Characterization of Leu777Pro and Ile865Thr Type IIA von Willebrand Disease Mutations

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Type IIA von Willebrand disease (vWD) is an autosomal dominant bleeding disorder characterized by a qualitative defect in von Willebrand factor (vWF). A number of missense mutations responsible for type IIA vWD have recently been identified. This report examines the type IIA vWD mutations Leu777→Pro and Ile865→Thr by expression of recombinant vWF containing mutant and wild-type (WT) sequences. Recombinant vWF containing the L777P mutation (vWF(L777P)) showed markedly impaired secretion compared with that for wild-type vWF (vWF WT) after DNA transfection into mammalian cells. Multimer analysis of secreted vWF(L777P) showed predominantly low molecular weight forms. In contrast, recombinant vWF containing the I865T mutation (vWF(I865T)) was processed in a pattern similar to vWF WT, with secretion of the full spectrum of vWF multimers. Thus, L777P and I865T are subclassified as type IIA group I and group II mutations, respectively. Analysis of platelet vWF from a patient heterozygous for the L777P mutation shows reduced large vWF multimers in a pattern similar to plasma, consistent with the intracellular transport defect predicted for a group I mutation. An increase in the proportion of high molecular weight multimers observed in type IIA vWD patient plasma, after renal transplantation from a normal donor, suggests that the kidney endothelium may be a major source of plasma vWF.

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degradation to lower molecular weight vWF forms in plasma (group II mutations). In this report, we characterize the biosynthesis of vWF containing each of 2 previously reported type IIA vWD mutations, Leu777 → Pro (L777P) and Ile865 → Thr (I865T), leading to their subclassification as group I and group II, respectively. In addition, analysis of plasma vWF from a Type IIA vWD patient with the L777P mutation after kidney transplantation suggests that renal endothelial cells are a major site of plasma vWF synthesis.

MATERIALS AND METHODS

Patient material. Patients A7 and A12 were diagnosed with type IIA vWD based on decreased plasma vWF antigen, decreased ristocetin cofactor activity (disproportionately decreased compared with vWF antigen level), and an abnormal vWF multimer pattern. Patient A7 was originally reported as part of a large pedigree with "variant von Willebrand disease" by Green and Philip (corresponding to individual IV-46 in the original pedigree). Later, clinical analysis of plasma vWF multimers from patient A7 (Blood Center of Southeastern Wisconsin, Milwaukee, WI) showed loss of HMW but not of intermediate-sized vWF multimers (see Fig 4A). This pattern was interpreted as consistent with type IIB or an acquired form of vWD. However, the clinical phenotype of this patient and the autosomal dominant inheritance pattern in this family is most consistent with type IIA vWD. None of the family members showed thrombocytopenia or other characteristics of type IIB vWD. Patient A7 also has type I diabetes mellitus and, as a result, developed end-stage renal disease. In July 1991, the patient received a kidney transplant from one of her sisters previously determined not to have type IIA vWD based on normal vWF antigen and ristocetin cofactor activity (corresponding to patient IV-48 in the original pedigree). Since transplantation, the patient has been maintained on immunosuppressive therapy consisting of steroids, azathioprine, and mycophenolate mofetil. After 1 year after transplant are shown in Table 1.

Patient A12 has also been previously reported as a member of a large pedigree with hereditary hemorrhagic telangectasia and type IIA vWD. This patient corresponds to individual II-6 from family A in the original report.

DNA analysis. Patient A7 was previously reported to be heterozygous for a T → C mutation at nucleotide (nt) 4619\(^{17}\) (based on the numbering of Bonthron et al,\(^{26}\) where the A of the initiator ATG codon is designated +1), resulting in the substitution of proline for leucine at amino acid 777 of the mature vWF subunit. This mutation results in loss of a Pst I site. Genomic DNA from patient A7 and her mother was prepared from peripheral blood (PB) lymphocytes, as previously described. DNA was amplified using the polymerase chain reaction (PCR; primers A and C\(^{17}\)). The PCR product was digested with Pst I and electrophoresed on a 2% agarose gel. Patient A12 was previously shown to have a T → C transition at nt 4883, resulting in a substitution of threonine for isoleucine at amino acid 865 (I865T).\(^{19}\)

