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## Role of tumor cell sialylation in pancreatic cancer progression

Michael P. Marciel,

Barnita Haldar,

Jihye Hwang,

Nikita Bhalerao,

Susan L. Bellis\*

Department of Cell, Developmental and Integrative Biology, University of Alabama at Birmingham, Birmingham, AL, United States

### Abstract

Pancreatic ductal adenocarcinoma (PDAC) is one of the deadliest malignancies and is currently the third leading cause of cancer death. The aggressiveness of PDAC stems from late diagnosis, early metastasis, and poor efficacy of current chemotherapies. Thus, there is an urgent need for effective biomarkers for early detection of PDAC and development of new therapeutic strategies. It has long been known that cellular glycosylation is dysregulated in pancreatic cancer cells, however, tumor-associated glycans and their cognate glycosylating enzymes have received insufficient attention as potential clinical targets. Aberrant glycosylation affects a broad range of pathways that underpin tumor initiation, metastatic progression, and resistance to cancer treatment. One of the prevalent alterations in the cancer glycome is an enrichment in a select group of sialylated glycans including sialylated, branched N-glycans, sialyl Lewis antigens, and sialylated forms of truncated O-glycans such as the sialyl Tn antigen. These modifications affect the activity of numerous cell surface receptors, which collectively impart malignant characteristics typified by enhanced cell proliferation, migration, invasion and apoptosis-resistance. Additionally, sialic acids on tumor cells engage inhibitory Siglec receptors on immune cells to dampen anti-tumor immunity, further promoting cancer progression. The goal of this review is to summarize the predominant changes in sialylation occurring in pancreatic cancer, the biological functions of sialylated glycoproteins in cancer pathogenesis, and the emerging strategies for targeting sialoglycans and Siglec receptors in cancer therapeutics.

### 1. Introduction

Pancreatic cancer is one of the most aggressive epithelial malignancies. The most common and deadly form, pancreatic ductal adenocarcinoma (PDAC), has a dismal 5-year survival rate of less than 10% (Siegel, Miller, Fuchs, & Jemal, 2021). The high mortality of patients is due to the early invasion of tumor cells into adjacent tissue, early metastasis, and late diagnosis; together these features limit the only potential curative treatment for PDAC, surgical resection (Kabashi, Dedushi, Ramadani, Mucaj, Hoxhaj, & Jerliu, 2016; Rahib, Smith, Aizenberg, Rosenzweig, Fleshman, & Matrisian, 2014). Current treatments including

\*Corresponding author. bellis@uab.edu.

chemotherapies, targeted therapies, and immunotherapies have failed to substantially improve PDAC patient survival, therefore new avenues for treatment must be considered. One of the areas of pancreatic cancer biology that has received limited attention is the role of cell surface glycans in tumor cell behavior. Aberrant glycosylation was one of the earliest observed characteristics of a cancer cell (Almeida & Kolarich, 2016; Helenius & Aebi, 2001; Reis, Osorio, Silva, Gomes, & David, 2010; Rudd, Woods, Wormald, Opendakker, Downing, & Campbell, 1995; Vajaria & Patel, 2017) and surface glycans have been implicated in chemoresistance, tumor aggressiveness and metastasis (Laubli & Borsig, 2019; Munkley & Elliott, 2016).

Abnormal sialylation is one of the predominant glycan alterations observed during carcinogenesis, and is associated with malignant properties including invasion and metastasis (Shah, Telang, Shah, & Patel, 2008). Sialic acid, a negatively-charged monosaccharide, is added to the non-reducing terminal position of glycoconjugates. Sialic acids are linked through either  $\alpha$ 2,3 or  $\alpha$ 2,6 bonds to galactose or an  $\alpha$ 2,6 bond to N-acetylgalactose (GalNAc). Sialic acid can also be added in an  $\alpha$ 2,8 linkage to another sialic acid, forming polysialic acid. To date, twenty different sialyltransferases have been identified in humans (Harduin-Lepers, Krzewinski-Recchi, Colomb, Foulquier, Groux-Degroote, & Delannoy, 2012). These enzymes add sialic acid to either glycolipids or to the N- or O-linked sugar chains of glycoproteins. Sialyltransferases are subdivided into four general families: (1) the ST3Gal enzymes, ST3Gal1-6, which add  $\alpha$ 2,3-linked sialic acid to galactose; (2) ST6Gal1 and 2, which add  $\alpha$ 2,6-linked sialic acid to galactose; (3) ST6GalNAc1-6, which add  $\alpha$ 2,6 sialic acid to GalNAc, and (4) ST8Sia1-6, which generate the polysialic acid structure. While  $\alpha$ 2,8-linked polysialylation is increased in some types of cancer (e.g., neuroblastoma) (Pietrobono & Stecca, 2021; Sato & Kitajima, 2021), malignant epithelial cells more commonly exhibit an enrichment in  $\alpha$ 2,3 and  $\alpha$ 2,6 sialic acids (Bellis, Reis, Varki, Kannagi, & Stanley, 2022). The hypersialylation of tumor cells can be caused by the upregulation of select sialyltransferases, increased availability of CMP-sialic acid, or decreased neuraminidase levels in the cell (Bhide & Colley, 2017; Bull, Stoel, den Brok, & Adema, 2014; Rodrigues & Macauley, 2018). An extensive literature has underscored the importance of sialoglycans in fundamental processes such as cell-cell communication, cell-extracellular matrix communication and intracellular signaling induced by cell surface receptors.

Dysregulated sialylation is a hallmark feature of pancreatic and other malignancies. Examples of tumor-associated sialoglycans found on glycoproteins include hypersialylated N-glycans, sialyl Lewis antigens, and sialylated forms of truncated O-glycans (sialyl-Tn and sialyl-T antigens) (Bellis et al., 2022; Christiansen, Chik, Lee, Anugraham, Abrahams, & Packer, 2014; Dall'Olio, Malagolini, Trinchera, & Chiricolo, 2014; Dobie & Skropeta, 2021; Munkley, 2019). Changes in the sialylation of gangliosides are also common in cancer, however these have been described elsewhere (Kannagi, Cai, Huang, Chao, & Sakuma, 2018; Kasprovicz, Sophie, Lagadec, & Delannoy, 2022), and will not be a focus of this review. Sialoglycans play a critical role in regulating tumor cell phenotype by modulating the activity of transmembrane and secreted glycoproteins. Additionally, the hypersialylation of tumor cells can dampen the immune response through sialic acid binding to Siglecs (Sialic acid-binding immunoglobulin-type lectins) on the surface of various immune cells.

The presence of sialic acids on tumor cells has been associated with a Siglec-mediated reduction in effector T cells, an increase in regulatory T cells (Perdicchio, Cornelissen, Streng-Ouwehand, Engels, Verstege, & Boon, 2016), and differentiation of monocytes into macrophages with an immunosuppressive phenotype (Rodriguez, Boelaars, Brown, Eveline Li, Kruijssen & Bruijns, 2021). Together these effects facilitate tumor escape from immune surveillance.

The lack of effective treatments for pancreatic cancer underscores the need for a better understanding of the molecular mechanisms that drive cancer initiation and progression. Elucidating the mechanisms by which sialoglycans promote carcinogenesis may reveal important new targets for therapeutic intervention or biomarkers that can be used to track disease advancement or recurrence. In this review, we summarize the changes in sialylation occurring in pancreatic cancer, the functional contribution of aberrantly-sialylated glycoproteins to pathogenesis, and the corresponding role of Siglec receptors in directing immunosuppression in response to hypersialylation.

