Evidence That an Abnormality in the Glycoprotein Ib alpha Gene Is Not the Cause of Abnormal Platelet Function in a Family With Classic Bernard-Soulier Disease

By Clara N. Finch, Jonathan L. Miller, Vicki A. Lyle, and Robert I. Handin

The underlying molecular basis for Bernard-Soulier Disease (BSD) is currently unknown. Platelets from patients with this autosomal recessive bleeding disorder have multiple abnormalities, including a markedly reduced von Willebrand factor-dependent adhesiveness due to a deficiency of the platelet membrane glycoprotein (GP) Ib/IX complex. In the present studies, we have used an intragenic restriction fragment length polymorphism (RFLP) for Taq I in the GPlba gene to study linkage between this gene and the inheritance of BSD in a family with two affected siblings. Whereas the proband was heterozygous, showing both the 0.7 and 4.0 kb bands of this polymorphism (A/A), her affected brother was homozygous for the 0.7 kb band (A/A). Accordingly, these siblings did not inherit the same pair of GPlba alleles from their parents. Additionally, one child of the proband was A/A, while the second studied child was A/B, with neither showing any evidence of BSD. No construct of heterozygosity or homozygosity for GPlba alleles in this family is consistent with a model in which one or more defective GPlba alleles could produce BSD. RFLP analysis with BamHI or HindIII showed entirely normal patterns in the patients, indicating the absence of any gross deletion of the GPlba gene. GPlba mRNA from patient platelets was reverse transcribed and subsequently amplified by the polymerase chain reaction, demonstrating the presence of GPlba transcript. Furthermore, trace amounts of GPlb could be shown on the surface of patient platelets. Based on these results, a defect in the GPlba gene is unlikely to be the cause of BSD in this family.

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Table 1. Routine Hemostatic Studies

<table>
<thead>
<tr>
<th>Bleeding episodes</th>
<th>Tonsillectomy, menorrhagia, epistaxis, ear piercing</th>
<th>Severe epistaxis</th>
<th>NH</th>
<th>NH</th>
<th>NH</th>
<th>NH</th>
<th>NH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bleeding time (2-8 min)</td>
<td>19</td>
<td>12</td>
<td>6</td>
<td>2.5</td>
<td>5.5</td>
<td>—</td>
<td>5.5</td>
</tr>
<tr>
<td>Platelet count (150-400 k/μL)</td>
<td>26-51</td>
<td>38-91</td>
<td>248</td>
<td>235</td>
<td>353</td>
<td>258</td>
<td>256</td>
</tr>
<tr>
<td>Platelet volume (7.5-11.0 fl)</td>
<td>11.7</td>
<td>15.6</td>
<td>—</td>
<td>—</td>
<td>8.2</td>
<td>9.3</td>
<td>9.6</td>
</tr>
<tr>
<td>Platelet diameter (blood film)</td>
<td>Increased</td>
<td>Increased</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td>PRP platelet aggregation</td>
<td>Ristocetin (1.2 mg/L)</td>
<td>Decreased</td>
<td>Decreased</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td></td>
<td>Ristin + PNP</td>
<td>Decreased</td>
<td>Decreased</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>Asialo-vWF (10 μg/mL)</td>
<td>Decreased</td>
<td>Decreased</td>
<td>—</td>
<td>N</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td>Collagen</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>—</td>
<td>N</td>
</tr>
<tr>
<td>ADP (8 μmol/L)</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>—</td>
<td>N</td>
</tr>
<tr>
<td>Epinephrine (8 μmol/L)</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>—</td>
<td>N</td>
</tr>
</tbody>
</table>

Abbreviations: Rist, ristocetin; PNP, pooled normal plasma; Asialo-vWF, desialylated von Willebrand factor; NH, negative history; N, normal.

Fluorography. Densitometric analysis of bands was done using a Helena Laboratories (Beaumont, TX) gel scanner.

