GCMa Regulates the Syncytin-mediated Trophoblastic Fusion*

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The human placental trophoblast cell can be classified as either a cytotrophoblast or a syncytiotrophoblast. Cytotrophoblasts function as stem cells for the development of the syncytiotrophoblast layer via cell fusion. An envelope gene of the human endogenous retrovirus family W (HERV-W) called syncytin is specifically expressed in the syncytiotrophoblast layer. Syncytin is a fusogenic membrane protein; therefore, it can mediate the fusion of cytotrophoblasts into the syncytiotrophoblast layer, which is essential for pregnancy maintenance. GCMa is a placenta-specific transcription factor and is required for placental development. To study the placenta-specific fusion mediated by syncytin, we tested whether GCMa is involved in this process by regulating syncytin gene expression. In this report, we demonstrate that GCMa was able to regulate syncytin gene expression via two GCMa-binding sites upstream of the 5′-long terminal repeat of the syncytin-harboring HERV-W family member in BeWo and JEG3 cells but not in HeLa cells. Furthermore, adenovirus-directed expression of GCMa enhanced syncytin gene expression and syncytin-mediated cell fusion in BeWo and JEG3 cells but not in HeLa cells. Therefore, the integration site of the syncytin-harboring HERV-W family member in the human genome is close to the functional GCMa-binding sites by which GCMa can specifically transactivate syncytin gene expression in trophoblast cells. Our results may help to explain the mechanism underlying the cell fusion event specific for syncytiotrophoblast formation.

The human placenta contains a specialized cell type called a trophoblast, which is the first lineage to differentiate in embryo development and plays key roles during implantation and placenta formation. The human trophoblast cell can be further classified as cytotrophoblasts and syncytiotrophoblasts. In the early gestation stage, trophoblast stem cells facing the maternal decidua proliferate and fuse to form a syncytiotrophi, i.e. the syncytiotrophoblast. Later on, vascular spaces called trophoblastic lacunae appear in the syncytiotrophi around day 8–9. The cytotrophoblast layer under the syncytiotrophi can rapidly proliferate into these spaces, which results in the formation of the primary chorionic villi. Subsequently, proliferation of the cytotrophoblasts, growth of chorionic mesoderm (under the cytotrophoblast layer), and blood vessel development transform the primary villi into secondary and tertiary villi, which are composed of a core of mesenchyme cells surrounded by an inner layer of cytotrophoblasts and an outer layer of multinucleate syncytiotrophoblasts (1, 2). The syncytiotrophoblast layer (syncytiotrophi) transports nutrients and gases and produces hormones such as placental lactogen and chorionic gonadotrophin, which are indispensable for the further progression of pregnancy (1).

Recently, a membrane protein termed syncytin has been demonstrated to mediate cell fusion of the human BeWo trophoblastic cell line (3). Syncytin is an envelope protein of the newly identified human endogenous retrovirus family W (HERV-W) and is a polypeptide of 538 amino acids (3, 4). After synthesis, a post-translational cleavage is predicted to separate the syncytin polypeptide into surface protein and transmembrane protein. The latter contains the membrane-spanning segment and a hydrophobic fusion domain. In situ hybridization has demonstrated that syncytin is specifically expressed in the syncytiotrophoblast layer (3–5). These studies suggest that syncytin can mediate fusion of cytotrophoblasts into the syncytiotrophoblast layer, and the expression of syncytin is tightly regulated in a temporal and spatial manner to maintain an integral and functional syncytiotrophoblast layer.

GCM (glial cell missing) was originally isolated from a Drosophila melanogaster mutant line that produces additional neurons at the expense of glial cells (6, 7). Currently, two GCM-like genes (GCMa and GCMb) have been reported in mouse, rat, and human (8, 9). Altogether these GCM homologues form a novel family of transcription factors, which all share sequence homology in the amino-terminal region that constitutes the DNA-binding domain called the GCM motif. Although sequence homology is less preserved outside the GCM motif, a transactivation domain (TAD) has been identified in the extreme carboxyl terminus of GCM proteins (10, 11). The optimal recognition sequence for the GCM motif is 5′-(A/G)CCC(T/G)CAT-3′ or its 5′-ATG(A/C)GGG(T/C)-3′ complement (10, 12). Drosophila GCM mRNA is transiently detected in glial precursors and immature glial cells, except for mesodermal midline glia during a short period of gliogenesis within the central nervous system (6, 7). In contrast, mouse GCMa mRNA is highly expressed in the labyrinthine trophoblast cells (13). GCMa is required for placental development because genetic ablation of mouse GCMa leads to a failure of labyrinth layer formation and the fusion of trophoblasts to syncytiotrophoblasts (14, 15).

