Intracellular reprogramming of expression, glycosylation, and function of a plant-derived antiviral therapeutic monoclonal antibody.

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Intracellular Reprogramming of Expression, Glycosylation, and Function of a Plant-Derived Antiviral Therapeutic Monoclonal Antibody

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Abstract

Plant genetic engineering, which has led to the production of plant-derived monoclonal antibodies (mAb’s), provides a safer and economically effective alternative to conventional antibody expression methods. In this study, the expression levels and biological properties of the anti-rabies virus mAb’s SO57 with or without an endoplasmic reticulum (ER)-retention peptide signal (Lys-Asp-Glu-Leu; KDEL) in transgenic tobacco plants (Nicotiana tabacum) were analyzed. The expression levels of mAb’s SO57 with KDEL (mAb’sK) were significantly higher than those of mAb’s SO57 without KDEL (mAb’s) regardless of the transcription level. The Fc domains of both purified mAb’s and mAb’sK and hybridoma-derived mAb (mAbH) had similar levels of binding activity to the FcγRI receptor (CD64). The mAb’sK had glycan profiles of both oligomannose (OM) type (91.7%) and Golgi type (8.3%), whereas the mAb’s had mainly Golgi type glycans (96.8%) similar to those seen with mAbH. Confocal analysis showed that the mAb’sK was co-localized to ER-tracker signal and cellular areas surrounding the nucleus indicating accumulation of the mAb’s with KDEL in the ER. Both mAb’s and mAb’sK disappeared with similar trends to mAbH in BALB/c mice. In addition, mAb’sK was as effective as mAbH at neutralizing the activity of the rabies virus CVS-11. These results suggest that the ER localization of the recombinant mAb’sK by KDEL reprograms OM glycosylation and enhances the production of the functional antivirus therapeutic antibody in the plant.


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Introduction

Rabies virus causes a neuroinvasive disease that is typically fatal in humans. After the penetration of the virus and the subsequent onset of the associated clinical symptoms, there is no effective treatment. Recombinant rabies virus vaccines provide an effective method for the prevention of virus infections [1,2]. However, after a rabies exposure, the currently recommended intervention strategy is to neutralize and clear the virus with antibodies or immunoglobulins (IgGs) through post-exposure prophylaxis (PEP) before the virus enters the nervous system. The use of human or equine rabies immune globulin has saved the lives of countless patients who would have died if treated with vaccine alone. Unfortunately, the worldwide shortage of the IgGs has hampered global efforts to provide PEP against rabies [3].

Typically, recombinant pharmaceutical proteins such as antibodies and therapeutic proteins are produced in animal systems. Alternatively, keep plant systems can be used for the large-scale production of these proteins. Plant systems offer several advantages including low upstream cost inputs, an absence of human or animal pathogen contaminants, and the ability to employ post-translational modifications such as glycosylation [4–8]. Many therapeutic and diagnostic mAbs have been expressed successfully in plants, including full-length IgGs, Fab fragments, single variable domains, antibody-fusion proteins, and single-chain antibodies [5,9,10].
The biosynthesis of N-linked glycans in plants differs from that of mammalian cells [11]. Although plants synthesize complex N-linked glycans containing a core Manα1,3GlcNAc2 that bears 2 terminal N-acetylgalactosamine (GlcNAc) residues, which are similar to those found in mammals, a β[1,2]-xylose (Xyl), Lewis’s epitopes, and an α[1,3]-fucose (Fuc) exist on the Manα1,3GlcNAc2 core in plants. These plant-specific epitopes are absent on mammalian glycans and are therefore recognized by allergen-reactive mammalian IgEs [12,13].

Glycoproteins are N-glycosylated in the ER and the Golgi complex and then secreted into subcellular compartments such as vacuoles and the extracellular space. Glycosylation processing in the ER is conserved amongst almost all species and restricted to OM (Manα1,6GlcNAc2)-type glycans, whereas the Golgi-generated glycans are highly diverse [14]. In plants, the addition of KDEL at the C-terminal end of a protein is sufficient for the protein to be retained in the ER [15,16]. mAbPs with KDEL fused to their light chain (LC) therefore contain exclusively non-immunogenic, OM type glycans with stable ER accumulation [17]. Gradinaru et al. [18] found that their protein of interest accumulated in the ER when it contained the KDEL in mammalian cells, and this ER retention of proteins in plants usually improved the production levels [19,20]. However, an in vitro study in mice demonstrated that the anti-rabies mAb with OM type glycans was cleared from serum more rapidly than mAbH [5]. The rapid clearance might be due to a number of possibilities, including immunogenicity resulting from KDEL itself acting as an epitope, a glycan residue-derived conformational alteration of the Fc domain [21], the OM structure being easily accessible to Man binding lectin [22], and a lack of terminal sialylation, which contributes to protein instability [23]. It has not been clearly understood whether the shorter half-life is due to the OM or lack of sialylation on the glycoproteins [5]. Unlike mAbs for cancer therapy, an anti-rabies mAb for PEP with rapid clearance is beneficial because interference between the mAbs and the vaccine can then be avoided [3].

