Identification and Characterization of a Phospholipid-binding Site of Bovine Factor Va*

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Coagulation factor Va is a cofactor which combines with the serine protease factor Xa on a phospholipid surface to form the prothrombinase complex. The phospholipid-binding domain of bovine factor Va has been reported to be located on the light chain of the molecule and more precisely on a fragment of \( M_r = 30,000 \) which is obtained after digestion of factor Va light chain by factor Xa. This proteolytic fragment is located in the NH\(_2\)-terminal part of factor Va light chain (residues 1664–1765). In order to further characterize the lipid-binding domain of bovine factor Va, isolated bovine light chain was preincubated with synthetic phospholipid vesicles (75% phosphatidylcholine, 25% phosphatidylserine) and digested with trypsin, chymotrypsin, and elastase. Two peptide regions protected from proteolytic cleavage were identified and characterized from each proteolytic digestion. A comparison of the NH\(_2\)-terminal sequence and amino acid composition of the two tryptic peptides with the deduced sequence of the bovine factor Va light chain this lipid-binding region of the bovine factor Va is further localized to amino acid residues 1667–1765.

The presence of calcium ions. This enzyme complex catalyzes the activation of prothrombin to thrombin at a rate >300,000-fold greater than that of factor Xa alone (3–6). The procofactor, factor V, circulates in plasma as a large monomeric protein with a molecular weight of 330,000 (7, 8). The cDNA sequence for human factor V includes a 6672-base pair coding region and the deduced amino acid sequence consists of 2224 amino acids inclusive of a 28-amino acid leader peptide (9).

Proteolytic cleavage of factor V by thrombin produces factor Va which is the active cofactor of the prothrombinase complex (7, 8, 10). The activation of factor V to factor Va by thrombin involves three enzymatic cleavages and gives rise to two heavily glycosylated activation peptides (\( M_r = 71,000 \) and 120,000) and the active cofactor (\( M_r = 168,000 \)). Factor Va is a heterodimer composed of a heavy chain derived from the NH\(_2\)-terminal part of factor V (\( M_r = 94,000 \)) and a light chain (\( M_r = 74,000 \)) derived from the COOH-terminal end of the factor V molecule. The two chains are non-covalently associated in the presence of divalent ions (8, 11–13). Although thrombin is the principal activator of factor V, factor Xa likely serves as the initial activator of factor V during early stages of coagulation when little or no thrombin is present. This activation catalyzed by factor Xa requires significantly higher enzyme to substrate ratios than that required for the thrombin-catalyzed reaction (14). Recent data have shown that factor Xa activates human factor V in a time-, phospholipid-, and calcium ion-dependent manner (15). Furthermore, the factor Xa cleavage pattern differed markedly from the one obtained in the bovine system whereas the activation profile obtained using thrombin instead of factor Xa for the activation was slightly different. Moreover, these data indicated that activation by factor Xa gives rise to a cofactor which is as active as the thrombin–activated factor V (15). Once formed factor Va may be inactivated by plasmin or activated protein C (APC)1 (16, 17). The specific peptide bonds within bovine factor Va which are hydrolyzed by factor Xa and APC have been previously reported, and the derived fragment have been isolated and characterized (18).

A complete understanding of the assembly of the prothrombinase complex and the expression of its activity requires the exact definition of the parameters of the interactions within the complex. A great deal of information now available concerning the factor V/Va membrane interaction has indicated that the factor V- or the factor Va-phospholipid interaction

1 The abbreviations used are: APC, activated protein C; PCPS, phospholipid vesicles; Pyr-Va, factor Va modified with pyrene mal- emide; PS, phosphatidylserine; PC, phosphatidylcholine; SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis; HPLC, high performance liquid chromatography; PPACK, D-phenylalanylproplyarginyl chloromethyl ketone; TPCK, L-1-tosylamido-2-phenylethyl chloromethyl ketone; Heps, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid.