To study the placenta-specific fusion mediated by syncytin, we tested whether GCMa can activate the promoter activity of syncytin.
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the long terminal repeats (LTRs) of the syncytin-harboring HERV-W family member to specifically drive syncytin expression in trophoblasts. In this study, we demonstrated that GMCA recognizes two GMCA-binding sites (GBSs) in the upstream region of the 5'-LTR of the syncytin-harboring HERV-W family member, activating syncytin gene expression and consequently enhancing the syncytin-mediated cell fusion. Our data help to explain the regulatory mechanism underlying the placenta-specific trophoblastic fusion mediated by syncytin.

**EXPERIMENTAL PROCEDURES**

**Library Screening and Plasmid Constructs**—The human syncytin and GMCA cDNAs were cloned by PCR using a human placental cDNA library as template. The syncytin cDNA fragment was radiolabeled and used to screen a ADASH II human genomic library (Strategene, La Jolla, CA). A genomic clone, L13, covering the entire proviral genome of the syncytin-harboring HERV-W family member was isolated and used to build promoter constructs (Fig. 1A). The human BAC clone, 083M05 (GenBank accession no. AC000064), was used to isolate more distal genomic regions upstream and downstream of the proviral genome of the syncytin-harboring HERV-W family member (Fig. 1A).

A GMCA cDNA fragment containing an amino-terminal HA epitope sequence was subcloned into the pReCMV plasmid (Invitrogen) to generate pCAG-HA-GMCA. Genomic fragments were subcloned into the pE1bCAT reporter plasmid, which is derived from pCAT3-Basic (Promega, Madison, WI) by insertion of the adenovirus E1B TATA box in front of the bacterial CAT (chloramphenicol acetyltransferase) gene. For simplicity, the range of genomic fragments used for these constructs was based on the numbering of nucleotide (nt) residues in the 083M05 BAC clone. Genomic fragments of nt 25468–25545, 25649–25726, and 25820–26033, or both were subcloned into pCAG-Basic to generate deletion constructs pCATA6p–25545, pCATA6p–25649–25726, or pCATA6p–25820–26033, respectively.

**Cell Culture, Transfection, and Reporter Gene Assays**—The mammary cell lines used in this study were obtained from the American Type Culture Collection (Manassas, VA). BEWo cells were grown at 37 °C in F-12K, 15% fetal bovine serum, and 100 μg/ml streptomycin, and 100 units/ml penicillin. JEG3 and HeLa cells were grown at 37 °C in minimum Eagle’s medium, 10% fetal bovine serum, and the same antibiotics as mentioned above. BeWo or HeLa cells were transfected by using the Geneporter system (GTS, San Diego, CA). CAT assays were performed as described (16). The Student’s t test was used to determine statistical significance for differences between means of relative CAT activities. A p value of less than 0.05 was considered statistically significant. HAGCMa proteins in transfected cells were subject to immunoblotting with an horseradish peroxidase-conjugated rat monoclonal anti-HA antibody (Roche Molecular Biochemicals) and Protein A-agarose beads (Oncogene, Boston, MA). Specific sequences of regions upstream of the 5'-LTR of HERV-W in the immunoprecipitates were detected by PCR with specific primers. PCR products were analyzed on 2% MetaPhor agarose gels (FMC, Rockland, ME). Sequences of primers are 5'-CTCAGTCGGGCTTACAGTTTCGTTC-3' and 5'-GAATAGAAGCGCCCTCTTGGACCCTTCTCCTCT-3' for region 22473-22371; 5'-GGGCGTGCACTGCTATTACTGTAGG-3' and 5'-AAATTAGATCGGCCTTGAGGGTCTCGG-3' for region 25461-25686; 5'-GCCATTTCTAGATTCAATCTGCGCAC-3' and 5'-GCAAGATAAATCCTGACTTCTCAGGCGGCAC-C3 for region 27890-28064.

