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Lack of the multidrug transporter MRP4/ABCC4 defines the PEL-negative blood group and impairs platelet aggregation

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Key Points

- *ABCC4* encoding the multidrug resistance protein 4 specifies the novel PEL human blood group system
- The rare PEL-negative phenotype is associated with impaired platelet aggregation

Abstract

The rare PEL-negative phenotype is one of the last blood groups with an unknown genetic basis. By combining whole-exome sequencing and comparative global proteomic investigations, we found a large deletion in the *ABCC4*/*MRP4* gene encoding an ATP-binding cassette (ABC) transporter in PEL-negative individuals. The loss of PEL expression on *ABCC4*-CRISPR-Cas9 K562 cells and its overexpression in *ABCC4*-transfected cells provided evidence that *ABCC4* is the gene underlying the PEL blood group antigen. Although *ABCC4* is an important cyclic nucleotide exporter, red blood

cells from *ABCC4*_{null}/PEL-negative individuals exhibited a normal cGMP level, suggesting a compensatory mechanism by other erythroid ABC transporters. Interestingly, PEL-negative individuals showed an impaired platelet aggregation, confirming a role for *ABCC4* in platelet function. Finally, we showed that loss-of-function mutations in the *ABCC4* gene, associated with leukemia outcome, altered the expression of the PEL antigen. Besides *ABCC4* genotyping, PEL phenotyping could open a new way toward drug dose adjustment for leukemia treatment.

Introduction

Blood group phenotypes are defined by the presence or absence of specific antigens on the surface of the red blood cell (RBC) membrane and are inherited characteristics resulting from genetic polymorphism at the 38 currently identified blood group loci¹. Most blood group systems are carried by glycoproteins or glycolipids, with the antigen specificity determined by either an amino acid sequence or an oligosaccharide moiety (e.g., ABO). The majority of blood antigen-carrying proteins has important functions not only in RBCs but also in other tissues. Hence, because of their polymorphisms and the existence of natural null phenotypes, blood groups also represent powerful tools to investigate human diseases²⁻⁴. However, some null phenotypes are not accompanied by any evident pathologies, suggesting that some redundancy and compensatory mechanism occur in individuals with the corresponding null phenotype^{5,6}. For example, some blood group antigens are carried by members of the ABC transporter family and we have recently demonstrated that null alleles of *ABCB6* and *ABCG2* are responsible for the Lan- and Jr(a-) blood phenotypes, respectively^{7,8}. Despite the important physiological role of ABC transporters, individuals with both those phenotypes are apparently healthy.

Although the genetic loci of most blood group antigens have been identified, the genetic basis of some high-frequency blood group antigens remains unknown. In 1980, Daniels described a

new high-frequency red cell antigen, provisionally called PEL, after the proband's name⁹. Sixteen years later, it was shown that some other rare French-Canadian individuals made an antibody against a high-prevalence blood group antigen reacting with all RBCs tested, except their own and other PEL-negative probands⁹. Anti-PEL was never reported to cause hemolytic disease of the fetus and newborn. The clinical significance of this antibody in case of an incompatible transfusion is unknown, however, a reduced survival of transfused ⁵¹Cr-labeled incompatible red cells was observed⁹. Family studies showed that the PEL-negative phenotype was inherited as an autosomal recessive trait, but the *PEL* locus remained undetermined until now⁹.

In this study, we demonstrated that the ABC transporter ABCC4 (also called MRP4 for multidrug resistance protein 4) carries the PEL antigen and that a large deletion in the *ABCC4* gene is responsible for the PEL-negative blood type. These findings elucidate the molecular basis of a new human blood group system. In agreement with the proposed role of ABCC4 in mouse models^{10,11}, we reported an impairment of platelet aggregation in four PEL-negative individuals.

Methods

Samples

Blood samples from previously characterized PEL-negative individuals were cryopreserved in the rare blood collection of Héma-Québec and the National Reference Center for Blood Group (CNRGS) (biocollection, DC-2016-2872). Informed consent was obtained for the PEL-negative subjects in accordance with the Declaration of Helsinki protocols and approved by the Ethical Committee of Héma-Québec.

Antibodies

The anti-PEL were sourced from Mrs. "Pel" described in 1980 and from "HugS" subject, both described in the original paper⁹. By indirect antiglobulin testing at 37°C on papain-treated

RBCs, HugS and Pel sera were found to react 3+ (titer 64, score 69) and 2+ (titer 2, score 12), respectively. Anti-PEL was purified after adsorption of human polyclonal anti-PEL from the serum sample of Mrs. ‘HugS’⁹ onto a pool of three group O papain-treated RBCs at 37°C, followed by an acid elution test with the Gamma ELU-KIT II device (Immucor). The PEL specificity of the eluate was verified as well as the absence of contaminating ABO antibodies. This eluate was used to confirm the PEL-negative phenotype of all individuals from the four families previously described in the original manuscript⁹. The investigation by flow cytometry of the antibody class and subclass of the eluate was consistent with a mix of IgG1 and IgG2, with no IgG3, IgG4 and IgM. The monoclonal anti-ABCC4 antibody targeting N-terminal amino acids 1–110 of the ABCC4 protein was purchased from Abcam (ab56675; Abcam, Cambridge, MA)^{12,13}.

