetic pathway to some extent to meet the increased demands for sialoconjugate synthesis (Go et al. 2007), but upon progression, cancer cells tend to rely more on the salvage pathway, which reutilizes the sialic acid residues cleaved from exogenous glycoconjugates in lysosomes. Sialin is a lysosomal sialic acid transporter that pumps in free sialic acids released in lysosomes to cytoplasm and is closely involved in the salvage pathway. In humans, sialic acid species provided by the de novo synthetic pathway is limited to NeuAc but not NeuGc, because humans lack the enzyme which converts NeuAc to NeuGc. On the other hand, sialic acids transported by sialin contain NeuGc, the nonhuman sialic acid derived from fetal calf serum under cell culture conditions and from a dietary origin under in vivo conditions. Consequently, the amount of glycans containing NeuGc in cancer cells having enhanced sialin activity is usually higher than that in nonmalignant cells. A glycan containing NeuGc was sometimes known to be antigenic to humans and was termed Hanganatziu-Deicher antigen. This antigen was for a long time counted as a member of cancer-associated glycans, as cancers have a higher amount of NeuGc-containing glycans than normal tissues. The Hanganatziu-Deicher antigen occurs late during cancer progression, mainly in the advanced stages of cancers, because its appearance is driven by HIF-1 $\alpha$ , which starts to work in the advanced stages. Recently, cultured ovarian cancer cells having an extremely high NeuGc content were reported, and other mechanisms, in addition to enhanced sialin transcription, were suggested to be involved in this extremely high NeuGc expression (Inoue et al. 2010).

## 9.7 Glycan Alteration by Epithelio-Mesenchymal Transition of Cancer Cells in Advanced Stages of Cancers

Epithelio-mesenchymal transition (EMT) is a critical event in the advanced stages of cancers which prepares cancer cells for metastasis. EMT is caused by a well-defined set of transcription factors and is found to induce several genes related to glycan expression such as sialyltransferases, fucosyltransferases, and galactosyltransferases, which are also involved in the synthesis of sialyl Lewis A and sialyl Lewis X glycans (Sakuma et al. 2012). Consequently, cancer cells which had undergone EMT have a higher expression of the sialyl Lewis A and sialyl Lewis X glycans and strongly bind to vascular E-selectin (Fig. 9.5). Several decades ago, it had been noticed that cancer cells in the invasion front having a mesenchymal cell-like morphology frequently express these glycans strongly (Ono et al. 1996). Judging from the recent findings mentioned above, this must have been due to the EMT-induced transcription of glycan-related genes.

The best-known function of cancer-associated glycans is that sialyl Lewis A and sialyl Lewis X glycans serve as vascular E-selectin and mediate hematogenous metastasis of cancer cells (Phillips et al. 1990; Takada et al. 1991, 1993). For adhesion to occur, however, these glycans need to be expressed in a density high



**Fig. 9.5** Induction of cancer-associated glycans sialyl Lewis A and sialyl Lewis X in cancer cells underwent epithelio-mesenchymal transition (EMT). Human colon cancer cells DLD-1 were cultured with EGF/bFGF in serum-free medium to induce EMT. Morphological changes (*left panel*) and results of flow-cytometric analyses of sialyl Lewis A and sialyl Lewis X expression (*right panel*) upon EMT are shown (Adopted from reference Sakuma et al. 2012)

enough to be recognized by E-selectin. As disialyl Lewis A and sialyl 6-sulfo Lewis X are only minor components among the glycans in nonmalignant epithelial cells, their interconversion through the “incomplete synthesis” mechanism, i.e., epigenetic silencing of *ST6GalNAc6* or *SLC26A2*, would confer, although significant, only a weak expression of sialyl Lewis A and sialyl Lewis X glycans. The high-density expression of these cancer-associated glycans could be achieved only after further enhancement of their synthesis through transcriptional induction by hypoxia and/or EMT of additional glycan-related genes, the mechanism defined as “*neosynthesis*” in our previous proposition. The two mechanisms, “incomplete synthesis” and “*neosynthesis*,” are not mutually exclusive; they sometimes work on the same glycans in a stepwise manner during the multistep progression of cancers. In contrast, appearance of the NeuGc-containing glycans (Hanganatziu-Deicher antigens) in cancer cells can be regarded to have stemmed exclusively from the “*neosynthesis*” mechanism, which specifically occurs in the advanced stages of cancer progression.

## 9.8 Glycans Associated with Cancer Stem Cells and Embryonic Stem Cells

Characteristics of EMT-induced cancer cells are known to be very similar to those of so-called cancer stem cells (Mani et al. 2008). Expression of sialyl Lewis A and sialyl Lewis X was enhanced in cancer cells after EMT, while a paradoxical decrease was noted in the expression of some other glycans that had been assumed to be cancer associated, such as Lewis Y glycan (Sakuma et al. 2012). This unexpected finding suggested that some hitherto known cancer-associated glycans, exemplified by sialyl Lewis A/X, are linked to a more malignant population of cancer cells such as cancer stem cells, whereas others are not. Examples of glycan-related genes which have been reported to exhibit altered transcription levels in EMT-induced cancer cells and/or cancer stem cells are shown in Table 9.2, together with the candidate glycan species which are expected to be affected by these alterations.