**Construction of Ad-HAGCMa—**Recombinant HAGCMa adenoviruses (Ad-HAGCMa) were generated in CRE8 cells by cotransfection of the linearized vector transfer (pAdlox-HAGCMa) and the φ5 genomic DNA (19). For a control, an empty recombinant adenovirus (Adlox) was generated using a linearized pAdlox and φ5 genomic DNA. AdHAGCMa and Adlox were grown and amplified in CRE8 cells for two consecutive cycles. Cells in culture plates were transfected with AdHAGCMa or Adlox at an multiplicity of infection of 100 or 200 at 37 °C for 90 min. After that, the virus was removed, and fresh culture media were added and incubated for an additional time until analysis. RNA was isolated using RNeasy reagents (Qiagen, Hilden, Germany). RNA (20 μg) were assayed for Northern analysis using human GMCA or β-actin cDNA probes. To detect syncytin transcripts, 15 μg of RNA from Ad-HAGCMa-transduced cells were analyzed by ribonuclease protection assays using the RPA III kit (Ambion, Austin, TX). The syncytin riboprobe contains nucleotides 417–821 relative to the translation start site. A kit-provided β-actin riboprobe was used as an internal control. The protected syncytin bands were quantified by BAS-1500. HAGCMa and syncytin proteins in transduced cells were subject to immunoblotting with an anti-HA antibody and a syncytin antibody, respectively. Antiserum against syncytin was induced in guinea pigs using a His-tagged surface protein (amino acids 21–215) expressed in BL21(DE3).

**Fusion Assay and Fluorescence Microscopy—**293 cells were transfected with the red fluorescent protein plasmid pDsRed1-N1 (Clontech) 24 h before cell fusion assay. HeLa, JEG3, or BeWo Cells were transfected with Adlox or Ad-HAGCMa. Four hour post-infection, cells were trypsinized, and 8 × 105 infected cells and 1 × 105 transduced 293 cells were cocultured onto a 60-mm culture dish. After another 30 h at 37 °C, cell fusions were examined under an Olympus microscope (Tokyo, Japan) equipped with a cooled charge-coupled device camera (DP20). Images were prepared for presentation using Adobe Photoshop 6.0.

**RESULTS**

**Promoter Analysis of the syncytin Gene—**Syncytin is encoded by the envelope (env) gene of an HERV-W family member with a genomic configuration of 5'-LTR-gag-pro-pol-env-LTR-3' (Fig. 1A) (4). To investigate the placenta-specific expression of syncytin, promoter analysis was performed to identify potential elements and transcription factors that could enhance the LTR promoter activity of the syncytin-harboring HERV-W family member. For simplicity, we refer to the syncytin-harboring HERV-W family member as HERV-W for the rest of this report. A ADASH II genomic clone (L13) containing the HERV-W genome was isolated using the syncytin cDNA probe (Fig. 1A). A human BAC clone, 083M05, which encompasses the L13 clone, was used together with L13 to build a series of promoter constructs covering genomic regions up to 14.8-kb upstream of the 5'-LTR and 5.1-kb downstream of the 3'-LTR of HERV-W (Fig. 1, A and B).

The role of the placenta-specific transcription factor GMCA in the expression of syncytin gene was investigated, because GMCA is known to play an important role in murine placental development (14, 15). Transient expression experiments of the promoter constructs were performed in BeWo cells. As shown
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**Fig. 1. Promoter analysis of the syncytin gene.** A, schematic representation of the human BAC clone 083M05, the λDASH II clone L13, and HERV-W. The numbers above and underneath 083M05 denote the positions of the numbered nucleotides. B, schematic representation of promoter constructs used in this study. The genomic fragment inserted in pE1bCAT is indicated on the left by a horizontal filled bar, denoting its location in the BAC clone 083M05 as listed in panel A. The numbers on the right indicate the ranges of the genomic fragments in the BAC clone 083M05. C, promoter analysis for the syncytin gene. BeWo cells were transfected with 0.5 μg of the indicated promoter construct in the absence (black bar) or presence (gray bar) of 0.5 μg of pCMVHAGCMa. Mean values and S.E. obtained from six independent transfection experiments are provided. Asterisks denote statistically significant differences (**, p < 0.01) between mock- and pCMVHAGCMa-transfected groups. HAGCMa proteins in the total cell lysate of mock- and pCMVHAGCMa-transfected groups were analyzed by Western analysis with a horseradish peroxidase-conjugated rat monoclonal anti-HA antibody. As a loading control, actin proteins in the lysate were detected with a rabbit polyclonal anti-actin antibody.