## 2. Hypersialylation of N-glycosylated proteins

An increase in highly-sialylated, branched N-glycans (Fig. 1A) is one of the prevalent glycan alterations observed in epithelial cancers including PDAC (Bellis et al., 2022). Hypersialylation of tumor cells has been reported for decades, however more recent glycan profiling studies have provided important insights into the overall structure of tumor sialoglycans. Comprehensive glycomics analyses using mass spectrometry approaches have confirmed that N-glycans expressed by cancer cells carry elevated levels of both  $\alpha$ 2,3 and  $\alpha$ 2,6 sialylation. For example, analyses of PDAC patient tissues using MALDI imaging mass spectrometry indicated that  $\alpha$ 2,3 and  $\alpha$ 2,6 sialylated N-glycans were enriched in the malignant, compared to healthy, pancreas (McDowell, Klamer, Hall, West, Wisniewski & Powers, 2020). Interestingly, while  $\alpha$ 2,3 sialylation was more abundant than  $\alpha$ 2,6 sialylation in cancer tissues,  $\alpha$ 2,6 sialylation appeared to be more specific for adenocarcinoma cells (McDowell, Klamer, Hall, West, Wisniewski, & Powers, 2020). The N-glycans on serum glycoproteins isolated from PDAC patients also displayed increased levels of sialic acid (Zhao, Qiu, Simeone, & Lubman, 2007), and the ratio of  $\alpha$ 2,6 sialylation versus  $\alpha$ 2,3 sialylation on the serum glycoproteins was higher for patient samples than for healthy controls (Vreeker, Hanna-Sawires, Mohammed, Bladergroen, Nicolardi, & Dotz, 2020). Studies of N-glycan composition are reinforced by lectin microarray results (Kurz, Chen, Vucic, Baptiste, Loomis & Agrawal, 2021; Rodriguez, Boelaars, Brown, Eveline Li, Kruijssen, & Bruijns, 2021; Wagatsuma, Nagai-Okatani, Matsuda, Masugi, Imaoka, & Yamazaki, 2020). In a microarray incorporating lectins for numerous glycan structures, an increase in  $\alpha$ 2,3 and  $\alpha$ 2,6 sialylation was one of the dominant modifications identified in tissues from PDAC patients as well as the “KC” PDAC mouse model (Kurz, Chen, Vucic, Baptiste, Loomis, & Agrawal, 2021). The KC model, which expresses oncogenic KRas (KRas<sup>G12D</sup>) (Hingorani, Petricoin, Maitra, Rajapakse, King, & Jacobetz, 2003), recapitulates human PDAC in that more than 90% of PDAC patients have activating mutations in KRas (Wood & Hruban, 2012). These collective studies showing cancer-related enrichment in  $\alpha$ 2,3 and  $\alpha$ 2,6 sialylated N-glycans are consistent with a wealth of literature highlighting functional roles for these sialoglycans in cancer pathogenesis.

The  $\alpha$ 2,3-linked sialylation of N-glycans is elaborated by three main sialyltransferases, ST3Gal3, ST3Gal4 and ST6Gal6 (Chung, Yin, Wang, Chuang, Chu, & Betenbaugh, 2015). Of these, ST3Gal3 and ST3Gal4 are reportedly overexpressed in pancreatic cancer (Perez-Garay, Arteta, Llop, Cobler, Pages & Ortiz, 2013; Perez-Garay, Arteta, Pages, de Llorens, de Bolos & Vidal-Vanaclocha, 2010; Rodriguez et al., 2021). The expression of ST3Gal3 and ST3Gal4 is increased by TGF $\beta$  (Zhang, Zhang, Holst, Blochl, Madunic, & Wuhrer, 2022), a well-known inducer of epithelial to mesenchymal transition (EMT), as well as pro-inflammatory cytokines found within the tumor microenvironment including TNF $\alpha$  and IL-1 $\beta$  (Bassaganas, Allende, Cobler, Ortiz, Llop, & de Bolos, 2015). The high expression of ST3Gal4 in combination with ST3Gal1 correlates with significantly lower survival rates for PDAC patients (Rodriguez et al., 2021). Heightened activity of ST3Gal3 and ST3Gal4 is associated with enhanced pancreatic cancer cell migration, invasion and metastasis (Bassaganas, Carvalho, Dias, Perez-Garay, Ortiz, & Figueras, 2014; Guerrero, Miro, Wong, Massaguer, Martinez-Bosch, & Llorens, 2020; Perez-Garay, Arteta, Llop, Cobler, Pages, & Ortiz, 2013; Perez-Garay, Arteta, Pages, de Llorens, de Bolos, & Vidal-Vanaclocha, 2010). Some of these behaviors may relate to the increased production of sialyl Lewis X structures, given that sialoglycans generated by ST3Gal3 and ST3Gal4 serve as substrates for subsequent fucosylation (as discussed in the next section). The forced overexpression of ST3Gal3 and ST3Gal4 in MDAPanc-28 pancreatic cancer cells was shown to promote cell adhesion and motility (Perez-Garay et al., 2010, 2013), whereas knockdown of ST3Gal3 or ST3Gal4 in the BxPC-3 and Capan-1 PDAC lines inhibited migratory capacity (Guerrero, Miro, Wong, Massaguer, Martinez-Bosch, & Llorens, 2020). These enzymes were further implicated in metastasis in studies utilizing the splenic injection metastasis model. Mice injected intrasplenically with MDAPanc-28 cells engineered with ST3Gal3 or ST3Gal4 overexpression developed more metastatic tumors in the liver and other organs, and had decreased survival (Perez-Garay et al., 2010, 2013). Surface levels of  $\alpha$ 2,3 sialylation on tumor cells were similarly correlated with metastasis. N-glycan profiling of four different pancreatic cancer cell lines showed that lines with higher  $\alpha$ 2,3 sialylation had more metastatic potential compared to cells with low  $\alpha$ 2,3 sialylation (Holst, Belo, Giovannetti, van Die, & Wuhrer, 2017).

The  $\alpha$ 2,6 sialic acid linkage on N-glycans is directed primarily by the ST6Gal1 sialyltransferase. ST6Gal2 can also sialylate N-glycans in an  $\alpha$ 2,6 linkage, however, ST6Gal2 expression is either embryonic or largely confined to the brain after birth (Takashima et al., 2003). ST6Gal1 expression is upregulated in numerous malignancies including pancreatic cancer (Dorsett, Marciel, Hwang, Ankenbauer, Bhalerao, & Bellis, 2021; Garnham, Scott, Livermore & Munkley, 2019; Lu & Gu, 2015). Upregulation occurs, in part, through transcriptional activation of *ST6GAL1* by oncogenic forms of ras (Dalziel, Dall'Olio, Mungul, Piller, & Piller, 2004; Seales, Jurado, Singhal, & Bellis, 2003). Increased ST6Gal1-mediated sialylation has widespread effects on tumor cell phenotype. High expression of ST6Gal1 in cancer cells promotes cell migration and invasion (Britain, Bhalerao, Silva, Chakraborty, Buchsbaum, & Crowley, 2021; Hait, Maiti, Wu, Andersen, Hsu, & Wu, 2022; Isaji, Im, Gu, Wang, Hang, & Lu, 2014; Lin, Kemmner, Grigull, & Schlag, 2002; Ranjan & Kalraiya, 2013; Rao, Beggs, Ankenbauer, Hwang, Ma, & Salaita, 2022; Seales, Jurado, Brunson, Wakefield, Frost, & Bellis, 2005; Zhu, Srivatana, Ullah,

