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Essential role of gastric gland mucin in preventing gastric cancer in mice

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Gastric gland mucin secreted from the lower portion of the gastric mucosa contains unique O-linked oligosaccharides (O-glycans) having terminal α1,4-linked N-acetylglucosamine residues (αGlcNAc). Previously, we identified human α1,4-N-acetylglucosaminyltransferase (α4GnT), which is responsible for the O-glycan biosynthesis and characterized αGlcNAc function in suppressing Helicobacter pylori in vitro. In the present study, we engineered A4gnt+/− mice to better understand its role in vivo. A4gnt+/− mice showed complete lack of αGlcNAc expression in gastric gland mucin. Surprisingly, all the mutant mice developed gastric adenocarcinoma through a hyperplasia-dysplasia-carcinoma sequence in the absence of H. pylori infection. Microarray and quantitative RT-PCR analysis revealed upregulation of genes encoding inflammatory chemokine ligands, proinflammatory cytokines, and growth factors, such as Ccl2, Il-11, and Hgf in the gastric mucosa of A4gnt+/− mice. Further supporting an important role for this O-glycan in cancer progression, we also observed significantly reduced αGlcNAc in human gastric adenocarcinoma and adenoma. Our results demonstrate that the absence of αGlcNAc triggers gastric tumorigenesis through inflammation-associated pathways in vivo. Thus, αGlcNAc-terminated gastric mucin plays dual roles in preventing gastric cancer by inhibiting H. pylori infection and also suppressing tumor-promoting inflammation.

Introduction

Gel-forming mucins covering the gastric mucosa are heavily glycosylated glycoproteins that form a barrier between the stomach and the external environment. Gastric mucins are divided into surface mucin and gland mucin (1). The former is secreted from surface mucous cells lining the gastric mucosa, whereas the latter is produced by gland mucous cells, such as mucous neck cells and pyloric gland cells located in lower layer of the mucosa. Gland mucin characteristically contains O-linked oligosaccharides (O-glycans) with terminal α1,4-linked N-acetylglucosamine residues (αGlcNAc), largely attached to a MUC6 scaffold (2, 3). Interestingly, gland mucin distribution in mammals, including humans, is limited to gland mucous cells of the stomach and Brunner’s glands of the duodenum (1, 4).

Previously, we used expression cloning to identify a human A4GNT cDNA encoding α1,4-N-acetylglucosaminyltransferase (α4GnT), which is responsible for biosynthesis of these O-glycans (5). We also found that α4GnT expression in humans is limited to glandular mucous cells and duodenal Brunner’s glands, in which αGlcNAc is secreted (3). It is well known that Helicobacter pylori is a causative microbe for gastric cancer (6). We then demonstrated in vitro that αGlcNAc suppresses growth and motility of H. pylori by inhibiting biosynthesis of the bacterial cell wall constituent, cholesteryl-α-D-glucopyranoside (7). In fact, H. pylori rarely colonizes the gastric gland mucin containing αGlcNAc but instead solely colonizes the surface mucin (8). However, the role of αGlcNAc in vivo remained undefined.

Here we generated A4gnt+/− mice and found that null mice showed loss of αGlcNAc and developed gastric adenocarcinoma in the absence of H. pylori infection. Microarray and quantitative RT-PCR analysis showed upregulation of numerous genes encoding inflammatory chemokine ligands, proinflammatory cytokines, and growth factors in the gastric mucosa of mutant mice. These results demonstrate that αGlcNAc loss in itself is sufficient to trigger gastric tumorigenesis, most likely through inflammation-associated pathways.

Results

A4gnt+/− mice show complete lack of αGlcNAc expression in gastric gland mucin. To understand the role of αGlcNAc in vivo, we disrupted the A4gnt gene encoding α4GnT in mice (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI59087DS1). After birth, A4gnt+/− mice developed to adulthood and reproduced normally. Immunohistochemistry of the gastroduodenal mucosa with an αGlcNAc-specific antibody revealed loss of αGlcNAc in gastric gland mucous cells and in duodenal Brunner’s glands in A4gnt+/− mice (Figure 1A). Mass spectrometry analysis of O-glycans from the gastric mucosa of the glandular stomach demonstrated that the 9 peaks of oligosaccharides carrying αGlcNAc typically detected in wild-type mice were completely absent in A4gnt−/− mice (Figure 1B). However, 2 peaks of O-glycans, having both sialic acid and fucose residues, appeared, and 2 peaks indicative of oligosaccharides terminated with β-galactose residues were apparently increased in A4gnt−/− mice.