In Fig. 1C, the CAT activity directed by pE1bCAT-(25468–30953) is higher than those of the other constructs examined. In addition, a statistically significant 3.3-fold transactivation by GCMa on pE1bCAT-(25468–30953) was observed when it was cotransfected with pCMVHAGCMa. This up-regulation was not due to a differential expression of HAGCMa proteins in transfected cells because comparable amounts of HAGCMa proteins were detected (Fig. 1C). When the pE1bCAT-(25468–30953) was divided into pE1bCAT-(25468–28066) and pE1bCAT-(28067–30953), transcriptional activation by HAGCMa was not observed with either construct. pE1bCAT-(28067–30953) contains the 5′-LTR; therefore, these results suggest that potential GBSs are present in nucleotides 25468–30953, which, in conjunction with 5′-LTR, can be up-regulated by HAGCMa. The positive effect of pCMVHAGCMa on pE1bCAT-(25468–30953) was also observed in another human trophoblastic cell line, JEG3 (data not shown). The optimal recognition sequence for the DNA binding domain of Drosophila GCM is 5′-(A/G)GCC(T/G)CAT-3′ or its 5′-ATG(A/C)GGG(T/A)CG-3′ complement (10, 12). Indeed, close scrutiny of GBS(s) in nucleotides 25468–30953 revealed two potential GBSs (25538–25545 and 28026–28033) upstream of the 5′-LTR of HERV-W. The sequences for GBS-(25538–25545) and GBS-(28026–28033) are TCCCTCAT and ATGAGGGC, respectively.

Analysis of the Binding Elements of GCMa in the syncytin Promoter—To test whether GCMa directly binds the two potential GBSs, we performed EMSA with radiolabeled (25488–25587) and (27978–28077) DNA fragments and a recombinant GCMa-FLAG protein (Fig. 2A). GCMa-FLAG specifically bound to radiolabeled (25488–25587) and (27978–28077) DNA fragments (Fig. 2B, lanes 2 and 8) because the unlabeled oligonucleotide pGCMa, consisting of the GBS-(28026–28033) at a 100-fold excess, competed with complex formation (Fig. 2B, lanes 3 and 9). However, a pGCMa mutant oligonucleotide, Mut, containing mutated nucleotide residues in GBS-(28026–28033) could not compete with complex formation (Fig. 2B, lanes 4 and 10). Furthermore, the GCMa antiserum, but not the control serum, was able to supershift the DNA-protein complex (Fig. 2B, lanes 5, 6, 11, and 12). These results suggest that GBSs are present in (25488–25587) and (27978–28077) DNA fragments.

To localize the binding sites of GCMa in (25488–25587) and (27978–28077) DNA fragments, DNase I footprinting analyses were performed using GCMa-FLAG and the radiolabeled probes of the two fragments. As shown in Fig. 2C, the regions protected by GCMa-FLAG in both fragments encompass the GBS core sequence and some immediate 5′-flanking nucleotides (Fig. 2C). We further verified the footprinting results by EMSA using GCMa-FLAG and labeled dGCMa and pGCMa oligonucleotides spanning the GCMa-FLAG-protected regions GBS-(25538–25545) and GBS-(28026–28033), respectively (Fig. 2D). Specific complexes were observed in lanes without
pGCMa and dGCMa, derived from the footprinting analysis, were radiolabeled as probes for GCMa-FLAG in EMSA. On the left, G/H11032 analysis of GBSs in the 5'-flanking region were asymmetrically radiolabeled. The labeled DNA probe was incubated with GCMa-FLAG protein, digested with DNase I, and detected by Coomassie Blue R-250 staining. Comp, the presence or absence (−) of unlabeled pGCMa or Mut oligonucleotide in a 100-fold (100×) excess. NPGS, normal guinea pig serum. The arrow and arrowhead indicate the GCMa-FLAG-DNA complex and its supershifted complex, respectively. C, DNase I footprinting analysis of GBSs in the 5'-flanking region of HERV-W 5'-LTR. Two genomic fragments (nt 25488–25587 and nt 27978–28077) in the HERV-W 5'-flanking region were asymmetrically radiolabeled. The labeled DNA probe was incubated with GCMa-FLAG protein, digested with DNase I, and analyzed on 8% polyacrylamide-urea gels. The vertical lines on the right denote the protected regions of which sequences are listed and underlined on the left. G+A, Maxam and Gilbert G plus A sequencing reaction of the probe. B, bound or protected probe. F, free probe. D, oligonucleotides pGCMa and dGCMa, derived from the footprinting analysis, were radiolabeled as probes for GCMa-FLAG in EMSA.

pGCMa and dGCMa competitor oligonucleotides and in lanes with the Mut negative control oligonucleotide (Fig. 2D, lanes 2, 5, 9, and 12). A supershifted complex was only observed using the GCMa antiserum (Fig. 2D, lanes 7 and 14). Taken together, the EMSA and footprinting results suggest that GCMa specifically recognizes GBS-(25538–25545) and GBS-(28026–28033) in the 5'-flanking region of HERV-W 5'-LTR.