Whole-exome sequencing and data analysis

Genomic DNA was extracted from leukocytes using the MagnaPure system (Roche). Exome capture was performed with the Sure Select Human All Exon Kit (Agilent Technologies). A detailed protocol is provided in Supplemental Methods.

Sanger sequencing and PCR genotyping

PCR primer pairs ABCC4-FWD1 (forward) and ABCC4-AS1 (reverse) were used to amplify the region containing the breakpoint between exon 20 and downstream of the 3’UTR caused by a deletion in the *ABCC4* gene. PCR products were purified with SureClean Plus (Bioline) and sequenced by ABI BigDye terminator chemistry (GATC Biotech) with the primer ABCC4-AS2 (Primer sequences are available in supplemental Table 1). For PCR genotyping of PEL-negative samples, two PCRs were performed with specific forward primers, WT-F and BK-F and a common reverse primer BK-R (Primer sequences are available in supplemental Table 2).

Plasmid construction

The coding sequence of *ABCC4* cDNA was amplified using a forward primer containing the *NheI* restriction site at the 5' end and a reverse primer containing the *XhoI* restriction site at the 5' end, from the pcDNA3-*ABCC4* plasmid provided by Dr Gabriele Jedlitschky. The *ABCC4* sequence was verified (identical to NM_005845) and cloned as a *NheI/XhoI* fragment into the pCEP4 vector.

Cell culture and transfection

HEK 293 cells and K562 cells were grown in DMEM/Glutamax I (Invitrogen) and IMDM/GlutaMax/HEPES (25 mM), respectively, supplemented with 10% (vol/vol) fetal calf serum (Dutscher, Brumath, France), and 1× antibiotic-antimycotic solution (Invitrogen) at 37°C under a humidified atmosphere containing 5% CO₂. HEK293 cells were first transfected with the pCEP4-*ABCC4* plasmid by nucleofection using the Cell Line Nucleofector Kit V (Amaxa). Stable HEK293 transfectants were obtained after 10 days of selection with hygromycin B (0.15 mg/ml, Invitrogen).

SDS-PAGE and Western blotting

RBC membranes (ghosts) were prepared from frozen blood samples that were previously washed in PBS buffer. Briefly, ghosts were obtained by hypotonic lysis of RBCs with 5P8 buffer (5 mM Na₂HPO₄ pH 8.0 and 0.35 mM EDTA pH 8.0 containing 1 mM PMSF), followed by four washes with the same buffer and then stripped by incubation with 10 mM NaOH (40 min at 4°C). Ghost proteins were solubilized in Laemmli buffer and then separated by SDS-PAGE and transferred to nitrocellulose membranes. The membrane was then blocked and incubated with a monoclonal antibody to *ABCC4* (1:500; Abcam) for 120 min at RT. Anti-*ABCC4* labeling was revealed with an anti-mouse IgG(H+L) horseradish-peroxidase-linked goat antibody (1:800; P.A.R.I. S Biotech) for 30 min at 21 °C. The membrane was also probed with rabbit antiserum to p55, which was used as a loading control.

Immunoprecipitation of the PEL antigen

The immunoprecipitation of the PEL antigen was performed as described previously¹⁴. Briefly, RBC ghosts from PEL+ and PEL- subjects were lysed for 1 h at 4°C with gentle shaking in Na₂HPO₄ 5 mM, NaCl 150 mM pH 8.0, Triton X-100 2% with a protease inhibitor cocktail. Supernatant and pellet were separated by centrifugation (15,000 g 15 min at 4°C). Supernatant was incubated overnight at 4°C with the anti-PEL eluate. Immune complexes were purified with UltraLink Immobilized Protein A/G (Pierce), and the immunoprecipitated proteins were eluted in Laemmli buffer at 90°C for 5 min and analyzed by Western blot as described above.

Disruption of ABCC4 in K562 by CRISPR/Cas9

Gene editing by CRISPR/Cas9 technology was performed as described previously^{15,16}. The pSpCas9(BB)-2A-Puro (PX459) expression vector was purchased from Addgene (plasmid #48139). Three guides were selected with CRISPRdirect: <http://crispr.dbcls.jp/>¹⁷. Oligonucleotides (see supplemental Table 3) were ligated into the BbsI linearized PX459 plasmid. The integrity of each cloned guide sequence was checked by Sanger sequencing with PX459 plasmid sequencing primer (see supplemental Table 3). Five micrograms of purified plasmid were electroporated with 10⁶ K562 cells using Nucleofector II and the V/program T-016 kit (Lonza). Cells were seeded at a density of 150 000 cells per mL 48 hours before electroporation. Viability was >95% on the day of transfection. Transfected K-562 cells were grown with puromycin (5 µg/mL) in the culture medium 24 hours after transfection for 4 days. Then, the cells were grown without puromycin. The generation of INDEL events in the ABCC4 gene was assessed using T7 endonuclease I enzyme (New England Biolabs) fifteen days after transfection.

Platelet aggregation studies

Platelet aggregation was measured with an optical platelet aggregometer (Chronolog model 490 4+4, Chrono-log Corporation) according to the manufacturer's instructions.

***In vitro* erythropoiesis**

Peripheral blood mononuclear cells (PBMCs) were obtained from the peripheral blood samples of healthy donors using a Ficoll density gradient separation (Pancoll 1.077 g/ml, PAN BIOTECH). CD34⁺ cells were then purified using anti-CD34 conjugated microbeads and manual cell separation columns (Miltenyi). The cell culture procedure was comprised of 2 phases as described by Freyssinier *et al*^{18,19}.