A4gnt−/− mice spontaneously develop gastric adenocarcinoma. To further analyze the consequences of αGlcNAc loss, we undertook morphological examination of A4gnt−/− mice. Surprisingly, histology indicated abnormal proliferation of pyloric epithelial cells in the gastric antrum of mutant mice, even in the absence of oral H. pylori administration. In all A4gnt−/− mice, tumor growth was noted in the antrum as early as postnatal week 5, and tumor
size gradually increased as mice aged (Figure 2, A and B). These tumors were localized to the pyloric mucosa and were never seen in the fundic mucosa of the gastric corpus (Figure 2B and Supplemental Figure 2). Histological examination of the pyloric mucosa revealed that the mucosal thickness of the tumorous portion of A4gnt<sup>−/−</sup> mice was significantly increased compared with that of age-matched wild-type mice (P < 0.01) (Figure 2C), and the number of epithelial cells in the tumorous portion was also increased (P < 0.01) (Figure 2D). By 5 weeks of age, all A4gnt<sup>−/−</sup> mice developed hyperplasia of both surface mucous cells and pyloric gland cells of the antrum but did not show cellular atypia (Figure 2E). By 10 weeks, gastric lesions developed low-grade dysplasia, which showed slight glandular distortion, such as crypt serration or papillary enfolding, with decreased mucin production (Figure 2E). At 20 weeks, gastric pathology proceeded to high-grade dysplasia, characterized by marked glandular complexity, including well-packed tubular gland proliferation with prominent cellular atypia but no intramucosal invasion (Figure 2E). Well-differentiated gastric adenocarcinomas invading the lamina propria developed at 30 weeks in 2 out of 6 A4gnt<sup>−/−</sup> mice, and the incidence of adenocarcinoma increased by 50 weeks of age (Figure 2E and Supplemental Figure 3). All 50-week-old and 60-week-old A4gnt<sup>−/−</sup> mice exhibited adenocarcinoma, with cancer cells mostly located within the gastric mucosa (Figure 2E). Focal submucosal invasion by cancer cells was found in one A4gnt<sup>−/−</sup> mouse at 60 weeks of age (Figure 2B). No distant metastasis was detected in mice observed up to 60 weeks. Undifferentiated types of adenocarcinoma, such as signet ring cell carcinoma, had not developed by 60 weeks of age. Goblet cells expressing MUC2, which are indicative of intestinal metaplasia (9), were rarely detected in the gastric mucosa of the A4gnt<sup>−/−</sup> mice or control A4gnt<sup>+/+</sup> mice during the 60-week observation period (Supplemental Figure 4). No significant abnormality was found in organs other than the glandular stomach (Supplemental Figure 5). These results indicate that loss of αGlcNAc promotes tumor formation of differentiated-type gastric adenocarcinomas, even in the absence of H. pylori infection.
Figure 2

Gastric pathology of A4gnt+/– mice. (A) Gross appearance of the stomach isolated from A4gnt+/+ and A4gnt–/– mice. Scale bar: 5 mm. (B) H&E staining. Low-power view of histology of gastroduodenal mucosa of A4gnt+/+ and A4gnt–/– mice, where c, a, and d indicate the gastric corpus, gastric antrum, and duodenum, respectively. Scale bar: 1 mm. (C) Comparison of mucosal thickness of the pyloric mucosa between A4gnt+/+ and A4gnt–/– mice at different ages. Each group consists of 6 mice, and data represent the mean ± SEM. **P < 0.01. (D) Comparison of epithelial cell number in the pyloric mucosa of A4gnt+/+ and A4gnt–/– mice at different ages. Each group consists of 6 mice, and data represent the mean ± SEM. **P < 0.01. (E) Histology of hyperplasia (at 5 weeks), low-grade dysplasia (at 10 weeks), high-grade dysplasia (at 20 weeks), and differentiated type of adenocarcinoma (at 40 weeks, 50 weeks, and 60 weeks) seen in the pyloric mucosa of A4gnt–/– mice as well as normal pyloric mucosa of 5-week-old A4gnt+/+ mice. For adenocarcinoma, the desmoplastic reaction in 40-week-old mice, cribriform glands in 50-week-old mice, and irregularly oriented tubular glands in 60-week-old mice are shown. Scale bar: 100 μm. Boxed areas are enlarged in lower panels. Scale bar: 50 μm.
A4gnt<sup>+/−</sup> mice show enhanced proliferation of gastric epithelial cells. We next compared the proliferative activity of gastric epithelial cells between A4gnt<sup>+/−</sup> and A4gnt<sup>+/+</sup> mice at various ages by injecting BrdU into the abdominal cavity 1 hour prior to sacrifice and undertaking BrdU immunohistochemistry. The number of BrdU-labeled S-phase cells significantly increased in A4gnt<sup>+/−</sup> mice that were older than 6 weeks, compared with that in age-matched wild-type mice (P < 0.01) (Figure 3A). The labeling indices of BrdU-labeled cells in A4gnt<sup>+/−</sup> mice were also significantly higher than those in A4gnt<sup>+/+</sup> mice at both 40 and 50 weeks of age (P < 0.01 at 40 weeks; P < 0.05 at 50 weeks) (Figure 3B), indicating active proliferation of epithelial cells in these periods. In wild-type mice, the distribution of BrdU-labeled S-phase cells was restricted to the generating zone of the pyloric mucosa, whereas, in A4gnt<sup>+/−</sup> mice, they were widely distributed (Figure 3C). In the latter, BrdU-labeled cells were detected primarily in the upper layer of the mucosa; however, a small but substantial number was seen in the glandular base, indicating abnormal distribution of S-phase cells. By contrast, apoptotic cells, as detected by immunohistochemistry with anti-cleaved caspase-3 antibody, were rarely seen in either A4gnt<sup>+/−</sup> or A4gnt<sup>+/+</sup> mice, and there was no significant difference in their number between the 2 genotypes (Supplemental Figure 6). These results indicate that tumor growth in A4gnt<sup>+/−</sup> mice is largely the result of increased epithelial cell proliferation rather than decreased apoptosis.