In the present study, we expressed and characterized a human anti-rabies mAb derived from plants with or without the C-terminal KDEL tag for ER retrieval and demonstrated its effectiveness in vitro and in vivo. Both mAbK and mAbS were compared with the mAbH for the rabies virus in their expression level, ER localization, N-glycan processing, neutralization activity, and protein stability. The KDEL-tagged mAb became predominantly localized in the ER, thus enhancing the mAb assembly in the plant cells. Therefore, the KDEL tagging to the mAb helped to enhance the final mAb yield in plants.

Results

Expression of mAb SO57 in Tobacco Transgenic Plants

Transgenic tobacco lines were obtained by Agrobacterium-mediated transformation with plant expression vectors carrying HC, HCK, and LC of the human mAb SO57. Both HC and HCK cDNA were placed downstream of the alfalfa mosaic virus untranslated leader sequence (AMV) under the control of the enhanced cauliflower mosaic virus 35S promoter (Ca2p), while LC cDNA was under control of the potato protease inhibitor II gene (Pin2) promoter (Figure 1A). PCR amplification was conducted to confirm the presence of HC, HCK, and LC genes in genomic DNA isolated from the randomly selected transgenic plants (Figure 1B). The amplified HC (1,431 bp), and LC (729 bp) fragments were detected in all samples, whereas the HCK (1,443 bp) genes were detected only in the transgenic plants with the KDEL-tagged mAb P; mAbP K, KDEL-tagged mAbP.

Figure 1. Expression of mAb SO57 in transgenic plants. (A) A schematic diagram of the mAb SO57 HC and LC DNA constructs [7]. (B) PCR analysis of LC (729 bp), HC (1431 bp) and HC fused to KDEL (HCK, 1443 bp) in the genomic DNA. NT, non-transgenic plant; mAbK, non-KDEL-tagged mAbB; mAbK K, KDEL-tagged mAbB.

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HC (Figure 1B). None of the transgenes were detected in the non-transgenic plants.

Evaluation of mAb SO57 HC and LC Expression Levels by Real-Time Quantitative Reverse Transcription-PCR (RT-qPCR) and Immunoblotting

A RT-qPCR assay was performed to determine the transcription levels of HC and LC in randomly selected transgenic plants (Figure 2A). RT-qPCR products of the expected sizes for the mAb SO57 HC (67 bp; Left) and LC (66 bp; Right) were detected in the transgenic plants (Figure 2A). When normalized against actin mRNA, transcription levels of both HC and LC were not significantly different between mAbB and mAbB K (p>0.05) (Figure 2A). The expression of the HC and LC proteins in the transgenic plants was confirmed by immunoblot (Figure 2B). Both the HC (50 kDa) and LC (25 kDa) bands were identified in the total leaf soluble protein extracts from the transgenic plants by the anti-human Fcγ and anti-F(ab)2-specific secondary IgGs, respectively. In the immunoblot with the anti-human Fcγ-specific IgG, HC was detected in both mAbP and mAbB K samples. In the immunoblot with the anti-F(ab)2-specific IgG, LC was detected in all transgenic samples. In addition, the expression levels of HC (Left) and LC (Right) were higher in the mAbB K sample than that in the mAbP sample (Figure 2B).