Transactivation of HERV-W 5'-LTR by GCMa Depends on the Two GBSs and Is Cell Type-dependent—Transient expression experiments were performed in BeWo cells, using GBS-deletion promoter constructs, to test whether transactivation of HERV-W 5'-LTR by GCMa depends on GBSs-(25538–25545) and GBS-(28026–28033) (Fig. 3A). As shown in Fig. 3B, transcriptional activation by HAGCMa of both pCATΔd-(25468–30953) and pCATΔp-(25468–30953) was observed; however, this activation was lower than that observed with pCATΔd-(25468–30953). Moreover, transactivation was abolished in pCATΔdp-(25468–30953). In contrast, no transcriptional activation by HAGCMa of these constructs was observed in HeLa cells. These results suggest that transactivation of HERV-W 5'-LTR by GCMa depends on the two GBSs and is cell type-dependent.

In Vivo Interaction between GCMa and GBSs Upstream of the HERV-W 5'-LTR—Because GBSs-(25538–25545) and GBSs-(28026–28033) could be functionally transactivated by GCMa, we further tested whether GCMa interacts with both sites in vivo by means of a ChIP assay. BeWo cells were transfected with pCMVHAGCMa, and the DNA-HAGCMa complexes were immunoprecipitated by anti-HA antibody for PCR analysis (Fig. 4A). Positive signals were detected when regions 25461–25686 and 27800–28064 were amplified by PCR (Fig. 4B). These two regions encompass GBSs-(25538–25545) and GBSs-(28026–28033), respectively. No signal was detected when a more distal upstream region, 22473–22731, was amplified. These results suggest that GCMa associates with the two GBSs in the 5'-flanking region of HERV-W 5'-LTR in the nuclei of BeWo cells.

GCMa Transactivates syncytin Gene Expression—We next tested whether the expression of GCMa increases the synthesis of syncytin proteins. A recombinant HAGCMa adenovirus, Ad-HAGCMa, and an empty recombinant adenovirus, Adlox, were generated. Expression of HAGCMa in BeWo, JEG3, or HeLa cells transduced with Ad-HAGCMa was analyzed by Northern and Western analyses at different time points. As shown in Fig. 5A, Northern analyses revealed that HAGCMa transcripts in HeLa and BeWo cells were detected from 16 h to at least 72 h post-transduction. In JEG3 cells, HAGCMa transcripts were detected from 24 to 72 h post-transduction. Correspondingly, increasing levels of HAGCMa protein were detected in the transduced cells (Fig. 5A, lower panel). To investigate the effect of HAGCMa on syncytin expression, ribonuclease protection assays were performed to specifically detect the syncytin transcripts in Ad-HAGCMaC-transduced cells at 24 or 48 h post-transduction. In comparison with untransduced cells, the level of syncytin transcripts in transduced JEG3 and BeWo cells at 48 h post-transduction increased ~4.2- and 3.4-fold, respectively (Fig. 5B). Interestingly, no syncytin transcript was detected in transduced HeLa cells in the presence of a higher level of the HAGCMa protein. Western analyses on the syncytin proteins in BeWo and HeLa cells, transduced with Ad-HAGCMa or Adlox, were performed at 48 h post-transduction. As shown in Fig. 5C, HeLa cells transduced with the control