**Human gastric adenoma and adenocarcinoma show decreased αGlcNAc expression.** We next asked whether αGlcNAc expression on its scaffold, MUC6, is reduced in human gastric differentiated-type adenocarcinoma or in the potentially premalignant lesion tubular adenoma. As we demonstrated previously (3) and confirmed here, gland mucous cells expressing MUC6 in non-neoplastic gastric mucosa also expressed αGlcNAc (Figure 4A).

**Figure 3** Detection of BrdU-positive S-phase epithelial cells in the pyloric mucosa of A4gnt<sup>+/−</sup> and A4gnt<sup>+/+</sup> mice. (A) Comparison of the number of BrdU-positive, S-phase epithelial cells in the pyloric mucosa of A4gnt<sup>+/−</sup> and A4gnt<sup>+/+</sup> mice at different ages. Each group consists of 6 mice, and data represent the mean ± SEM. **P < 0.01. (B) Comparison of the BrdU-labeling index between A4gnt<sup>+/−</sup> and A4gnt<sup>+/+</sup> mice. Each group consists of 6 mice, and data represent the mean ± SEM. *P < 0.05; **P < 0.01. (C) Localization of S-phase cells in pyloric mucosa. Scale bar: 100 μm.

Immunohistochemical analysis of gastric adenocarcinoma from 54 patients with differentiated-type early gastric adenocarcinoma (Supplemental Table 1) revealed that MUC6 was expressed in 48 (88.8%) tissue specimens. Among them, 41 (85.4%) patients showed reduced numbers of αGlcNAc-positive cancer cells compared with those of MUC6-positive cancer cells in the same tissue sample (Figure 4, B and C). Notably 19 (39.5%) out of these 48 MUC6-positive patients were completely negative for αGlcNAc (Figure 4D). Semiquantitative analysis showed that the reduction in the number of αGlcNAc-positive cancer cells seen in differentiated types of early gastric cancer is statistically significant compared with the number of MUC6-positive cancer cells (P < 0.01) (Figure 4F, left panel). When we used histopathology to classify gastric adenocarcinomas into 2 groups—namely, adenocarcinoma with or without papillary component—significant reductions in αGlcNAc were seen irrespective of the papillary component (Figure 4F, middle and right panels). Subsequently, the same analysis was done on 12 patients with gastric tubular adenoma. Compared with the gastric adenocarcinoma group, both the proportion of MUC6-positive tumors and MUC6 levels were much lower in the gastric adenoma group; specifically, 6 out of 12 (50%) patients were MUC6 positive (Supplemental Table 2). When αGlcNAc expression was compared with that of MUC6 in adenoma cells from MUC6-positive patient specimens (n = 6), 5 out of 6 (83.3%) showed no or reduced expression of αGlcNAc (Figure 4E). Semiquantitative analysis showed that αGlcNAc-positive adenoma cells were significantly reduced relative to MUC6-positive adenoma cells (P < 0.05) (Figure 4G). Overall, these results suggest that reduced αGlcNAc expression on MUC6 occurs not only in differentiated-type adenocarcinoma but also in tubular adenoma in the human stomach.

The gastric mucosa of A4gnt<sup>+/−</sup> mice shows upregulated gene expression of inflammatory chemokine ligands, proinflammatory cytokines, and growth factors. To elucidate pathways linking αGlcNAc to tumor suppression, DNA microarray analysis was carried out using RNA isolated from gastric mucosa of A4gnt<sup>+/−</sup> and A4gnt<sup>+/+</sup> mice at 5, 10, and 50 weeks of age. Using approximately 2.5 × 10<sup>4</sup> probes, we identified 209 consistently upregulated genes and 222 consistently downregulated genes in A4gnt<sup>+/−</sup> mice compared with those in A4gnt<sup>+/−</sup> mice during these periods (Supplemental Tables 3 and 4). Gene ontology analysis of these 431 upregulated and downregulated genes identified 22 upregulated genes that encode proteins with receptor binding properties (Table 1). Among them were genes encoding 7 representative molecules, including inflammatory chemokine ligands Cxcl1, Ccl2, and Cxcl5; proinflammatory cytokines IL-1β and IL-11; and growth factors Hgf and Fgf7. Upregulation of all 7 was validated by quantitative RT-PCR analysis of independent samples of glandular stomach mRNA and found to be statistically significant at 10 weeks of age, a time point coinciding with low-grade dysplasia (Figure 5A). Transcript levels encoding the
bone morphogenetic protein antagonist gremlin 1 (Grem1) also increased at the 10-week time point, but that upregulation was not statistically significant. Statistically significant upregulation of all 7 genes plus Grem1 was seen at 50 weeks of age, a time point coinciding with adenocarcinoma. Overall, gene expression changes noted above were not significant at the 5-week time point, except those for Hgf, which showed a significant increase in A4gnt–/– samples relative to that in controls. The same gene ontology analysis also identified 9 consistently downregulated genes in mutant mice at 5, 10, and 50 weeks of age; these genes encoded proteins with receptor binding properties (Table 2). Significant downregulation of Amb and Egf in A4gnt–/– mice, compared with that in age-matched A4gnt+/+ mice, was confirmed by quantitative RT-PCR analysis at as early as 5 weeks prior to development of gastric adenocarcinoma (Figure 5B). Pthlh was also significantly downregulated in mutant mice relative to that in controls at 10 and 50 weeks. 