Southern blot analysis of genomic DNA. Human genomic DNA was isolated from white blood cells by modification of the method of Bell et al. From 20 mL of blood, 100 to 600 μg of DNA was obtained. Genomic DNA was digested with restriction endonucleases BamHI, HindIII, BglII, or TaqI (all from Boehringer Mannheim Biochemicals, Indianapolis, IN), the resulting DNA fragments were electrophoresed in a 0.8% agarose gel and transferred to a nylon membrane (Gene Screen Plus; NEN Research Products, Boston, MA), and the membrane was then hybridized at 42°C for 16 hours with GPβc DNA probe labeled with [32P]dCTP. The membrane was then taken through a series of washes (two washes at room temperature for 5 minutes each in 0.3 mol/L NaCl-0.03 mol/L sodium citrate; two washes at 65°C for 30 minutes each in 0.3 mol/L NaCl-0.03 mol/L sodium citrate-1% SDS; two washes at room temperature for 30 minutes each in 0.015 mol/L sodium chloride-0.0015 mol/L sodium citrate), as recommended by the manufacturer of the membrane (NEN Research Products). The membrane was then exposed to Kodak X-Omat AR X-ray film for 1 to 3 days at –70°C.

Analysis of platelet RNA. From ACD anticoagulated blood of patients or of normal volunteers, PRP was prepared by multiple centrifugations, as described above. After several washes with PBS containing 2 mmol/L EDTA, platelet suspensions (1 to 10 × 10⁷ platelets/mL) were centrifuged at room temperature for 10 minutes at 1,000 g. The resulting cell pellets were lysed by adding 3.6 mL of a solution containing 4 mol/L guanidinium isothiocyanate, 5 mmol/L sodium citrate (pH 7.0), 0.1 mol/L β-mercaptoethanol and 0.5% N-lauroylsarcosine (sarkosyl). RNA was isolated using a guanidium/cesium chloride gradient essentially as described by Maniatis et al. From 100 mL of patient blood or 50 mL of blood from normal controls, 10 to 14 μg of total RNA was obtained. To this RNA was added 1 unit of RQ1 RNase-free DNase (Promega Corp, Madison, WI) in a final volume of 20 μL. After incubation at 37°C for 15 minutes, phenol/chloroform/isooamyl alcohol extraction, followed by ethanol precipitation, was done for the recovery of RNA. For first-strand cDNA synthesis and subsequent amplification of the cDNA by the polymerase chain reaction (PCR), two DNA 17-mer primers were obtained from Genetic Designs, Inc (Houston, TX). J9 (5'-TTGCTGTCGGCTGGGCTAG-3'), included bases 737 to 753 of the cDNA sense strand sequence published by Lopez et al., and J10 (5'-GGCTGTCGAGAAGACGT-3') corresponded to the anti-sense strand from bases 1035 to 1051. First strand GPβc cDNA was synthesized by adding oligonucleotide primer J10 (50 pmol) to 1 μg of total platelet RNA and 500 U of Moloney murine leukemia virus (M-MLV) reverse transcription (BRL) in a final volume of 50 μL, essentially as described by Newman et al. After the addition of 100 pmol of primer J9 and 50 pmol more of primer J10, together with KCl and gelatin, the reaction mix (100 μL) was heated to 94°C for 2 minutes and cooled; amplification was then started by adding 5 U of Taq polymerase (Perkin-Elmer Cetus Corp, Norwalk, CT). Amplification was performed for 50 cycles using a programmable heating and cooling system (Microcycler; Eppendorf Corp, Fremont, CA) under the following conditions: denaturation of strands at 94°C for 1 minute, annealing at 58°C for 1 minute, extension at 72°C for 1.5 minutes, and a final extension step at 72°C for 5 minutes. After heating the reaction mixture to 94°C, the reaction was cooled to 58°C and the DNA samples were separated under denaturing conditions on a 8% polyacrylamide gel (5 mmol/L EDTA, 0.1% w/v sodium dodecyl sulfate (SDS), 0.5 mmol/L N-lauroylsarcosine (sarkosyl)). The gel was stained with ethidium bromide and photographed under UV light. The resulting gel picture was used for the quantitation of bands using a PhosphorImager system.
for 45 seconds, primer annealing at 49°C for 1 minute, and primer extension at 72°C for 3 minutes. No additional Taq polymerase was added to the reaction during the PCR cycles. After the PCR reaction, both intact PCR product and product digested for 4 hours at 37°C with Hae III restriction endonuclease were analyzed by agarose gel electrophoresis.