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requires the presence of negatively charged phospholipid (19, 20) and is not dependent on the presence of exogenously added calcium ions (19). Fluorescence polarization studies using factor Va modified with pyrene maleimide (Pyr-Va) have indicated a dissociation constant between Pyr-Va and the phospholipid vesicles of 2.7 x 10^{-9} M with 42 mol of PCPS required/mole of factor Va, which added to a tether (21). The stoichiometry between factor Va and the PCPS vesicles was proportionally altered with increasing PS concentration, but the Kd was essentially independent of the PS content of the vesicles (21). In the case of bovine factor Va the lipid-binding event is mediated by the light chain of the cofactor (21-23) and more precisely by a fragment of M, = 30,000 (21). This fragment, which contains the NH2-terminal part of factor Va light chain, is produced when the light chain is cleaved by factor Xa, or APC (18). The fragment of M, = 30,000 inhibits Pyr-Va binding to phospholipid vesicles (21), and essentially all the lipid binding capacity of the light chain is accounted for by this NH2-terminal fragment. Conflicting reports are available in the literature regarding the contribution of hydrophobic and electrostatic interactions toward stabilization of the factor Va-phospholipid complex (20, 22, 23). Also some results have led to a hypothesis that factor Va binding to platelets is intrinsically different from the binding of factor Va to phospholipid vesicles and may involve specific receptors on the platelet surface (24). In addition the results obtained using Pyr-Va are surprising because the fragment of M, = 30,000 contains a major part of the A3 domain of factor Va which is highly homologous to the A1 and A2 domains of the heavy chain of the cofactor (9) which do not bind to phospholipid vesicles.

In the present paper we study the membrane-binding site of factor Va. We used the assumption that at least part of the factor Va light chain is protected by the phospholipid bilayer. This study identifies an element of the light chain which accounts for the interaction of factor Va with the phospholipid vesicles.

**EXPERIMENTAL PROCEDURES**

**Materials**—All proteolytic enzymes used in this study were purchased from Worthington. Heps, L-α-phosphatidylethanol (hen egg) and L-α-phosphatidylinositol (bovine brain) were from Sigma. d-Phenylalanylmaleimidylchloromethyl ketone (PFAK) was from Calbiochem. Phospholipid vesicles (PCPS), composed of 75% phosphatidylethanolamine and 25% phosphatidylinositol were prepared as previously described (22, 25), and stored in 20 mM Heps, pH 7.4 (Heps-saline buffer or HBS). Phospholipid vesicles composed of 100% phosphatidylethanolamine (PC) were prepared in the same manner except that phosphatidylserine was omitted from the preparation. For PCPS alone was collected and lyophilized. This procedure was repeated three times for each enzyme. The lyophilized sample was resuspended in 3 ml of H2O, 0.05% trifluoroacetic acid, centrifuged at 10,000 rpm in an HBI microcentrifuge for 5 min, and filtered through 0.45-μm filters (Millipore) in preparation for reverse-phase HPLC analysis.

HPLC analysis was performed by injecting 1 ml of sample onto a 4.6-mm x 7.0-cm Beckman Ultragel RPSC-3 gel filtration column (Beckman) equilibrated in Heps-saline buffer. The column was monitored with a Waters model 450 absorbance detector operated at 280 nm. The flow rate was 1 ml/min, and the data were collected on a strip chart recorder operated at 5 mm/min. The protein fraction which comigrates with the PCPS vesicles as determined by running PCPS alone was collected and lyophilized. This procedure was repeated three times for each enzyme. The lyophilized sample was resuspended in 3 ml of H2O, 0.05% trifluoroacetic acid, centrifuged at 10,000 rpm in an HBI microcentrifuge for 5 min, and filtered through 0.45-μm filters (Millipore) in preparation for reverse-phase HPLC analysis.