The gastric mucosa of A4gnt–/– mice shows increased inflammation and angiogenesis. The above analysis suggests that tumor-promoting inflammation in the gastric mucosa of A4gnt–/– mice underlies tumorigenesis of gastric adenocarcinoma seen in mutant mice. To evaluate the extent of that inflammation, we calculated inflammation scores based on gastric mucosa histology. As expected,
infiltration of mononuclear cells was progressively increased as A4gnt−/− mice aged and showed significant increases when comparing scores at 5 weeks of age and those at time points later than 10 weeks (Figure 6A). Similarly, neutrophil infiltration was increased but less so than that of mononuclear cells (Figure 6B).

Immunohistochemical analyses revealed that the number of F4/80-positive macrophages in the pyloric mucosa of A4gnt−/− mice increased at as early as 5 weeks compared with that in age-matched A4gnt+/+ mice, and significant numbers of those cells were infiltrated around the atypical glands of 50-week-old A4gnt−/− mice (P < 0.01) (Figure 6C). The number of CD31-positive endothelial cells in the pyloric mucosa also increased at as early as 5 weeks compared with that in age-matched A4gnt+/+ mice, and significant numbers of CD31-positive cells were seen in 50-week-old A4gnt−/− mice relative to those in wild-type mice (P < 0.01) (Figure 6D).

Our microarray data show that Ptgs2 (encoding prostaglandin-endoperoxide synthase 2, otherwise known as cyclooxygenase-2 [Cox-2]), which plays a key role in inflammation-associated gastric tumorigenesis (10), was substantially upregulated in A4gnt−/− mice (Table 1). The data obtained in the present study clearly indicate that Cox-2 pathways, although upregulated in this mouse model, do not play a significant causative role in tumor-promoting inflammation.

### Discussion

To characterize the role of αGlcNac-terminated mucins in gastric mucosa, we generated A4gnt−/− mice. Our studies revealed that α4GnT is the sole enzyme responsible for the biosynthesis of αGlcNac: both immunohistochemical staining and oligosaccharide analysis (see Figure 1) indicated that αGlcNac residues are not detected in the gastric mucin secreted from mutant mice. Interestingly, in mutant mice, newly appearing O-glycans, exhibiting sialic acid and fucose residues and increased expression of O-glycans terminated with β-galactose residues in the gastric mucin, indicate remodeling of O-glycans in the gastric mucosa.

More interestingly, abnormal proliferation of gastric pyloric epithelial cells was seen in A4gnt−/− mice, and pathology analysis revealed gastric adenocarcinoma through a hyperplasia-dysplasia-carcinoma sequence in the absence of H. pylori infection (see Figure 2). Since few gastric cancer models are available, A4gnt−/− mice should be useful for in vivo studies of gastric cancer biology. It is also noteworthy that the MUC2-positive goblet cells were rarely seen in the gastric mucosa of either A4gnt−/− or control A4gnt+/+ mice during the 60-week observation period. It remains controversial whether intestinalization of gastric mucosa is preneoplastic or not (11, 12), but the present study clearly indicates that intestinal metaplasia is not associated with gastric tumorigenesis in this model.

The data obtained in the present study clearly indicate that αGlcNac suppresses gastric tumors in mice, suggesting that αGlcNac loss has a causative role in gastric cancer. Our findings

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### Table 1

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a Gene names are listed in descending order based on fold change seen in 5-week-old mice.
The research article strongly suggests that this conclusion may also apply to human disease, as expression of αGlcNAc was reduced in human gastric adenocarcinoma and its potentially premalignant lesion adenoma (see Figure 4). Similar results were reported in our previous study, in which 11 patients with the differentiated type of early gastric adenocarcinoma were examined (13). That study also analyzed 9 patients with an undifferentiated type of early gastric cancer and revealed that the number of αGlcNAc-positive adenocarcinoma cells was greater than that of MUC6-positive adenocarcinoma cells. Thus, these findings, combined with results reported here, suggest that αGlcNAc suppresses tumorigenesis of gastric adenoma as well as differentiated-type adenocarcinoma but not undifferentiated gastric adenocarcinoma in humans. Previously, we demonstrated that α4GnT protein is detected in the Golgi apparatus of gastric adenocarcinoma cells expressing αGlcNAc (3, 13). Molecular mechanisms regulating α4GnT expression in gastric cancer cells remain to be determined.