Flow cytometric analysis of PEL and Jr^a antigen expression

Thawed RBCs or fresh cells (K562 and HEK293) were washed 3 times in PBS (Gibco) and then resuspended in low-ionic strength buffer (BFI) supplemented with 1% BSA and incubated with anti-PEL eluate (1:2) or mouse anti-ABCG2 (5D3, 1:20, Ozyme). Anti-PEL labeling was revealed with anti-human IgG-PE (1:50, Beckman Coulter), and anti-Jr^a (ABCG2) labeling was revealed with anti-mouse IgG-PE (1:100, Beckman Coulter). A FACSCantoII flow cytometer (BD Bioscience) and FlowJo software were used for data acquisition and analysis, respectively.

Label-free quantification mass spectrometry analysis

Ghosts from 4 healthy donor control samples and three PEL individuals were obtained as described above and then lysed by heating for 5 min at 95°C in the same volume of 2X lysis buffer (100 mM Tris/HCl pH 8.5, 2% SDS). Proteomic analyses were performed by using the label free proteomic method. Raw data were analyzed by label-free quantification on MaxQuant software. A detailed protocol for this analysis is provided in Supplemental Methods.

Intracellular cGMP measurements

The intraerythrocytic cGMP level was measured as described previously²⁰. Briefly, packed and washed RBCs were lysed, and then the intracellular cGMP was measured following the enzyme immunoassay (EIA) procedure according to the instructions provided by the supplier (code RPN226, Kit Biotrak, Amersham Pharmacia Biotec.).

Statistical analysis

Differences between groups were analyzed by the Mann-Whitney test (GraphPad Prism V7).

Results

A large deletion in the *ABCC4* gene causes the PEL-negative blood type

To identify the molecular basis of the PEL blood group, whole-exome sequencing (WES) was performed using genomic DNA from leukocytes of one French-Canadian PEL-negative individual in each of the four unrelated families described in the original paper⁹. Variant filtering strategies failed to reveal any single-mutations or indel variants common to the four PEL-negative individuals. We hypothesized that the PEL-negative phenotype could be due to a deletion of one or several exons in a candidate gene encoding a red cell membrane protein. We then used a comparative global proteomic strategy to analyze the differential expression of membrane proteins in RBC membranes (ghosts) from three PEL-negative and three PEL-positive individuals as controls. Only one missing membrane protein was identified, *ABCC4*/MRP4, which was absent in the ghosts from all three PEL-negative samples compared to the control ghosts (Supplemental Excel file). We then verified the exon coverage in *ABCC4* genes by analyzing copy number variation (CNV) data. Integrative Genomics Viewer analysis revealed a large homozygous deletion in the *ABCC4* gene [GenBank: NM_005845] in the four PEL-negative individuals (Figure 1A). The 67,528-bp deletion identified in the *ABCC4* gene of PEL-negative samples removed the last 10 exons of the gene and part of the downstream 3'UTR region. Using a primer walking approach and Sanger sequencing, the precise breakpoints of the deletion were identified between intron 21 and the

intergenic region, with coordinates from chromosome 13:95,018,454-95,085,982 (GRCh38/hg38 assembly) (Figure 1B). This deletion was accompanied by the insertion of an intervening 18-bp sequence that corresponds to an intronic sequence repeated 62 times in the *ABCC4* gene (Figure 1B). We next performed Sanger sequencing of the *ABCC4* gene in eight additional PEL-negative individuals from the four families. All these individuals were homozygous for the same deletion/insertion, although the family investigation showed no relationship over the last five generations.

To validate the *ABCC4* gene as the yet unidentified genetic locus encoding the PEL antigen, we first performed Western blot analysis using a monoclonal antibody specific for the first 110 amino acids of ABCC4. We showed that ABCC4 was present in the membrane of PEL-positive control RBCs but totally absent in the PEL-negative RBCs (Figure 1C). According to the mass spectrometry data which failed to detect any ABCC4-derived peptide in the PEL-negative sample (supplemental Figure 1), no truncated protein was detected in these samples (supplemental Figure 2). These results strongly suggested that the large deletion in the *ABCC4* gene may be responsible for the PEL-negative phenotype. To confirm that the ABCC4 protein carries the PEL antigen, we assessed whether exogenous ABCC4 expression in a transfected cell line would generate the expression of the PEL antigen. Flow cytometry analyses of HEK293 cells stably transfected with *ABCC4* cDNA using the anti-PEL eluate revealed a significant increase of PEL antigen cell-surface expression (Figure 2A and 2C, left panel). To fully confirm the molecular basis of the PEL antigen, we generated three *ABCC4*-knockout K562 cell lines using the CRISPR-Cas9 strategy with different RNA guides (gRNAs) targeting exons 8 and 18 of *ABCC4* gene (Supplemental Figure 3 and Figure 2C, lane 4). Flow cytometry analysis using the anti-PEL eluate showed that the complete loss of ABCC4 abolished the expression of the PEL antigen in all three knockout cell lines (Figure 2B). Finally, the ABCC4 protein was immunoprecipitated using anti-PEL eluate from RBC

membrane extracts of PEL-positive subjects, but not from PEL-negative subjects (Figure 2D). All these genetic, molecular and cellular data indicated that the PEL blood group is carried by the ABCC4 protein and that homozygosity for a large deletion in the *ABCC4* gene is responsible for the rare PEL-negative phenotype.

