

5. 病因・病態

- 1) GPIアンカーの生合成およびタンパク質への付加に必要な遺伝子の変異によるもの (PIG遺伝子欠損症)
PIGA, PIGQ, PIGL, PIGW, PIGM, PIGV, PIGN, PIGO, PIGT欠損症など
- 2) GPIアンカーの修飾に必要な遺伝子の変異によるもの (PGAP遺伝子欠損症)
PGAP1, PGAP3, PGAP2欠損症など
- 3) その他の遺伝子の変異によるもの

GPIアンカー型タンパク質の欠損と病態

アルカリホスファターゼ(ALP)の発現低下とてんかん

GPIアンカー型タンパク質であるALPは、細胞表面でビタミンB6の1つピリドキサルリン酸を脱リン酸化して細胞内に取り込める形のピリドキサルにし、細胞内に入ったピリドキサルは再びリン酸化されてピリドキサルリン酸となり、抑制性ニューロンにおいて γ -アミノ酪酸 (GABA) 合成酵素の補酵素として働く。細胞膜上のALPが発現が低下すると、細胞内のピリドキサルリン酸が不足し、GABA合成が抑制され、けいれん発作が誘発されることが考えられる。ビタミンB6はGABA合成だけでなく様々なアミノ酸代謝に関わっているので、ビタミンB6欠乏による代謝異常が起こる可能性がある。

6. 検査所見

- 高ALP血症
高ALP血症を伴う知的障害、運動発達障害はIGDである可能性が高いが変異遺伝子のステップによっては正常の場合もある。逆にPIGT欠損症では低値になり共通の症状に加えて骨の形成異常を示す。
- 手指・足趾のX線写真で末節骨欠損
- 聴性脳幹反応 (ABR) の異常、脳波の異常
- 脳MRIの拡散強調画像 (DWI) にて基底核に高信号、小脳萎縮、
- 顆粒球のフローサイトメトリーにてCD16の発現低下

7.重症度分類

Barthel Indexが85点(%)以下を重症とする。

8.治療

てんかんを合併している症例では、通常の抗てんかん薬や治療では難治に経過することが多い。しかし、ビタミンB6（ピリドキシン）の投与がてんかん発作に著効する症例が報告されている（文献8）。注意すべきは、ビタミンB6製剤の選択である。ピリドキサルリン酸はGPIアンカー型タンパク質であるALPを介して細胞内に取り込まれるため、IGDでは細胞内への取り込みが低下し無効であると考えられる。一方、ピリドキシンは前述のALPを介さずに細胞内に取り込まれるために有効と考えられる。

商品名：アデロキシシン(鳥居薬品株式会社、ゾンネボード製薬株式会社)

投与量：Pyridoxine 10-15mg/kg/day分3で投与を開始。副作用等確認した後に 20-30mg/kg/day分3まで増量

現在大阪大学小児科にて臨床研究が行われているので投与をお考えの先生は下記までご連絡ください。

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Ⅱ. 研究成果の刊行に関する一覧表

研究成果の刊行に関する一覧表

書籍

著者氏名	論文タイトル名	書籍全体の編集者名	書籍名	出版社名	出版地	出版年	ページ
Inoue, N., Kinoshita, T.	Pathogenesis of Clonal Dominance in PNH; Growth Advantage in PNH.	Kanakura, Y., Kinoshita, T., Nishimura, J.	Paroxysmal Nocturnal Hemoglobinuria-From bench to bedside	Springer-Verlag	Tokyo	2016	In press
井上徳光	PNH型細胞のクローン性拡大の機序	金倉譲、西村純一	発作性夜間ヘモグロビン尿症 (PNH) ~ 遺伝子異常の解析から新規治療の臨床・開発まで~	医薬ジャーナル社	大阪	2016	69-82
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Ⅲ. 研究成果の刊行物・別刷

***PIGN* mutations cause congenital anomalies, developmental delay, hypotonia, epilepsy, and progressive cerebellar atrophy**