Our DNA microarray analysis identified 209 upregulated genes in A4gnt−/− mice compared with those in wild-type mice between 5 and 50 weeks of age. Upregulated genes included 22 that encoded molecules with receptor binding properties (see Table 1). Overall, quantitative RT-PCR analysis demonstrated upregulation of Grem1, Cxcl1, Ccl2, Cxcl5, Il11, Hgf, Il1b, and Fgf7 genes in A4gnt−/− mice compared with that in control mice at 10 and 50 weeks of age (see Figure 5A). Among them, the CC chemokine CCL2 (also known as MCP-1) is of particular interest, because CCL2 attracts tumor-associated macrophages (TAMs) (14). Interestingly, F4/80-positive macrophages were increased in the pyloric mucosa of A4gnt−/− mice compared with those in age-matched A4gnt+/+ mice (see Figure 6C). CCL2 recruitment of TAMs also plays an important role in tumor angiogenesis (14, 17). Genes encoding CXC chemokines CXCL1/CXCL5, which are potent angiogenic factors (14), were also upregulated in A4gnt−/− mice (see Figure 5A). In fact, CD31-positive endothelial cells were increased in the pyloric mucosa of A4gnt−/− mice compared with those in age-matched A4gnt+/+ mice (see Figure 6D), indicating that active angiogenesis is occurring in mutant mice. Notably, Ohta et al. (18) demonstrated possible involvement of CCL2 in human gastric adenocarcinoma, showing that CCL2 expression in gastric cancer cells was increased with tumor cell invasiveness, and its expression levels were positively correlated with angiogenesis and macrophage recruitment.

We also observed upregulation of Il11 in mutant mice (see Figure 5A). Nakayama et al. (19) demonstrated that IL-11 is expressed in 72.6% of human gastric adenocarcinomas from 73 patients and that its expression is significantly higher in differentiated types of adenocarcinoma compared with that in undifferentiated adenocarcinoma. More recently, Howlett et al. (20) demonstrated that IL-11 functions in the progression of inflammation to gastric tumorigenesis via gp130 signaling, followed by STAT3 phosphorylation. The same study revealed that Grem1 is upregulated in both IL-11–treated mice and human gastric cancer. Here, we found that Grem1 was significantly upregulated in A4gnt−/− mice at 50 weeks of age, a time coinciding with development of adenocarcinoma (see Figure 5A).
Recently, Kosinski et al. (21) demonstrated that GREM1 functions to maintain the colonic stem cell niche by activating Wnt signaling and that it is expressed by tumor stromal cells in human colon cancer. Future studies are required to determine the significance of Grem1 expression in gastric tumorigenesis.

The gene encoding the proinflammatory cytokine IL-1β as well as the genes encoding HFG and FGF7 (also known as keratinocyte growth factor), both of which play important roles in gastric epithelial proliferation (22, 23), were also upregulated in A4gnt−/− mice (see Figure 5A). Notably, Palmieri et al. (24) demonstrated that IL-1β induces FGFR7 release from breast fibroblasts, and Tu et al. (25) reported that IL-1β overexpression in mouse gastric mucosa promotes spontaneous gastric inflammation and cancer by recruiting myeloid-derived suppressor cells. In human gastric adenocarcinoma, Kai et al. (26) demonstrated that tumor IL-1β expression levels are elevated more than 50 fold over those seen in normal gastric mucosa and that levels were significantly higher in nonscirrhous carcinomas compared with those in scirrhous carcinomas.

We also identified 9 genes encoding molecules with receptor binding properties that were consistently downregulated at 5, 10, and 50 weeks of age in A4gnt−/− mice compared with those in wild-type mice (see Table 2). Overall, quantitative RT-PCR analysis confirmed downregulation of Amh, Egf, and Pthlh genes in mutant mice between 5 and 50 weeks of age (see Figure 5B). Downregulation of Amh, which encodes anti-Mullerian hormone (also known as Mullerian-inhibiting substance [MIS]), is noteworthy, because MIS inhibits growth of ovarian and uterine cervical cancer cells (27). The role of MIS in gastric cancer remains unknown and should be addressed in future studies.

Collectively, our results suggest that tumor-promoting inflammation occurs in the gastric mucosa of A4gnt−/− mice. The lack of effect of celecoxib treatment on progression of gastric dysplasia in A4gnt−/− mice suggests involvement of other signaling pathways promoting inflammation. It remains to be determined how loss of αGlcNAc in gastric gland mucin leads to tumor-promoting inflammation in the stomach.

