

A complex between phosphatidylinositol 4-kinase II α and integrin α 3 β 1 is required for *N*-glycan sialylation in cancer cells

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Aberrant *N*-glycan sialylation of glycoproteins is closely associated with malignant phenotypes of cancer cells and metastatic potential, which includes cell adhesion, migration, and growth. Recently, phosphatidylinositol 4-kinase II α (PI4KII α), which is localized to the trans-Golgi network, was identified as a regulator of Golgi phosphoprotein 3 (GOLPH3) and of vesicle transport in the Golgi apparatus. GOLPH3 is a target of PI4KII α and helps anchor sialyltransferases and thereby regulates sialylation of cell surface receptors. However, how PI4KII α -mediated sialylation of cell surface proteins is regulated remains unclear. In this study, using several cell lines, CRISPR/Cas9-based gene knockout and short hairpin RNA-mediated silencing, RT-PCR, lentivirus-mediated overexpression, and immunoblotting methods, we confirmed that PI4KII α knockdown suppresses the sialylation of *N*-glycans on the cell surface, in Akt phosphorylation and activation, and integrin α 3-mediated cell migration of MDA-MB-231 breast cancer cells. Interestingly, both integrin α 3 β 1 and PI4KII α co-localized to the trans-Golgi network, where they physically interacted with each other, and PI4KII α specifically associated with integrin α 3 but not α 5. Furthermore, overexpression of both integrin α 3 β 1 and PI4KII α induced hypersialylation. Conversely, integrin α 3 knockout significantly inhibited the sialylation of membrane proteins, such as the epidermal growth factor receptor, as well as in total cell lysates. These findings suggest that the malignant phenotype of cancer cells is affected by a sialylation mechanism that is regulated by a complex between PI4KII α and integrin α 3 β 1.

Alteration of the sialylation of glycoproteins has often been observed in several types of malignant tumors, such as those found in breast, ovary, and colorectal cancers (1–3). Sialylation is linked via either an α 2,3 or an α 2,6 bond to Gal/GalNAc and

via an α 2,8 bond to sialic acid in glycoproteins through a group of sialyltransferases. The up-regulation of cell surface sialic acid is thought to control cell phenotypes such as cell adhesion, migration, immune response, apoptosis, and cell epithelial–mesenchymal transition (EMT).³ Sialylation is also believed to be essential for the differentiation potential of human mesenchymal stem cells (4, 5). The sialylation levels of glycoproteins on the cell surface are mainly determined by sialyltransferase, sialidase, and substrate expression (6, 7). Some transcription factors are critical for transcriptional activation of sialyltransferases in cancer cells. For example, the expression level of α 2,6-galactoside sialyltransferase 1 (ST6GAL1) is up-regulated by the *RAS* oncogene and increases the α 2,6 sialylation of β 1 integrins, which promotes integrin-mediated cell migration, adhesion, and cell proliferation (8, 9).

As described above, sialylation levels are mainly dependent on their gene expression levels, whereas other mechanisms for regulation are usually neglected. However, Popoff and co-workers (10) and our group (11) independently reported that Golgi phosphoprotein 3 (GOLPH3), which has been identified as an oncogenic protein and is increased in several human solid tumors (12), could anchor sialyltransferases to regulate sialylation on cell surface receptors without regulating the gene expression levels of sialyltransferases. In particular, suppression of GOLPH3 attenuated the levels of cellular sialylation and integrin-dependent cell migration. Furthermore, tumor formation was significantly reduced in mice implanted with GOLPH3 shRNA-expressing cells (11–13). GOLPH3 has multiple cellular functions in vesicle trafficking and in support of Golgi apparatus structure, which has specific affinity for phosphatidylinositol 4 (PI4P) (14, 15). PI4P is mainly catalyzed by phosphatidylinositol 4-kinase II α (PI4KII α), which is localized to the trans-Golgi network (TGN) (16). Given the importance of

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³The abbreviations used are: EMT, epithelial–mesenchymal transition; shRNA, short hairpin RNA; PI4P, phosphatidylinositol 4-phosphate; PI4K, phosphatidylinositol 4-kinase; TGN, trans-Golgi network; ECM, extracellular matrix; EGF, epidermal growth factor; PH, pleckstrin homology; DOX, doxycycline; KD, knockdown; SNA, *Sambucus nigra* agglutinin; WGA, wheat germ agglutinin; PA, pyridilaminated; SSA, *Sambucus sieboldiana* agglutinin; MAM, *Maackia amurensis* mitogen; ConA, concanavalin A; KO, knockout; EGFR, epidermal growth factor receptor; DMEM, Dulbecco's modified Eagle's medium; FBS, fetal bovine serum; cDNA, complementary DNA; mRFP, monomeric red fluorescent protein; SALSA, sialic acid linkage-specific alkylamidation; Ctrl, control.

Importance of the PI4K-integrin $\alpha 3\beta 1$ complex for sialylation

GOLPH3 in sialylation and cell functions, it is plausible that PI4P expression at the TGN may influence sialylation.

Integrins are heterodimeric cell surface adhesion receptors and major carriers of sialylation. The interaction between integrin and the extracellular matrix (ECM) is essential for cell adhesion, migration, viability, and proliferation (17, 18). In fact, glycosylation is a key regulator that plays important roles in modulating integrin functions. For example, integrin $\alpha 5\beta 1$ binding to fibronectin and integrin-mediated cell spreading and migration are modulated by overexpression of glycosyltransferase genes such as *N*-acetylglucosaminyltransferase III and V or ST6GAL1 (19–21). In addition, sialylated *N*-glycans on the membrane-proximal domain of integrin $\beta 1$ play crucial roles in integrin activation and in complex formation between integrin and EGF receptors and syndecan-4 to regulate cell migration and proliferation (22).

In contrast to the regulation of integrin functions from the extracellular domain, it is well known that integrin function is regulated by its association with cytoplasmic molecules such as focal adhesion kinase and phosphatidylinositol 3-kinase (23, 24). Other studies have detected PI4K activity in the immune complex with integrin $\beta 1$, suggesting that integrin might also regulate the biosynthesis of PI4P (25–27). Mammalian PI4Ks are classified as types II and III (28). PI4KII α plays important roles in clathrin-dependent molecular sorting and associates with TGN membranes (29–31), whereas PI4KIII β is enriched in the cis-medial Golgi in breast cancer cells (32).

In this study, to further understand the underlying mechanism for GOLPH3 expression on sialylation and cell functions, we investigated the effects of PI4KII α , which is one of the regulators of GOLPH3 in breast cancer MDA-MB-231 cells. We found that the sialylation on integrins, Akt phosphorylation, and integrin $\alpha 3$ -mediated cell migration all were significantly inhibited in PI4KII α knockdown cells. It was interesting that overexpression of both PI4KII α and integrin $\alpha 3$ greatly increased sialylation. Conversely, knockout of integrin $\alpha 3$ significantly inhibited sialylation in membrane proteins. These findings suggest a novel mechanism for sialylation, which suggests a new concept for the regulation of glycosylation in cell biology.

Results

We recently reported that the expression of GOLPH3 up-regulated cell surface sialylation and cell migration (11). However, the molecular mechanism of posttranslational modification of sialylation on the cell surface remains unclear. Considering that GOLPH3 exhibits a highly selective affinity for PI4P that is similar to the canonical pleckstrin homology (PH) domain in the TGN (33), we hypothesized that the expression of PI4P in the TGN could affect sialylation and cell properties. PI4P is produced mainly by PI4Ks, which are classified as type II and III according to their sensitivity to inhibitors (30). PI4KIII β is enriched in early Golgi compartments, whereas PI4KII α is localized mainly in the TGN and in the endosome (16), where sialyltransferases also are localized (34). Furthermore, PI4KII α is a dominant PI4K in mammalian cells (35). Therefore, we chose PI4KII α for functional analysis,

and established a line of doxycycline (DOX)-controlled PI4KII α silencing in MDA-MB-231 breast cancer cells.