Cell surface glycans are known to be good markers for embryonic stem (ES) cells in the field of stem cell research. Good examples are SSEA-1 for murine ES cells and SSEA-3/-4 for human ES cells. However, the mechanisms of how these glycans appear specifically on the surface of ES cells have not been elucidated yet. It is well known that a combination of several transcription factors such as OCT3/4, Nanog, and Sox-2 plays critical roles in maintaining the stemness in these cells (Takahashi et al. 2007), while transcriptional regulation of ES cell-associated glycan expression still remains largely unknown. There were sporadic publications reporting that SSEA-3/-4 glycans sometimes appear in human cancer cells (Schrump et al. 1988; Suzuki et al. 2013; Gottschling et al. 2013; Lou et al. 2014), and it was recently reported that these glycans are specifically expressed in cancer stem-like cells (Chang et al. 2008; Noto et al. 2013).

**Table 9.2** Examples of glycan-related genes reported to exhibit altered transcription levels in EMT-induced cancer cells and/or cancer stem cells

Genes	Glycans involved	Mechanisms	References
<i>B3GALT4</i> (decrease)	Gg4	EMT induced by hypoxia	Guan et al. (2010)
<i>HAS2</i> (increase)	Hyaluronan	EMT induced by TGF $\beta$	Craig et al. (2010)
<i>HAS2</i> , <i>HAS3</i> (increase)	Hyaluronan	EMT induced by EGF and IL-1 $\beta$	Chow et al. (2010)
<i>GCNT2</i> (increase)	I-branching	EMT induced by TGF $\beta$	Zhang et al. (2011)
<i>ST3GAL1/3/4</i> , <i>FUT3</i> (increase); <i>FUT2</i> (decrease)	Sialyl Lewis A/sialyl Lewis X	EMT induced by EGF/bFGF	Sakuma et al. (2012)
<i>MGAT3</i> (decrease)	<i>N</i> -glycan	EMT induced by TGF $\beta$	Xu et al. (2012)
<i>MGAT3</i> (decrease)	<i>N</i> -glycan	EMT induced by TGF $\beta$	Pinho et al. (2012)
<i>GCNT1</i> (increase)	<i>O</i> -glycan	Breast cancer tumor-initiating cells	Kim et al. (2012)
<i>ST8SIA1</i> (increase)	GD2	Cancer stem cells induced through EMT	Battula et al. (2012)
<i>UGCG</i> (increase)	Glycolipids, Gb3	Breast cancer stem cells	Gupta et al. (2012)
<i>HAS2</i> (increase)	Hyaluronan	Breast cancer stem cells	Okuda et al. (2012)
<i>MGAT5</i> , <i>FUT8</i> , and <i>B3GALT5</i> (increase); <i>MGAT3</i> (decrease)	Lectin binding	EMT induced by HGF	Li et al. (2013)
<i>ST6GAL1</i>	<i>N</i> -glycan	Colon cancer stem cells	Swindall et al. (2013)
<i>FUT8</i> (increase)	<i>N</i> -glycan	EMT induced by TGF $\beta$	Chen et al. (2013)
<i>ST3GAL5</i> (increase)	GM3	EMT induced by TGF $\beta$	Kim et al. (2013)
<i>ST3GAL5</i> , <i>B4GALNT1</i> , <i>ST8SIA1</i> , <i>ST3GAL2</i> (increase)	GD2, GD3, GM2, GD1a	Cancer stem cells induced through EMT	Liang et al. (2013)

Candidate glycans expected to be affected by these alterations are also included

SSEA-3/-4 glycans are classified into the globo-series glycolipids (Kannagi et al. 1983), which compose a unique series of glycolipids having glycan structures confined to glycolipids, and are not easily detectable in glycoproteins. Recently, another classical stem cell-specific glycan, TRA-1-60, was reported to be a type 1 chain glycan, having common backbone structures with glycans carried by both glycolipids and glycoproteins (Natunen et al. 2011). This glycan is structurally very similar to that of sialyl Lewis A, sharing the same enzymes in most steps of their synthetic pathways.

The recently introduced fucosylated stem cell-associated glycan, SSEA-5, again had the backbone structure of the type-1 chain glycan (Tang et al. 2011). Finally, sialyl Lewis A itself was shown to be expressed in human ES cells and to disappear upon ES cell differentiation, thus behaving as a stem cell-specific glycan (Tang et al. 2011). These findings strongly suggest that there are some common features between glycans specific to ES cells and those associated with cancer stem cells.

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