In conclusion, the present study reveals that αGlcNAc secreted from the gastric gland mucous cells prevents development of differentiated-type gastric adenocarcinoma. H. pylori infection is closely associated with gastric cancer in humans (6). We previously demonstrated that gastric gland mucin containing αGlcNAc inhibits H. pylori growth and motility, preventing infection of deeper portions of the gastric mucosa (7). The finding that A4gnt−/− mice spontaneously develop gastric adenocarcinoma without H. pylori infection strongly suggests that αGlcNAc plays dual roles in human gastric cancer development by blocking H. pylori infection and suppressing of tumor-promoting inflammation in gastric mucosa. In fact, pyloric gland atrophy, which is associated with reduction of αGlcNAc, reportedly enhances the risk of gastric cancer 2 to 3 fold compared with that of chronic gastritis without pyloric gland atrophy (28). The present study shows an essential role for gastric O-glycans that suppress inflammation-associated tumorigenesis, extending our understanding of the function of carbohydrates in pathogenesis (29). These investigations will provide us with new strategies to prevent gastric cancer in humans.

Methods

Patients and clinical gastric samples. The present study included 54 patients with early gastric cancer with differentiated-type adenocarcinomas (33 males and 21 females; age range, 52–90 years) and 12 patients with gastric tubular adenoma (9 males and 3 females; age range, 59–87 years), who underwent endoscopic resection of the primary tumor at Shinshu University Hospital, Matsumoto, Japan, and Iiyama Red Cross Hospital. In all 54 patients, cancer cells were limited to the gastric mucosa. Venous and lymph vessel invasion or lymph node metastasis was absent. Nonneoplastic pyloric mucosa contained in endoscopically resected gastric mucosa from a patient with early gastric cancer with undifferentiated-type adenocarcinoma served as the positive control of immunostaining for αGlcNAc and MUC6. Histopathological diagnosis of gastric tumors was done according to WHO guidelines for classification for gastric carcinoma (30). Formalin-fixed and paraffin-embedded tissue blocks from these patients were retrieved from the archives (between 2007 and 2009) of both hospitals and cut into 3-μm sections.

Generation of A4gnt−/− mice. The mouse A4gnt BAC clone, RP22-392L18, was selected from an RPCI-22 129S6/SvEv Tac mouse BAC library (BACPAC Resources Center at Children’s Hospital Oakland Research Institute) by hybridization of high-density arrayed nylon filters using a 3′ probe generated by PCR with A4GNT3PRF5 and A4GNT3PRR5 primers (Supplemental Table 5). The full-length A4gnt genomic sequence was verified by PCR using A4GNT3PRF4 and A4GNT3RRR4 primers for a region 4 kb upstream of exon 1 and A4GNT3PRFS and A4GNT3PRR5 primers for a region 10 kb downstream of exon 2. The neomycin resistance gene for ES cell selection was introduced into exons 2 and 3 of the BAC clone using a Red/ET Quick & Easy BAC Modification Kit (Gene Bridges). A neomycin-resistance selection cassette (PGK-gb2-neo) flanked on both
Subcloning Kit (Gene Bridges) as described previously (31). The 5′-4.4 kb upstream and 9.6 kb downstream of the PGK-gb2-neo cassette, produce mutant mice. Chimeric male offspring were identified on the mouse were cultured with mouse embryo fibroblasts as feeders in medium vector was constructed in pBluescript-MCA/DTA using a Red/ET BAC basis of coat color and bred with C57BL/6J female mice. Germ line transfecting System (GE Healthcare). C57BL/6J blastocysts injected with correctly probe, and neo-probe, respectively. The 5′-probe was generated by PCR –/– with A4GNTBIF1 and A4GNTBIR1 primers. The 3′-probe was cleaved by –probe, +/+, and –/– DNA isolated from G418-resistant clones was digested with EcoRI and subjected to Southern blot analysis with a 5′-recombination sites of the modified BAC clone were located in a region –/– –probe, and 3′-probe, respectively. The 5′-probe was generated by PCR –/– with A4GNT5PRF4 and A4GNT5PRR4 primers, and the neo-probe was –probe, 3′-probe, and 3′-probe, respectively. All probes used for Southern blotting were prepared by random-prime labeling using the Megaprime DNA Labeling System (GE Healthcare). C57BL/6J blastocysts injected with correctly targeted ES cells were implanted into pseudopregnant CD-1 females to produce mutant mice. Chimeric male offspring were identified on the basis of coat color and bred with C57BL/6J female mice. Germ line transmission of the mutant A4gnt locus was assessed by Southern blotting of BglII-digested tail DNA as described above. Heterozygotes were crossed to generate homozygous mutants. A4gnt–/– mice backcrossed into a C57BL/6J background for 6 generations (F6 mice) were used in this study. Southern blot analysis of genomic DNA isolated from the tails of F6 mice confirmed correct targeting of the A4gnt gene (Supplemental Figure 1). F6 mutant mice were genotyped by multiplex PCR using tail DNA and a set of 3 primers for the short arm (SAC-F and SAN-R or SAW-R), yielding 559-bp and 253-bp fragments, respectively, for the wild-type and mutant alleles. The set of 3 primers for the long arm were LAN-F or LAW-F and LAC-R, yielding 429-bp and 222-bp fragments for the wild-type allele and mutant alleles, respectively (Supplemental Figure 1).