Gagneja, Berenson, & Lance, 2001) as well as resistance to apoptosis induced by various forms of cell stress including hypoxia and serum growth factor deprivation (Britain et al., 2017; Jones, Dorsett, Hjelmeland, & Bellis, 2018). ST6Gal1 activity also facilitates tumor resistance to chemotherapy and radiotherapy (Chakraborty, Dorsett, Trummell, Yang, Oliver, & Bonner, 2018; Lee, Lee, Bae, & Lee, 2008; Lee, Lee, Seo, Park, & Lee, 2010; Schultz, Holdbrooks, Chakraborty, Grizzle, Landen, & Buchsbaum, 2016; Schultz, Swindall, Wright, Sztul, Landen, & Bellis, 2013; Smithson, Irwin, Williams, Alexander, Smythies, & Nearing, 2022). For instance, high expression of ST6Gal1 in MiaPaCa2 and BxPC3 PDAC cells protects cells from DNA damage induced by gemcitabine (Chakraborty, Dorsett, Trummell, Yang, Oliver, & Bonner, 2018), which is a frontline treatment for pancreatic cancer. One of the mechanisms by which ST6Gal1 enables cells to withstand cytotoxic stimuli may be through promoting cancer stem cell (CSC) characteristics. CSCs are notoriously resistant to apoptosis (Garcia-Mayea, Mir, Masson, Paciucci, & ME, 2020; Najafi et al., 2019; Safa, 2016). Increased ST6Gal1 activity endows cancer cells with all of the key features of a CSC including upregulation of CSC surface markers, enhanced spheroid growth, and increased expression of stem cell transcription factors such as Sox9 (Schultz, Holdbrooks, Chakraborty, Grizzle, Landen, & Buchsbaum, 2016; Swindall, Londoño-Joshi, Schultz, Fineberg, Buchsbaum, & Bellis, 2013). Moreover, knockdown of ST6Gal1 in MiaPaCa2 PDAC cells impairs tumor-initiating potential in in vivo limiting dilution assays (Schultz et al., 2016), the gold standard assay for establishing CSC status. Consistent with a role in imparting stem-like features, ST6Gal1 activity promotes EMT in the Suit2 and S2-LM7AA pancreatic cancer cell lines (Britain, Bhalerao, Silva, Chakraborty, Buchsbaum, & Crowley, 2021). Recent studies in mouse models strongly support a role for ST6Gal1 in pancreatic cancer progression.

In the KC PDAC model, deletion of *St6gal1* impeded the formation of early neoplastic lesions known as PanINs (Pancreatic intraepithelial neo-plasias) (Kurz et al., 2021). Additionally, Hsieh et al. reported that ST6Gal1 contributed to the transition between pancreatitis and PDAC development (Hsieh, Shyr, Liao, Chen, Wang, & Lu, 2017). Specifically, the administration of fructose to KC mice with cerulein-induced pancreatitis accelerated invasive PDAC, and ST6Gal1 activity was central to this process.

The mechanism by which enhanced  $\alpha$ 2,3 and  $\alpha$ 2,6 sialylation regulates tumor cell behavior depends, in large part, upon sialylation-induced changes in the activity of cell surface receptor glycoproteins. The hypersialylation of N-glycans can influence many aspects of glycoprotein structure and/or localization including conformation, oligomerization and cell surface retention. In turn, altered receptor sialylation modulates intracellular signaling cascades and gene expression. It is noteworthy that receptor tyrosine kinases (RTKs) seem to be particularly affected by modifications in sialylation (Duarte et al., 2022; Gao, Luan, Melamed, & Brockhausen, 2021). Some of the RTKs known to be activated by  $\alpha$ 2,3 sialylation include the Insulin Receptor and the oncogenic RTKs, MET and RON (Balmana, Diniz, Feijao, Barrias, Mereiter, & Reis, 2020; Gomes, Osorio, Pinto, Campos, Oliveira, & Reis, 2013; Mereiter, Magalhaes, Adamczyk, Jin, Almeida, & Drici, 2016). Reis and colleagues demonstrated that increased  $\alpha$ 2,3 sialylation of MET resulting from the overexpression of ST3Gal4 stimulated receptor activation, cell invasion and resistance to the tyrosine kinase inhibitor, crizotinib (Balmana et al., 2020; Gomes et al., 2013). RTKs

are similarly affected by alterations in  $\alpha$ 2,6 sialylation. An activating role for ST6Gal1-mediated  $\alpha$ 2,6 sialylation has been reported for EGFR, MET and ERBB2 (Her2) (Britain et al., 2021; Britain, Holdbrooks, Anderson, Willey, & Bellis, 2018; Liu, Liu, Pan, Huang, Qi, & Li, 2019; Liu, Zhu, Linhai, Song, Gui, & Tan, 2018; Qian, Zhu, Tang, Shen, Ai, & Li, 2009; Rao, Beggs, Ankenbauer, Hwang, Ma, & Salaita, 2022). In pancreatic cancer cells, the  $\alpha$ 2,6 sialylation of EGFR promoted cell invasiveness and EMT (Britain et al., 2021), and protected against the EGFR inhibitor, gefitinib (Britain et al., 2018). Along with RTKs, the pro-survival function of ST6Gal1 is mediated through the  $\alpha$ 2,6 sialylation of the TNFR1 and Fas death receptors. The  $\alpha$ 2,6 sialylation of TNFR1 and Fas blocks ligand-induced internalization of these receptors, thereby preventing apoptotic signaling (Holdbrooks et al., 2018; Swindall & Bellis, 2011). Finally, integrin cell adhesion receptors represent another key target for sialylation by ST6Gal1. Indeed, many of ST6Gal1's effects on tumor cell migration and invasion are driven by sialylation of the  $\beta$ 1 integrin subunit (Christie, Shaikh, Lucas, Lucas, & Bellis, 2008; Hou, Hang, Isaji, Lu, Fukuda, & Gu, 2016; Seales et al., 2005; Shaikh, Seales, Clem, Hennessy, Zhuo, & Bellis, 2008). Taken together, these studies point to the importance of receptor sialylation in tumor cell growth, apoptosis-resistance, migration and invasiveness.

In conjunction with well-established functional roles for receptor sialylation, emerging evidence suggests that the sialylation of N-glycans may be a pivotal determinant for the efficacy of therapeutic monoclonal anti-bodies (Duarte et al., 2022). Duarte et al. showed that the  $\alpha$ 2,6 sialylation of N-glycans on ERBB2 blocked the binding of Trastuzumab, and it was further suggested that high ST6Gal1 levels may be predictive of a poor patient response to Trastuzumab therapy (Duarte, Rodrigues, Gomes, Hensbergen, Ederveen, & de Ru, 2021). Likewise, the  $\alpha$ 2,6 sialylation of EGFR protected against cytotoxicity induced by Cetuximab (Rodrigues, Duarte, Gomes, Balmana, Martins, & Hensbergen, 2021). In light of the growing use of tumor-targeting therapeutic antibodies, these studies have significant implications for cancer treatment.