Expression vector construction. The type IIA vWD mutations identified in patients A7 (L777P) and A12 (I865T) were inserted into full-length vWF cDNA in the expression vector pMT2, under the control of the adenovirus major late promoter. Briefly, genomic DNA from patient A7 was amplified by PCR as previously described.\(^{17}\) An Nco I-Kpn I fragment (nts 4482-4752) containing the mutation was inserted into full-length vWF cDNA in pMT2 using standard methods.\(^{13,25}\) The mutation identified in patient A12 (I865T) was prepared by site-directed mutagenesis of a vWF Sac I fragment (+13086-+16676) subcloned into the phagemid pSE-Lect using a commercial kit (Promega Corp, Madison, WI). The 19-bp mutagenesis oligonucleotide, TGGTGGCCACTGAGTGGG (mutation is underlined), corresponds to the vWF cDNA sense strand beginning at nt 4878. A Kpn I-Kpn I fragment (nts 4752-5134) containing the mutation was subcloned into full-length vWF cDNA as above. In both constructions, all segments derived by PCR or mutagenesis were sequenced to verify the presence of the corresponding type IIA mutations and to exclude polymerase errors. pMT2-derived plasmids containing the full-length vWF cDNA with wild-type sequence, L777P, or I865T mutations are designated pWT-vWF, pL777P, and pI865T, respectively. The β-galactosidase (β-gal)–expression plasmid (p3β-Gal), which contains the SV40 origin and LacZ cDNA under the direction of an SV40 enhancer/promoter, was kindly provided by L. Spain (Whitehead Institute, Cambridge, MA).

Cell culture and transfection. COS-7 cells were maintained in Dulbecco’s modified Eagle’s medium (JRH Biosciences, Lenexa, KS) supplemented with 7.5% fetal bovine serum (GIBCO-BRL Life Technologies, Inc. Gaithersburg, MD). On the day of transfection, cells were split 1:7 from a near confluent plate and transfected within 1 to 4 hours by a modified standard calcium phosphate-mediated transfection method. For each transfection, 10 µg of vWF and 2 µg of β-gal expression plasmid were used. Approximately 36 hours after transfection, cells were rinsed twice with phosphate-buffered saline and transferred into 3-ml serum-free AIM-V medium (GIBCO-BRL). After 24 hours in serum-free medium, cell lysates and cell medium were harvested from transfections, essentially as previously described. A mixture of protease inhibitors was added to final concentrations of 0.5 mg/mL leupeptin, 0.2 mg/mL aprotinin, 10 mg/mL bovine trypsin inhibitor, 0.7 mg/mL peptatin, and 5 mmol/L iodoacetic acid (all purchased from Sigma Chemical Co, St Louis, MO) for both lysates and medium. Phenylmethylsulfonyl fluoride and EDTA were also added to final concentrations of 2 mmol/L and 5 mmol/L, respectively. vWF in cell lysates and cell medium was quantitated by enzyme-linked immunosorbent assay (ELISA), as previously described.\(^{27}\) using a commercial reference plasma (Bio/Data Corp, Horsham, PA) as a standard (assuming 10 µg/ml vWF concentration in normal plasma). β-gal ELISA was also performed as described\(^{28}\) using a commercial β-gal standard (Sigma). Wild-type vWF and vWF containing the mutations L777P or I865T will be referred to as vWFWT, vWFL777P, and vWF1865T, respectively.

Agarose gel electrophoresis. Preparation of samples from transfections and electrophoresis in vertical 1.5% sodium dodecyl sulfate (SDS)–agarose multimer gels were performed, as previously described,\(^{24}\) using chemiluminescence (Amersham Corp, Arlington Heights, IL) for detection of vWF multimers. After obtaining informed consent, PB was collected from patients into EDTA. For plasma and platelet lysates, PB was centrifuged at 100g for 10 minutes to obtain platelet-rich plasma, followed by centrifugation at

| Table 1. Clinical Evaluation of Patient A7 Before and After Renal Transplantation |
|-------------------------------------|-------------------------------------|
|                                      | Before Transplant | After Transplant |
| Factor VIII:C (normal, 50% to 150%) | 129               | 178              |
| vWF antigen (normal, 50% to 150%)   | 47                | 60               |
| Ristocetin cofactor activity (normal, 50% to 150%) | 28                | 41               |
| Serum creatinine (mg/dL)            | 2.2               | 1.4              |

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250μl to form a platelet pellet and platelet-poor plasma. Platelet-poor plasma was stored at −80°C. Platelet lysates were prepared as described. Washed platelet pellets derived from 1 mL of whole blood were resuspended in 15 μL of Tris-buffered saline (10 mmol/L Tris-HCl, pH 7.5, and 140 mmol/L NaCl) with 3% bovine serum albumin. Platelets were lysed at 37°C with 1/40 volume of 20% Triton X-100. The clinical multimer analysis of patient A7, shown in Fig 4A, was performed in the clinical reference laboratory at the Blood Center of Southeastern Wisconsin.