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Abstract Defects of the human glycosylphosphatidylinositol (GPI) anchor biosynthetic pathway show a broad range of clinical phenotypes. A homozygous mutation in *PIGN*, a member of genes involved in the GPI anchor-synthesis pathway, was previously reported to cause dysmorphic features, multiple congenital anomalies, severe neurological impairment, and seizure in a consanguineous family. Here, we report two affected siblings with compound heterozygous *PIGN* mutations [c.808T >C (p.Ser270Pro) and c.963G >A]

showing congenital anomalies, developmental delay, hypotonia, epilepsy, and progressive cerebellar atrophy. The c.808C >T mutation altered an evolutionarily conserved amino acid residue (Ser270), while reverse transcription-PCR and sequencing demonstrated that c.963G >A led to aberrant splicing, in which two mutant transcripts with premature stop codons (p.Ala322Valfs*24 and p.Glu308Glyfs*2) were generated. Expression of GPI-anchored proteins such as CD16 and CD24 on granulocytes from affected siblings was

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significantly decreased, and expression of the GPI-anchored protein CD59 in *PIGN*-knockout human embryonic kidney 293 cells was partially or hardly restored by transient expression of p.Ser270Pro and p.Glu308Glyfs*2 mutants, respectively, suggesting severe and complete loss of *PIGN* activity. Our findings confirm that developmental delay, hypotonia, and epilepsy combined with congenital anomalies are common phenotypes of *PIGN* mutations and add progressive cerebellar atrophy to this clinical spectrum.

Keywords Cerebellar atrophy · Compound heterozygous mutation · Glycosylphosphatidylinositol anchor · *PIGN*

Introduction

Defects of the biosynthetic pathway of the glycosylphosphatidylinositol (GPI) anchor cause broad clinical phenotypes [1]. The products of more than 20 genes in the phosphatidylinositol glycan (PIG) family are involved in GPI biosynthesis, whereas post-GPI-attachment to proteins (PGAP) gene products play a role in the structural remodeling of GPI glycan and lipid portions [2]. Mutations in eight genes involved in GPI biosynthesis and remodeling (*PIGA*, *PIGM*, *PIGN*, *PIGV*, *PIGL*, *PIGO*, *PIGT*, and *PGAP2*) have been identified in individuals with neurological abnormalities [1, 3–5], of which *PIGN* controls the addition of phosphoethanolamine to the first mannose in GPI [6]. To date, only one homozygous *PIGN* mutation has been reported to cause dysmorphic features, multiple congenital anomalies, severe neurological impairment, and seizures in a consanguineous family [7]. Here, we report a family with two affected siblings, possessing compound heterozygous *PIGN* mutations. Detailed clinical information and molecular and functional analyses are presented.

Patients and methods

Patients

We analyzed two affected siblings and their parents. Experimental protocols were approved by the Institutional Review Board of Yokohama City University School of Medicine. Clinical information and peripheral blood samples were acquired from the family members after obtaining written informed consent. Patient clinical features are summarized in Table 1. They showed dysmorphic facial features, developmental delay, intellectual disability, hypotonia, vertical nystagmus, and epilepsy.

Patient 1

This 9-year-old girl was born to nonconsanguineous healthy parents as a second child after 39 weeks of gestation (Fig. 1a). Her birth weight was 3,390 g [+1.40 standard deviation (SD)], body length of 49 cm (−0.03 SD), and head circumference of 35 cm (+1.35 SD). At 1 month of age, she showed vertical nystagmus without eye pursuit. She was hypotonic, and severe developmental delay was evident from early infancy. She was unable to control her head or utter words at 9 years of age. Abdominal echogram revealed bilateral vesicoureteral reflux as a cause of repeated urinary tract infections. Complex partial seizures developed at 8 months of age and were controlled by antiepileptic drugs. Tube feeding by gastrostomy was necessary for poor appetite at the age of 2 years.

Several dysmorphic features (prominent occiput, bitemporal narrowing, epicanthal folds, open mouth, tented upper lip, high arched palate, micrognathia, and deep plantar groove) were noted (Fig. 1b), but hypoplasia was absent from fingers and fingernails. Initial brain magnetic resonance imaging (MRI) at 6 months of age was normal, but cerebellar atrophy was observed at 2 and 6 years of age (Fig. 1c–f).

At present, her height is 122 cm (+1.1 SD), weight of 18.4 kg (−1.2 SD), and head circumference of 51.4 cm (−0.3 SD). Generalized muscle weakness and nystagmus were neurologically recognized. Laboratory examination showed a normal profile, including blood cell count and blood smear, renal and liver function, total bilirubin, uric acid, albumin, serum electrolytes, lactate, pyruvate, ammonia, amino acids, blood gasses, thyroid function, and cerebrospinal fluid study. Her serum alkaline phosphatase (ALP) activity has been normal for her age since infancy. Metabolic disorder screening including organic acid analysis, lysosomal enzymes, and mass spectrometry of transferrin was normal. G-banded analysis showed a normal karyotype (46, XX).