### 3. Sialyl Lewis antigens

A common feature of pancreatic tumors is an increase in expression of sialyl Lewis antigens (Fig. 1B) (Satomura, Sawabu, Takemori, Ohta, Watanabe, & Okai, 1991; Singh, Pal, Yadav, Tang, Partyka, & Kletter, 2015; Zhang, Yang, Li, Wu, Zhang, & Chen, 2015). Sialyl Lewis structures can be found on N- and O-linked glycans on glycoproteins, or on glycolipids (Trinchera et al., 2017). The Lewis X ( $Le^X$ ) antigen is generated by the addition of an  $\alpha$ 1,3-linked fucose to GlcNAc on type 2N-acetyllactosamine (LacNAc). The sialyl Lewis X ( $sLe^X$ ) structure contains both an  $\alpha$ 1,3-linked fucose and an  $\alpha$ 2,3-linked sialic acid on type 2 LacNAc. Alternatively,  $\alpha$ 1,4 fucosylation occurs on type 1 LacNAc, leading to Lewis A ( $Le^A$ ). The sialyl  $Le^A$  ( $sLe^A$ ) tetrasaccharide includes the  $\alpha$ 1,4-linked fucose and an  $\alpha$ 2,3-linked sialic acid on type 1 LacNAc. Multiple glycosyltransferases contribute to the synthesis of sialyl Lewis antigens, including various  $\alpha$ 1,3 fucosyl-transferases and  $\alpha$ 1,4 fucosyltransferases, which transfer fucose to type 2 and type 1 LacNAcs, respectively. Additionally, several  $\alpha$ 2,3 sialyltransferases direct the sialylation of type 1 and type 2 LacNAcs. Increased sialyl Lewis expression is one of the main changes to the glycome in pancreatic cancer, and functionally, sialyl Lewis antigens play a seminal

role in hematogenous metastasis (Natoni et al., 2016; Satomura, Sawabu, Takemori, Ohta, Watanabe, & Okai, 1991; Sozzani, Arisio, Porpiglia, & Benedetto, 2008). Sialyl Lewis antigens are preferentially expressed on the surface of metastatic adenocarcinoma cells (Hanski, Hanski, Zimmer, Ogorek, Devine, & Riecken, 1995). These structures mediate tumor cell interactions with the vascular endothelium, facilitating tumor cell extravasation and metastasis (Lowe, Stoolman, Nair, Larsen, Berhend, & Marks, 1990; Takada, Ohmori, Yoneda, Tsuyuoka, Hasegawa, & Kiso, 1993; Walz, Aruffo, Kolanus, Bevilacqua, & Seed, 1990).

The sLe<sup>A</sup> antigen is highly expressed in embryonic tissues, down-regulated in adult tissues, and then re-expressed in malignant lesions (Goonetilleke & Siriwardena, 2007; Lahdenne, Pitkanen, Rajantie, Kuusela, Siimes, & Lanning, 1995). FUT3 is the primary fucosyltransferase involved in generating sLe<sup>A</sup>, along with the ST3Gal3 sialyltransferase (Dall'Olio et al., 2021; Trinchera et al., 2017). FUT3 overexpression is associated with a poor patient prognosis in breast (do Nascimento et al., 2020) and renal carcinoma (Meng, Xu, Yang, Zhou, Chang, & Shi, 2017) and knockdown of FUT3 inhibits pancreatic cancer cell proliferation and invasion in vivo (Zhan et al., 2018). The sLe<sup>A</sup> antigen has been identified on a variety of proteins including carcinoembryonic antigen, circulating apo-lipoproteins, and mucins (Tang, Hsueh, Kletter, Bern, & Haab, 2015). The binding of tumor cell sLe<sup>A</sup> antigens to E-selectin on endothelial cells promotes tumor cell rolling, an event necessary for the subsequent arrest of tumor cells and exit from the vasculature (Kannagi, 2007; Takada, Ohmori, Takahashi, Tsuyuoka, Yago, & Zenita, 1991). Supporting a pro-metastatic role for sLe<sup>A</sup>, treatment with function-blocking antibodies against sLe<sup>A</sup> inhibited the development of liver metastases after intraperitoneal transplantation of SW1990 pancreatic cancer cells (Hosono, Narita, Kimura, Sato, Nakashio, & Kasai, 1998). Moreover, high sLe<sup>A</sup> expression on SUIT2 pancreatic cancer cells increased their adherence to endothelial cells after TNF $\alpha$  stimulation, and the sLe<sup>A</sup>-expressing SUIT2 cells more readily developed liver metastasis when implanted into nude mice after inflammatory insult (Nozawa, Hirota, Okabe, Shibata, Iwamura, & Haga, 2000). Levels of sLe<sup>A</sup> have been consistently correlated with metastasis across multiple pancreatic cancer cell lines. In carcinoma cell lines generated from 9 pancreatic cancer patients, the expression of sLe<sup>A</sup> was significantly associated with metastasis and strikingly, the intensity of surface sLe<sup>A</sup> on each cell line directly correlated with the number of metastatic colonies in the liver (Kishimoto, Ishikura, Kimura, Takahashi, Kato, & Yoshiki, 1996). Definitive evidence that sLe<sup>A</sup> antigens play a causal role in pancreatic cancer progression was provided by the Tuveson laboratory. This group generated a genetically-engineered mouse model that expressed sLe<sup>A</sup> antigens in the pancreas via the transgenic expression of the FUT3 and  $\beta$ 3GALT5 glycosyltransferases (Engle, Tiriatic, Rivera, Pommier, Whalen & Oni, 2019). Mice expressing sLe<sup>A</sup> antigens developed severe pancreatitis that, in the presence of oncogenic Kras, led to accelerated pancreatic cancer initiation and reduced survival when compared with mice expressing Kras alone (Engle, Tiriatic, Rivera, Pommier, Whalen, & Oni, 2019). In the aggregate, these results implicate the sLe<sup>A</sup> antigen as an attractive target for immunotherapeutic treatment of PDAC, and fully humanized sLe<sup>A</sup> antibodies have passed phase 1 A clinical trials for pancreatic cancer (Sawada, Sun, Wu, Hong, Ragupathi, & Livingston, 2011).

The sLe<sup>A</sup> structure is the epitope of the CA19-9 antigen, which was discovered in 1979 and has been widely used as a clinical biomarker for pancreatic cancer (Herlyn, Sears, Steplewski, & Koprowski, 1982; Herlyn, Steplewski, Herlyn & Koprowski, 1979; Koprowski, Steplewski, Mitchell, Herlyn, Herlyn, & Fuhrer, 1979; Magnani, Brockhaus, Smith, Ginsburg, Blaszczyk, & Mitchell, 1981; Magnani, Nilsson, Brockhaus, Zopf, Steplewski, & Koprowski, 1982; Magnani, Steplewski, Koprowski, & Ginsburg, 1983; Yue, Partyka, Maupin, Hurley, Andrews, & Kaul, 2011). CA19-9 is useful for monitoring patient response to cancer treatment but has limited utility in terms of diagnosis (Galli et al., 2013; Goonetilleke & Siriwardena, 2007; Tempero, Uchida, Takasaki, Burnett, Steplewski, & Pour, 1987; Yue, Maupin, Fallon, Li, Partyka, & Anderson, 2011). However, monitoring CA19-9 antigen on specific proteins, such as mucins, may improve the performance of the CA19-9 assay (Partyka, Maupin, Brand, & Haab, 2012; Tang, Partyka, Hsueh, Sinha, Kletter, & Zeh, 2016; Yue, Maupin, Fallon, Li, Partyka, & Anderson, 2011). CA19-9 antigen has been reported to be carried by MUC1, MUC5AC, and MUC16 in pancreatic cancer (Yue, Goldstein, Hollingsworth, Kaul, Brand, & Haab, 2009; Yue, Maupin, et al., 2011), and the presence of sialyl Lewis epitopes on MUC16 enhances the ability of circulating tumor cells to adhere to E and L-selectins (Chen, Dallas, Balzer, & Konstantopoulos, 2012).