**Peptide Isolation**—Isolated light chain was dialyzed against Hepes-saline buffer, and incubated with PCPS vesicles. Final concentrations were 3 μM light chain and 750 μM PCPS. The sample was incubated for 5 min at 37 °C to ensure that equilibrium had been attained. TPCK-treated trypsin, chymotrypsin, or elastase were added in separate reaction mixtures at a final concentration of 6.4, 8, and 10 μM, respectively. The mixture was incubated at 37 °C for 45 min to allow digestion of the exposed light chain. Preliminary experiments using a mixture of 125I light chain and unlabeled light chain had indicated that these conditions were optimum and gave rise to large amounts of peptides. The sample was then applied to a 5.0-ml x 30-cm TSK-3000 high performance liquid chromatography (HPLC) gel filtration column (Beckman) equilibrated in Heps-saline buffer. The column was monitored with a Waters model 450 absorbance detector operated at 280 nm. The flow rate was 1 ml/min, and the data were collected on a strip chart recorder operated at 5 mm/min. The protein fraction which comigrates with the PCPS vesicles as determined by running PCPS alone was collected and lyophilized. This procedure was repeated three times for each enzyme. The lyophilized sample was resuspended in 3 ml of H2O, 0.05% trifluoroacetic acid, centrifuged at 10,000 rpm in an HBI microcentrifuge for 5 min, and filtered through 0.45-μm filters (Millipore) in preparation for reverse-phase HPLC analysis.
were identical to those obtained using the Applied Biosystems computer program.

**Amino Acid Composition Analysis**—In a typical experiment, a known volume of purified peptide (usually a third or half of the amount used for the amino acid sequence) was transferred to an acid-washed borosilicate glass culture tube (6 x 50 mm). Noreleucine, 1 nmol, was added and the mixture was completely dried in a Savant Speed-Vac concentrator. The tube was then transferred into an acid washed 19 x 150-mm glass culture tube containing 600 µl of 6 N hydrochloric acid (Pierce Chemical Co.) and 2% thioglycolic acid to avoid oxidation of the methionine and tyrosine. Cysteine was determined as cysteic acid by performic acid oxidation prior to hydrolysis with 6 N HCl (27). The 19 x 150-mm hydrolysate tube was then purged with nitrogen and sealed under vacuum prior to heating for 24 h at 110 °C. The samples were dried completely, resuspended in 200 µl of 0.2 N sodium citrate buffer, pH 2.2, and filtered through 0.45-µm filters. Amino acid composition was determined using cation-exchange chromatography (Interaction Chemicals AA 911) and employing a pH gradient from 3.17 to 9.94, with post column detection using o-phthalaldehyde. The data were quantified using a computer program, Maxima 820 (Waters).

**Protein Labeling**—Proteins were labeled with [125I]-Na (Amersham Corp., using Iodo-Gen (Pierce Chemical Co.) as previously reported by Fraker and Speck (28). Free sodium iodide was removed by gel filtration using cellulose F5 desalting columns (Pierce Chemical Co.) or Sephadex G-10 columns (Pharmacia).

In some experiments a trace amount of iodinated light chain was added to a known concentration of unlabeled light chain, and the mixture was incubated with either PCPS or PC vesicles or HBS for 6 or 18 h at 37 °C. The final concentration was 3 µM light chain and 370 µM PCPS or PC. Then TPCK-treated trypsin or chymotrypsin were added to a final concentration of 6.4 and 8 µM, respectively, and the mixtures were incubated at 37 °C for 45 min. The reaction was stopped by adding 1% final concentration SDS (v/v) and bromphenol blue in 50% glycerol followed by heat at 90 °C for 5 min. In several experiments the time-dependent proteolysis of the light chain-PCPS complex was studied. For these experiments a mixture of [35S] labeled light chain and unlabeled light chain and PCPS vesicles was combined with trypsin, chymotrypsin, or elastase using the same conditions described above. After appropriate intervals of time an aliquot of the solution was withdrawn and SDS (1% final concentration) and bromphenol blue in 50% glycerol followed by heat at 90 °C for 5 min. The samples were subjected to SDS-PAGE analysis on 8-18% gradient gels (or as indicated). The gel was dried, and the proteins were visualized by autoradiography using Kodak X-Omat AR film.