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**FIG. 2.** Analysis of GCMa binding to GBSs in the 5'-flanking region of HERV-W 5'-LTR. A, GCMa-FLAG proteins were affinity purified from SF-9 cells infected by a recombinant GCMa-FLAG baculovirus. Approximately 0.2 µg of purified GCMa-FLAG was analyzed by SDS-PAGE and detected by Coomassie Blue R-250 staining. B, EMSA of GCMa-FLAG and radiolabeled genomic fragments containing potential GBSs. Comp, the presence or absence (−) of unlabeled pGCMa or Mut oligonucleotide in a 100-fold (100×) excess. NPGS, normal guinea pig serum. The arrow and arrowhead indicate the GCMa-FLAG-DNA complex and its supershifted complex, respectively. C, DNase I footprinting analysis of GBSs in the 5'-flanking region of HERV-W 5'-LTR. Two genomic fragments (nt 25488–25587 and nt 27978–28077) in the HERV-W 5'-flanking region were asymmetrically radiolabeled. The labeled DNA probe was incubated with GCMa-FLAG protein, digested with DNase I, and analyzed on 8% polyacrylamide-urea gels. The vertical lines on the right denote the protected regions of which sequences are listed and underlined on the left. G+A, Maxam and Gilbert G plus A sequencing reaction of the probe. B, bound or protected probe. F, free probe. D, oligonucleotides pGCMa and dGCMa, derived from the footprinting analysis, were radiolabeled as probes for GCMa-FLAG in EMSA.
virus Adlox or Ad-HAGCMa did not reveal any signals for syncytin proteins (lanes 3 and 4). However, two bands of 75 and 200 kDa were observed in Ad-HAGCMa-transduced BeWo cells (lane 2). The band of 75 kDa may represent the syncytin precursor, whereas the band of 200 kDa may represent trimeric syncytin (5). The endogenous syncytin proteins in the Adlox-transduced BeWo cells were detected after a longer exposure (data not shown). The results of ribonuclease protection assays and Western analyses also suggest that GCMa transactivates syncytin gene expression in a cell type-dependent manner.

Cell fusion assays were performed to investigate the effect of GCMa-activated syncytin expression on cell fusion. 293 cells expressing red fluorescent protein were cocultured with Adlox- or Ad-HAGCMa-transduced cells and examined under fluorescence microscopy 30 h after coculture. In comparison with Adlox-transduced cells (Fig. 6, A–C), fusion events were significantly increased in Ad-HAGCMa-transduced BeWo and JEG3 cells (Fig. 6, E and F). No fusion events were observed in Ad-HAGCMa-transduced HeLa cells (Fig. 6D). Taken together, our study indicates that GCMa up-regulates syncytin gene expression via two GBSs upstream of the HERV-W 5′-LTR and consequently enhances syncytin-mediated cell fusion.
DISCUSSION

The fusogenic activity of the syncytin protein has been demonstrated in a variety of primate cell lines including BeWo, COS, HeLa, and 293 (3, 5). In situ hybridization has revealed that the expression of the syncytin gene is restricted to the syncytiotrophoblast layer in human placenta (3). These observations suggest that syncytin can mediate fusion of cytотrophoblasts into the syncytiotrophoblast layer. Strict regulation of syncytin gene expression is important in maintaining an integral syncytiotrophoblast layer, because the overexpression of syncytin in cultured cells causes extensive cell fusion and leads to cell death.2

In this study, we identified GCMa as a transactivator for the trophoblast-specific expression of the syncytin gene. Several lines of evidence support this conclusion. First, GCMa associated with GBS-(25538–25545) and GBS-(28026–28033) in the 5′-flanking region of HERV-W 5′-LTR in vivo based on ChIP...
analysis. Second, the expression of GCMa specifically increased the levels of syncytin transcripts and proteins in trophoblastic cells. Third, syncytin-mediated cell fusion was increased after GCMa expression. Interestingly, expression of the syncytin gene was not detected in HeLa cells expressing a high level of GCMa protein. This suggests that regulation of syncytin expression by GCMa is cell type-dependent or that other placenta-specific factors may be involved in the trophoblast-specific expression of syncytin gene.

Mutation analysis revealed that nucleotide residues 2, 3, 6, 7, and 8 in the optimal GCM recognition sequence (5′-ATG(N/C)GGG(T/C)-3′) are important for interaction with Drosophila GCM and mouse GCMa. We demonstrated that two GCMa binding sites in the 5′-flanking region of HERV-W 5′-LTR were responsive to GCMa. The proximal site, GBS-(25538–25545), is 34 bp upstream of the 5′-LTR, and its sequence matches the optimal binding sequence perfectly. The distal site, GBS-(25538–25545), is 2522-bp upstream of the 5′-LTR, and its sequence has a mismatch in position 8 in comparison to the optimal binding sequence. Correspondingly, GBS-(25538–25545) has a lower binding efficiency with GCMa in EMSA compared to the 25538–25545 sequence. A recent clinical survey on the expression of syncytin in human placemtas has revealed a lower syncytin mRNA level in patients with placental dysfunction, including preeclampsia and hemolysis, elevated liver enzymes, low platelets (HELLP syndrome). Because syncytin is a target gene of GCM, this warrants an investigation into the role played by GCMa in the etiology of preeclampsia and HELLP syndrome.

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