As with sLe<sup>A</sup>, the sLe<sup>X</sup> antigen is overexpressed in both PDAC cell lines and tissues (Hosono, Narita, Kimura, Sato, Nakashio, & Kasai, 1998; Kim, Itzkowitz, Yuan, Chung, Satake, & Umeyama, 1988; Peracaula, Tabares, Lopez-Ferrer, Brossmer, de Bolos, & de Llorens, 2005; Satomura et al., 1991; Sinn, Brown, Oberle, & Thompson, 1992). A variety of  $\alpha$ 1,4 fucosyltransferases can participate in the biosynthesis of sLe<sup>X</sup> antigens including FUT4,5,6 and 7 (Dall'Olio et al., 2021; Trinchera et al., 2017). Of these, FUT6 is known to be upregulated in pancreatic cancer (Mas, Pasqualini, Caillol, El Battari, Crotte, & Lombardo, 1998). FUT3 can also generate sLe<sup>X</sup>, as this enzyme has both  $\alpha$ 1,3 and  $\alpha$ 1,4 fucosyltransferase activity (Kukowska-Latallo, Larsen, Nair, & Lowe, 1990; Trinchera et al., 2017).

The sialylation of sLe<sup>X</sup> is mainly elaborated by ST3Gal3,4 or 6 (Carvalho, Harduin-Lepers, Magalhaes, Machado, Mendes, & Costa, 2010). Elevated sLe<sup>X</sup> levels were documented in approximately 30% of pancreatic cancer tissues (Pour, Tempero, Takasaki, Uchida, Takiyama, & Burnett, 1988) and select proteins with enriched sLe<sup>X</sup> showed increased expression in PDAC patients compared to healthy controls (Balmana, Sarrats, Llop, Barrabes, Saldoval, & Ferri, 2015; Sarrats, Saldoval, Pla, Fort, Harvey, & Struwe, 2010). Numerous proteins implicated in pancreatic cancer, including Wnt7b and SPARC, express the sLe<sup>X</sup> antigen (Rho, Mead, Wright, Brenner, Stave, & Gildersleeve, 2014). Increased expression of sLe<sup>X</sup> is an efficient marker for predicting the postoperative progression of hepatic metastasis, where PDAC patients with high sLe<sup>X</sup> have a poor prognosis (Takahashi, Oda, Hasebe, Sasaki, Kinoshita, & Konishi, 2001a, 2001b). In one study, sLe<sup>X</sup> was found to be upregulated in only 13 of 69 pancreatic cancers, but co-expression of sLe<sup>A</sup> and sLe<sup>X</sup> enhanced the ability to differentiate pancreatic cancers from benign pancreatic diseases (Tang, Singh, Partyka, Kletter, Hsueh, & Yadav, 2015).

Interestingly, the expression of sLe<sup>X</sup> and sLe<sup>A</sup> antigens may be influenced by the activity of the  $\alpha$ 1,2 fucosyltransferases, FUT1 and FUT2, which add fucose to galactose (Abrantes,



Posada, Guillon, Esteves, & Le Pendu, 2009; Blanas, Sahasrabudhe, Rodriguez, van Kooyk, & van Vliet, 2018). Because FUT1/2 compete with  $\alpha$ 2,3 sialyltransferases for the galactose on LacNAc, high levels of FUT1/2 can inhibit the production of sialyl Lewis structures (Gorelik, Xu, Henion, Anaraki, & Galili, 1997; Goupille, Hallouin, Meflah, & Le Pendu, 1997; Prieto, Larsen, Cho, Rivera, Shilatifard, & Lowe, 1997). For example, the ectopic expression of FUT1 in pancreatic cancer cells suppressed the expression of sLe<sup>A</sup> and sLe<sup>X</sup>, which concomitantly attenuated E selectin-mediated cell adhesion as well as metastatic properties in vivo (Aubert, Panicot, Crotte, Gibier, Lombardo, & Sadoulet, 2000a,2000b). In another study, FUT1 overexpression in pancreatic (BxPC3), hepatic (HepG2), and colon (HT-29) cancer cell lines reduced sLe<sup>X</sup>, but not sLe<sup>A</sup>, expression. The FUT1-transduced HT-29 and HepG2 cells, but not BxPC3 cells, failed to bind to E-selectin or to activated endothelial cells (Mathieu, Prorok, Benoliel, Uch, Langlet, & Bongrand, 2004).

The bioavailability of particular sialyltransferases can also regulate sLe<sup>A</sup> and sLe<sup>X</sup> expression levels. Peracaula and colleagues examined sialyltransferases in the established PDAC cell lines, Capan-1, MDAPanc-3, MDAPanc-28 and Panc-1 (Perez-Garay et al., 2013). MDAPanc-28 cells had the lowest expression of ST3Gal3 and ST3Gal4 while the other lines had comparable transcript levels of both enzymes. ST3Gal6 was undetectable in all cell lines examined. All cell lines, with the exception of MDAPanc-28, demonstrated high ST3Gal3 and ST3Gal4 expression, which correlated with high  $\alpha$ 2,3 sialyltransferase activity. Accordingly, greater cell surface levels of sLe<sup>A</sup> and sLe<sup>X</sup> were noted in all cell lines except MDAPanc-28. The overexpression of ST3Gal4 in MDAPanc-28 cells resulted in heightened E-selectin-dependent cell adhesion and migration and a heterogeneous increase in sLe<sup>X</sup> levels. In another study, Capan-1 and MDAPanc-28 cells with forced overexpression of ST3Gal3 displayed upregulated surface sLe<sup>X</sup> expression and enhanced E-selectin binding capacity and cell migration (Perez-Garay et al., 2010). Conversely, knockdown of ST3Gal3 and ST3Gal4 expression in BxPC3 and Capan-1 cells led to significantly lower levels of sLe<sup>X</sup>, leading to inefficient binding to E-selectin as well as decreased cell migration and invasion (Guerrero et al., 2020).

Further underscoring the functional importance of sLe<sup>A</sup> and sLe<sup>X</sup> antigens, the establishment and growth of metastatic colonies of the human pancreatic carcinoma cell line, PCI-6, were reduced after antibody blockade of sLe<sup>A</sup> and sLe<sup>X</sup> (Kawarada, Ishikura, Kishimoto, Kato, Yano, & Kato, 2000). Consistent with this work, Aubert et al. knocked-down FUT3 expression in BxPC3 pancreatic cancer cells and found that this diminished the expression of sLe<sup>A</sup> and sLe<sup>X</sup>, and prevented cancer cell adhesion to E-selectin with a resultant decrease in metastasis (Aubert, Panicot-Dubois, Crotte, Sbarra, Lombardo, & Sadoulet, 2000a, 2000b). On the other hand, some data suggest a unique role for Lewis-negative pancreatic tumor cells. In a study including 853 patients with pancreatic cancer, 11.7% of patients were Lewis negative (Liu, Deng, Jin, Gong, Cheng, & Fan, 2020). The Lewis-negative patients had poorer outcomes and higher metastatic rates than Lewis-positive patients. Although there is robust evidence for the pro-invasive phenotype conferred by sLe<sup>A</sup> and sLe<sup>X</sup> antigen expression, more investigation is needed to elucidate the molecular mechanisms that account for the aggressiveness of Lewis antigen-negative pancreatic cancer.