**Gel Electrophoresis**—SDS-PAGE analysis was performed using homogeneous or 8-18% and 8-20% gradient gels following the method of Laemmli (29). The gels were stained with Coomassie Brilliant Blue R or silver-stained (30).

**Analysis of the Lipid-binding Peptide Amino Acid Sequence**—Sequence analysis was studied using the University of Wisconsin Genetics Computer Group sequence analysis computer program. Computer programs contained within this package were used in the analysis of the factor V sequence included "PEPTIDESTRUCTURE." This program makes secondary structure predictions for a protein or a peptide sequence. Predictions are based upon the rules developed by Chou and Fasman (31) for predicting helices, sheets, and turns. Options also allow for the determination of surface probability according to a formula developed by Emin et al. (32). The predictions are shown in a graphical form. It is stated clearly that such predictions may be far different from the actual protein structure.

**RESULTS**

The Light Chain-Vesicle "Footprint"—A mixture of unlabeled and iodinated factor Va light chain was incubated with PCPS, PC, or Hepes-saline buffer. The reaction mixtures were digested with trypsin or chymotrypsin as described under "Experimental Procedures." The resulting mixture was subjected to SDS-PAGE analysis and the proteins were displayed by autoradiography (Fig. 1). The intact native light chain appears as a large band with a Mr = 76,000, accompanied by fragments of Mr = 58,000, 42,000, and 30,000 (Fig. 1, lane 1). When the light chain was incubated with PCPS prior to the trypsin digestion the large band representing the light chain disappeared and two new fragments of Mr = 58,000 and 34,000 were present accompanied by two peptides of Mr = 18,200 and 14,000. Low molecular weight material is observed at the bottom of the gel which likely represents small peptides not resolved by the gel (Fig. 1, lane 2). When chymotrypsin replaced trypsin for the hydrolysis of the light chain in the presence of PCPS, trace amounts of a species of Mr = 58,000 were observed (Fig. 1, lane 5). In addition, a fragment of Mr = 36,000 was detected and was accompanied by two peptides of Mr = 17,500 and 14,500 (Fig. 1, lane 5). The same low molecular weight material as observed when using trypsin was present at the bottom of the gel. When the light chain was incubated with trypsin in the presence or absence of PC, only low molecular weight material at about 10,000 was present at the end of the digestion (Fig. 1, lanes 3 and 4). In the same manner when the light chain was incubated with chymotrypsin in the presence or absence of PC vesicles (Fig. 1, lanes 6 and 7) only low molecular weight material containing several bands at about 8,000 was present at the bottom of the gel. These data suggest that portions of the light chain are protected from proteolysis by the phospholipid vesicles composed of phosphatidylserine and phosphatidylycholine. Further, there are two smaller peptides in the factor Va light chain which are protected from enzymatic digestion and which may contain all or part of the phospholipid-binding domain of factor Va.

**Time Course Digestion of the Light Chain-Phospholipid Mixture by Various Enzymes**—A mixture of iodinated and unlabeled light chain was incubated with PCPS vesicles. Then trypsin, chymotrypsin, or elastase were added to separate reactions, and samples were removed at various times and prepared for SDS-PAGE as described under "Experimental Procedures." The native light chain had the same composition as described in Fig. 1, lane 1. When trypsin was added to the PCPS/light chain mixture, the doublet of Mr = 45,000/52,000 as well as a species of Mr = 39,000 and two peptides of Mr = 18,200 and 14,000 remained even after 24 h (data not shown). In contrast when chymotrypsin or elastase were used instead
of trypsin only the two peptides of $M_r = 17,500$ and $14,500$ remained after 24 h. It should be noted that regardless of the digestive enzyme used there is ultimately complete loss of the larger ($M_r > 18,200$) fragments. This observation is consistent with the reversible nature of the factor Va light chain interaction with phospholipid. Finally, a comparison of the time course digestion of the factor Va light chain using trypsin, chymotrypsin, and elastase shows that the concentration of all the fragments decreased with time. Therefore, the reaction was stopped at 45 min where the concentration of the set of peptides with $M_r = 18,200/14,000$ and $17,500/14,500$ was maximum.