Impact of genetic variation in the *ABCC4* gene on PEL antigen expression

The *ABCC4* gene is highly polymorphic, and numerous non-synonymous single-nucleotide polymorphisms (SNPs) were associated with multiple disease susceptibilities^{21,22}. We investigated the effect of the major loss-of-function SNPs, rs11568658 (G187W), rs2274407 (K304N) and rs3765534 (E757K), on the PEL antigen expression at the red cell surface (Figure 3A). These heterozygous *ABCC4* variants were selected from 85 whole exome-sequenced samples, available from our own cryopreserved RBC bio-collection; all mutations were confirmed by Sanger sequencing. Flow cytometry analysis using anti-PEL eluate showed a moderate decreased expression of the PEL antigen in the G187W variant (16%) but a stronger decrease expression in the K304N and E757K variants (30 and 33%, respectively) (Figure 3B). Interestingly, these latter variants have been shown to alter the membrane localization of ABCC4^{23,24}. These results indicated that a heterozygous mutation in the *ABCC4* gene could affect the expression of the PEL antigen.

Role of ABCC4 in erythroid cells

To better understand the function of ABCC4 in mature erythroid cells, we measured the intracellular cGMP level in frozen stored RBCs from 5 PEL-negative individuals and 5 controls. We showed that the cGMP level was not significantly impaired in the absence of ABCC4 (Figure 4A), which is consistent with the absence of erythroid defects in these patients (see supplemental Table 4). We then monitored the expression profile of ABCC4 during *in vitro* erythropoiesis (Supplemental Figure 4). Figure 4B showed a higher expression level of ABCC4 in immature erythroblasts (pro-erythroblast stage) followed by a gradual

decrease upon erythroid terminal differentiation, suggesting a potential role for this transporter in cyclic nucleotide regulation in early erythroblasts. This finding raised the hypothesis that another cGMP transporter could compensate for the absence of ABCC4 on the membrane of mature RBCs. Previous studies using murine models reported that the absence of an ABC transporter can elicit compensatory changes in functionally related ABC transporters^{25,26}. Therefore, we reanalyzed our proteomic data to compare the expression of different ABC transporters at the RBC membrane from PEL-negative individuals (P) and controls (C). We found that five other ABC transporters (ABCC1, ABCA7, ABCB6, ABCC5 and ABCG2) were expressed on the surface of RBC membranes, and we calculated the P/C (proband/control) expression ratio for each of them. ABCC1, ABCA7, ABCB6, and ABCC5 exhibited a P/C ratio near 1 while ABCG2 expression was found to be increased by 1.3-fold in PEL-negative/ABCC4_{null} RBCs (n=3) compared to controls (Figure 4C). ABCG2 overexpression in PEL-negative RBCs was confirmed by flow cytometry analysis using an anti-ABCG2 antibody. Although ABCG2 expression was variable among PEL-negative RBCs (n=7), it was significantly higher in this group than in controls ($p=0.0002$) (Figure 4D). These results suggested that the absence of ABCC4 in PEL-negative individuals could be compensated by the overexpression of ABCG2. We have recently shown that ABCG2 is the carrier of the JR blood group system and that the rare Jr(a-) (ABCG2_{null}) individuals did not exhibit any specific apparent clinical features⁸. To confirm our hypothesis, we analyzed ABCC4 expression in RBCs from ABCG2_{null} individuals (n = 11) and controls by flow cytometry (n=11). Figure 4E showed a significant upregulation of ABCC4 expression in the absence of ABCG2 ($p=0.0007$). Our data, together with previous studies indicating that both ABCC4 and ABCG2 export cGMP²⁷, suggest that the overexpression of ABCG2 in PEL-negative RBCs may represent a compensatory mechanism for the lack of ABCC4, which could explain the absence of erythroid disorder in PEL-negative individuals (supplemental

Table 4). To confirm that the upregulation of ABCG2 in these patients is actually due to the absence of ABCC4, we analyzed the expression of ABCG2 in the previous loss-of-function variants of ABCC4 (K304N, E757K, and G187W). We did not find any increase in the ABCG2 expression in these variants (data not shown), suggesting that the upregulation of ABCG2 in ABCC4_{null} RBCs could be specific for PEL-negative families.

Loss of ABCC4 results in impaired platelet aggregation in PEL-negative individuals

ABCC4 is highly expressed in platelets and was initially suggested as the ADP transporter in dense granules (DGs)²⁸. Two recent studies using ABCC4-knockout mice indicated a role for ABCC4 in platelet aggregation and involvement in cAMP rather than ADP transport^{10,11}. In addition, one of those studies localized ABCC4 to the plasma membrane by structured illumination microscopy and biochemical approaches. Since anti-PEL represents the only currently available probe to detect ABCC4 at the cell surface, we used it in flow cytometry and showed that this protein is expressed at the plasma membrane of platelets from controls but not from PEL-negative individuals (supplemental Figure 5). We then investigated platelet function in four PEL-negative individuals. These individuals showed similar complete blood count parameters compared to reference values, with a platelet count within the normal range and with no signs of easy bruising or increased bleeding tendency (supplemental Table 4). We then assessed platelet aggregation test in the four PEL-negative individuals. No difference was noted in platelet aggregation induced by collagen ($80\% \pm 4.9$ at $2 \mu\text{g/mL}$; normal range: 70-94%) and by a high ADP concentration ($67\% \pm 14$ at $10 \mu\text{M}$; normal range: 71-88%). Conversely, at lower ADP concentrations of 2.5 and 5 μM , platelet aggregation was decreased in the PEL-negative individuals ($9.5\% \pm 4.9$ and $27\% \pm 11$, respectively) compared to reference ranges (75-95% and 78-91%, respectively)²⁹. These findings suggest a potential role of ABCC4 in platelet aggregation.