Localization of mAbB and mAbB K in Plant Cells

The ER, labeled red with ER tracker was observed in cells of both mAbB and mAbB K transgenic plants (Figure 3, ER-tracker). mAbH SO57-immunoreactive green fluorescence was seen in cells from mAbB and mAbB K transgenic tobacco plants (Figure 3, and S1, Human IgG, respectively) whereas no green signal was found in cells from non-transgenic plants (NT; Figure S1, Human IgG, lower panel). The nuclei, which were labeled blue with TO-PRO-3, were observed in cells from all of the plant samples (Figure 3, TO-PRO-3). In the mAbB K transgenic plant, the strong green fluorescent signal of antibody closely overlapped with the red fluorescent signal of ER-Tracker in round shape (Figure 3, Human IgG and Merge, upper panel) whereas in the mAbB transgenic plant, the green fluorescent signal was roughly spread in cells without close overlapping to the red fluorescent signal (Figure 3, Human IgG and Merge, lower panel).
In the mAbPK transgenic plant, the antibody immunoreactivity disclosed a concentric green ring (Figure S1, Human IgG and Merge, upper panel, arrow heads) whereas in the mAbP transgenic plant, a strong green ring shape was not observed (Figure S1, Human IgG and Merge, middle panel). In the mAbPK transgenic plants, the merge of green and blue showed, surrounding the outside of the blue-labeled nucleus, a relatively strong green ring, where the ER is distributed (Figure S1, Merge, upper panel). In contrast, in the mAbP transgenic plants, the green did not surround the outside of the nucleus in the plant cells. In the non-transgenic plants, the nuclei labeled in blue were observed whereas the green was not detected (Figure S1).

Purification of Plant-derived mAb SO57

mAbs were purified from leaves harvested from mAbP and mAbPK transgenic tobacco plants. The protein A column purification yielded an average of 0.4 and 1.2 mg of mAbP and mAbPK per kilogram of fresh leaves from high mAb expressing lines, respectively. SDS/PAGE analysis of the purified mAb P revealed two major bands (50 and 25 kDa for the HC and LC, respectively) (Figure 4). The LC of mAbP was slightly heavier than that of mAbK (Figure 4). The discrepancy of mobility is due to the different buffer composition of purified samples between plant and human or the different signal peptide used to express the recombinant LC gene in transgenic plants. In this study, different

Figure 2. The RT-qPCR and immunoblot analysis of mAb SO57 HC and LC in transgenic tobacco plants. (A) Relative expression levels (Y axis) of the HC and LC gene as determined by RT-qPCR. Amplicons generated with the RT-qPCR were confirmed by 1% agarose gel electrophoresis (upper panel). The results of RT-qPCR are expressed as the average of three independent experiments after normalization with N. tabacum actin bands (lower panel). Error bars represents mean relative expression values (mean ± SD) of HC and LC to actin from the mAbP and mAbK samples. Transcript levels of HC and LC were not significantly different between the mAbP and mAbK (p>0.05). mAbP, non-KDEL-tagged mAb; mAbK, KDEL-tagged mAb (B) Western blot analysis of proteins extracted from leaves of randomly selected 4 transgenic plants without KDEL and 3 transgenic plants with KDEL, respectively. The bands for HC (50 kDa) and LC (25 kDa) were detected with HRP-conjugated goat anti-human Fcγ- or F(ab')2-specific antibodies, respectively. *p<0.05 compared to mAbP samples (Student’s t-test analysis). Error bars represent the mean ± SD.

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Figure 3. Confocal analysis of the subcellular localization of mAb SO57 and mAb SO57 K in plant leaves. Immunofluorescent confocal microscopic photomicrographs displayed localization of mAb SO57 in subcellular organelles of transgenic tobacco plant leaf cells. The red signal for ER-Tracker Blue-White DPX, a photo-stable probe selective for the ER in live cells, shows specific ER localization of mAb. The mAb SO57-immunoreactive green fluorescence was detected by FITC-conjugated anti-human IgG (green). The nuclei (blue) were labeled with TO-PRO-3. Each image was merged to analyze the subcellular localization of mAb SO57 in transgenic plants. The green fluorescent signal of mAb SO57 K closely overlapped with the blue fluorescent signal of ER-Tracker. Scale bars, 20 μm.

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Comparison of N-Glycan Structure and Neutralizing Activity of Purified mAb\(^{P}\) and mAb\(^{PK}\) S057

A DNA sequencer-based analysis was performed to compare the N-glycan profiles of mAb\(^{P}\), mAb\(^{PK}\), and mAb\(^{H}\) (Figure 5, S2, and S3). APTS ([8-amino-1,3,6-pyrenetrisulfonic acid]-labeled glycan profiles are shown in Figure 5, and the peaks were identified by exoglycosidase digestion and by the comparison to glycan profiles previously assigned. Relative percents (%) for OM and Golgi types were calculated from the sum of the corresponding peak areas (Table 1). As expected, mAb\(^{P}\) had very low percentage of OM-type glycans. In contrast, mAb\(^{PK}\) included a high portion of OM-type glycans (91.7%) together with Golgi-type glycans (8.3%). The mAb\(^{H}\) displayed a range of complex glycans, most of which (90%) contained a core \(\alpha(1,6)-Fuc\) (Figure S2). In addition, an in vitro comparison of the neutralizing activity of mAb\(^{P}\) and mAb\(^{PK}\) against cell culture-adapted rabies virus (CVS-11) indicated that both mAb\(^{P}\) and mAb\(^{PK}\) were as active against the CVS-11 as was mAb\(^{H}\) (Table 1).