#### 4. Sialylated forms of truncated O-glycans

Another major alteration in the glycome of neoplastic cells is the expression of immature, truncated O-glycans, exemplified by the Tn, sialyl-Tn (sTn), T and sialyl-T (sT) antigens (Fig. 1C). Truncated O-glycans arise from the disrupted elongation of mucin-type O-glycan chains. Mucin-type O-glycosylation is initiated by a family of N-acetylgalactosaminyltransferases (GALNTs) that transfer GalNAc to the hydroxyl group of serine or threonine residues to generate the Tn antigen (GalNAc $\alpha$ 1-Ser/Thr). Galactose is then added to the Tn antigen by the T synthase enzyme (core 1  $\beta$ 1,3 galactosyltransferase, C1GALT1) to produce the T antigen, specifically, the core 1 disaccharide, Gal $\beta$ 1-3GalNAc $\alpha$ 1. In normal tissues, the core 1 disaccharide is typically extended by an array of enzymes which together direct the synthesis of elongated, and often branched, O-glycan structures (Magalhaes et al., 2021). The dysregulated synthesis of O-glycans contributes to a number of pathologies including familial tumoral calcinosis (Ichikawa, Guignonis, Imel, Courouble, Heissat, & Henley, 2007; Kato, Jeanneau, Tarp, Benet-Pages, Lorenz-Depiereux, & Bennett, 2006; Topaz, Shurman, Bergman, Indelman, Ratajczak, & Mizrachi, 2004), Tn syndrome (Flores, Lemos, Rema, Taulescu, Seixas, & Reis, 2020; Ju & Cummings, 2005), IgA nephropathy (Allen, Bailey, Brenchley, Buck, Barratt, & Feehally, 2001), high-density lipoprotein metabolism (Kathiresan, Melander, Guiducci, Surti, Burt, & Rieder, 2008; Wang, Mao, Narimatsu, Ye, Tian, & Goth, 2019) and cancer (Ju, Aryal, Kudelka, Wang, & Cummings, 2014; Kim & Varki, 1997; Kolbl et al., 2015; Springer, 1997; Stowell et al., 2015).

The abnormal expression of immature, truncated O-glycans is a characteristic feature of nearly all epithelial cancers. One of the prime mechanisms underlying the synthesis of truncated O-glycans is a decrease in the activity of the T synthase, which leads to an accumulation in the Tn antigen. The Tn antigen can be sialylated by certain ST6GalNAc enzymes to produce the sTn disaccharide ( $\alpha$ 2,6 sialylated GalNAc), but cannot be further extended. The T synthase requires a molecular chaperone called COSMC (C1GALT1C1) for proper folding and export to the Golgi (Wang, Ju, Ding, Xia, Wang, & Xia, 2010). In the absence of COSMC, the T synthase is misfolded and targeted for degradation by the proteasome (Ju & Cummings, 2002). Indeed, knockdown of COSMC expression in Panc-1 PDAC cells prevented O-glycan elongation beyond the initial GalNAc addition (Hofmann, Schluter, Lange, Mercanoglu, Ewald & Folster, 2015). The increased levels of Tn antigen in the COSMC knockdown cells were associated with enhanced cell migration and resistance to apoptosis (Hofmann, Schluter, Lange, Mercanoglu, Ewald, & Folster, 2015). In the T3M4 PDAC cell line, genetic deletion of *C1GALT1C1* conferred oncogenic characteristics including cell invasiveness, apoptosis-resistance and EMT, along with enhanced tumor growth and invasion in xenograft models (Radhakrishnan, Dabelsteen, Madsen, Francavilla, Kopp & Steentoft, 2014; Thomas, Sagar, Caffrey, Grandgenett, & Radhakrishnan, 2019). A tumor-promoting function for COSMC was further confirmed in a genetically-engineered mouse model. Chugh et al. crossed the COSMC knockout mouse line to the “KPC” PDAC mouse model, which expresses oncogenic KRas (Kras<sup>G12D</sup>) and mutated p53 (Trp<sup>53R172H</sup>) (Chugh, Barkeer, Rachagani, Nimmakayala, Perumal & Pothuraju, 2018). KPC mice with COSMC knockout exhibited significantly accelerated PDAC progression, metastasis and

mortality. The more advanced malignancy noted in COSMC knock-out mice was attributed, at least in part, to the activation of the ERBB family receptors, EGFR and Her2.

The *CIGALTIC1* gene is silenced in many types of cancers including PDAC through hypermethylation (Ju, Lanneau, Gautam, Wang, Xia & Stowell, 2008; Radhakrishnan, Dabelsteen, Madsen, Francavilla, Kopp, & Steentoft, 2014). Radhakrishnan et al. suggested that increased expression of Tn and sTn could be attributed to *CIGALTIC1* hypermethylation in 38% of PDAC tumors (Radhakrishnan et al., 2014). Loss-of-function mutations or deletions in *CIGALTIC1* constitute another major conduit for increased expression of Tn/sTn (Ju, Lanneau, Gautam, Wang, Xia, & Stowell, 2008). Inactivating mutations in *CIGALTIC1* have been documented in many human cancers and are consistently correlated with reduced expression of the T synthase and increased abundance of Tn and sTn (Sun et al., 2018). However, in one study of PDAC patient tissues, no mutations were detected in *CIGALTIC1*, whereas hypermethylation of *CIGALTIC1* was prevalent (Radhakrishnan et al., 2014).

Truncations in O-glycan structure can also occur as a consequence of increased expression of ST6GalNAc1, which appears to be the principal enzyme responsible for generating sTn (Ogawa, Hirohashi, Murai, Nishidate, Okita, & Wang, 2017). The upregulation of ST6GalNAc1 in pancreatic and other cancers has been widely reported (Hruban, Goggins, Parsons, & Kern, 2000; Schuessler, Pintado, Welt, Real, Xu, & Melamed, 1991). Because ST6GalNAc1 and the T synthase both use Tn as a substrate, high levels of ST6GalNAc1 may out-compete the T synthase, resulting in an enrichment in sTn. Tn and sTn antigens are not usually detected in the healthy pancreas, however, these O-glycan structures are markedly upregulated in PDAC tissues (Hofmann et al., 2015; Remmers, Anderson, Linde, DiMaio, Lazenby, & Wandall, 2013; Romer, Aasted, Dabelsteen, Groen, Schnabel & Tan, 2021). The overexpression of Tn and sTn has been associated with enhanced PDAC growth and metastatic dissemination, as well as poor patient prognosis (Burchell et al., 2001; Hofmann et al., 2015; Mereiter, Balmana, Gomes, Magalhaes, & Reis, 2016; Radhakrishnan et al., 2014).

The sTn antigen has served as an important cancer biomarker for decades (Munkley, 2016). Elevated levels of sTn are detectable in tissue sections and sera from PDAC patients (Motoo, Kawakami, Watanabe, Satomura, Ohta, & Okai, 1991; Nanashima, Yamaguchi, Nakagoe, Matsuo, Sumida, & Tsuji, 1999; Thomas et al., 2019) and have both diagnostic and prognostic significance. Mucins are major carriers of sTn, and much of the sTn present in serum is present on shed forms of mucins such as MUC1 and MUC16 (Aithal, Rauth, Kshirsagar, Shah, Lakshmanan, & Junker, 2018; Chen, Zhang, Zhang, Zhu, Ko, & Yung, 2021; Rajesh, Sagar, Rathinavel, Chemparathy, Peng, & Yeh, 2022). In tandem with biomarker function, sTn is receiving increasing attention as a therapeutic target. Humanized antibodies are in development for use in antibody-drug conjugate treatments and other types of immunotherapy (Eavarone, Al-Alem, Lugovskoy, Prendergast, Nazer, & Stein, 2018; Loureiro, Sousa, Ferreira, Chai, Lima, & Pereira, 2018; Prendergast, Galvao da Silva, Eavarone, Ghaderi, Zhang, & Brady, 2017). Additionally, sTn is currently being investigated as a target molecule for vaccines (Ibrahim, Murray, Zhou, Mittendorf, Sample,

& Tautchin, 2013) and CAR-T cell therapies (Abrantes, Duarte, Gomes, Walchli, & Reis, 2022; Loureiro, Feldmann, Bergmann, Koristka, Berndt, & Arndt, 2018).