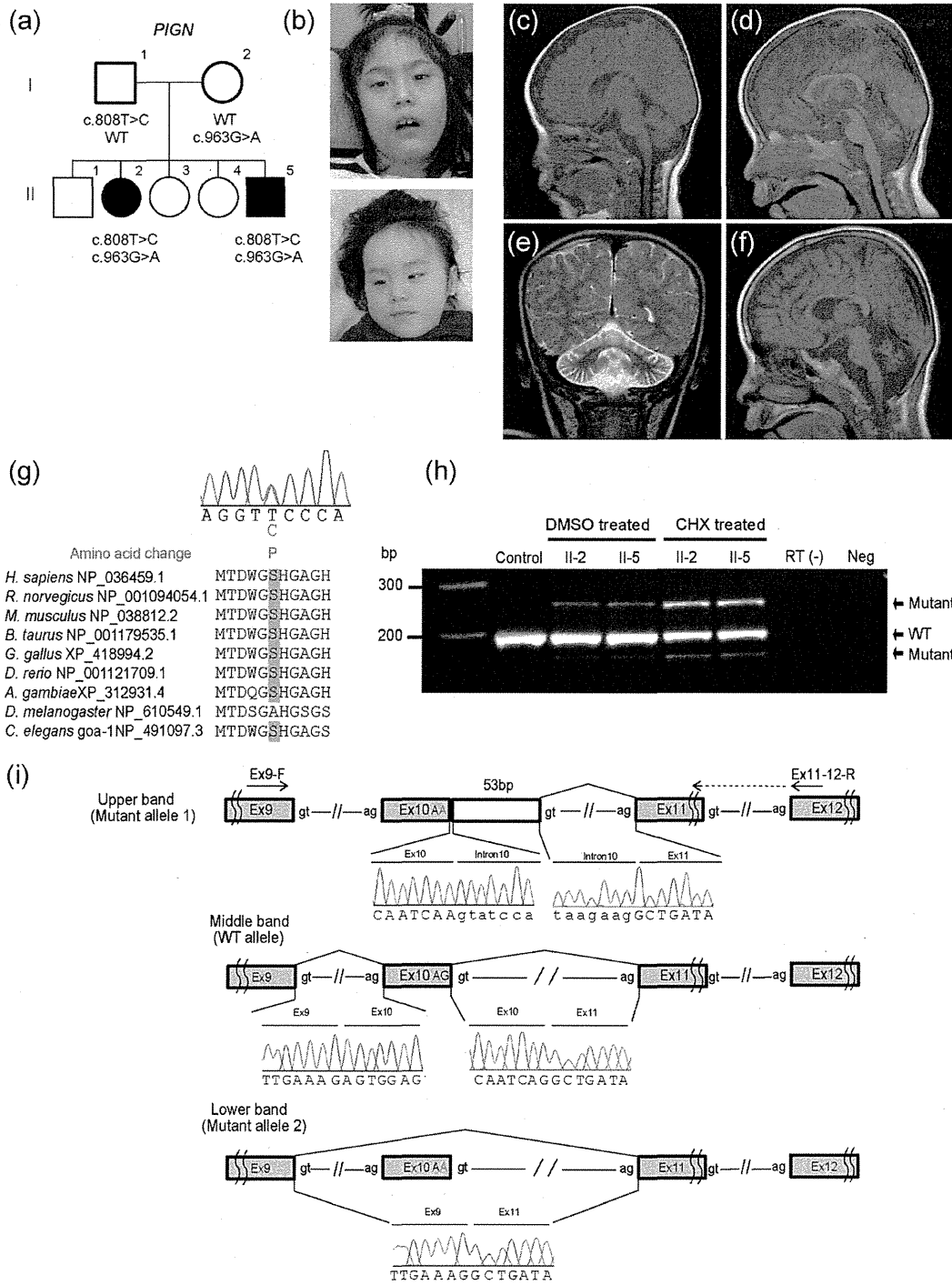
Patient 2

This 2-year-old boy was born after 37 weeks of gestation as a younger brother to patient 1 (Fig. 1a). His birth weight was 3,252 g (+1.3 SD), body length of 50 cm (+1.2 SD), and head circumference of 35 cm (+1.6 SD). He also showed vertical nystagmus at 1 month of age. Complex partial seizures developed at 5 months of age. He was hypotonic, and his developmental milestones were severely delayed with no head control at 1 year and 10 months of age. At present, his height is 92.3 cm (+2.5 SD), weight of 10.9 kg (−0.6 SD), and head circumference of 48.8 cm (+0.4 SD). He showed similar dysmorphic features to patient 1. Brain MRI at 2 months of age revealed no significant abnormalities.