Clearance of Plant-derived mAb S057

An in vivo comparative clearance test of mAbs was conducted in mice i.p. administered mAb\(^{P}\), mAb\(^{PK}\), and mAb\(^{H}\). The blood samples were collected between days 1 and 10 after injection. Serum antibody concentrations were determined by ELISA. To exclude the possibility to miscalculate clearance rate due to difference in the initial antibody concentrations, the initial values were considered as 100% at day 1 after injection. The concentrations of antibodies in serum were expressed as relative percent (Figure 6). Between days 1 and 10, mAb concentrations slowly declined until day 10. The clearance trend of all three antibodies was similar between days 1 and 10. At day 10 after injection, the % value of mAb\(^{H}\) (36%) was statistically not different to mAb\(^{PK}\) (39%).

Discussion

Our data demonstrate that plant cell reprogramming with the addition of an ER retention signal to mAb enhanced the expression of the antibodies, which had a virus neutralizing activity comparable to that of mAb\(^{H}\). In addition, the ER retention signal allowed control of the subcellular localization of the mAb and generated different glyco-structural patterns. The expression level of the mAb and its biological activities are essential elements for effective heterologous production of such a highly valuable therapeutic protein. In this study, two different plant expression vectors for the anti-rabies mAbs with and without the KDEL (mAb\(^{K}\) and mAb\(^{H}\), respectively), which was fused to the HC, were designed in order to investigate the resulting expression levels and biological activities of the ER-retained and default secreted mAbs. The HC and LC were controlled under two different promoters, G\(\alpha\)2p and P\(\alpha\)2p, respectively, in order to avoid promoter-targeted transcriptional gene silencing [24]. The HCK had about 2 times greater protein accumulation than the HC without KDEL (HC). However, the relative transcription level of the HCK was not significantly different. These data indicate that the higher HC level in transgenic plants with mAb\(^{PK}\) is due to ER accumulation of the mAb. The LC protein expression in transgenic plants with HCK was slightly higher compared to transgenic plants without KDEL, whereas the LC transcriptional level was relatively lower in HCK compared to HC transgenic plants. These results suggest that the LC protein was assembled together with the HCK, and consequently retained and accumulated in the ER. Taken together, in transgenic plants with HCK, protein expression levels were increased regardless of the similar transcription level, when compared to transgenic plants with HC. Thus, the KDEL can be applied to enhance the protein accumulation level [25].

In the glycosylation profiles of the mAbs analyzed using the DNA sequencer, mAb\(^{PK}\) and mAb\(^{H}\) showed 91.7% and 3.2% of OM-type glycan structures, respectively, which indicates that the KDEL influences the glycan structure through the retention of the mAb in the ER and supports the present confocal analysis results. The mature glycan structures of plant proteins are characterized by the presence of \(\beta(1,2)-Xyl\) and/or \(\alpha(1,3)-Fuc\) residues, which can cause allergic and immunogenic responses [28,29]. Thus, the KDEL has been added to the C-termini of proteins retained in the ER in order to yield OM-type glycans that avoid such glycopeptides. Our previous studies demonstrated that OM-type glycans of mAb\(^{PK}\) are associated with more rapid clearance in vivo compared with mAb\(^{H}\) [3]. It has been proposed that the increased clearance rate might be due to immunogenicity resulting from the KDEL itself acting as an epitope and/or due to the glycan residue-derived conformational alterations of the IgG Fc domain [21].