Similar to Tn and sTn, the T antigen and sT antigen are frequently enriched in cancer cells (Cervoni, Cheng, Stackhouse, Heimbürg-Molinari, & Cummings, 2020; Munkley & Elliott, 2016). The sT antigen is elaborated primarily by the ST3Gal1 enzyme, which adds sialic acid in an  $\alpha$ 2,3 linkage to the galactose of the T antigen. Both ST3Gal1 and the sT antigen are overexpressed in an array of cancers, including pancreatic cancer (Hugonnet, Singh, Haas, & von Gunten, 2021; Rodriguez et al., 2021). However, the T antigen is also expressed in the healthy pancreas (albeit at lower levels) (Doi, Ino, Angata, Shimada, Narimatsu, & Hiraoka, 2020; Osako, Yonezawa, Siddiki, Huang, Ho, & Kim, 1993), which limits its usefulness as a cancer-specific biomarker. Furthermore, the expression of the T antigen in PDAC tissues is much lower than that of the Tn antigen (Chugh, Barkeer, Rachagani, Nimmakayala, Perumal, & Pothuraju, 2018).

Truncated O-glycans are frequently expressed in early stage, pre-malignant lesions that harbor potential to develop into adenocarcinomas (Burchell et al., 2001; Freitas, Campos, Gomes, Pinto, Macedo, & Matos, 2019; Ju et al., 2014; Ju, Wang, Aryal, Lehoux, Ding, & Kudelka, 2013; Julien et al., 2012; Radhakrishnan et al., 2014). Intriguingly, the expression of Tn and sTn is often reduced with increasing tumor progression (Romer, Aasted, Dabelsteen, Groen, Schnabel, & Tan, 2021). It has been suggested that the expression of Tn/sTn and T/sT antigens may be inversely correlated. Tn/sTn antigens are upregulated in premalignant cells, promoting early events in tumorigenesis, whereas the expression levels of T-synthase, and thus T antigen, appear to increase with tumor progression (Bergstrom, Liu, Zhao, Gao, Wu, & Song, 2016; Gao, Bergstrom, Fu, Xie, Chen, & Xia, 2016). Therefore, Tn and sTn may be useful biomarkers or therapeutic targets for early stages in neoplasia, while targeting T and sT antigen may be more effective in established tumors.

## 5. Activation of Siglec receptors by tumor sialoglycans

The sialylation of surface receptors has profound effects on tumor cell signaling and phenotype, however tumor sialylation also plays a major role in regulating the behavior of immune cells within the tumor microenvironment. Sialic acids present on the surface of tumor cells serve as ligands for the Siglec family of mammalian lectins (Fig. 1D) (Varki & Angata, 2006). Hypersialylated N-glycans, sialyl Lewis structures, and sTn antigens all serve as important ligands for Siglecs (Gonzalez-Gil & Schnaar, 2021). Siglecs are expressed by a diversity of immune cells including tumor-infiltrating T cells, B cells, NK cells, dendritic cells, and macrophages (Crocker & Varki, 2001; Duan & Paulson, 2020; Gonzalez-Gil & Schnaar, 2021; Varki & Angata, 2006). Siglecs are categorized into two subtypes according to sequence homology, CD33-related Siglecs that show high sequence identity (50–99%) and the others (Siglec-1, Siglec-2, Siglec-4, and Siglec-15) sharing 25%–30% sequence identity (Gonzalez-Gil & Schnaar, 2021; Laubli, Kawanishi, George Vazhappilly, Matar, Merheb, & Sarwar Siddiqui, 2021; Lim et al., 2021). Fourteen Siglecs have been identified in humans (Gonzalez-Gil & Schnaar, 2021). Thirteen of these are found on overlapping immune cell types, and one (Siglec-4) on myelinated neurons. Structurally, Siglecs have an extra-cellular N-terminal V-set immunoglobulin (Ig) domain

with a conserved sialic acid-binding site, followed by varying numbers of C2-set Ig-like domains (Crocker, Clark, Filbin, Gordon, Jones, & Kehrl, 1998; Crocker et al., 2007; Duan & Paulson, 2020; Gonzalez-Gil & Schnaar, 2021). The extracellular domain is connected to a single membrane-spanning domain and a cytosolic domain containing multiple regulatory motifs. Based on the intracellular motifs, Siglecs can exert activating or inhibitory effects to modulate the immune system. Siglecs that carry intracellular immunoreceptor tyrosine-based inhibitory (ITIM) motifs are major drivers of inhibitory immune responses (Gonzalez-Gil & Schnaar, 2021; Jiang, Qi, Kang, & Wang, 2022). Immune cells infiltrating into the tumor bind to tumor sialic acids through their surface Siglecs; this interaction consequently suppresses the immune response leading to tumor escape from immune surveillance (Hudak et al., 2014; Laubli, Pearce, Schwarz, Siddiqui, Deng, & Stanczak, 2014). Hence, Siglecs serve as immune checkpoint molecules much like the well-known immunotherapy targets, programmed cell death protein 1 (PD-1) and cytotoxic T lymphocyte-associated protein 4 (CTLA-4) (Fraschilla & Pillai, 2017; Macauley, Kawasaki, Peng, Wang, He, & Arlian, 2015; Sharma & Allison, 2015). There is currently growing interest in exploiting the sialoglycan-Siglec axis as a novel avenue for immune checkpoint therapy (Adams, Stanczak, von Gunten, & Laubli, 2018; Bull, Heise, Adema, & Boltje, 2016; Daly et al., 2019), and several Siglec inhibitors have entered into clinical trials.

PDAC has an aggressive and complex tumor microenvironment (Dougan, 2017; Rodriguez et al., 2021) and anti-PD1 immunotherapy shows little effectiveness for treatment of this malignancy (Dougan, 2017; Feng, Xiong, Cao, Yang, Zheng, & Song, 2017). Recently, Rodriguez et al. uncovered a role for the inhibitory Siglecs, Siglec-7 and Siglec-9, in PDAC progression (Rodriguez et al., 2021). It was demonstrated that the engagement of Siglec-7 and Siglec-9 on monocytic cells with sialic acids on PDAC cells induced the conversion of monocytes into immunosuppressive macrophages within the microenvironment. In this same report, the Siglec-dependent reprogramming of monocytes was associated with poor patient outcomes. This work established Siglec activation as a key mechanism underlying PDAC-mediated immunosuppression, and also identified Siglecs as promising new immunotherapy targets that could potentially serve as alternatives to PD1-targeting treatments. Notably, CAR-T cell therapies have been developed that incorporate Siglec-7 or Siglec-9 to enable targeting of sialic acid-expressing tumor cells. Siglec-7/9-based CAR-T cell therapy is currently being tested for potential treatment of melanoma (Meril, Harush, Reboh, Matikhina, Barliya, & Cohen, 2020), however there is hope that this strategy may have efficacy in PDAC. Humanized monoclonal antibodies against Siglecs also hold promise for treatments utilizing antibody-drug conjugates (Lim et al., 2021; Smith & Bertozzi, 2021).

A role for Siglec-4 (also called Myelin Associated Glycoprotein or MAG) has been reported in the recurrence of PDAC after surgical resection (Lim et al., 2021; Swanson, McDermott, Singh, Eggers, Crocker, & Hollingsworth, 2007). Siglec-4 is mainly expressed in myelinated neurons and auto-antibodies against Siglec-4 have been observed in several neuropathic syndromes (Dougan, 2017). Apart from the brain, an interaction between Siglec-4 and MUC1 expressed on tumor cells is involved in pancreatic cancer perineural invasion (Swanson et al., 2007). Perineural invasion is a common pathologic manifestation in PDAC, whereby cancer cells invade the endoneurium of pancreatic nerves. This process leads to

significant lower back pain in PDAC patients and is a source of local recurrence after the resection of primary tumor masses (Liu, Ma, Xu, Lei, Li, & Wang, 2012; Swanson et al., 2007; Takahashi, Hasebe, Oda, Sasaki, Kinoshita, & Konishi, 2001a, 2001b). Swanson et al. showed that Siglec-4 binds to pancreatic cancer cells in a sialic acid-dependent manner and interacts with the MUC1 adhesive mucin (Swanson et al., 2007). MUC1 is overexpressed and aberrantly glycosylated in PDAC and is responsible for the adhesion of PDAC cells to Siglec-4-expressing pancreatic nerves. Future studies of the Siglec-4 and MUC1 interaction could provide new avenues for developing treatments for pancreatic cancer pain and recurrence.