RESULTS

Routine hemostatic studies. Routine laboratory studies are shown in Table 1. Patient II-1 and patient II-4 presented with prolonged bleeding times, thrombocytopenia, and giant platelets on peripheral blood films. Platelet aggregation studies showed decreased responsiveness with ristocetin and with asialo-vWF, but normal responses to all other agents. Normal bleeding time, platelet count, platelet size, and platelet aggregation studies were obtained in all other family members available for study, including patient III-5, a newborn male child of patient II-1.

Glycoprotein analysis. Glycoprotein analysis was done using platelets from a normal control or from BSD patient II-4, with ³H-labeled platelet lysates electrophoresed nonreduced on SDS-PAGE. Labeled polypeptides were detected by fluorography. After a 5-day exposure, absence of GPIb was demonstrated in the patient as compared with the normal control (Fig 1A). After a 7-week exposure (Fig 1B), GPIb could be detected in the patient. While not well visualized in the figure, a trace amount of GPIX could also be seen in the 7-week exposure of the original autoradiograph. However, the 82 Kd band corresponding to GPV remained

Fig 2. Taq I RFLP analysis by Southern blotting of GPIbα genomic DNA. There is a constant 1.1 kb fragment in all lanes. Individuals are either homozygous for the 0.7 kb band (Type A/A, lanes B through E), homozygous for the 4 kb band (Type B/B, lane G), or heterozygous for this polymorphism (Type A/B, lanes A and F). Lanes: A through D, normal controls; E, classic BSD-affected male sibling (patient II-4); F, classic BSD-affected female sibling (patient II-1); G, normal control.
Absence of linkage between GPIbα Taq I polymorphism and inheritance of BSD. Patients with a history of thrombocytopenia and giant platelets are shown in hatched symbols; asymptomatic individuals, open symbols. Individuals homozygous for the presence of the polymorphic site are denoted as A/A; heterozygous individuals, A/B. Note that BSD patients II-1 and II-4 have different Taq I polymorphic patterns. Two children of patient II-1, patients III-1 and III-2, also show different Taq I polymorphic patterns, but neither has clinical or laboratory evidence of BSD.

Undetectable in the patient. Additionally, when 3H-labeled platelets from patient II-1 or II-4 were immunoprecipitated with the anti-GPIb MoAbs AP-1 or AS-7, bands comigrating with normal GPIb were seen by fluorography; however, by densitometry, the patient GPIb bands showed only 1% to 5% as much intensity as the normals.

Southern blot analysis. For study of the genomic structure of the GPIbα gene in the affected patients, DNA was isolated from leukocytes, digested with restriction endonucleases, and hybridized with 32P-labeled full-length GPIbα cDNA probes. Genomic DNA digested with restriction enzyme BamHI revealed a single 6.4 kb band both in normal controls and in the affected patients. When genomic DNA was digested with HindIII, a single 12.9 kb band was seen, both in patients and in normal controls. These findings suggested that there was no gross deletion of the GPIbα gene in the affected patients.

When genomic DNA was digested with Taq I, a constant 1.1 kb band was always seen in all persons studied. However, a Taq I polymorphism was also seen in the normal population, resulting in individuals homozygous for a 0.7 kb band, individuals heterozygous for both a 0.7 and a 4.0 kb band, and individuals homozygous for a 4.0 kb band (Fig 2). Double digestion of genomic DNA with Bgl II and Taq I, followed by probing with labeled cDNA fragments representing only the 3’ end or the 5’ end of the cDNA confirmed localization of the Taq I polymorphic site approximately 75 bp downstream from the 3’ end (bp 2420) of the published cDNA sequence. The presence of the polymorphic site resulted in the 0.7 kb band (designated Allele A), shown schematically in Fig 3. Lack of the polymorphic site resulted in the 4.0 kb band (designated Allele B).