On the other hand, OM structures can be easily internalized into endocytic pathways in macrophages and dendritic cells upon which the surface carrying Man receptors bind the OM of mAb [30–32]. This internalization can be associated with faster clearance of circulating oligomannosylated antibodies [33]. In this
study, however, both mAbPs, regardless of their OM or plant-specific complex type glycostructures had similar disappearance trends with mAbH. The mAb clearance trends observed in this study are similar to the previous report where plant-derived anti-hepatitis B virus mAbs with KDEL and without KDEL showed a similar clearance trend in mice from 1 to 10 day after injection [34]. These results suggest that the KDEL or OM glycan structures are not closely related to the clearance trend of mAb in mice sera. It is speculated that the non-sialylation of both mAbPs did not affect the faster clearance of mAbs in blood circulation regardless of OM or plant-specific complex glycan structures from 1 day to 10 day after injection. The interaction of the Fc portion of the antibody with the Fc receptor of the immune cells is essential to elicit ADCC, a mechanism of cell-mediated immunity whereby natural killer cells actively promote cell death in a target cell by triggering apoptosis. Previous studies have shown that anti-colorectal cancer mAbs with plant-specific glycostructures had similar in vitro interactions of Fc and the Fc Receptor I (CD64) to their parental mAbM [7,35] and in vivo anti-tumor activity [36]. In this study, the binding activities of mAb P, mAbPK and mAb H to U937 cells (Human leukemic monocyte lymphoma cell line) [37] expressing the Fc Receptor I (CD64) were determined by flow cytometric assay (Figure 7). The FL2-H fluorescence peak (bold line) of mAbPK (bottom) were located similarly to the mAb H (upper), whereas the peak (bold line) of mAb P (center) was located slightly more to the left as compared to the peak (bold line) of mAbH (upper). Binding activity to the Fc receptor is also essential for anti-rabies immunotherapy since the neutralization activity, which physically blocks the rabies virus particles by mAb SO57, is the only one required to acquire the anti-virus activity [38]. These results indicate that an OM-type of antibody can have slightly better interaction between Fc and Fc receptors compared to the plant-specific glycan type.

In this study, direct comparison of clearance time and biological activities of plant-derived anti-rabies virus monoclonal antibodies with high mannose and plant-specific glycan structure were performed, which has not been reported previously. Through these data, we now see that glycan structures might not significantly alter antibody stability. Certainly ER localization affects glycan structure and expression of recombinant mAbs in this plant expression system. The current results highlight the potential of OM glycomodifications of therapeutic anti-rabies virus mAbs produced in plants with KDEL-mediated subcellular ER localization. Even though mAbP (plant-specific glycans) and mAbPK (OM-type glycans) had relatively similar virus neutralizing activity compared to mAbH, and thus similar potential for rabies PEP application, expression in the ER can overcome concerns about plant-specific glycoepitopes expressed by others [29] and provide the additional benefits of higher expression and relatively better effectiveness of Fc receptor-Fc interaction.

### Materials and Methods

**Ethics statement**

BALB/c mice (female, 6–8 wk) were obtained from Daihan Biolink (Eumsung, Korea) and injected i.p. with plant-derived monoclonal antibody (mAbP) or hybridoma-derived monoclonal antibody (mAbH). After injection, blood samples were collected from the orbital sinus twice during the entire time period (10 days). The animal experiments were approved by the Institutional Animal Care and Use Committee (IACUC) of Wonkwang University, Iksan, Korea (Approval ID: WKKU11-28). All efforts were made to minimize suffering of the animals.

### Table 1. Comparison of profiled glycan of mAbP, mAbPK, and mAbH, and their virus-neutralizing activity against rabies virus CVS-11.

<table>
<thead>
<tr>
<th>Sample</th>
<th>% of total peak area</th>
<th>Neutralizing Activity (IU/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Glgoi type</td>
<td>OM type</td>
</tr>
<tr>
<td>mAbH</td>
<td>~90</td>
<td>~10</td>
</tr>
<tr>
<td>mAbP</td>
<td>96.8</td>
<td>3.2</td>
</tr>
<tr>
<td>mAbPK</td>
<td>8.3</td>
<td>91.7</td>
</tr>
</tbody>
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OM type, oligomannose type.

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**Figure 5. N-glycan profiles of anti-rabies mAbPK and mAbP.** mAbs were expressed from transgenic tobacco plants as dual forms with mAbPK or mAbP. Glycan profiles of mAbP (A) and mAbPK (B) were obtained by DNA sequencer-based method for the plant N-glycan analysis. Golgi-type and OM-type glycans were classified and confirmed by hexosaminidase (H) and α(1,2)-mannosidase (α,1,2-Man) digestions. The symbols of the glycan structures are as follow: GlcNAc, black square; Man, white circle; Xyl, white triangle; Fuc, diamond with a dot inside. Non, non-digested sample.