Mice were housed in autoclaved cages under specific pathogen-free conditions, fed commercially prepared pellet diet, given UV-irradiated water ad libitum, and maintained on a 12-hour-light/12-hour-dark cycle.

Histopathology of mouse samples. To label S-phase cells in wild-type and mutant mice, BrdU (50 mg/kg body weight) was injected into the peritoneal cavity as described previously, with a modification (32). One hour after injection, mice were killed by cervical dislocation. Along with duodenum, stomachs were removed, opened along the greater curvature, flattened by pinning, and fixed in 20% buffered formalin for 48 hours. Each stomach was cut longitudinally into 5 pieces of equal width and embedded in paraffin. Serial 3-μm sections were prepared and stained with H&E and Alcian blue (pH 2.5)/PAS (AB-PAS). In addition, tissues, such as the jejunum, proximal and distal colons, pancreas, liver, kidney, lung, heart, and spleen, were removed, and sections for H&E staining were similarly prepared. Gastric mucosal thickness was analyzed on images of AB-PAS-stained sections. Briefly, a well-oriented representative pyloric gland was selected for each mouse, and mucosal thickness was measured. Mucosa

Figure 6
Inflammation and angiogenesis in the gastric mucosa of A4gnt–/– mice. (A) Inflammation score for mononuclear cell infiltration in the antrum of A4gnt–/– mice. Each group consists of 6 mice, and data represent the mean ± SEM. *P < 0.05; **P < 0.01. (B) Inflammation score for neutrophil infiltration in the antrum of A4gnt–/– mice. Each group consists of 6 mice, and data represent the mean ± SEM. *P < 0.05; **P < 0.01. (C) Detection of F4/80-positive macrophages in gastric mucosa. Immunohistochemistry with anti-F4/80 antibody (left panel). Scale bar: 50 μm. Comparison of number of F4/80-positive macrophages in gastric mucosa of A4gnt–/– and A4gnt+/+ mice (right panel). Each group consists of 6 mice, and data represent the mean ± SEM. **P < 0.01. (D) Detection of CD31-positive endothelial cells in gastric mucosa. Immunohistochemistry with anti-CD31 antibody (left panel). Scale bar: 50 μm. Comparison of number of CD31-positive endothelial cells in gastric mucosa of A4gnt–/– and A4gnt+/+ mice (right panel). Each group consists of 6 mice, and data represent the mean ± SEM. *P < 0.05.
al thickness of the fundic mucosa was also measured in a similar way. Histopathology of mouse gastric mucosa was done basically according to WHO classification criteria for human gastric cancer (30). Inflammation scores in the gastric antrum were determined according to criteria of Nolan et al. (33). Briefly, inflammatory cell infiltration of the gastric mucosa by mononuclear cells and neutrophils was scored as follows: 1, mild multifocal; 2, mild widespread or moderate multifocal; 3, mild widespread and moderate multifocal or severe multifocal; 4, moderate widespread; 5, moderate widespread and severe multifocal; and 6, severe widespread.

**Immunohistochemistry.** Expression of αGalNAc and MUC6 in human samples, and αGalNAc, MUC2, BrdU, cleaved caspase-3, CD31, and the pan-macrophage marker F4/80 in mouse samples, was analyzed by immunohistochemistry. Deparaffinized tissue specimens were subjected to immunohistochemistry using primary antibodies, including anti-gastric mucosa (gastric mucosa, the number of positive cells was determined by scanning the entire pyloric mucosa area in each mouse and determining cell number—namely, hyperplasia at 5 weeks of age, low-grade dysplasia at 10 weeks, and adenocarcinoma at 50 weeks (see Supplemental Figure 3). RNA quality was assessed using an Agilent 2100 BioAnalyzer, and Cy3-labeled cRNA was synthesized using a Quick Amp Labeling Kit (Agilent Technologies), according to the manufacturer’s protocol. 1.65 µg Cy3-labeled cRNA were heat fragmented and applied to Agilent Whole Mouse Genome Oligo ver. 2 (4 x 44 K) arrays using a Gene Expression Hybridization Kit (Agilent Technologies), and hybridization was carried out at 65°C for 17 hours. Washing was performed using a Gene Expression Wash Pack (Agilent Technologies). Slides were scanned using an Agilent Technologies Microarray Scanner, and images were processed by Feature Extraction software (Agilent Technologies) with background correction. After normalization and data filtering of the raw date output files, log-fold changes in gene expression in A4gnt+/− and A4gnt−/− mice compared to those in A4gnt−/− mice at each age were analyzed to determine consistently upregulated and downregulated genes, using a 2-fold change as the cut-off using GeneSpring GX 11.0 software (Agilent Technologies). Upregulated and downregulated genes were further clustered into functional gene groups using ontology analysis with GeneSpring GX 11.0 software. Microarray data are available on the MIAME-compliant GEO database (accession number GSE31074; http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE31074).

