Two TaqI polymorphisms in the 5' region of the von Willebrand factor (vWF) gene

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SOURCE AND DESCRIPTION OF CLONE: The 368 bp Bam HI/Sac I fragment of pvWH22 was used as a probe. pvWH22 is a 4 kb partial cDNA clone for human vWF inserted into pUC 13 (Ginsburg et al, 1985).

POLYMORPHISMS: Two. Digestion with Taq I (TCGA) (New England Biolabs) identified several invariant bands and two variant bands with alleles at 2.2 (A1) and 1.3 (A2) and 1.75 kb (B1) and 0.75 kb (B2) (see Figure 1).

FREQUENCY: 60 unrelated individuals

2.2 kb (A1) - 0.25	1.3 kb (A2) - 0.75
1.75 kb (B1) - 0.06	0.75 kb (B2) - 0.94

NOT POLYMORPHIC FOR: Eco RI, Bam HI, Sac I, in a panel of 10 unrelated individuals.

CHROMOSOMAL LOCALIZATION: 12p12-12pter (Ginsburg et al, 1985). The region of vWF cDNA contained in the Bam HI/Sac I fragment corresponds exclusively to sequences on chromosome 12 (Ginsburg et al, 1985 ; Sadler et al, 1987). We constructed a partial genomic library and cloned, mapped, and sequenced a 4.5 kb fragment of genomic DNA that was covered by the Bam HI/Sac I probe and spanned the Taq I site. The Taq I site yielding the B1/B2 RFLP was mapped to an intron 50 bp upstream from an intron/exon boundary.

MENDELIAN INHERITANCE: Co-dominant segregation was demonstrated for each of the RFLPs in four families with 11 individuals.

PROBE AVAILABILITY: Available from Robert I. Handin.

OTHER COMMENTS: There was no problem with RFLP analysis under normally stringent conditions.

REFERENCES: Ginsburg et al (1985) Science 228:1405.
Sadler et al (1987) J Clin Invest 79:1459.

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Figure 1: Southern blot of human genomic DNA digested with Taq I and hybridized with a 368 bp Bam HI/Sac I fragment of vWF cDNA. The size of the variant fragments is shown on the right and the four different alleles are depicted in lanes 1-4. The 2.2 kb fragment is A1, 1.3 kb fragment A2, 1.75 kb fragment B1, 0.75 kb fragment B2. Lane 1-A2/A2, B1/B1; Lane 2-A1/A1, B2/B2; Lane 3-A2/A2, B2/B2; Lane 4-A1/A2, B1/B2.