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Plant Transformation Vector and Generation of Transgenic Plants

The mAb SO57 HC and LC genes were amplified by PCR with forward and reverse primers containing Ncol and Xbal, and Pdi and BamHl sites in the 5’ and 3’ ends, respectively. The HC and HCK cDNA were placed with AMV translational enhancer element under the control of the Ca2p, and the LC cDNA were under the control of the Pm2p in a pBI121-based plant expression vector (Figure 1A). The two different types of HC genes were cloned with and without fusion to the KDEL. Binary vectors for Agrobacterium-mediated plant transformation were obtained according to the protocol employed by a previous study [5]. The transgenic tobacco plants were selected on kanamycin (100 µg/ml), transplanted into soil, and maintained for subsequent generations.

Polymerase Chain Reaction (PCR)

Genomic DNA was isolated from leaves by a DNeasy kit (Qiagen, Valencia, CA), according to the manufacturer’s recommendations. PCR amplification was applied in order to confirm the presence of the genes encoding for mAb SO57 HC (1431 bp), LC (729 bp) and HCK (1443 bp) using the forward (F) and reverse (R) primers shown in Table S1. PCR amplification was applied in order to confirm the presence of the genes encoding for mAb SO57 HC (1431 bp), LC (729 bp) and HCK (1443 bp) using the forward (F) and reverse (R) primers shown in Table S1. The PCR reaction was subjected to 30 cycles of 94°C for 20 sec, 53°C for 20 sec and 72°C for 90 sec. Non-transgenic plants were used as a negative control. Analysis of mRNA expression by RT-qPCR was performed as described in SI Materials and Methods.

SDS-PAGE and Immunoblot Analysis

Leaf tissue (100 mg) was homogenized in Bradley buffer (50 mM Tris, 7.5 pH, 10 mM KCl, 20% glycerol, 0.4 M sucrose, 5 mM MgCl2, and 10 mM β-mercaptoethanol). The proteins in the homogenates were resolved by 12.5% SDS-PAGE and either stained by using Coomassie brilliant blue R250 or transferred to a nitrocellulose membrane (Millipore, Billerica, MA). Membranes were incubated in 3% skim milk (Fuka, Buchs, Switzerland) in PBS plus 0.5% (v/v) Tween 20 followed by goat anti-human Fc and F(ab’)2 fragment-specific antibodies conjugated to horseradish peroxidase (Jackson Immunolab, West Grove, PA) to detect HC and LC, respectively. Protein bands were visualized by exposing the membrane to X-ray film (Fuji, Tokyo, Japan) using a chemiluminescence substrate (Pierce, Rockford, IL). Non-transgenic plants and mAbH SO57 (Bayrab, Bayer, Elkhart, IN) were used as negative and positive controls, respectively. Antibody levels were densitometrically analyzed using ImageQuant v2005 software (GE Healthcare, Freiburg, Germany).

Confocal Fluorescence Analysis

Leaf samples were fixed for 5 days with 4% paraformaldehyde in 0.1 M phosphate buffer (pH 7.2). The fixed leaves were dehydrated with ethanol, cleared with xylene, and embedded in paraffin to make a paraffin block. The paraffin-embedded sample was sectioned into 10 µm slices and attached to gelatin-coated slides. The primary antibody (goat anti-human IgG; Animal Genetics, Daejeon, Korea) was applied to the coated slides, and the slides were then treated with green fluorescent Alexa-488 conjugated to a rabbit anti-goat IgG in order to detect the mAb SO57. The slide was then incubated with the nuclear stain TO-PRO-3 (Molecular Probes, Eugene, OR), which fluoresces blue at 633 nm.

Purification of mAbP SO57

Plant leaves (300 g) were homogenized on ice with extraction buffer (37.5 mM Tris-HCl, 50 mM NaCl, 15 mM EDTA, 75 mM sodium citrate, and 0.2% sodium thiocyanate) and centrifuged at 15,000 g for 30 min at 4°C. The supernatant was filtered through a Miracloth (Calbiochem, Darmstadt, Germany), and solid ammonium sulfate (AS) was added to produce a solution with 16% saturation. After 2 h of incubation at 4°C, the solution was centrifuged at 15,000 g for 30 min at 4°C, the precipitate was discarded, and AS was added to the supernatant to produce a solution with 40% saturation. After incubation at 4°C overnight, the solution was centrifuged as before, and the pellet was resuspended in an extraction buffer to one-fifth of the original volume. Soluble proteins were applied to a protein A column (GE Healthcare), and the mAb was eluted according to the manufacturer’s recommendations. After overnight dialysis against 1 × PBS, the mAb was concentrated by using an Amicon Ultra spin column with a 10 kDa cut-off (Millipore) and then stored at −80°C.
N-glycan Analysis by DNA Sequencer