Discussion

Since the initial description of the PEL antigen and despite efforts that have been made toward finding its molecular basis, the elucidation of the PEL blood group system has remained an enigma for almost 40 years. Here, we combined multiple omics approaches to demonstrate that a large deletion in the *ABCC4* gene is responsible for the PEL-negative blood type and we provided evidence that *ABCC4* underlies the PEL blood group antigen. Thus, these findings elevate PEL to a novel blood group system to be joined to the 38 currently known systems. The discovery of a novel human blood group system is an exceptional event, representing a milestone in transfusion medicine and in genetic fields. As an example, the recent characterization of the molecular basis of the VEL antigen and the rare Vel-negative blood type, particularly found in Northern Scandinavia, allowed to set up a genotyping program at the Regional Blood Center in Lund, Sweden³⁰. Interestingly, since the PEL-negative blood type has been found only in the French-Canadian population, a mass-screening genotyping program in Canada, especially in the Quebec province, would probably make it possible to identify other *ABCC4* null individuals. This could add value to estimate the prevalence of this rare blood type as well as to help in the search for compatible blood for potentially immunized patients against the PEL antigen. The identification of the *ABCC4* deletion breakpoint in PEL-negative individuals allowed us to develop a PCR genotyping assay (supplemental Figure 6).

The multidrug resistance protein *ABCC4*/MRP4 belongs to the ATP-binding cassette family of membrane transporters and is expressed in blood cells as well as in several tissues, including the kidney, liver, lung, pancreas, and prostate, and particularly in blood cells. PEL-negative individuals are the first ever-reported people lacking the complete expression of the *ABCC4* protein. Surprisingly, despite the expected biological importance of *ABCC4* as a cyclic nucleotide transporter, no apparent mutual symptoms or diseases were identified after

investigation of the clinical history of the 12 PEL-negative members within the 4 families analyzed in this study. Although the intracellular cyclic nucleotides is crucial for the proliferation and differentiation of early erythroblasts and for hemoglobin synthesis^{31,32}, no erythroid disorders were reported in the PEL-negative individuals. The overexpression of ABCG2 in the mature PEL-negative RBCs and its involvement in a potential compensatory mechanism need to be confirmed in erythroid precursors of PEL-negative individuals.

ABCC4 regulates the cellular efflux of cGMP and cAMP involved in cellular signaling and, more recently, in platelet activation^{10,11,28,33}. *In vitro* platelet aggregation test performed in four ABCC4_{null}/PEL-negative blood samples suggests an impaired platelet aggregation at low ADP concentration due to the absence of ABCC4. These results are in total accordance with previous studies showing that the inhibition of ABCC4 leads to a decrease in human platelet function and that an inhibitor of ABCC4 (MK 571) can be used as a therapeutic molecule to potentiate the aggregating effects of some guanylate cyclase activators usually used in thrombotic complications³⁴. The role of ABCC4 in platelet function has also been demonstrated in ABCC4-deficient mice in which the cytosolic level of cAMP in platelets is higher than in wild-type mice^{10,11}.

In malignant diseases, ABC transporters contribute to chemotherapy resistance due to their drug-efflux capabilities in cancer cells³⁵. The overexpression of ABC transporters represents a powerful prognostic marker in acute myeloid leukemia (AML)³⁶⁻³⁸. An exciting hypothesis would be that the expression of these transporters on red cells, an easily available biological material through a simple peripheral blood sample, could reflect their overexpression in other blood cells. Since ABCC4 (carrying the PEL antigen) can now be considered the third ABC transporter coding for a human blood group system, after ABCB6 (carrying the Lan antigen) and ABCG2 (carrying the Jr^a antigen)^{7,8}, a pilot study is required to determine whether red blood cell typing may help to predict poor or good prognosis in AML patients. On the other

hand, *ABCC4* exports a wide variety of drugs and confers resistance to thiopurines, such as methotrexate (MTX), cyclophosphamide and thiopurines (e.g., 6-thioguanine and 6-mercaptopurine (6-MP)). *ABCC4* is strongly expressed in hematopoietic cells, and some variants of this gene are associated with a higher toxicity of MTX and 6-MP anticancer drugs, which have an impact on the clinical outcome in childhood acute lymphoblastic leukemia (ALL)^{22,39-42}. Notably, the loss-of-function *ABCC4* variant p.Glu757Lys (rs3765534) known to impair the membrane localization of *ABCC4*, is frequently present in the Japanese population (MAF 18%) where it is associated with severe leukopenia in pediatric patients with ALL treated with the 6-MP drug^{24,43}. Consistently, our results showed that this variant alters the expression of the PEL antigen at the red cell surface. Since genotyping of *ABCC4* is strongly recommended prior to thiopurine administration in patients with ALL⁴³, it could also be interesting to propose a PEL phenotyping for optimal drug dose adjustment and prevention of chemotherapy side effects.