RESULTS

Steady-state analysis of recombinant vWF containing type IIA vWD mutations L777P or I865T. The previously identified type IIA vWD mutations, T4619 → C (L777P) and T4883 → C (I865T), were inserted into full-length vWF cDNA in the expression vector pMT2. To examine the synthesis of vWF containing these mutations, COS-7 cells were transfected with the vWF expression constructs pWTvWF, pL777P, or pI865T, and vWF in cell media and in cell lysates from transfected cells was quantitated by ELISA. Cells were cotransfected with a β-gal expression vector (pβ3Gal) as an internal control for transfection efficiency. vWF-ELISA values in lysates and media were normalized for transfection efficiency using intracellular β-gal levels from each transfection. Comparisons of the vWF level in conditioned media between WT and each mutant showed that vWF secretion was similar to vWFWT, whereas the level of vWF was markedly reduced (Fig 1). Intracellular levels of each mutant were greater than that of vWFWT.

The defective secretion of vWF is similar to that previously observed with the group I IIA mutations V844D, S743L, and G742R. Intracellular L777P was entirely sensitive to digestion with endoglycosidase H (data not shown), indicating that mutant vWF was retained in the ER, which is similar to results with the other group I IIA mutations. In contrast, the relative quantity of extracellular vWF secretion in steady-state analysis is indistinguishable from that of vWFWT, which is consistent with classification of this mutation as a group II defect. However, the apparent intracellular accumulation of vWF when compared with normal control. The T4619C mutation reported in this family results in a loss of the level of the extracellular vWF when compared with that of vWFWT.

Multimer analysis of secreted recombinant vWF. Recombinant vWF secreted from cells transfected with pWTvWF, pL777P, and pI865T was analyzed by SDS-agarose gel electrophoresis to assess the effect of these mutations on multimer structure. The multimer pattern of extracellular vWF was indistinguishable from that of WT (Fig 2). However, only trace amounts of vWF were seen in the conditioned medium (Fig 2B), and these were predominantly low molecular weight multimer species. When equal amounts (as quantitated by ELISA) of vWF were analyzed, larger multimers were observed, although reduced in quantity (Fig 2A).

Multimer analysis of plasma vWF from a type IIA vWD patient after renal transplantation. To evaluate the potential contribution of endothelial cells in the renal vasculature to circulating vWF, we analyzed plasma from patient A7 after kidney transplant. Because pretransplant plasma was unavailable for direct comparison in our laboratory, blood was obtained from patient A7's mother (corresponding to individual III-25 in the original pedigree) who is also affected with a moderately severe bleeding diathesis. The T4619C mutation reported in this family results in a loss of the T4619C restriction site. DNA restriction analysis with T4619C is shown in Fig 3. DNA restriction analysis with T4619C is shown in Fig 3. shows that both patient A7 and her mother are heterozygous for the T4619C mutation. Clinical analysis (Blood Center of Southeastern Wisconsin) of plasma vWF from patient A7 before renal transplant is shown in Fig 4A.

Fig 1. Steady-state analysis of recombinant vWF containing type IIA vWD mutations L777P or I865T. The previously identified type IIA vWD mutations, T4619 → C (L777P) and T4883 → C (I865T), were inserted into full-length vWF cDNA in the expression vector pMT2. To examine the synthesis of vWF containing these mutations, COS-7 cells were transfected with the vWF expression constructs pWTvWF, pL777P, and pI865T, and vWF in cell media and in cell lysates from transfected cells was quantitated by ELISA. Cells were cotransfected with a β-gal expression vector (pβ3Gal) as an internal control for transfection efficiency. vWF-ELISA values in lysates and media were normalized for transfection efficiency using intracellular β-gal levels from each transfection. Comparisons of the vWF level in conditioned media between WT and each mutant showed that vWF secretion was similar to vWFWT, whereas the level of vWF was markedly reduced (Fig 1). Intracellular levels of each mutant were greater than that of vWFWT.