Interaction of the Factor Va Light Chain or Heavy Chain with the PCPS Vesicles—High performance liquid chromatography gel filtration data obtained from five different mixtures of light chain or heavy chain and PCPS are illustrated in Fig. 2. Fig. 2A indicates the position at which PCPS vesicles were eluted from the gel filtration column, which is presumably at the void volume of the column. When the PCPS vesicles (750 μM) were incubated with the light chain (3 μM final concentration) prior to the TSK gel filtration, a net increase in the 280-nm absorbance of the void volume peak was observed (Fig. 2B). This increase was the result of the interaction between the light chain and the PCPS vesicles. It must be noted, however, that measurement of the absorbance at 280 nm in Fig. 2B is the result of the intrinsic absorbance of the light chain and the contribution of high scatter due to the phospholipid vesicles. Fig. 2C indicates the position at which native light chain alone was eluted from the column and shows, in comparison with Fig. 2B, that the light chain binds specifically to phospholipid vesicles. The amount of the light chain recovered after HPLC gel filtration of the light chain-phospholipid complex (Fig. 2B, first peak) was verified by silver stained SDS-PAGE and compared with the peak of light chain alone (Fig. 2C) and with the material which does not bind to the PCPS vesicles (Fig. 2B, second peak). More than 95% of the starting material was found to coelute with the PCPS vesicles (Fig. 2B, first peak). Fig. 2D illustrates the chromatogram obtained when the heavy chain of factor Va was incubated with the phospholipid vesicles. A comparison of this chromatogram with that obtained with the heavy chain alone (Fig. 2E) or with PCPS alone (Fig. 2A) indicates no interaction between the factor Va heavy chain and PCPS vesicles. This was also confirmed by SDS-PAGE analysis of the fractionated material (data not shown). These data indicate that this technique can be used to isolate lipid-bound protein or peptide in a qualitative manner. This technique can also give a qualitative answer as to whether or not a protein binds to the phospholipid vesicles and shows that the heavy chain of factor Va does not bind to the PCPS. The slight increase in the absorption of the PCPS peak was the result of the coelution of the high molecular weight contaminant of the factor Va heavy chain preparation with the PCPS peak.

Proteolytic Processing of Factor Va Light Chain by Trypsin and Chymotrypsin in the Presence of PCPS Vesicles—When trypsin alone was incubated with PCPS vesicles and subjected to HPLC gel filtration analysis two separate peaks were observed corresponding to free PCPS and to free trypsin (Fig. 3A); no interaction occurs between the PCPS vesicles and trypsin. Fig. 3B illustrates the profile obtained when the light chain-lipid complex was incubated with trypsin (45 min) prior to chromatographic analysis. The net increase in the 280-nm absorbance of the PCPS peak is attributed to the portion of the factor Va light chain which remains associated with the phospholipid vesicles. Similarly, chymotrypsin shows no interaction with the PCPS vesicles (Fig. 3C). The greater absorbance of the second peak which represented free chymotrypsin compared with the trypsin peak in Fig. 3A is the result of the higher chymotrypsin concentration and the higher extinction coefficient of chymotrypsin ($E_{280} = 20.4$) compared with $E_{280} = 14.3$ for trypsin. When the light chain was incubated with the PCFS vesicles prior to the chymotrypsin digestion and analyzed by gel filtration, an increase of the 280-nm absorbance of the phospholipid peak (Fig. 3D) was observed which was presumably the result of the interaction of the lipid binding portion of the light chain with the PCPS vesicles. Therefore, it appeared that this technique could be used to isolate the lipid-bound peptide of the factor Va molecule.