Knockdown of PI4KII α affected the sialylation of *N*-glycans

First, we verified the expression levels of PI4KII α and sialyltransferases (ST3GAL3, ST3GAL4, and ST6GAL1) that involve major sialylated *N*-glycans (36). RT-PCR analysis showed that the expression levels of PI4KII α mRNA were significantly decreased in knockdown cells, whereas the expression levels of ST6GAL1 for $\alpha 2,6$ sialylation and those of ST3GAL3 and ST3GAL4 for $\alpha 2,3$ sialylation were all similar in both cells (Fig. 1A). Second, we verified the expression levels and the distributions of PI4P in KD cells. The PH domain of four-phosphate adaptor protein 1 (FAPP1), which preferentially recognizes PI4P, is known for its use as a monitor for PI4P distribution (37). In control cells, PI4P was localized near the medial Golgi marker GM130, as expected (Fig. 1B). In contrast, PI4P staining was significantly decreased in knockdown (KD) cells (Fig. 1B). These data confirmed that PI4KII α is mainly involved in the synthesis and localization of PI4P in the TGN, which agrees with previous reports (35).

Next, we tested whether decreased PI4P affects sialylation expression on the cell surface. As shown in Fig. 1C, top panels, the intensities of the staining in KD cells with *Sambucus nigra* agglutinin (SNA) lectin, which preferentially recognizes $\alpha 2,6$ sialylation of glycoproteins, was weaker than that in control cells. However, the intensities of staining with WGA lectin, which preferentially recognizes GlcNAc residues and hybrid-type and lactohexose *N*-glycans (38), were almost equal in both cells (Fig. 1C, bottom panels). These data suggested that the expression levels of sialylated glycans were decreased in KD cells. Furthermore, the decrease was confirmed by quantitative analysis using HPLC. Total pyridylaminated (PA) *N*-glycans of cells were examined via anion exchange chromatography, and the ratios of sialylated *N*-glycans versus total *N*-glycans were calculated. The expression levels of sialylated *N*-glycans were significantly suppressed in KD cells (Fig. 1D). A similar change in $\alpha 2,6$ sialylation on specific membrane proteins such as integrin $\beta 1$ was also consistently observed (Fig. 1E) using *Sambucus sieboldiana* agglutinin (SSA)-agarose. These data suggest that the expression levels of PI4P in the TGN are important for sialylation.

Knockdown of PI4KII α significantly inhibited cell migration and Akt phosphorylation

Alterations in *N*-glycosylation affect many cellular events involved in cellular signaling and cell migration. Here we examined the effects of PI4KII α KD on cell migration and Akt activation. As shown in Fig. 2A, cell migration on laminin-332 in a Transwell assay was significantly reduced in KD cells compared with control cells. The expression levels of integrin $\alpha 3\beta 1$, a major receptor for laminin-332 and $\alpha 5\beta 1$ on the cell surface were similar in both cells (Fig. 2B). Activation of Akt is required for integrin-mediated cell migration (39). As shown in Fig. 2C, the level of phosphorylated Akt was apparently decreased in KD cells compared with control cells. These data suggest that PI4P in the TGN plays an important role in Akt activation and in integrin $\alpha 3$ -mediated cell migration.