Purified mAbs were digested into glycopeptides with 0.1 mg of pepsin in 10 mM HCl buffer (pH 2.2) for 12 h at 37°C and then incubated for an additional 12 h after the addition of a second batch of 0.1 mg pepsin [39]. From the resulting glycopeptide mixtures, N-glycans were released using peptide N-glycosidase (PNGase) A (Roche, Mannheim, Germany). After the deglycosylation, the glycans were labeled by APTS and purified, as previously described [39]. The resulting APTS-labeled glycans were dissolved in 5 μl ultrapure water, and 1:20 diluents were dispensed into a 96-well plate. The plate was loaded onto an ABI 3130 sequencer (Applied Biosystems, Foster City, CA) equipped with a standard 56 cm capillary array filled with POP-7 polyacrylamide linear polymer. The running parameters for the sequencer were the same as the previously described protocol [39,40]. The resultant electropherograms were then analyzed using GeneMapper software (Applied Biosystems). N-glycan analysis by permethylation and mass spectrometry was performed as described in SI Materials and Methods.

In Vitro Rabies Virus Neutralization Assay

The fluorescent antibody virus neutralization (FAVN) test was carried out as previously described [41]. Each mAb and standard reference serum containing a titer of 0.5 international units (IU)/ml was tested in 4 replicates in a 96-well tissue culture plate. Three-fold serial dilutions of mAbH, mAbPK, and mAbH were incubated with the rabies virus cell cultured adapted standard strain (CVS-11) [41] for 60 min at 37°C. After incubation, a cell suspension containing 4×10⁴ BHK-21 (baby hamster kidney cells) [42] cells/ml were added, and the mixture was allowed to incubate for 40 h at 37°C under 5% CO₂. The plate was washed, fixed, and stained with the FITC-labeled anti-rabies mAb (Jeno Biotech, Chuncheon, Korea) and examined under a fluorescent microscope. Every well that showed specific fluorescence was considered to be positive. The median titer (D₅₀) of the 4 replicate wells was calculated by the Spearman-Karber formula. The titer of each mAb was expressed as IU/ml after comparison with that of standard serum.

In Vivo Clearance of mAbs

BALB/c mice (female, 6–8 wk, n = 10 for each mAb, Daihan, Eumsung, Korea) were injected i.p. with 7 μg of mAbP, mAbPK, or mAbH in 100 μl of 1× PBS buffer. After injection, blood samples were collected from the orbital sinus every day for 10 days; each mouse was bled twice during the entire time period. Serum levels of mAbP, mAbPK and mAbH were detected by sandwich ELISA. Plates were coated with 2 μg/ml of rabbit anti-human IgG-Fc antibody (Bethyl Labs, Montgomery, TX) overnight at 4°C. The stimulated cells were then incubated for 1 h at 4°C with 10 μg/ml of purified mAbH SO57, mAbP SO57 or mAbPK SO57 in PBS containing 0.1% BSA and 0.02% sodium azide (immunofluores-
eluates were collected by adding 400 ml centrifugation at 400 g. The resulting mixtures were passed eight times over a column containing permethylated glycans was dried and resuspended in 1 mM sodium acetate aqueous solution. Equal volumes of the liquid-liquid extraction step was repeated twice. The chloroform layer was carefully removed after centrifugation. This liquid-liquid fractionation for enhancing the sensitivity, the mass of glycans prepared which provided the possible glycan structures. After permethylation, the glycan structures are as follows: GlcNAc, black square; mannose, white circle; fucose, diamond; galactose diamond with a dot inside. Non, no glycosidase treatment; S, pre-treatment with (1–2, 3, 4, 6) fucosidase; S+G, S pre-treatment with β1–4 galactosidase; S+G+F, S+G pre-treatment with β1–2, 3, 4, 6) fucosidase; S+G+F+H, S+G+F pre-treatment with of β-N-acetylhexosaminidase.