Enzyme Digests Isolated by Gel Filtration—The fragments which were coeluted with the PCPS vesicles were lyophilized, filtered, and subjected to reverse-phase high performance liquid chromatography. Fig. 4 illustrates a chromatogram obtained when the undigested light chain-phospholipid complex was analyzed. The peak at the beginning of the chro-

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**Fig. 2. HPLC gel filtration of the protein/phospholipid mixture.** HPLC gel filtration was performed on a TSK-3000 gel filtration column operated at a flow rate of 1 ml/min in Hepes-saline buffer. Chromatograms were obtained from various mixtures of either light chain or heavy chain with the phospholipid vesicles. Flow rate and chart speed were kept constant to facilitate direct comparison of elution profiles. Absorbance was monitored at 280 nm as indicated on the left. A, PCPS alone; B, PCPS and light chain; C, light chain alone; D, PCPS and heavy chain; E, heavy chain alone.
A Phospholipid-binding Domain of Factor Va

46,000 which bound to the fragment of $M_r = 30,000$ copurified with the light chain.

Fig. 5 shows the results obtained from reverse-phase HPLC when the lipid-peptide complex resulting from trypsin digestion and resolved by gel filtration was analyzed. The chromatogram illustrates a peak at 27.6 min which represents a peptide of $M_r = 18,200$ (t₁) as shown in Fig. 5, inset, lane 1. A second peak at 28.3 min contained intermediates resulting from the incomplete digestion of the light chain with trypsin (Fig. 5, inset, lane 2). A third peak occurs at 30.0 min and contained a peptide of $M_r = 14,000$ (t₂, Fig. 5, inset, lane 3). The fourth peak at 33.5 min with the small shoulder at 32.5 min contained the residual light chain and a fragment of $M_r = 46,000$ (Fig. 5, inset, lanes 4 and 5).

The chromatogram resulting from reverse-phase HPLC analysis of the PCPS-light chain chymotrypsin mixture gave products which eluted at 28.1 min (Fig. 6) and contained a peptide of $M_r = 17,500$ (ct₁, Fig. 6, inset, lane 2). A second peak at 29.7 min represented a peptide of $M_r = 14,500$ (ct₂,

The conditions for the enzymatic digestion of the light chain-PCPS complex are described under “Experimental Procedures.” HPLC gel filtration was performed as described in the legend for Fig. 2. Elution profiles of samples and controls are illustrated as follows: A, PCPS and trypsin; B, PCPS-light chain after trypsin treatment; C, PCPS and chymotrypsin; D, PCPS-light chain after chymotrypsin treatment.

Fig. 4. Reverse-phase HPLC of the light chain-lipid complex. The samples were analyzed on a 4.6-mm x 7.5-cm Ultrapore RPSC C-3 reverse-phase HPLC column operated at a flow rate of 1 ml/min at 22 °C. A gradient of 0% buffer B to 60% buffer B over 40 min was initiated at the same time the sample was injected (time 0). All samples were prepared in buffer A. Elution was monitored by absorbance at 214 nm as shown on the left of the chromatogram. The inset shows a silver-stained 8 to 20% gradient SDS-PAGE. Lane 1, corresponds to the peak 1 of the chromatogram; lane 2, peak 2. The position of the molecular weight standards is indicated on the left.

Fig. 5. Reverse-phase HPLC analysis of the phospholipid-peptide mixture after trypsin degradation. The sample was prepared as described under “Experimental Procedures,” and the HPLC analysis was performed as described in the legend of Fig. 4. The inset shows a silver-stained 8 to 20% gradient SDS-PAGE. Lanes 1–5 correspond to peaks 1 to 5 of the chromatogram. The position of the molecular weight markers is indicated on the left.

Fig. 6. Reverse-phase HPLC analysis of the lipid-peptide mixture after chymotrypsin digestion. The sample was prepared as described under “Experimental Procedures,” and the HPLC analysis was performed as described in the legend for Fig. 4. The inset shows a silver-stained 8 to 20% gradient SDS-PAGE. Lanes 1–4 correspond to the peaks 1–4 of the chromatogram. The position of the molecular weight standards is indicated on the left.
Fig. 6, inset, lane 2). Fig. 6 (inset) lanes 3 and 4, illustrates the proteins included in the third peak at 32.0 min and in the shoulder at 33.5 min. These proteins were the remaining light chain and a species of $\text{M}_r = 46,000$.