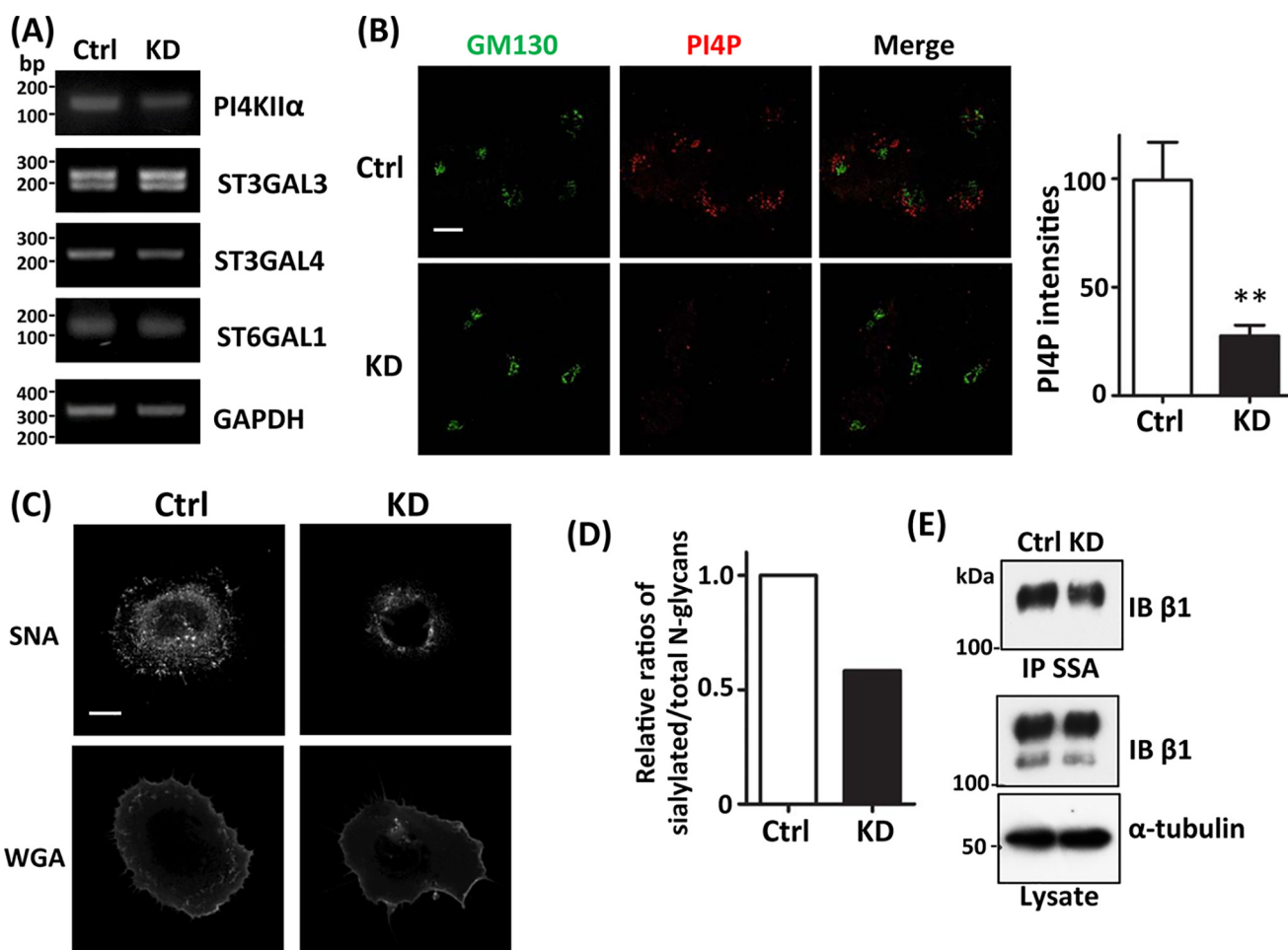


Figure 1. Effects of PI4KII α gene knockdown on the sialylation of N-glycans. A, RT-PCR using total RNA extracted from the control (Ctrl) and PI4KII α KD of MDA-MB-231 cells were carried out to examine the expression levels of PI4KII α and sialyltransferases that involve sialylated N-glycans. The expression level of glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was used as a loading control. ST3GAL, β -galactoside $\alpha 2,3$ -sialyltransferase. B, the amounts and distribution of PI4P in KD and Ctrl cells were examined by expressing mRFP-FAPP, which specifically binds to PI4P. These cells were also immunostained with anti-GM130 antibody, which is a medial Golgi marker. The immunostaining intensities for PI4P were quantified using ImageJ software, averaged by cell numbers, and normalized to the control values (percent). Values represent the means \pm S.E. ($n = 10$). **, $p < 0.01$ (Welch's t test). Scale bar = 10 μ m. C, Cells were incubated with biotin-conjugated SNA or WGA and then fixed and visualized by Alexa Fluor-streptavidin conjugates. Scale bar = 20 μ m. D, preparation of PA oligosaccharides and calculation of ratios of sialylated N-glycans versus total N-glycans as described under "Experimental procedures." Data were normalized to the control. E, equal amounts of cell lysates from Ctrl and KD cells were precipitated by SSA-agarose (preferentially recognizes the $\alpha 2,6$ sialylation) and probed with anti- $\beta 1$ antibody (top panel). The expression levels of integrin $\beta 1$ in total cell lysates were verified by Western blotting with anti- $\beta 1$ antibody (center panel). α -Tubulin was used as a loading control. KD and Ctrl cells refer to transfectants with DOX-inducible knockdown of PI4KII α cultured with or without DOX, respectively. IB, immunoblot.

Complex formation between integrin $\alpha 3$ and PI4KII α is important for sialylation

As described above, PI4KII α regulated sialylation and the integrin $\alpha 3$ -mediated phenotype. Therefore, we examined the interaction between PI4KII α and integrin $\alpha 3$ in the Golgi apparatus. First, we used immunostaining to assess the intracellular distributions of PI4KII α and $\alpha 3$. Immunostaining showed that PI4KII α was localized in the vicinity of GM130 and that it was extensively co-localized with integrin $\alpha 3$ (Fig. 3A). Notably, co-immunoprecipitation with anti-integrin $\beta 1$ showed that it was $\alpha 3$, rather than $\alpha 5$, that interacted with PI4KII α in 293T cell stable expression of PI4KII α and/or either integrin $\alpha 3$ or $\alpha 5$ (Fig. 3B). The interaction between PI4KII α and $\alpha 3$ was further reciprocally confirmed by immunoprecipitation with either anti- $\alpha 3$ antibody (Fig. 3C) or anti-GFP antibody (Fig. 3D).

Next we wondered whether this interaction was required for efficient sialylation. To address this question, we precipitated

those cell lysates with SSA or *Maackia amurensis* mitogen (MAM) agarose, which preferentially recognize $\alpha 2,6$ -sialylated and $\alpha 2,3$ -sialylated N-glycans, respectively, and then performed Western blotting against integrin $\beta 1$. Interestingly, both sialylated N-glycans were up-regulated on integrin $\beta 1$ in cells that expressed both PI4KII α and integrin $\alpha 3$ but not in those that expressed PI4KII α and $\alpha 5$ (Fig. 3E, top and center panels). In contrast to SSA or MAM lectin blotting, ConA lectin blots showed a similar level in both integrin $\alpha 3$ - and $\alpha 5$ -expressing cells (Fig. 3E, bottom panel). ConA lectin equally recognized both mature and immature forms of integrin $\beta 1$ in $\alpha 3$ -expressing cells but only the most immature form of $\beta 1$ in $\alpha 5$ -expressing cells. These data further suggest the importance of $\alpha 3$ for sialylation. Data obtained from flow cytometry analysis via MAM lectin consistently supported this observation, although SSA lectin showed no significant changes in these cells (Fig. 3F). Therefore, these results clearly suggest that intracellular com-

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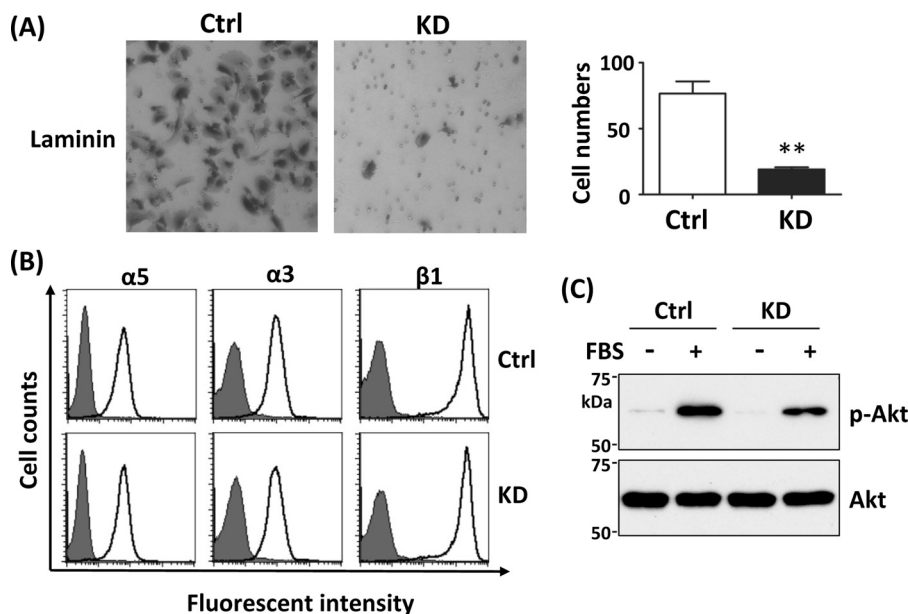


Figure 2. Comparison of cell migration and cellular signaling between Ctrl and KD cells. A, cell migration toward laminin-332 was determined by a Transwell assay as described under "Experimental procedures." The quantitative data were obtained by counting the cell number of five random fields. The p values were calculated using Welch's t test. Values represent the means \pm S.E. **, $p < 0.01$. B, comparison of the expression levels of $\alpha 3\beta 1$ and $\alpha 5\beta 1$ integrins on the cell surface between Ctrl and KD cells. Both Ctrl and PI4KII α KD cells were incubated with (bold line) or without (gray shadow) antibodies against integrin $\alpha 3$, $\alpha 5$, or $\beta 1$ and subjected to FACS analysis. C, comparison of Akt activation upon FBS stimulation between Ctrl and KD cells. After starvation, cells were supplied with fresh medium with (+) or without (-) 3% FBS. The cell lysates were then analyzed by Western blotting with anti-p-Akt or total Akt antibody.

plex formation between PI4KII α and $\alpha 3$ regulates the biosynthesis of sialylated N -glycans.

Expression of integrin $\alpha 3$ is important for efficient sialylation

To further verify the importance of complex formation between PI4KII α and integrin $\alpha 3$ for cellular sialylation, we used the CRISPR/Cas9 system to construct an integrin $\alpha 3$ knockout (KO) MDA-MB-231 cell line. Flow cytometric analysis revealed a KO efficiency of more than 95% (Fig. 4A), which also was confirmed by Western blotting with anti-integrin $\alpha 3$ (Fig. 4B). Notably, the band mobility of integrin $\beta 1$ on SDS-PAGE in KO cells was faster than in the control cells, suggesting that integrin $\alpha 3$ deficiency leads to an accumulation of the immature $\beta 1$ form without sialylation. It is well known that integrin $\alpha 3$ is important for laminin-mediated cell adhesion, migration, and several forms of cellular signaling (40–42). Consistent with previous reports (42, 43), expression of $\alpha 3\beta 1$ regulated cell morphology and that of the actin cytoskeleton by promoting lamellipodium and filopodium formation on laminin-332, a specific ligand for integrin $\alpha 3$, whereas lack of $\alpha 3$ blocked their formation (Fig. 4C). There were no significant differences between two cells spread on collagen, which is a specific ligand for integrin $\alpha 1$ and $\alpha 2$. Furthermore, cell spreading and migration on laminin-332 were inhibited in KO cells compared with control cells (Fig. 4, D and E).