Table 1 Clinical features of patients with *PIGN* mutations

Patient	1	2	Reported by Maydan et al. [7]							Total	
			V-1	V-2	V-4	V-5	V-8	V-9	V-10		
Age (years)	9	2	N.D.	Diseased at 14	Diseased at 1	Diseased at 5		Diseased at 3	Diseased at 17	Diseased at 39	
Sex	Female	Male	Male	Male	Male	Female		Female	Female	Male	
Size at birth (percentile)											
Weight (g)	3,390 (90–97)	3,252 (90–97)	3,566 (95)	4,065 (97)	3,850 (95)	3,410 (40)		4,250 (99)	4,300 (98)	4,800 (>99)	
Head circumference (cm)	35 (90)	35 (90–97)	37 (>97)	37 (97)	35.5 (75)	34.5 (10)		N.D.	N.D.	N.D.	
Abnormalities											
Facial features	+	+	+	+	+	+		+	+	+	9/9
Fingers/foot	+	+	+	+	+	-		-	+	+	6/9
Heart	-	-	+	+	+	+		-	+	-	5/9
Urinary tract	+	-	+	+	+	-		-	-	-	4/9
Gastrointestinal tract	GER	-	GER	GER	Anal stenosis	Imperforate anus, ano-vestibular fistula, GER		-	Feeding and swallowing difficulties	Feeding and swallowing difficulties	7/9
Neurological features											
Developmental delay	+	+	+	+	+	+		+	+	+	9/9
Hypotonia	+	+	+	+	+	+		+	+	+	9/9
Nystagmus	+	+	+	+	-	+		-	+	+	7/9
Tremor	+	+	+	+	+	+		+	-	-	7/9
Seizure	+	+	+	-	+	+		+	+	+	8/9
Brain CT	Normal	Normal	Normal	N.D.	Normal	Multiple small subdural hematomas		N.D.	N.D.	N.D.	1/5
Brain MRI				N.D.	N.D.			N.D.	N.D.	N.D.	
Delayed myelination	+	-	-			+					2/4
Thin corpus callosum	-	-	-			+					1/4
Cerebellar atrophy	+	-	Minimal loss of vermis parenchyma			-					1/4
Enlargement of the ventricle	+	-	-			+(Mild)					2/4

GER Gastroesophageal reflux, N.D. not determined



Whole exome sequencing (WES)

Genomic DNA was isolated from peripheral blood leukocytes, captured using the SureSelect Human All Exon v4 Kit (51 Mb;

Agilent Technologies, Santa Clara, CA), and sequenced on an Illumina HiSeq2000 (Illumina, San Diego, CA) with 101 bp paired-end reads. Data processing, variant calling, and variant annotation were performed as previously described [8].

Fig. 1 **a** Familial pedigree and mutations. **b** Photographs of the faces of patient 1 (*upper*) and patient 2 (*lower*). Frontal narrow temporal, frontal bossing, hypertelorism, epicanthal folds, down-slanting palpebral fissures, high nasal bridge, bilateral low set ears, thin philtrum, downturned mouth, and microretrognathia are noted in both patients. **c, d, f** T1-weighted midline sagittal images and **e** T2-weighted coronal images of patient 1 (**c** at 6 months, **d** and **e** at 2 years, and **i** at 6 years). Progressive vermis atrophy (**c, d, f**) and hemispheres atrophy (**e**) were observed. **g** Sequence chromatography showing heterozygous c.808C >T mutation, which alters an evolutionarily conserved amino acid. Homologous sequences were aligned using CLUSTALW. **h** RT-PCR analysis using cDNA of LCLs derived from two patients (II-2 and II-5) and a control. **i** Schematic representation of wild-type (WT) and mutant transcripts and primers used for the analysis. Primer of ex11-12-R spans exons 11 and 12. A single band (200 bp), corresponding to the WT allele, was amplified using control cDNA. Upper and lower bands were detected from patient cDNA. The upper band (253 bp) has a 53-bp insertion of intron 10 sequences, leading to a frameshift mutation. The lower band has a 41-bp deletion of the entire exon 10, also leading to a frameshift mutation

Reverse transcriptase-PCR

Lymphoblastoid cell lines (LCLs) were established from the two patients. RT-PCR using total RNA extracted from LCLs was performed as previously described [9].