**Quantitative RT-PCR.** RNA samples were prepared from formalin-fixed, paraffin-embedded tissue blocks from glandular stomachs (n = 5 for 5-week-old A4gnt−/− mice; n = 6 for other groups). To avoid contamination of the forestomach and duodenum adjacent to the glandular stomach, the borders between these areas were marked as described previously on H&E-stained tissue slides (38). By referring to the marked areas on the laser-induced dissociation was performed according to the manufacturer’s operation manual.

**DNA microarray analysis.** Total RNA was isolated from gastric mucosa stripped from the muscular layer of the glandular stomachs of A4gnt−/− and A4gnt−/− mice at 5, 10, and 50 weeks of age using an RNeasy Kit (Qiagen). One mouse per genotype and age was examined, since gastric mucosa of A4gnt−/− mice showed consistent histopathology in each group examined—namely, hyperplasia at 5 weeks of age, low-grade dysplasia at 10 weeks, and adenocarcinoma at 50 weeks (see Supplemental Figure 3). RNA quality was assessed using an Agilent 2100 BioAnalyzer, and Cy3-labeled cRNA was synthesized using a Quick Amp Labeling Kit (Agilent Technologies), according to the manufacturer’s protocol. 1.65 µg Cy3-labeled cRNA were heat fragmented and applied to Agilent Whole Mouse Genome Oligo ver. 2 (4 x 44 K) arrays using a Gene Expression Hybridization Kit (Agilent Technologies), and hybridization was carried out at 65°C for 17 hours. Washing was performed using a Gene Expression Wash Pack (Agilent Technologies). Slides were scanned using an Agilent Technologies Microarray Scanner, and images were processed by Feature Extraction software (Agilent Technologies) with background correction. After normalization and data filtering of the raw date output files, log-fold changes in gene expression in A4gnt−/− mice compared to those in A4gnt−/− mice at each age were analyzed to determine consistently upregulated and downregulated genes, using a 2-fold change as the cut-off using GeneSpring GX 11.0 software (Agilent Technologies). Upregulated and downregulated genes were further clustered into functional gene groups using ontology analysis with GeneSpring GX 11.0 software. Microarray data are available on the MIAME-compliant GEO database (accession number GSE31074; http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE31074).
H&E-stained tissue slides, shallow incisions were made into the relevant tissue blocks along borders using a razor blade. Then, 3 slices of 10-μm thickness were prepared and transferred to a sterile 1.5 ml tube for total RNA extraction using an RNeasy FFPE Kit plus deparaffinization solution (Qiagen), according to the manufacturer's protocol. Thirteen μl of a solution containing 3 μg of RNA isolated from the glandular stomach of mice, 0.5 μl of 0.5 mg/ml random primers (Promega), 0.5 μl of 0.5 mg/ml oligo-dT primers (Promega), and 1 μl of a 2.5 μM dNTP mixture was denatured at 65°C for 5 minutes and then placed on ice. For single-stranded cDNA synthesis, samples were incubated with 1 μl of 200 U/ml SuperScript III (Invitrogen), 1 μl of 0.1 M dithiothreitol, 1 μl of 40 U/ml RNasin Plus RNase inhibitor (Promega), and 4 μl of 5X Fast Strand buffer (Invitrogen) at 50°C for 1 hour. Heating at 70°C for 10 minutes terminated the reaction.

Quantitative RT-PCR analysis was achieved using the 7300 Real-Time PCR System (Applied Biosystems). Premixed reagents containing primers and TaqMan probes for selected genes, including Grem1 (Assay ID MM00488615_s1), Cxcl1 (Mm00433859_m1), Cxcl2 (Mm00441242_m1), Cxcl5 (Mm00436451_g1), Il1 (Mm00431462_m1), Hgf (Mm01135193_m1), Il1b (Mm01336189_m1), Fgf7 (Mm00433291_m1), Amb (Mm00431795_g1), Egr (Mm00483696_m1), and Phb (Mm00436057_m1), plus GAPdh (Mm99999915_g1) for normalization, were purchased from Applied Biosystems. Using 96-well optical plates, a 20 μl solution containing 10 μl of 2X TaqMan Universal Master Mix (Applied Biosystems), 9 μl of cDNA sample, and 1 μl of 20X premixed reagents containing primers and TaqMan probe were added to each well. Plates were heated at 50°C for 2 minutes and 95°C for 10 minutes and then subjected to 50 thermal cycles (95°C, 15 seconds; 60°C, 1 minute). Specific mRNA expression was normalized to RNA extraction using an RNeasy FFPE Kit plus deparaffinization solution (Qiagen), and 0.5 μg/ml oligo-dT primers (Promega), and 1 μl of 200 U/ml SuperScript III (Invitrogen), 1 μl of 0.1 M dithiothreitol, 1 μl of 40 U/ml RNasin Plus RNase inhibitor (Promega), and 4 μl of 5X Fast Strand buffer (Invitrogen) at 50°C for 1 hour. Heating at 70°C for 10 minutes terminated the reaction.

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