Next, we compared total sialylated N -glycan levels between KO and control cells, which were quantified using HPLC. Consistent with the data from PI4KII α KD cells, the ratios of sialylated N -glycans versus total N -glycans were greatly suppressed in KO cells (Fig. 5A). Because N -glycans of integrin $\beta 1$ could be directly influenced by $\alpha 3$ knockout (Fig. 4B, center panel), here we also analyzed sialylation on the EGF receptor, which has been reported to affect receptor activation (44). As expected,

sialylation of EGF receptors obtained from KO cells was also decreased compared with control cells (Fig. 5B). To investigate whether the phenomenon also occurred in other cell lines, we examined HeLa cells. The knockout efficiency of $\alpha 3$ was assessed via flow cytometry analysis (Fig. 5C). Interestingly, a similar tendency of sialylation decline was observed in $\alpha 3$ KO HeLa cells compared with control cells (Fig. 5D). To thoroughly examine the glycosylation states caused by knockout of integrin $\alpha 3$ or knockdown of PI4KII α , we utilized MS-based approaches to identify the N -glycan and O -glycan structures (Fig. 6, A and B). Consistently, hyposialylation in N -glycans was observed by attenuation of either integrin $\alpha 3$ or PI4KII α (Fig. 6A), which further suggests the importance of this pathway in the biosynthesis of sialylated N -glycans. In contrast to N -glycans, there were no significant changes in the sialylation of O -glycans among these cells (Fig. 6B). It was also notable that a decrease in $\alpha 2,3$ sialylation in N -glycans could slightly increase $\alpha 2,6$ sialylation in total cell lysates of $\alpha 3$ KO and PI4KII α KD cells (Fig. 6A), which seems contrary to the observation for integrin $\beta 1$ (Fig. 3E). Further study is needed to fully elucidate the mechanism. Nevertheless, these data suggest that complex formation of $\alpha 3$ and PI4KII α could act as a novel regulator for the sialylation of N -glycans.

Discussion

In this study, we found that PI4KII α expression played an important role in $\alpha 3\beta 1$ integrin-mediated cell migration, cellular signaling, and the expression of sialylation; PI4KII α could specifically associate with $\alpha 3$ but not $\alpha 5$, and complex formation between PI4KII α and $\alpha 3$ enhanced sialylation; and deletion of integrin $\alpha 3$ significantly inhibited not only cell adhesion and migration but also sialylation. These observations are the first to directly demonstrate a novel regulatory mechanism for sia-

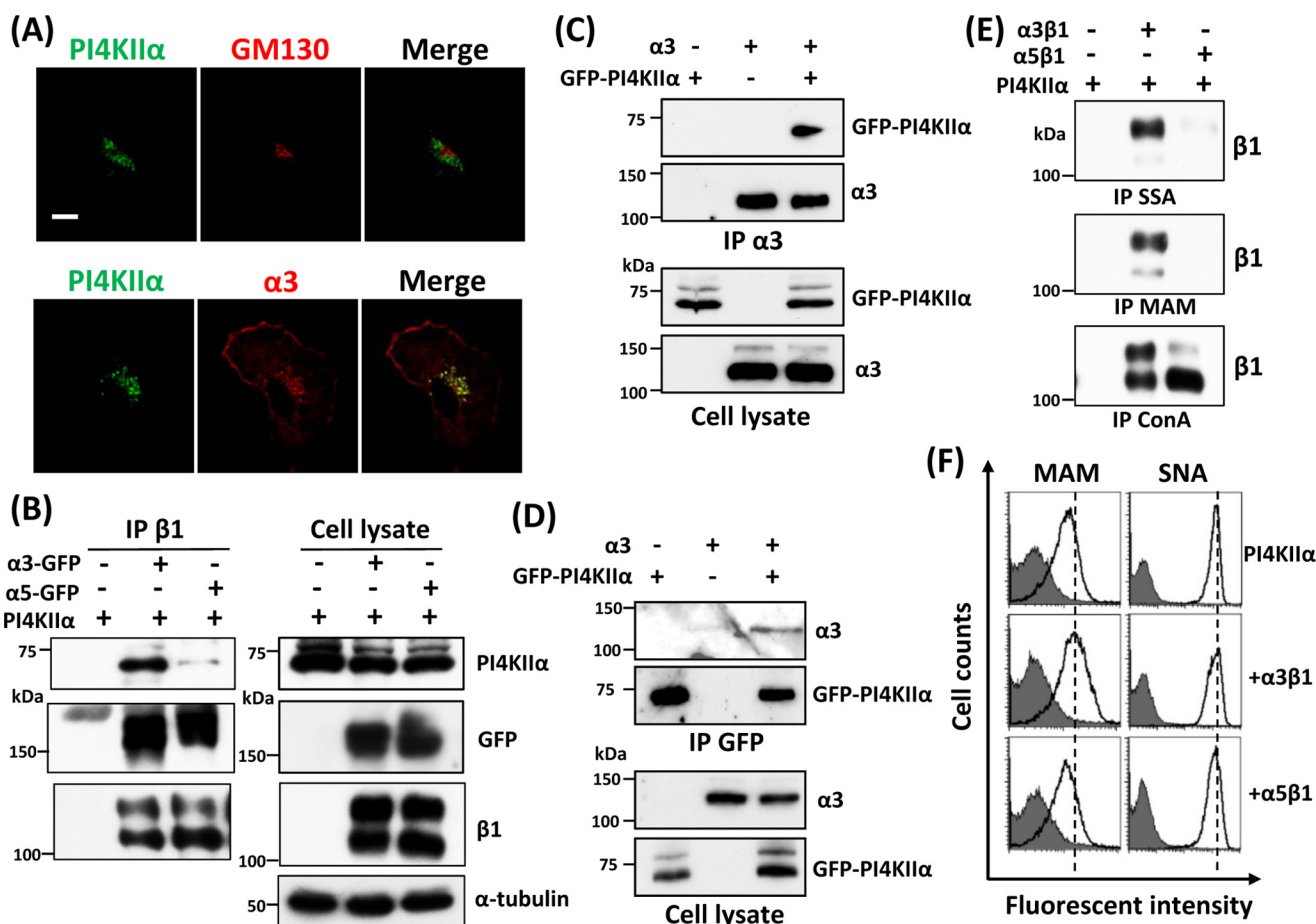


Figure 3. Interaction between integrin $\alpha 3\beta 1$ and PI4KII α and the effect on sialylation. A, MDA-MB-231 cells overexpressed with GFP-PI4KII α were fixed and then stained with either anti-GM130 (top panel) or anti-integrin $\alpha 3$ (bottom panel) antibody, followed by detection using anti-mouse Alexa 647 conjugates. Scale bar = 20 μ m. B, three overexpressed 293T cells were established by lentivirus infection: PI4KII α alone; PI4KII α , GFP-tagged $\alpha 3$ and $\beta 1$; and PI4KII α , GFP-tagged $\alpha 5$ and $\beta 1$ integrin. Equal amounts of cell lysates were immunoprecipitated (IP) with anti-integrin $\beta 1$ antibody, followed by detection with the indicated antibodies. The cell lysates were used as input to show similar expression levels of PI4KII α , integrin $\alpha 3\beta 1$, or $\alpha 5\beta 1$ among these cells. C and D, reciprocal immunoprecipitation was performed using either anti- $\alpha 3$ antibody (C) or anti-GFP for tagged PI4KII α (D) using cell lysates from 293T cells stably overexpressed with or without GFP tagged PI4KII α , which were further transiently transfected with or without $\alpha 3$ and $\beta 1$ integrin. The cell lysates were used as input to show similar expression levels of integrin $\alpha 3$ and GFP-PI4KII α . E, equal amounts of cell lysates were precipitated with either SSA-, MAM-, or ConA-conjugated agarose, followed by detection with antibody against integrin $\beta 1$. F, 293T cells expressing the indicated genes were incubated with (bold line) or without (gray shading) biotin-conjugated MAM or SNA and subjected to FACS analysis.

lylation, which may also partially explain the previous observation that GOLPH3 is a special regulator in the sialylation of *N*-glycans and a part of the signaling events that could influence mTOR signaling and tumor progression (11).