Briefly, total RNA was extracted using the RNeasy Plus Mini kit (Qiagen, Tokyo, Japan) from LCLs with or without incubation in 30 μ M cycloheximide (CHX; Sigma, Tokyo, Japan) for 4 h. Four micrograms of total RNA was subjected to reverse transcription, and 2 μ l cDNA was used for PCR. Primer sequences were ex9-F (5'-TCCTTTAGTCACTGGGAGCTGGA-3') and ex11-12-R (5'-AATCCACAGGAA GGATTCCCCTGA-3') (Supplementary Table 1). PCR products were electrophoresed on a 10 % polyacrylamide gel and sequenced. PCR bands were purified by the E.Z.N.A. poly-Gel DNA Extraction kit (Omega Bio-Tek, Norcross, GA).

Fluorescence-activated cell sorting (FACS) analysis

Surface expression of GPI-anchored proteins (GPI-APs) was determined by staining cells with Alexa 488-conjugated inactivated aerolysin [fluorescently-labeled inactive toxin aerolysin (FLAER); Protox Biotech, Victoria, BC, Canada] and appropriate primary antibodies: mouse anti-decay accelerating factor (DAF; IA10), -CD16 (3G8), -CD24 (ML5), -CD59 (5H8), and -CD48 (BJ40) followed by a PE-conjugated anti-mouse IgG antibody (3G8, ML5, BJ40, and secondary antibodies; BD Biosciences, Franklin Lakes, NJ). Cells were analyzed by flow cytometry (Cant II; BD Biosciences) with Flowjo software (v9.5.3, Tommy Digital, Tokyo, Japan).

Functional analysis in HEK293 cells

PIGN-knockout cells were generated from HEK293 cells using the CRISPR/Cas System [10]. We obtained the human codon-optimized *Streptococcus pyogenes* Cas9 and chimeric guide RNA expression plasmid pX330 from Addgene (Cambridge, MA). The seed sequence for the SpCas9 target site in *PIGN* exon 4 (CCA-GGTCATGTAGCTCTGATAGC) was selected and a pair of annealed oligos designed according to this sequence and cloned into the *Bbs* I sites of pX330. HEK293 cells were transfected with pX330 containing the target site using Lipofectamine 2000 (Invitrogen, Carlsbad, CA). Cells were stained with anti-CD59 antibody 14 days after transfection, and *PIGN*-knockout clones were obtained by limiting dilution.

PIGN-knockout HEK293 cells (clone PIGNKO2-12) were transiently transfected with a wild-type or mutant (S290P or exon 10 skipping) *PIGN* cDNA cloned into the SR α promoter-driven expression vector pME HA-*PIGN*. Restoration of the surface expression of CD59, DAF, and GPI-APs was assessed 2 days later by flow cytometry.

Results

WES detected 288 and 292 rare protein-altering and splice-site variants in patients 1 and 2, respectively. We filtered out common single nucleotide polymorphisms (SNPs) that met the following two criteria: variants showing minor allele frequencies ≥ 1 % in dbSNP 135 and variants found in more than two of our in-house 406 control exomes (Supplementary Table 2). All genes were surveyed for compound heterozygous or homozygous mutations consistent with an autosomal recessive trait, and only *PIGN* (GenBank accession number NM_176787.4) met this criterion, possessing compound heterozygous mutations in two patients. The missense mutation c.808T >C (p.Ser270Pro) was inherited from the patients' father, while c.963G >A is a synonymous mutation inherited from their mother but located at the last base of exon 10 (Fig. 1i). Neither of the two mutations was present in the 6,500 exomes sequenced by the National Heart, Lung, and Blood Institute exome project. In our 406 in-house control exomes, c.808T >C was absent, but c.963G >A was found in one, as a heterozygous mutation. c.808T >C occurred at evolutionary conserved amino acids (Fig. 1g) and was predicted to be pathogenic using online software (Supplementary Table 3). To examine the actual effects of c.963G >A on splicing, RT-PCR was performed (Fig. 1h, i) and a single band (200 bp) corresponding to the wild-type *PIGN* allele was amplified from control LCL cDNA template (Fig. 1h). By contrast, two aberrant faint bands were detected in addition to a wild-type band from patient cDNA (Fig. 1h). Sequencing of the upper aberrant band indicated a 53-bp insertion of intron 10 sequences that had