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Multimer analysis of plasma vWF from a type IIA vWD patient after renal transplantation. To evaluate the potential contribution of endothelial cells in the renal vasculature to circulating vWF, we analyzed plasma from patient A7 after kidney transplant. Because pretransplant plasma was unavailable for direct comparison in our laboratory, blood was obtained from patient A7's mother (corresponding to individual III-25 in the original pedigree) who is also affected with a moderately severe bleeding diathesis. The T4619C mutation reported in this family results in a loss of the T4619C restriction site. DNA restriction analysis with T4619C is shown in Fig 3. shows that both patient A7 and her mother are heterozygous for the T4619C (L777P) mutation. Clinical analysis (Blood Center of Southeastern Wisconsin) of plasma vWF from patient A7 before renal transplant is shown in Fig 4A. Although analyzed in different gel systems, plasma from the mother of patient A7 shows a type II vWD multimer pattern similar to that of patient A7 before renal transplant, with decreased intermediate and HMW multimers when compared with that for normal controls (Figs 4B and C). Even on long exposure of the lane containing the mother's plasma, intermediate molecular weight multimers are greatly decreased, and HMW multimers are absent (Fig 4C). By comparison, the vWF multimer pattern seen in patient A7 plasma after renal transplantation has a greater relative proportion of intermediate and HMW multimers (Figs 4B and C) compared with
that for the patient's mother. Comparison of patient A7's plasma multimer pattern with that of a normal control shows HMW multimeric species, similar to that of normal controls; however, it is present in relatively reduced quantity. Examination of platelet vWF from patient A7 (Fig 4D) shows a relative decrease in the large and intermediate-sized multimers compared with a normal platelet control, closely resembling the pattern observed in the plasma of patient A7's mother and in patient A7's plasma before transplant. We hypothesize that the increased HMW and intermediate vWF multimers seen in patient A7's plasma but not in her platelets result from the contribution of the normal transplanted kidney to circulating vWF. Comparison of patient A7's vWF multimer pattern before and after renal transplantation shows an increase in circulating HMW vWF multimers in the presence of the normal renal allograft.

DISCUSSION

In this report, two type IIA vWD mutations, L777P and I865T, are subclassified into groups I and II, respectively, based on steady-state analysis of recombinant mutant vWF expressed in heterologous cells. The group I type IIA mutations cause selective retention of HMW vWF in the ER. Expression of vWF-L777P in COS-7 cells showed impaired transport/secretion, with more pronounced effects on the HMW vWF forms, which is consistent with the group I classification. This is similar to our previous observations for the mutations V844D, S743L, and G742R.17 The decrease in large vWF multimers observed in patient A7's platelet lysate is consistent with a transport defect in vivo that also affects the storage of HMW vWF multimers in the a-granule.

In contrast, I865T can be categorized as a group II mutation, similar to R834W and G742E,17 based on its normal synthesis and secretion in COS-7 cells. The location of the I865T mutation within the region of clustered type IIA mutations, the coinheritance with type IIA vWD in a large pedigree, and its absence from a panel of 134 normal alleles19 all support the characterization of this amino acid substitution as an authentic type IIA vWD mutation. However, the occurrence of a rare, private DNA sequence polymorphism cannot be completely excluded. To date, a total of 15 type

Fig 2. Multimer analysis of recombinant vWF containing L777P or I865T is shown. vWF secreted from COS-7 cells transfected with pL777P, pI865T, or pWT-vWF was analyzed on a 1.5% nonreducing SDS-agarose gel. Conditioned media, adjusted so that each lane contains 1.5 ng of vWF-L777P (100 µL), vWF-I865T (4 µL), and vWF-WT (4 µL), are shown in (A). Similar analysis of equal volumes of conditioned media (4 µL) from vWF-L777P, vWF-I865T, and vWF-WT is shown in (B).

Fig 3. DNA analysis of patient A7 and her mother is shown. Genomic DNA was amplified by PCR, digested with Pst I, and electrophoresed on a 2% agarose gel. The T → C mutation reported in this family results in a loss of a Pst I restriction site (see Materials and Methods). This is depicted schematically in the lower portion of the figure, where loss of the restriction site (indicated by the asterisk) results in the creation of a novel 871-bp fragment. DNA restriction analysis from patient A7 (PT A7), her mother, a normal control (NI), and a type IIB patient (Arg545Cys) (IIB) are shown.
IIA vWD mutations have been reported. Of these mutations, 9 (including those in the current report) have been characterized by transfection analysis, with 5 mutations resulting in a normal group I pattern of secretion.