Many cancers are associated with sialylated structures such as sialyl Tn, sialyl Lewis antigen (sLe), $\alpha 2,6$ -sialylated lactosamine, polysialic acid, and gangliosides (45–48). The altered expression of these structures in cancer cells could be the result of multiple mechanisms. Loss of expression or excessive expression of certain sialyltransferases is frequently observed. For example, up-regulated expression of $\alpha 2,3$ and $\alpha 2,6$ sialyltransferases has been observed in many cancers, such as colon cancer, breast cancer, liver cancer, cervical cancer, choriocarcinomas, acute myeloid leukemias, and some malignancies of the brain (49), and this type of change can affect the structures and functions of some important target *N*-glycoproteins such as integrin $\beta 1$ (50), EGFR (44), and platelet endothelial cell adhesion molecule (51).

Recent studies have suggested that activation of the EMT programs serves as a major mechanism for generating cancer

stem cells (52). Interestingly, high expression of ST6GAL1 has been correlated with human-induced pluripotent stem cells and cancer stem cells, indicating that sialylation may be involved in maintaining some aspects of stem cell behavior (4, 5, 53). In fact, ST6GAL1 expression is required for transforming growth factor β -induced EMT. Knockdown of ST6GAL1 prevented a transforming growth factor β -induced increase in cell migration (54).

Given the accumulating evidence of the importance of sialylation in cancer progression, much attention has been paid to elucidating the regulatory mechanisms of its expression. The expression of sialylation on a tumor cell surface can be modulated at different levels (49). The most frequently observed mechanism is modulation of transcription. For example, ST6GAL1 expression is induced by the *ras* oncogene in NIH3T3 cells via its promoter (8). Beyond its promoter activity, in this study, we clearly showed that sialylation could also be regulated by complex formation of PI4KII α and integrin $\alpha 3\beta 1$ on a posttranscriptional level. In fact, the PI4P-binding Golgi protein GOLPH3, which functions in secretory trafficking in

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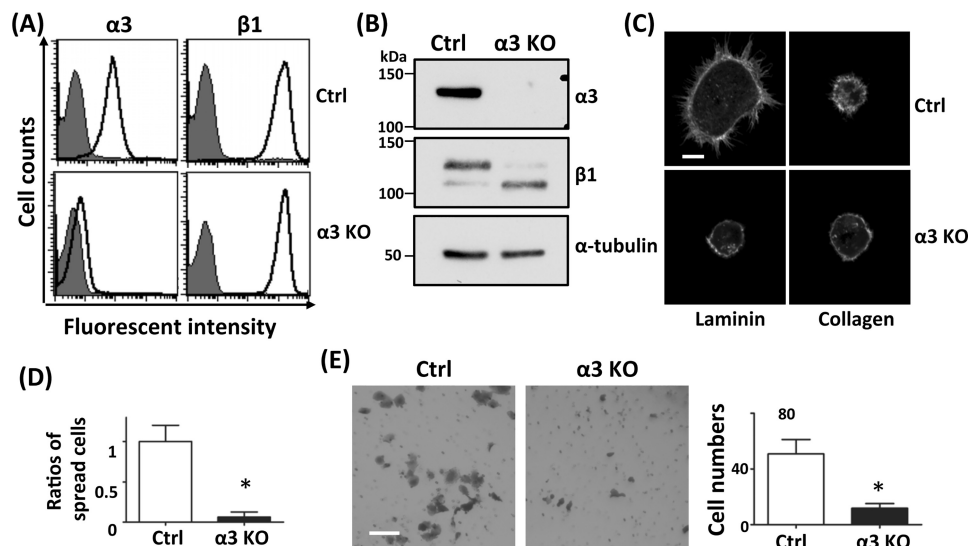


Figure 4. Effects of integrin $\alpha 3$ deficiency on cell spreading and migration. Establishment of integrin $\alpha 3$ KO MDA-MB-231 cells using the CRISPR/Cas9 system is described under “Experimental procedures.” The efficiency of $\alpha 3$ KO was assessed via flow cytometric analysis (A) and Western blotting (B). A, Both $\alpha 3$ KO and Ctrl cells were stained with (bold line) or without (gray shading) anti- $\alpha 3$ or $\beta 1$ integrin antibody and subjected to FACS analysis. B, the same amount of cell lysate was subjected to Western blotting to detect the indicated antibodies. C, cells were replated on coverslips coated with the indicated ECM, followed by incubation for 30 min, and were then fixed and stained with Alexa Fluor–conjugated phalloidin. Representative images are shown. Scale bar = 10 μm . D, cells were detached and then replated on laminin 332-coated dishes. After incubation for 15 min, the cells were fixed. The ratios of cell spreading were calculated. Cell spreading was defined as a cell spread of more than 0.025 μm^2 . Values represent the means \pm S.E. ($n = 5$). *, $p < 0.05$ (Welch’s t test). E, cell migration toward laminin-332 was determined using a Transwell assay. Scale bar = 100 μm . The quantitative data were obtained from three independent experiments. Values represent the means \pm S.E. ($n = 6$). *, $p < 0.05$ (Welch’s t test).

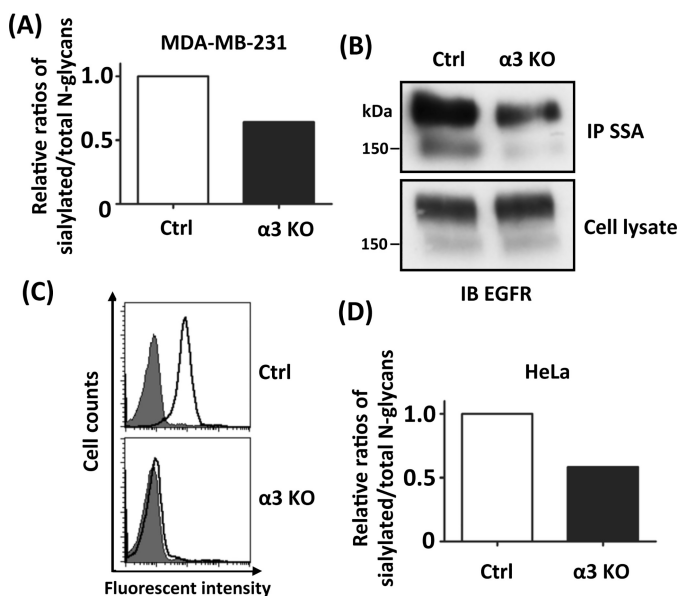


Figure 5. Deficiency of integrin $\alpha 3$ decreased sialylation of N -glycans in different cell lines. A, N -glycans released from both Ctrl and $\alpha 3$ KO MDA-MB-231 cells were pyridylaminated and verified as populations of sialylated N -glycans. The relative ratios of sialylated N -glycans versus total N -glycans were calculated by subtracting the neutral portions from the total and then dividing by the total. The control data were set as 1. B, equal amounts of cell lysates for control and $\alpha 3$ knockdown cells were precipitated via SSA-agarose and probed with anti-EGFR antibody (top panel). The same cell lysates were also probed with anti-EGFR antibody as a loading control (bottom panel). IP, immunoprecipitation. C, $\alpha 3$ KO of HeLa cells was established using the CRISPR/Cas9 system and verified via flow cytometric analysis. D, the ratios of sialylated N -glycans were analyzed as described in A.

the Golgi, is also important for the localization of several glycosyltransferases (10, 55, 56). Our previous study showed that knockdown of GOLPH3 leads to down-regulation of both $\alpha 2,3$ and $\alpha 2,6$ sialylation but has no effect on the transcription of

sialyltransferases. Therefore, regulation of biosynthetic glycan is not only dependent on the expression levels of glycosyltransferases but also on those of substrates, chaperones, and on the environment of the Golgi apparatus.