used a cryptic splice donor site within intron 10, producing a premature stop codon (p.Ala322Valfs*24). Sequencing of the lower band demonstrated the deletion of exon 10 from wild-type *PIGN* mRNA, also producing a premature stop codon (p.Glu308Glyfs*2). Therefore, these two mutant transcripts are likely to be degraded by nonsense-mediated mRNA decay (NMD). In fact, CHX treatment, which inhibits NMD, increased the intensity of the aberrant bands, suggesting that NMD was indeed involved.

To examine the functional impairment of *PIGN* caused by compound heterozygous mutations, the surface expression of various GPI-APs was analyzed by flow cytometry. CD16 and CD24 expression on blood granulocytes was decreased to 26–54 % of normal levels in both patients (Fig. 2a). No abnormal GPI-APs expression was observed on LCLs from either patient (Supplementary Fig. 1).

Transient expression of p.Ser270Pro and exon 10 skipping (p.Glu308Glyfs*2) mutants in *PIGN*-knockout HEK293 cells, in which expression of GPI-APs CD59 was decreased,

was confirmed by immunoblotting. Expression of the exon 10 skipping mutant was decreased compared with that of wild-type and p.Ser270Pro mutant (Supplementary Fig. 2). CD59 expression was only partially or hardly restored by the transient expression of p.Ser270Pro and exon 10 skipping mutants, respectively, suggesting severe or complete loss of *PIGN* activity (Fig. 2b).

Discussion

Herein, we report a second family with *PIGN* mutations that showed clinical features common to a previous affected family, including congenital anomalies, developmental delay, hypotonia, and epilepsy [7]. In addition, nystagmus was an early symptom of patients in this study and was also observed in five of seven patients previously [7]. Of note, progressive cerebellar atrophy was observed in the current patient 1, and this appears to be a novel phenotype associated with *PIGN*