In conclusion, we characterized the molecular basis of the novel human blood group system PEL and demonstrated that a null allele of *ABCC4* specifies the PEL-negative phenotype by an innovative approach combining whole-exome sequencing and global comparative proteomic analysis. The elucidation of this novel blood group system should prove of high clinical interest, both in transfusion medicine and in chemotherapy treatment.

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Authorship Contributions

S.A., C.L.V.K., Y.C., J.P. C and T.P. conceived the project. S.A., C.L.V.K., O.H., and T.P. designed the research study. S.A., M. M, P.H., C.V., and A.R. performed the experiments. S.A., C.L.V.K., Y.C., and T.P. analyzed the data. A.W and G.N designed and performed the CRISPR Cas-9 experiments. E.F.G., V.S. and P.M. realized the mass spectrometry and proteomic analyses. C.B-F. coordinated the WES procedure. P.N. gave bioinformatics support. G.J., M.C., C.E., J.C.Y., N. R and M.S.L. contributed essential material. M.S.L. and J.C.Y. collected the clinical history of PEL-negative individuals. Y. C, T. P, C.L.V.K., and S. A wrote the paper.

Data Sharing Statement

For original proteomic data, please contact patrick.mayeux@inserm.fr

Footnotes

This PEL blood group research study is dedicated to the memory of Corinne Nadeau Larochelle, 1988-2018.

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Figure Legends

Figure 1. The null allele of the *ABCC4* gene is responsible for the PEL-negative phenotype.
A. Integrative Genomics Viewer analysis reveals homozygous loss of exons from 21 to 31 of

the *ABCC4* gene in four PEL-negative individuals (P1, P2, P3, and P4). **B.** Schematic representation of the deletion in the *ABCC4* gene and Sanger sequencing confirmation of the 67528-pb deletion/18-bp insertion in genomic DNA of PEL-negative individuals. **C.** Western blot analyses of *ABCC4* in the RBC membranes from PEL-positive (controls 1, 2, and 3) and PEL-negative (P1, 2, and 3) individuals. Immunoblotting was performed with a mouse monoclonal antibody directed against *ABCC4*. The p55 antibody was used as a loading control.

Figure 2. A. Cell surface expression of the PEL antigen in *ABCC4*-transfected HEK293 cells. HEK293 cells stably transfected with *ABCC4* cDNA (thick lines) or an empty vector (dotted lines) were labeled with an anti-PEL and analyzed by flow cytometry. The gray profile corresponds to cells incubated with the secondary antibody only. **B.** Surface level of PEL antigen on K562 cells transfected with plasmid allowing expression of *Cas9* nuclease in combination with guide RNA-*guide* targeting exon 8 of *ABCC4* (thick line) or *Cas9* nuclease alone without guide RNA-*guide* (dotted lines). The gray profile corresponds to cells incubated with the secondary antibody only. **C.** Western blot analysis of *ABCC4* expression in HEK293 and K562 cells. Fifty micrograms of proteins from lysates of *ABCC4*-transfected (lane 2) or control (lane 1) HEK293 cells and *ABCC4*-knockout (lane 4) or control (lane 3) K562 cells were resolved by SDS-PAGE under reducing conditions and probed with a monoclonal anti-*ABCC4* antibody. GAPDH was used as a loading control. **D.** Anti-PEL eluate is able to immunoprecipitate *ABCC4* from RBC membrane extracts of PEL+ subjects, but not from two PEL-negative subjects. Immune complexes were analyzed by polyacrylamide gel electrophoresis under reducing conditions with heat denaturation, followed by western blot analyzes using the monoclonal anti-*ABCC4*.

Figure 3: A. Flow cytometry profiles of PEL expression in different red cell variants of *ABCC4*. **B.** Corresponding GMFI of PEL antigen expression in different variants of *ABCC4*.

PEL expression was analyzed using an anti-PEL eluate. Heterozygous variants in *ABCC4* were selected from our own RBC bio-collection. All mutations were confirmed by Sanger sequencing. Statistical analyses for significance were performed using the Mann-Whitney test. ** $P < 0.005$.

Figure 4. A. cGMP levels in RBCs from control (n=7) and PEL-negative individuals (n=7). Data are mean \pm standard error of the mean. **B.** *ABCC4* expression during terminal erythroid differentiation. Erythropoiesis was monitored via CD49d and band3 levels of GPA^{pos} cells and May-Grunwald Giemsa (MGG)-staining. The *ABCC4* expression was determined on the GPA^{pos} cells using the anti-PEL eluate. **C.** P/C ratios for ABC transporter expression in RBC membranes from 3 PEL-negative *ABCC4*_{null} individuals (P) and 3 controls (C). The P/C ratio was determined after normalization of the LFQ intensity of ABC transporter proteins by the LFQ intensity of actin. **D.** The geometric mean of fluorescence (GMFI) of ABCG2 expression in *ABCC4*_{null} (n=7) and control (n=8) RBCs was analyzed by flow cytometry using an anti-ABCG2 antibody. *** $P = 0.0002$ using the Mann-Whitney test. **E.** The geometric mean of fluorescence (GMFI) of *ABCC4* expression in *ABCG2*_{null} (n=11) and control (n=11) RBCs was analyzed by flow cytometry using an anti-PEL. *** $P = 0.0007$ using the Mann-Whitney test.