More recently, Siglec-15 has been implicated in pancreatic cancer progression and prognosis. High Siglec-15 mRNA expression was associated with worse overall survival of PDAC patients (Li, Huang, Chen, Yao, Ke, & He, 2020). Siglec-15 has also been reported to promote PDAC immune evasion. Li et al. showed that sialic acids on PDAC cells interacted with Siglec-15 to potentiate the immunosuppressive properties of tumor-associated macrophages within the PDAC microenvironment (Li, Jin, Li, Ye, Li, & Jiang, 2022). However, a separate study suggested that Siglec-15 was associated with favorable patient outcomes (Chen, Mo, Zhang, Ma, Lu, & Yu, 2022). In this latter report, Siglec-15 was primarily expressed by moderate to well-differentiated tumors, and was found to be a good prognostic indicator for PDAC. Further studies will be needed to resolve this discrepancy. Like Siglec-15, Siglec-10 has emerged as a potential mediator of immunosuppression in PDAC. In this case, Siglec-10 appears to exert its biological effects by binding to the CD24 surface receptor (Yin & Gao, 2020). The binding of Siglec-10 to sialylated forms of CD24 expressed by pancreatic cancer cells facilitated tumor cell escape from immune recognition. CD24 is a well-known marker for cancer stem cells, and is a major player in the malignant behavior of pancreatic cancer (Ikenaga, Ohuchida, Mizumoto, Yu, Kayashima, & Hayashi, 2010). The identification of a Siglec-10-CD24 interaction highlights a new glycosylation-dependent mechanism by which CD24 may promote tumor progression.

## 6. Concluding remarks

Despite advances in our understanding of the molecular mechanisms underlying pancreatic cancer, little progress has been made in the treatment of this cancer and the 5-year survival rate remains dismal. Although it is well-recognized that large scale changes in the glycome occur during pancreatic cancer, this knowledge has not been effectively utilized to develop new therapeutics to combat this disease. In this review, we have summarized the evidence supporting functional roles for tumor-associated sialoglycans in pancreatic cancer, with a particular focus on hypersialylated N-glycans, sialyl Lewis antigens, and sialylated, truncated O-glycans. These sialylated structures have a significant impact on tumor cell phenotype, and also contribute to immune suppression through the engagement of Siglec receptors. Although studies of tumor glycosylation have historically lagged behind other areas of cancer research, recent developments in the field are illuminating the enormous potential for glycans, including sialoglycans, to serve as cancer biomarkers and clinical targets. Targeting sialoglycans offers a novel approach for treating pancreatic cancer, providing an alternative to current therapeutic modalities which remain largely ineffective.

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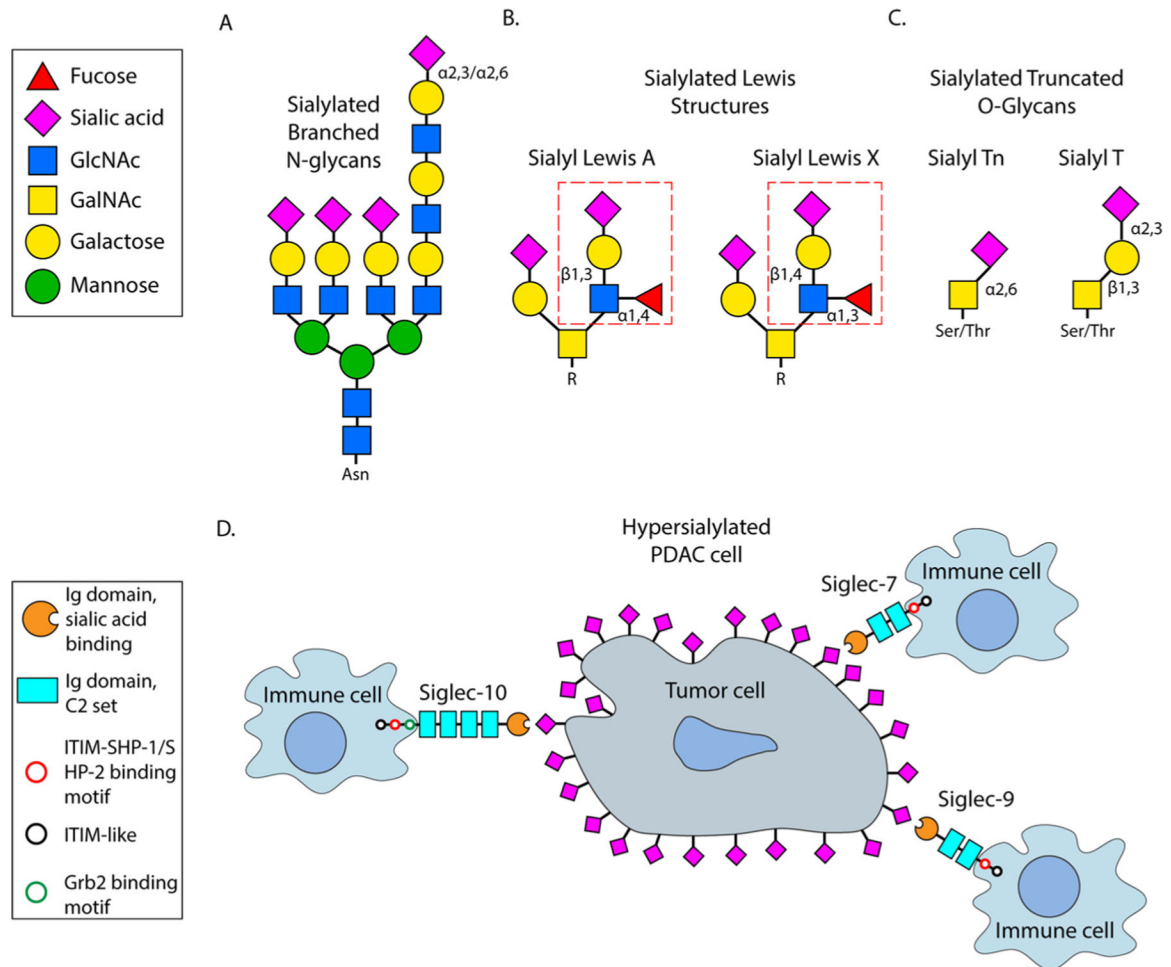
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**Fig. 1. Sialoglycans enriched in tumor cells and their cognate receptors, Siglecs.**  
 (A) N-linked, branched glycan terminating with either an  $\alpha 2,3$  or  $\alpha 2,6$  linked sialic acid. (B) Sialylated Lewis structures including sialyl Lewis A (left) and sialyl Lewis X (right). Dashed red box indicates the sialyl Lewis tetrasaccharide. (C) Sialylated forms of truncated O-glycans typified by sialyl Tn (left) and sialyl T (right) antigens. (D) Schematic demonstrating a hypersialylated pancreatic cancer cell and immune cells expressing various inhibitory Siglecs (Siglec-7, Siglec-9, and Siglec-10).