Considering that PI4P is a relatively abundant phosphoinositide that is required for the maintenance and function of the Golgi apparatus, which includes intracellular trafficking, it is plausible that PI4K could be involved in membrane transport from the trans-Golgi network to the plasma membrane. In fact, PI4KII α is known to associate with several cellular receptors such as EGFR, E-cadherin, LDL receptor-related protein, and the Fas receptor (57–60). In addition, alteration of the N -glycosylation of such receptors also regulates the functions of these receptors. For example, N -glycosylation is required for EGFR trafficking and has an effect on its endocytosis (61, 62). N -glycans of the LRP ectodomain also regulate the conformation and bending angle of the receptor (63). Cell surface sialylation protects Fas ligand-induced apoptosis by modification of the Fas ligand receptor (64), which could partially explain why enhancement of apoptosis has been observed in PI4KII α knockdown cells (60). Thus, the various phenotypes associated with PI4P and membrane proteins might be partially due to alteration of glycosylation.

The expression level of integrin $\beta 1$ is negatively correlated with the survival rates of patients with invasive breast cancer (65, 66), particularly $\alpha 3\beta 1$ expression in breast carcinoma associated with metastasis (41). During tumor progression, PI4KII α is also significantly up-regulated along with tumor growth compared with corresponding normal tissue (67). Given the importance of sialylation as described here, it is reasonable to expect up-regulation of both $\alpha 3\beta 1$ and PI4KII α in cancer cells.

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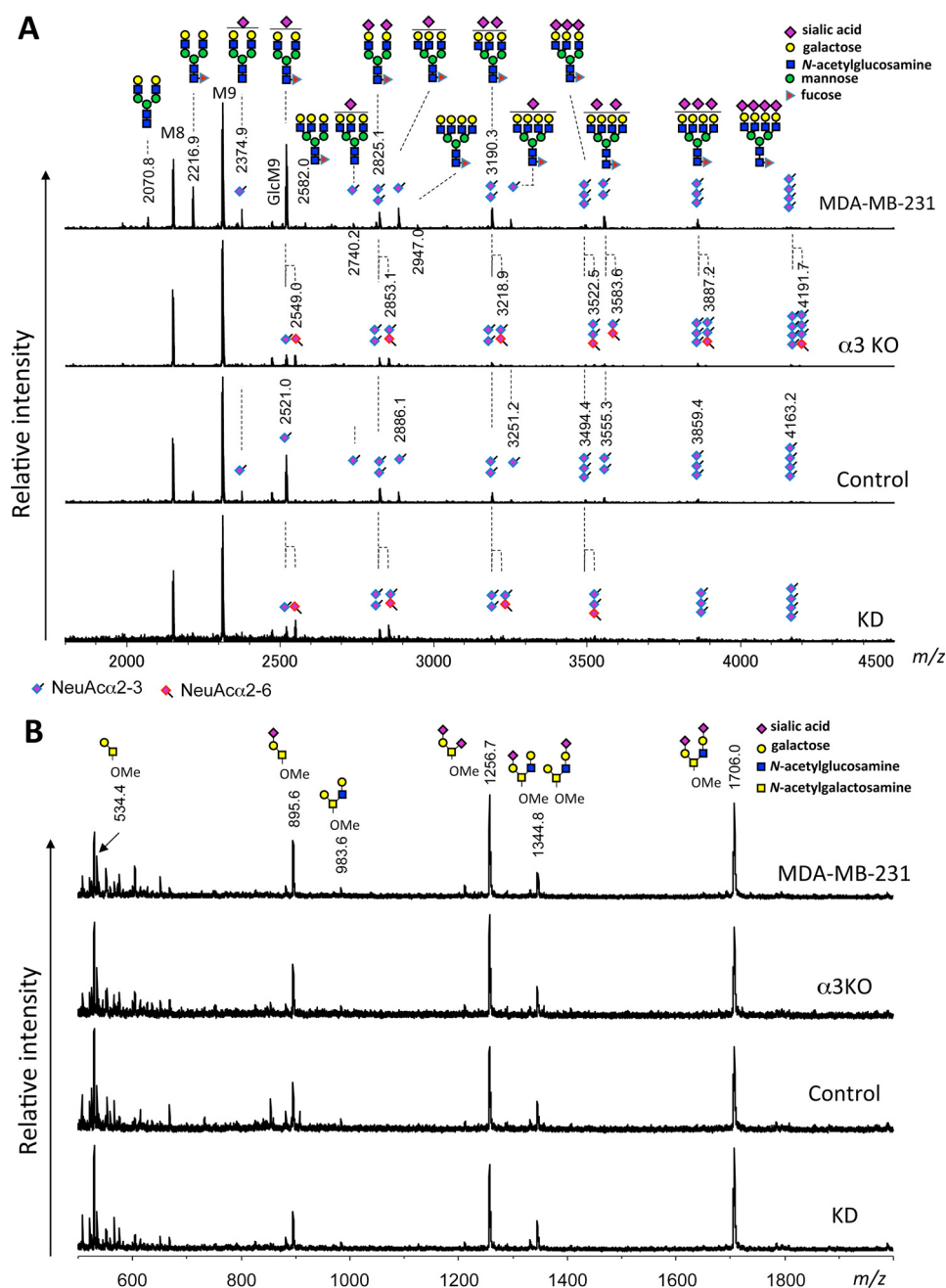


Figure 6. MS spectra of glycans obtained from cultured cells. *A*, MS spectra of *N*-linked glycans. The reducing ends of the *N*-linked glycans were derivatized with aoWR (86). The sialic acids of the *N*-linked glycans were differentially amidated with methylamine (+13.0 Da) for $\alpha 2,3$ -sialic acids and isopropylamine (+41.1 Da) for $\alpha 2,6$ -sialic acids via the SALSA method (87). MDA-MB-231 and $\alpha 3$ KO cells refer to parent and $\alpha 3$ knockout cells, respectively. KD and control cells of MDA-MB-231 cell line refer to transfectants with DOX-inducible knockdown of PI4KII α cultured with or without DOX, respectively. *B*, MS spectra of *O*-linked glycans. The *O*-linked glycans were obtained as the corresponding alditols and then permethylated.

These facts raise the question of why the interaction of PI4KII α with integrin $\alpha 3\beta 1$ but not of $\alpha 5\beta 1$ regulates sialylation. So far, the association underlying the mechanism between $\alpha 3\beta 1$ and PI4KII α remains unclear. However, the specificity of $\alpha 3\beta 1$ could be due to its interaction with the tetraspanin family, such as CD151, CD63, and CD9. In fact, other studies have reported that integrin $\alpha 3\beta 1$ and the tetraspanin family can interact with type II of PI4K (25–27). In addition, palmitoylation could also be a plausible factor because PI4Ks are proteins with membrane association and activity that are highly dependent on such a modification (68, 69), and palmitoylation also

plays an important role in the association between integrin and several molecules, such as tetraspanin and c-Met (70, 71). We assume that the association between PI4KII α and $\alpha 3$, but $\alpha 5$, might also relate to tetraspanin or palmitoylation.