Figure 1

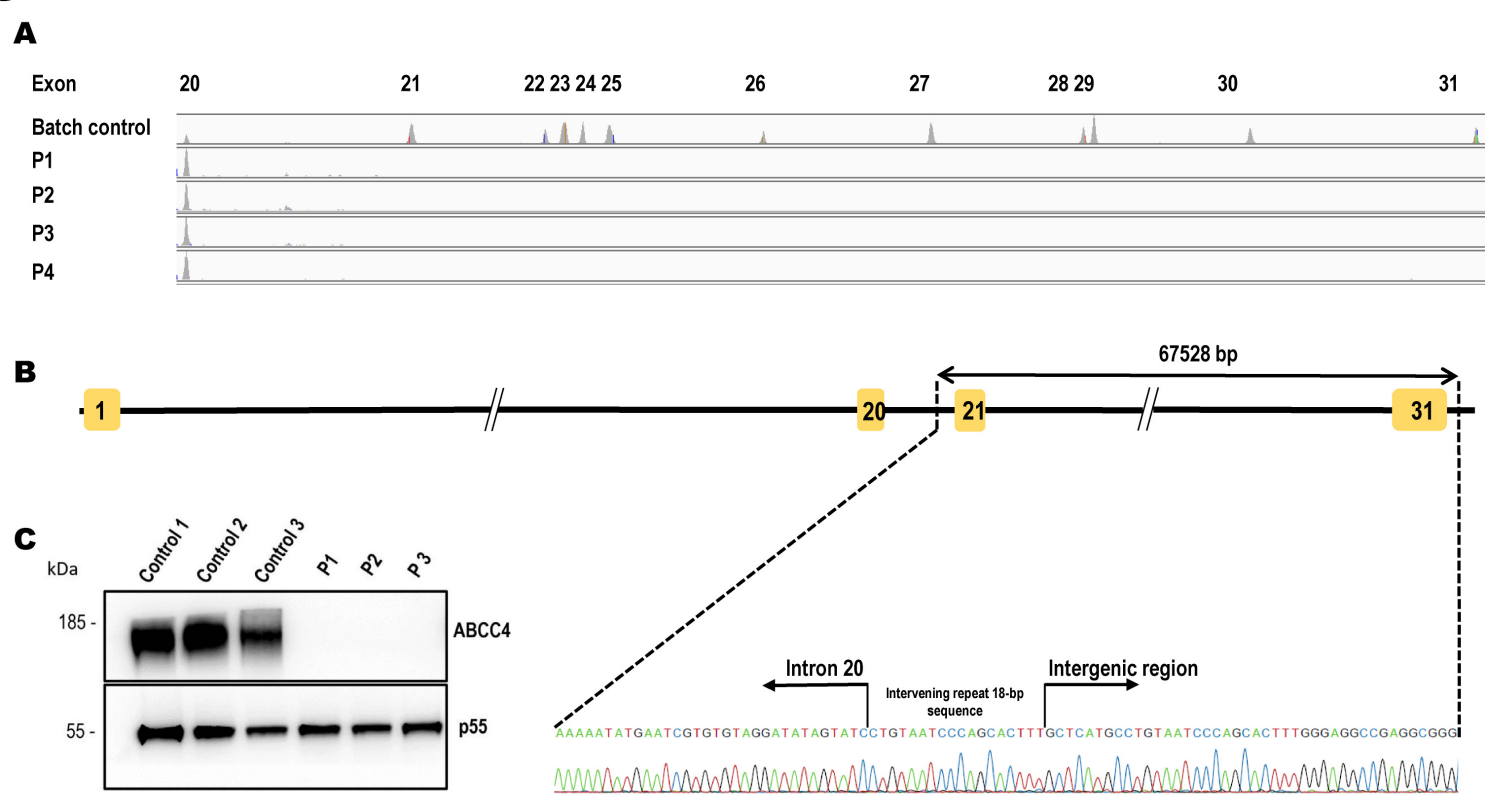


Figure 2

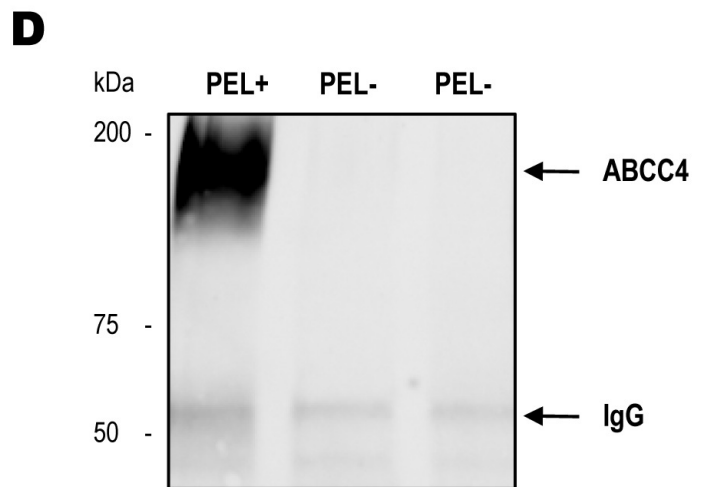
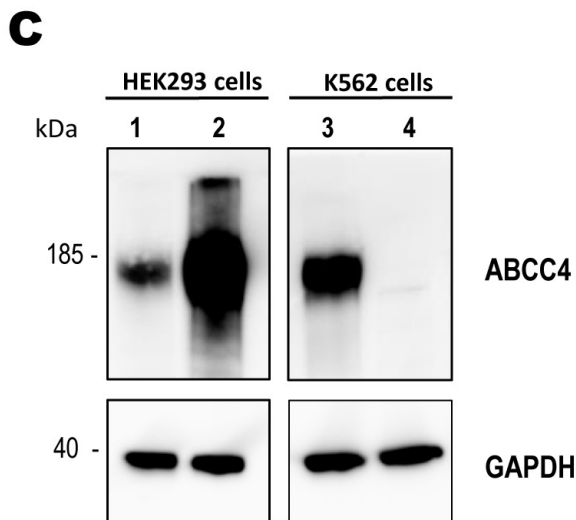