RT-qPCR

The mRNA expression of the mAb HC and LC was quantified by using RT-qPCR. Total RNA was extracted from leaves with TRIzol reagent according to the manufacturer’s protocol. To remove genomic DNA, 600 ng of total RNA was treated using a TURBO DNA-free kit (Ambion, Austin, TX) in a reaction volume of 20 μl. Each RNA sample was used as a template for RT reactions performed with AccuPower RT/PCR PreMix (Bioneer, Daejeon, Korea). A total volume (20 μl) contained 120 ng of template DNA-free RNA and oligo d(T)16 primer and random hexamers. Primers for RT-qPCR were designed with the aid of Primer Express software (Applied Biosystems) using default parameters. The cDNA samples (2 μl) were used for the RT-qPCR reaction, and the quantification was conducted on the StepOne™ Real-Time PCR System (Applied Biosystems) using Taqman 2x Universal PCR Master Mix, and primers and probe sets specific for the mAb SO57 HC and LC. The reporter FAM™ and nonfluorescent quencher BHQ™ dyes formed 5’ and 3’ modifications, respectively. A StepOne™ Real-Time PCR System was set for 1 cycle at 50°C for 2 min, 1 cycle at 95°C for 5 min, and 40 cycles of denaturation at 95°C for 15 sec and annealing/extension at 60°C for 1 min. A Nicotiana tabacum actin gene [44] was used as an endogenous control in the RT-qPCR reactions. The relative mAb SO57 HC and LC mRNA levels in each sample have been expressed as a ratio with the relative mRNA levels of actin for each sample. Primers used for RT-qPCR are listed in Table S2.

N-glycan analysis by permethylation and mass spectrometry

Prior to mass spectrometric analysis, glycans were permethylated for enhancing sensitivity by solid phase permethylation using spin-column method [45]. First, dried glycans were dissolved in a mixture of 90 μl DMSO, 2.7 μl distilled water, 35 μl iodo-methane. The resulting mixtures were passed eight times over a spin-column packed with sodium hydroxide mesh beads using the centrifugation at 400 g. After the washing step with acetonitrile, eluates were collected by adding 400 μl chloroform. One ml of 500 mM NaCl solution was added, mixed well and then the upper layer was carefully removed after centrifugation. This liquid-liquid extraction step was repeated twice. The chloroform layer containing permethylated glycans was dried and resuspended in 4 μl of 50% aqueous methanol solution for mass analysis. MALDI-TOF mass spectrometry was performed in the reflector positive ion mode using a Microflex TOF (Bruker Daltonik GmbH, Bremen, Germany). For preparation of matrix solution, DHB (2,5-dihydroxybenzoic acid) was dissolved at a 10 mg/ml concentration in 1 mM sodium acetate aqueous solution. Equal volumes of permethylated glycans in 50% methanol solution and the prepared matrix solutions were mixed and then applied onto a MALDI MSP 96 polished steel Chip (Bruker Daltonik). After drying, mass spectra were acquired with the method recommended by the manufacturer.

Statistical analysis

All experiments were repeated at least three times. Asterisks (*) in the figures indicate differences deemed significant (P<0.05) by a two-tailed Student’s t test. Data were shown as mean ± SD.

N-glycan analysis by mass spectrometry

Glycan profiles were cross-checked by mass spectrometric analysis, which provided the possible glycan structures. After permethylation for enhancing the sensitivity, the mass of glycans prepared from mAb P (A) and mAb P (B) were analyzed. The symbols of the glycan structures are as follows: GlcNAc, black square; mannose, white circle; xylose, white triangle; fucose, diamond with a dot inside.

Figure S2 N-glycan profiles of human-derived antibodies monoclonal antibodies (mAbH) obtained by DNA sequencing. The symbols of the glycan structures are as follows: GlcNAc, black square; mannose, white circle; lucose, diamond; galactose diamond with a dot inside. Non, no glycosidase treatment; S, pre-treatment with (1–2, 3, 4, 6) fucosidase; S+G, S pre-treatment with β1–4 galactosidase; S+G+F, S+G pre-treatment with β1–2, 3, 4, 6) fucosidase; S+G+F+H, S+G+F pre-treatment with of β-N-acetylhexosaminidase.

Figure S3 N-glycan analysis by mass spectrometry. Glycan profiles were cross-checked by mass spectrometric analysis, which provided the possible glycan structures. After permethylation for enhancing the sensitivity, the mass of glycans prepared from mAb P (A) and mAb P (B) were analyzed. The symbols of the glycan structures are as follows: GlcNAc, black square; mannose, white circle; xylose, white triangle; fucose, diamond with a dot inside.

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Author Contributions

Conceived and designed the experiments: Kinsung Ko YSL HK RB YKK. Performed the experiments: JHL DYP KJL YKS JSP SHO SJP KKL. Analyzed the data: Kinsung Ko YSL JHL DYP KJL Kinarm Ko KAH. Contributed reagents/materials/analysis tools: YSH YKC DBO. Wrote the paper: Kinsung Ko YSL JHL DYP.
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