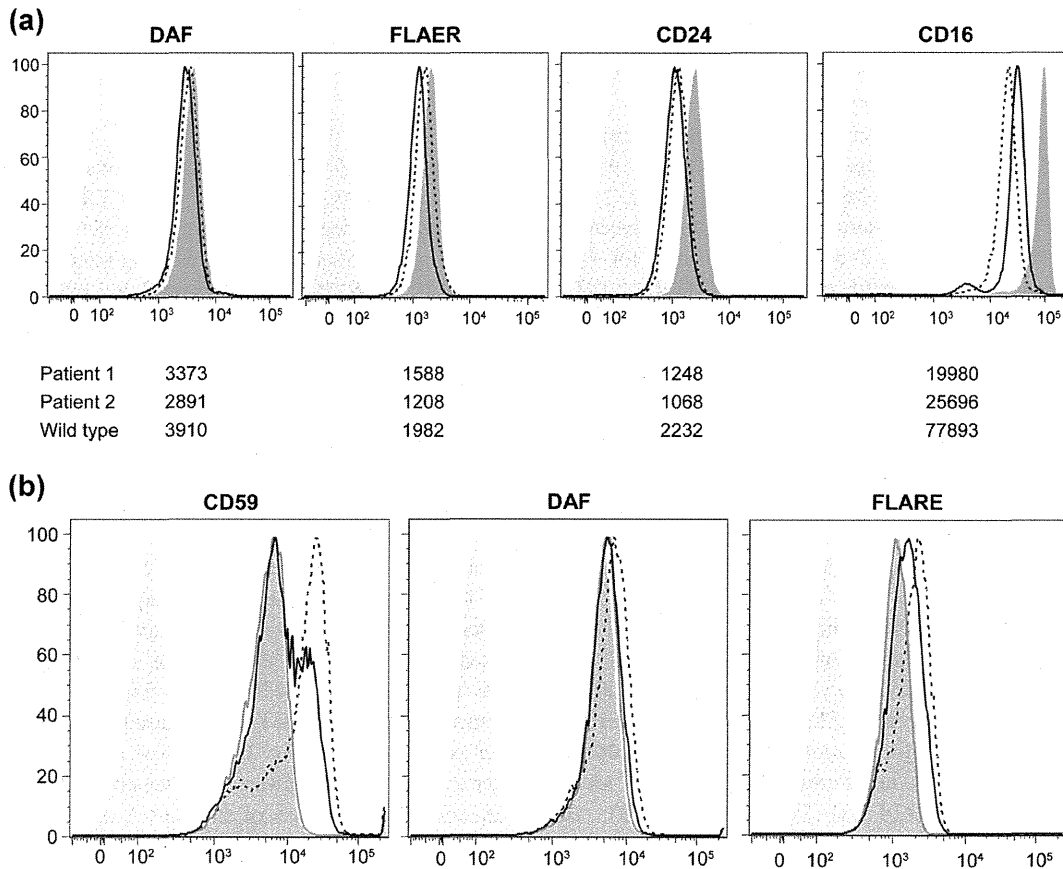


Fig. 2 **a** Surface expression of various GPI-APs on patient granulocytes (patient 1: dotted lines, patient 2: solid lines), a normal control (dark shadow) and an isotype control (light shadows). Numbers represent mean fluorescent intensities. Expression of DAF and FLAER in both patients did not significantly change compared with the control. However, CD16 and CD24 expression decreased to 26–54 % of normal levels. **b**

PIGN-knockout HEK293 cells were transiently transfected with wild type (dotted lines) or mutants (exon 10 skipping: gray line, p.Ser270Pro: black line) of pME HA-*PIGN* vectors. Empty vector: dark shadow, isotype control: light shadow. Expression of CD59 was only partially or hardly restored by p.Ser270Pro and exon 10-skipping vectors, respectively

mutations as two patients examined by MRI showed no cerebellar atrophy but only minimal loss of vermis parenchyma in one patient (patient V-1) in the previous report [7].

PIGN is involved in the addition of phosphoethanolamine to the first mannose in GPI [6]. In *Pign*-knockout mouse F9 embryonal carcinoma cells, the first mannose in GPI precursors is not modified by phosphoethanolamine. Nevertheless, further biosynthetic steps continue and the cell surface expression of GPI-anchored proteins is only partially affected [6], suggesting that this modification may not be essential for GPI-anchored protein biosynthesis [6]. By contrast, the *gonzo* mouse line, which harbors the splice donor site mutation in *Pign*, showed abnormal forebrain development resembling holoprosencephaly [11], and patients with *PIGN* mutations show severe phenotypes such as multiple congenital anomalies, neurological impairment, and even lethality [7]; this indicates that particular defects of *PIGN/Pign* cause abnormal development both in mice and humans. Although the overall amount of GPI-anchored proteins might not be significantly affected by *PIGN* defects, as revealed by the minimal decrease in DAF and FLAER expression on patient granulocytes in the present study, changes to a subset of GPI-anchored proteins such as CD16 and CD24 can be sufficient to cause severe neurological phenotypes. Additionally or alternatively, GPI-APs expressed on *PIGN*-defective cells lack the phosphoethanolamine-side branch, and this abnormal structure of the glycan part of the anchor might affect functions of GPI-APs. Functional analysis using neuronal cells may provide novel insights into the pathogenesis of neurological phenotypes caused by *PIGN* mutations.

Seven genes (*PIGA*, *PIGM*, *PIGN*, *PIGV*, *PIGL*, *PIGO*, and *PGAP2*) have been identified as being mutated in patients with neurological abnormalities. Mutations in three of these (*PIGV*, *PIGO*, and *PGAP2*) cause hyperphosphatasia [3, 12–14], suggesting that ALP is a useful marker for suspected GPI anchor-synthesis pathway deficiencies. However, mutations of the other four genes (*PIGA*, *PIGM*, *PIGN*, and *PIGL*) did not cause hyperphosphatasia [7, 14, 15], so clinical diagnosis might be difficult in the absence of specific biomarkers. Even in clinically unsuspected patients, WES may identify mutations in genes involved in the GPI anchor-synthesis pathway. Current advances in next generation sequencing should find more comprehensive answers for unsolved GPI anchor-related diseases.

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