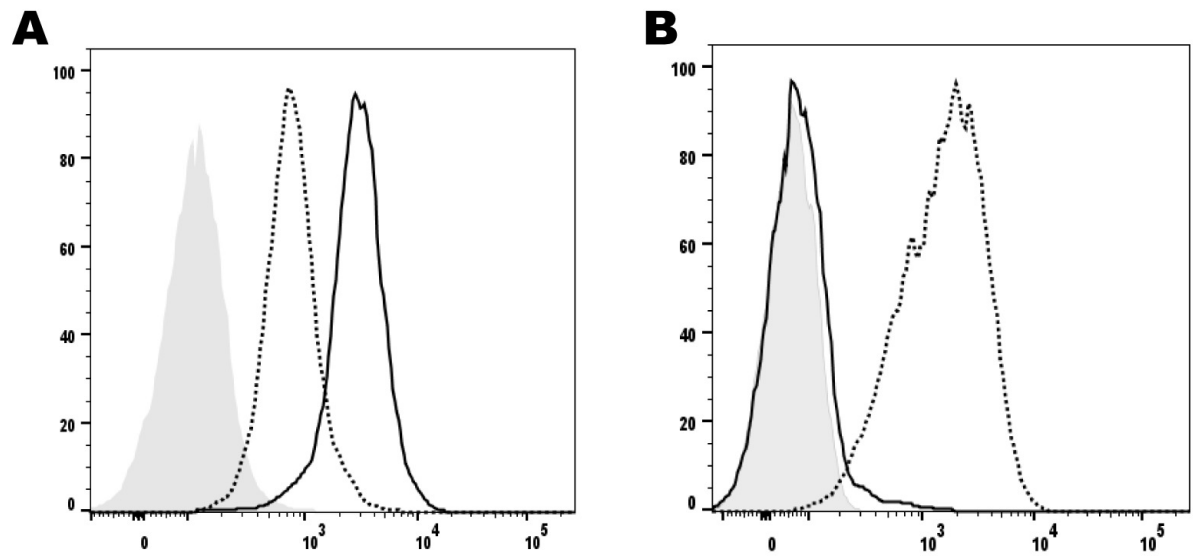
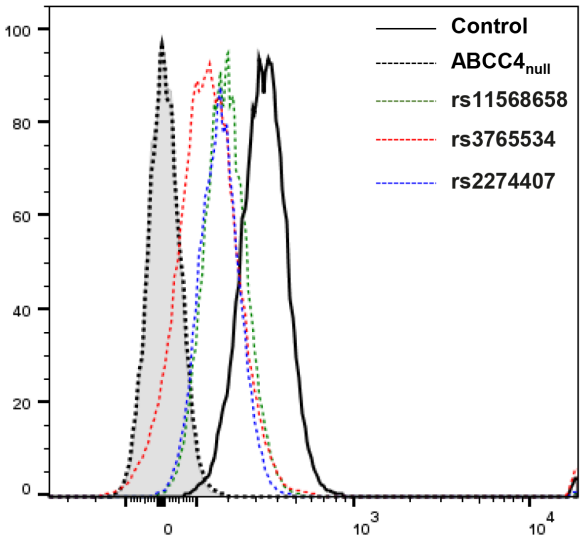


Figure 3

A



B

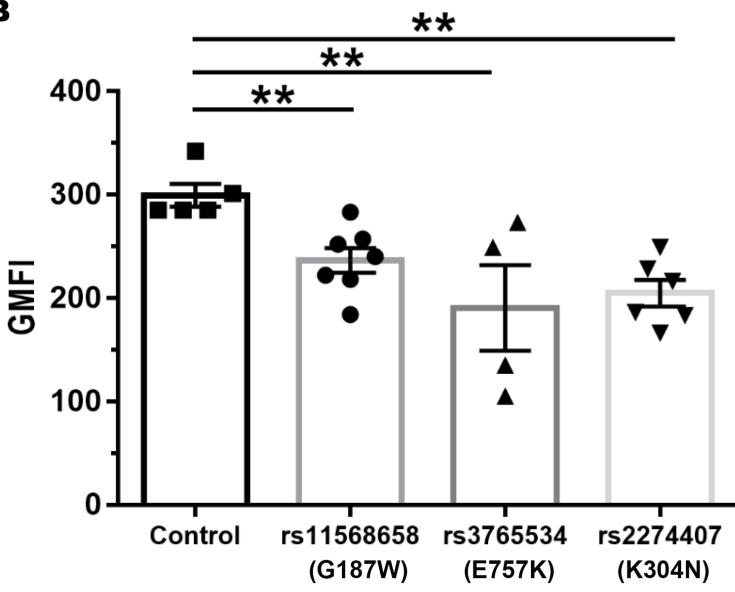


Figure 4