It is noteworthy that both cell spreading and migration on laminin 332 of integrin $\alpha 3$ KO cells were significantly suppressed (Fig. 4), which further supports the notion that $\alpha 3\beta 1$ is a major receptor of laminin-332 compared with integrin $\alpha 6\beta 1$ and $\alpha 6\beta 4$ in epithelial cells (43, 72). Accumulating evidence shows that integrin $\alpha 3\beta 1$ is important for tumor metastasis in human breast and prostate cancer cell lines (40, 41) and sialy-

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lation of adhesive molecules such as integrin $\beta 1$, which, in turn, contributes to tumorigenesis (73). In this study, $\alpha 3$ deficiency significantly inhibited sialylation, indicating a novel link between sialylation and this integrin, which demonstrated the importance for both forms of functional expression. Although the MS analysis clearly showed that the complex between PI4KII α and integrin $\alpha 3$ regulates the biosynthesis of sialylation on *N*-glycans but not *O*-glycans, we could not completely exclude other possibilities for the regulation of *N*-glycan structures other than sialylation or gangliosides. In addition, it has been reported that GOLPH3 containing a PI4P binding domain could control Golgi localization of core 2 *N*-acetylglucosaminyltransferase 1 for the biosynthesis of *O*-glycans (74). Thus, further studies are required to explain the underlying mechanism for different influences, such as localization of glycosyltransferase, pH environment (75), and cholesterol homeostasis (76) through this system. Taken together, this study may provide a new concept for the regulation of glycosylation and could suggest insights for the development of cancer treatment.

Experimental procedures

Cell lines and cell culture

The HeLa and 293T cells were obtained from the RIKEN Bioresource Research Center (Japan). The MDA-MB-231 cells were purchased from the ATCC. All cell lines were maintained at 37 °C in DMEM containing 10% FBS in a humidified atmosphere of 5% CO₂.

PCR for mRNA expression analysis

Total RNA was prepared with TRIzol (Invitrogen), and 1.0 μ g of RNA was reverse-transcribed using the PrimeScript RT reagent kit (Takara Bio Inc.) according to the manufacturer's instructions. PCR primers against ST3GAL3, ST3GAL4, ST6GAL1, and GAPDH have been described previously (54). The following primers were used for PI4KII α : 5'-CTCCAGCGGAAGCTACTTCG-3' and 5'-TCCACTTAGGATTAAGATGCCCA-3'.

shRNA-mediated silencing of PI4KII α in MDA-MB-231 cells

Conditional knockdown of the target gene was achieved using the DOX-inducible CS-RfA-ETBsd lentivirus vector (RIKEN) with minor modifications (11, 54). The following oligonucleotides were inserted into pENTR/H1/TO (Invitrogen): 5'-CACCAGAAGCAGAACCTCTTCCTGATGATATGTGCATCAGGAAGAGGTTCTGCTTCT-3' and 5'-AAAAAGAAGCAGAACCTCTTCCTGATGCACATATCATCAGGAAGAGGTTCTGCTTCT-3' (29). The use of LR Clonase allowed the inserted oligo to be transferred to CS-RfA-ETBsd, which is an encoding DOX-dependent transactivator for shRNA expression. The resultant vector was then transfected into 293T cells with packaging plasmids of calcium phosphate for the preparation of viruses. MDA-MB-231 cells were then infected with the obtained viruses and selected for stable integration with 1 μ g/ml blasticidin. shRNA-mediated silencing of PI4KII α was induced by addition of 1 μ g/ml DOX for 72 h in the established cell line, and cells cultured in DOX-free medium were used as a control.

Gene introduction using the lentivirus system

The cDNA sequences for the PH domain of human FAPP1, PI4KII α , and integrin $\alpha 3$ were cloned from HeLa cells and inserted into pENTR vectors (pENTR/D-TOPO cloning kit, Invitrogen). To obtain the *N*-terminal GFP-tagged PI4KII α , C-terminal mRFP-tagged FAPP1 and a C-terminal GFP-tagged integrin $\alpha 3$, in-fusion enzyme (Clontech) was used with standard PCR protocols. The linkers for GFP-PI4KII α , mRFP-FAPP1, and $\alpha 3$ -GFP were 5'-GGGGS-3', 5'-KNPPVAT-3' (37), and 5'-LELKLRLQSTVPRARDPPVAT-3', respectively. The resultant cDNAs were confirmed by DNA sequencing using an ABI Prism 3130 sequencer (Applied Biosystems Japan Ltd., Tokyo, Japan). The subcloned cDNAs were transferred into CSII-EF-Rfa (11) via LR Clonase (Invitrogen) for lentivirus production. The resultant vectors (CSII-EF-GFP-PI4KII α /mRFP-FAPP1/ $\alpha 3$ -GFP) and the previously constructed integrins of either $\alpha 5$ -GFP- or $\beta 1$ -overexpressed lentiviral vectors (CSII-EF- $\alpha 5$ GFP (77)/ $\beta 1$ (78)) were then transfected into 293T cells with packaging plasmids via calcium phosphate during the preparation of viruses. Either MDA-MB-231 or 293T cells were then infected with the obtained viruses for further experiments.

Cell migration (Boyden chamber assay)

Cell Migration was performed as described previously with minor modifications (11, 79). Each Transwell (BD BioCoat control inserts, 8.0- μ m inserts; BD Biosciences) was coated only on the bottom side with 1 μ g/ml laminin-332 (Oriental Yeast Co., Ltd.) in PBS containing 0.1% BSA at 4 °C for 24 h and then blocked with 5% BSA in DMEM at 37 °C for 1 h. Cells were trypsinized and suspended in DMEM containing 1% FBS. The suspended cells were centrifuged, and the cell pellets were resuspended in an assay medium (0.1% BSA in DMEM containing 1% FBS) and diluted to 3×10^5 cells/ml; cell viability was confirmed by trypan blue staining. Cell suspensions were then added to the Transwell. Following incubation, the membranes were fixed with 4% paraformaldehyde and stained with 0.5% crystal violet solution (Merck) for 24 h. After washing the Transwells with PBS, cells that migrated to the lower side were counted using a phase-contrast microscope.

Immunostaining

Cells (1×10^5) were plated on glass coverslips (MatTek), precoated with or without ECM for 24 h, fixed with 4% paraformaldehyde for 15 min, permeabilized with 0.1% Triton X-100 for 10 min, and blocked with PBS containing 3% BSA and 0.01% Tween 20 (PBSBT) for 1 h. Cells were then incubated with the indicated primary antibodies (GM130, BD Biosciences, 610822; $\alpha 3$, Millipore, P1B5) at 4 °C overnight, followed by incubation with Alexa Fluor 647-conjugated secondary antibodies (Molecular Probes) for 1 h. For lectin staining, cells on coverslips were incubated with either biotinylated SNA lectin (Vector Laboratories, B-1305) or wheat germ agglutinin (WGA) lectin (J-Oil Mills, J220) at 4 °C for 30 min in DMEM, fixed and blocked with PBSBT for 1 h, followed by incubation with streptavidin-conjugated Alexa Fluor 647 at 4 °C for 1 h in the dark. All samples were mounted using Prolong Diamond Antifade mounting medium (Molecular Probes). Images were acquired by sequential excitation using an Olympus FV1000 laser-scanning confo-

cal microscope with an UPlanSApo $\times 60/1.35$ oil objective operated with F10-ASW version 4.02 software.

Cell spreading and adhesion experiment

Coverslips were coated with 1 $\mu\text{g}/\text{ml}$ laminin-332 or 2 mg/ml gelatin in PBS containing 0.1% BSA at 4 °C for 24 h and then blocked with 5% BSA in DMEM at 37% for 1 h. Cells were replated on the coverslips in DMEM with 0.1% BSA. After incubation for 10 min, the areas of adherent cells were measured using ImageJ. We defined cells spread at more than 0.025 μm^2 as adherent cells. After incubation for 30 min, the cells were fixed with 4% paraformaldehyde and stained with phalloidin–Alexa Fluor 647 (Molecular Probes).