Several lines of evidence suggest that extracellular proteolysis of vWF multimers may result in the type IIA vWD phenotype in group I patients. The groups I and II mutations are clustered near the proteolytic cleavage site between Tyr842 and Met843. Cleavage at this site generates a 176-carboxyl-terminal fragment that is markedly increased in type IIA vWD plasma compared with that in normal plasma. In addition, the full spectrum of vWF multimers has been observed in platelet lysates from two individuals with group II mutations, supporting the hypothesis that a postsecretory defect accounts for the absence of plasma HMW multimeric species in these patients. Two additional type IIA vWD mutations (E875K and S850P), characterized via analysis of recombinant vWF, can also be classified as group II mutations. However, correlation with platelet vWF multimers from patients with these mutations is not available.

Group I or group II type IIA vWD mutations cannot be distinguished on the basis of the location or type of amino acid substitution. Both severe group I mutations, L777P and V844D, result from nonconservative amino acid substitutions. Other group I and II mutations include both nonconservative substitutions, such as G742E (group II) and G742R (group I), and conservative ones, such as I865T (group II) and S743L (group I). We hypothesize that all of these mutations perturb the same sensitive structure exposed on the surface of the vWF molecule. The altered structure that results from group I mutations interferes with intracellular transport, possibly through increased affinity for a resident ER protein(s). In contrast, the altered conformation produced by group II mutations escapes recognition by the ER machinery but results in increased susceptibility of vWF to a plasma protease(s) after secretion into plasma.

Most subtypes of type I vWD are currently classified based on differences in plasma vWF multimer patterns. The large number of multimer variants observed with both low- and high-resolution gel analysis and the occurrence of inconsistencies between clinical laboratory assays and multimer analyses have made subtype assignment difficult.

Patient A7 shows the potential problem of vWD classification based largely on use of vWF multimer pattern. Although the multimers were initially interpreted as most consistent with type IIB or acquired vWD, the other clinical features, the location of the identified mutation (L777P) and the results of transfection analysis, taken together, are most consistent with the diagnosis of group I type IIA vWD.

The distinction between group I and group II may have important implications for the treatment of type IIA vWD. Type IIA vWD patients have a variable response to 1-deamino 8-D-arginine vasopressin (DDAVP), an analogue of...
vasopressin used to treat various forms of vWD, via release of stored vWF. Some investigators have reported little effect of this drug in type IIA vWD patients, whereas others document good clinical responses. Intracellular storage pools in group I patients would not be predicted to contain HMW vWF multimers, and, thus, DDAVP would not be expected to increase the amount of circulating HMW vWF multimers. However, because storage granules from group II patients should contain the full range of vWF multimers, DDAVP would be expected to result in a transient increase in plasma HMW vWF multimers and improved hemostasis. Thus, the division of type IIA vWD into group I and group II may have significant implications for therapy; however, this hypothesis remains to be tested.

Of note, patient A7 had an improvement in her vWF antigen level and bleeding symptoms (menorrhagia and bruising) after transplantation of a normal kidney from her unaffected sister. In patients without vWD, previous investigators have reported that vWF antigen levels increase after placement of a renal allograft, but levels appear to return to baseline approximately 4 to 6 months after transplant. Others report that this increase in vWF may be partially caused by cyclosporine nephrotoxicity, although this is controversial. In addition to an increase in vWF antigen (persisting for >16 months after transplant), patient A7 also appears to have a greater percentage of circulating HMW vWF multimers (Fig 4). We hypothesize that the quantitative and qualitative changes in plasma vWF observed in this patient may be caused by the contribution of the transplanted kidney to circulating vWF. Webster et al previously reported no improvement in factor VIII levels or bleeding times in two pigs with severe vWD, who received normal porcine kidney allografts; however, these two animals lived for 6 and 7 days. During this time, the animals apparently suffered from continual hemorrhage that eventually led to their deaths. Similarly, Mannucci et al described a type III vWD patient who underwent a liver transplant for management of chronic hepatitis and hepatocellular carcinoma. Three months after transplantation, the patient’s vWF antigen was approximately twenty times higher than before transplantation, although still remarkably low (1.02%; with normal range, 50% to 150%). However, no clinical information was provided to document the status of the transplanted organ or the drug regimen used for immunosuppression. It has been previously shown that endothelial cells remain of donor origin in transplanted organs, except in the setting of organ rejection and cyclosporine toxicity. In patient A7, we have documented both a quantitative as well as a qualitative improvement in circulating vWF after successful placement of a normal renal allograft, which was also associated with a subjective improvement in bleeding symptomatology. These observations suggest that, with continued improvement in organ transplantation and endothelial cell graft procedures, such approaches may eventually have a role in the management of severe forms of vWD.

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