Study of the Taq polymorphism in this family indicated non-linkage with the GPIbα gene. The affected brother, patient II-4 (Fig 2, lane E), was homozygous for the 0.7 kb band (A/A), while his affected sister, patient II-1 (lane F), was heterozygous, showing both the 0.7 and the 4.0 kb bands (A/B). Thus, the brother and sister, both of whom have autosomal recessive BSD, did not inherit the same pair of alleles for GPIbα from their parents (Fig 4). Furthermore, DNA analysis of two of the children of patient II-1 revealed...
that one (patient III-2) was homozygous for the 0.7 kb band (A/A), while the other (patient III-2) was heterozygous for the polymorphic site (A/B), but neither had any clinical or laboratory evidence of BSD.

**Platelet RNA studies.** To establish whether specific mRNA coding for GPIbα was indeed present in the thrombocytopenic BSD patients, and to facilitate its analysis, the PCR technique was used to amplify the GPIbα RNA sequence. RNA samples were treated with RNase-free DNase to remove any possible contaminating genomic DNA. Two oligonucleotide primers, J9 and J10, were used to sequence. RNA samples were treated with RNase-free DNase to remove any possible contaminating genomic DNA. A 314 bp fragment (from bases 737 to 1051) of the RNA coding sequence for GPIbα was reverse transcribed and subsequently amplified, both for patient II-4 and for a normal control (Fig 5). For further confirmation that the 314 bp cDNA PCR product was an amplified copy of the corresponding region in the platelet GPIbα mRNA, the amplified DNA was digested with restriction endonuclease HaeIII. After ethidium bromide staining, the predicted major band corresponding to a 230 bp DNA restriction fragment was shown in both the patient and the normal control (Fig 5). Accordingly, these studies provide evidence at the RNA level for the expression of GPIbα in the platelets of these patients with BSD.

**DISCUSSION**

Using DNA and RNA analysis, we have studied possible abnormalities of the GPIbα gene in a family with BSD. Based upon clinical and laboratory evidence, this BSD family demonstrates a classic autosomal recessive pattern of inheritance, with the implication that a pair of defective alleles is needed in order to express disease. DNA analysis after digestion with BamHI or HindIII showed no rearrangements or deletions of the GPIbα gene in these BSD patients. Using restriction fragment length polymorphism (RFLP) analysis, we were able to show that these patients have different Taq I polymorphic patterns, indicating that they each inherited a different pair of GPIbα alleles from their parents. Patient II-4, who is homozygous (A/A), has BSD; patient II-1, who is heterozygous (A/B), is also affected. Furthermore, DNA analysis of two of the children of patient II-1 revealed that one (III-1) is homozygous (A/A), while the other (III-2) is heterozygous (A/B), and neither has evidence of BSD. No construct of heterozygosity or homozygosity for GPIbα alleles in this family is consistent with a model in which one or more defective GPIbα alleles could produce BSD. Thus, the BSD phenotype in this family is not linked to the RFLP that marks the GPIbα gene.

We have also shown the presence of mRNA encoding for GPIbα in the platelets of the BSD patients. This finding is not unexpected, since by the use of sensitive detection procedures, we have also been able to demonstrate GPIbα on the surface of their platelets. Detection of small amounts of platelet GPIbα in other patients with BSD has also been demonstrated recently.31

This report documents the usefulness of RFLP linkage analysis to identify which of several potential genes might be abnormal in a disorder characterized by the absence of a multisubunit membrane complex. Recent studies of other membrane complexes, such as platelet GPIb-IIIa33 and the T-cell receptor/CD3 complex,34 show that normal receptor assembly may require coordinate expression of multiple subunits. Thus, in BSD a defect in the separate genes encoding any one of several membrane glycoproteins, including GPIbα, GPIbβ, GPIX, and, possibly, GPV, could prevent the assembly and cell surface expression of the von Willebrand factor receptor complex.

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Evidence that an abnormality in the glycoprotein Ib alpha gene is not the cause of abnormal platelet function in a family with classic Bernard-Soulier disease

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