Immunoprecipitation and Western blotting

Immunoprecipitation was performed as described previously with minor modifications (11, 80). Briefly, cells were gently rinsed three times with PBS at room temperature and solubilized in cold lysis buffer A (20 mM Tris-HCl (pH 7.4), 150 mM NaCl, and 1% Brij98), which included protease inhibitors. Protein concentrations of lysates were determined via BCA assay (Pierce). The lysates were immunoprecipitated using either anti-GFP-agarose (MBL), anti-integrin $\alpha 3$ antibody (Millipore, P1B5), or anti-integrin $\beta 1$ (P5D2, DSHB) with Ab-Capcher Protein A-R28 (Protenova, Tokushima, Japan) for 1 h at 4 °C and gentle rotation. After washing with lysis buffer, the immunoprecipitates were subjected to SDS-PAGE. The proteins were probed with anti-integrin $\alpha 3$ (Santa Cruz Biotechnology, sc-6592) or anti-GFP antibody (Rockland, 600-101-215) and then detected using anti-goat IgG-conjugated horseradish peroxidase (Santa Cruz Biotechnology) with an Immobilon Western chemiluminescent horseradish peroxidase substrate (Millipore). For analysis of the lectin precipitates, we used lysis buffer B (20 mM Tris-HCl (pH 7.4), 150 mM NaCl, and 1% Triton X-100). Cell lysates were precipitated with either SSA-agarose (J-Oil Mills, J318), MAM (also called MAL-1)–agarose (J-Oil Mills, J310) or concanavalin A (ConA)–agarose (J-Oil Mills, J303), which specifically recognize either $\alpha 2,6$ - and $\alpha 2,3$ -sialylation or total *N*-glycans, respectively. The precipitants were detected using either anti-integrin $\beta 1$ (BD Biosciences, 610468) or anti-EGFR (Cell Signaling Technology, 4267). Antibody agents against Akt (9272) and p-Akt (4060) were purchased from Cell Signaling Technology. α -Tubulin (Sigma, T6199) was used as a loading control.

Flow cytometric analysis

Flow cytometric analysis was performed as described previously with minor modifications (11, 79, 80). Briefly, semiconfluent cells were detached from the culture dishes using trypsin containing 1 mM EDTA. The cells were subsequently stained with or without primary mouse anti- $\alpha 3$ (P1B5), anti- $\beta 1$ (P5D2), and anti- $\alpha 5$ integrin (Millipore, HA5) in PBS, followed by incubation with Alexa Fluor 647–conjugated secondary antibodies. For staining cells with biotin-conjugated lectins (MAM and SNA), we used PBS buffer containing 0.5 mM CaCl_2 and MgCl_2 . Flow cytometric analysis was performed using a FACSCalibur flow cytometer and Cell Quest Pro software (BD Biosciences).

PA oligosaccharide preparation of *N*-glycosylation and quantitative analysis of sialylated *N*-glycans by anion exchange HPLC

To release *N*-glycans from glycoproteins, the lyophilized cell pellets (1–2 mg) were heated with 200 μl of anhydrous hydrazine at 100 °C for 10 h using an oil bath. Removal of hydrazine and acetylation of *N*-glycans were carried out with a graphite carbon column (81). The released *N*-glycans were then 2-pyridylaminated using the Pyridylation Manual Kit (Takara Bio Inc.), and then the excess 2-aminopyridine was removed via phenol–chloroform extraction (81) with a gel filtration column (82). The prepared PA oligosaccharides treated with or without neuraminidases were subjected to a HPLC system (JASCO) equipped with a TSKgel DEAE-5PW column (7.5 \times 75 mm, Tosoh) and analyzed as described previously (19). HPLC chromatogram data were analyzed using chromNAV software (JASCO). The amounts of total and neutral *N*-glycans were calculated based on the peak area of neutral fraction with or without neuraminidase treatment. Relative ratios of sialylated *N*-glycans *versus* total *N*-glycans were calculated by subtracting the neutral portions from the total and then dividing by the total. The data were normalized to the control as 1.

Generation of CRISPR/Cas9-based integrin $\alpha 3$ KO cells

CRISPR/Cas9-based integrin $\alpha 3$ cells were established as described previously (83, 84). Briefly, the single guide RNA-specifying oligo sequences spanning human integrin $\alpha 3$ (forward, 5'-CACCGCATCGGGCACAGCGAGCTCC-3'; reverse, 5'-AAACGGAGCTCGCTGTGCCCGATGC-3) were chosen from the human KO library (85). Then the oligos were cloned into pSpCas9 (BB)-2A-GFP, which was a kind gift from Dr. Feng Zhang (Addgene plasmid ID 48138). The plasmid was transfected into cells according to the manufacturer's instructions (Amaya Cell Line Nucleofector kitV). After 4 days of transfection, GFP-positive cells were sorted using a FACSAria II (BD Bioscience). Following 10-day culture, $\alpha 3$ -negative and GFP-negative cells were sorted, and the procedure was repeated twice. The KO cells were defined by flow cytometry and Western blot analysis as described above.

Mass spectrometry of glycans

Total plasma membrane proteins of cells were prepared using a plasma membrane protein extraction kit (101Bio). For *N*-glycan analysis, a previous report (86) suggests that the pellets are dissolved and denatured and then digested by glycopeptidase F (Takara Bio Inc.). The released *N*-glycans were captured on hydrazide beads (BlotGlyco, 5 mg, Sumitomo Bakelite Co., Ltd.) using a process recommended by the manufacturer. Sialic acids of the *N*-glycans on the beads were then differentially amidated with methylamine for $\alpha 2,3$ -sialic acids and isopropylamine for $\alpha 2,6$ -sialic acids using the sialic acid linkage-specific alkylamidation (SALSA) method (87). The derivatized *N*-glycans were liberated, labeled with aWR (a component of BlotGlyco, Sumitomo Bakelite Co., Ltd.) (86), and purified according to the manufacturer's instructions. The obtained glycan solutions were mixed with a 2,5-dihydroxybenzoic acid solution (10 mg/ml in 30% acetonitrile) at a ratio of 1:10. Aliquots (0.5 μl) of the mixed solutions were deposited onto a

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MALDI target plate and dried. MS spectra were acquired with a MALDI quadrupole ion trap TOF mass spectrometer (AXIMA-QIT, Shimadzu Corp.). For O-glycan analysis, pellets of the membrane fractions were dissolved in a 1% SDS solution. Aliquots (10 μ l) of the solution were transferred into 90 μ l of 0.6 M sodium borohydride containing 60 mM NaOH and incubated at 45 °C for 16 h. Then the mixtures were neutralized, diluted to 1 ml, and applied onto a solid-phase extraction cartridge (Sep-Pak C18 Vac 1cc, 50 mg, Waters Corp.), and then the cartridge was washed with distilled water (1 ml). The eluents and washings were combined and lyophilized. The obtained residues were dissolved in 1% acetic acid in methanol (100 μ l) and evaporated using a centrifuge evaporator. The procedure of dissolution and evaporation was repeated. The obtained residues were permethylated according to previous reports (88). The permethylated glycans were dissolved in a 2,5-dihydroxybenzoic acid solution (20 μ l, 10 mg/ml in 30% acetonitrile), and aliquots (0.5 μ l) of the mixed solutions were deposited onto a MALDI target plate and dried. MS spectra were acquired with a MALDI-TOF mass spectrometer (Ultraflex, Bruker Daltonik).

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