An identical digestion/isolation procedure was used with elastase and gave rise to results similar to those obtained using chymotrypsin. A peptide of $\text{M}_r = 17,500$ ($\text{e}_1$) was eluted at approximately the same acetoni-trile concentration as $\text{c}_1$, a second peak containing a peptide of $\text{M}_r = 14,100$ ($\text{e}_2$) was recovered at about 30.0 min, and a third peak containing fragments of $\text{M}_r = 42,000, 39,000$, and 35,000 was eluted close to the end of the chromatogram (data not shown).

**NH$_2$-terminal Sequence of $\text{t}_1$, $\text{t}_2$, $\text{c}_1$, $\text{c}_2$, $\text{e}_1$, and $\text{e}_2$—Edman degradation** followed by phenylthiohydantoin analysis was employed to determine the NH$_2$-terminal sequence of the isolated peptides. The resulting sequences are presented in Table I. The peptide $\text{t}_1$ which is generated when the light chain/lipid complex is incubated with trypsin yields a sequence which matches with the portion of human factor $\text{V}$ sequence starting at amino acid residue 1657 (Table I). The second tryptic peptide ($\text{t}_2$) has an NH$_2$-terminal sequence identical to the sequence previously reported by our laboratory for the NH$_2$-terminal end of the bovine or human factor $\text{V}$ light chain and for the fragment of $\text{M}_r = 30,000$ produced after factor $\text{Xa}$ and/or APC digestion of bovine factor $\text{V}$ light chain (Table I).

The NH$_2$-terminal sequence of peptides $\text{c}_1$ and $\text{e}_1$ which are the peptides isolated after chymotrypsin and elastase digestion of the lipid/light chain mixture was identified with a sequence which matches with a portion of human factor $\text{V}$ starting at amino acid residue 1667 (Table I). The second peptide isolated after chymotrypsin and/or elastase digestion had the same NH$_2$-terminal sequence as $\text{t}_3$, which is the NH$_2$-terminal end of the bovine factor $\text{V}$ light chain (Table I). An important observation is that each time that the potential amino acid expected was asparagine at position 1675 of the light chain (indicated by an arrow on the first column in Table I), no residue was detected, and no quantification was possible for the next cycle. In addition the recovery of the three or four following amino acids was 80% less than expected. This residue corresponds to a potential glycosylation site in the human factor $\text{V}$ molecule. It is most likely that the peptide binds to the glass fiber filter of the sequencer by this carbohydrate moiety, and most of the peptide is washed out following Edman degradation of this residue.

**Amino Acid Composition Analysis of the Tryptic and Chymotryptic Peptides**—The results obtained from amino acid composition analysis of the tryptic and chymotryptic peptides are presented in Table II, and are compared with the composition found in the corresponding regions of human factor $\text{V}$. The difference between the calculated amino acid composition and the number of residues expected is attributed to 1) a comparison of the sequence of the same peptide region but from two different species (human and bovine), and 2) the accuracy of the method which is 5 to 10%. The only significant difference was the number of glycine (and alanine residues in the case of $\text{t}_1$ and $\text{c}_1$). Most other quantifications are in good agreement with respect to the two major reasons reported above. It must be noted that no methionine or cysteine were found either in $\text{t}_3$ and $\text{c}_3$ as well as in the corresponding regions of human factor $\text{V}$ (Table II).

**Direct Binding of the Peptides to PCPS Vesicles**—The four isolated peptides from the trypsin and chymotrypsin digests were assayed for their ability to bind directly to PCPS

### Table I

**Sequence of NH$_2$-terminal amino acid residues of the tryptic, chymotryptic, and elastase peptides**

The numbers in the parenthesis indicated picomoles at the given cycle.

<table>
<thead>
<tr>
<th>Human light chain 1557–1688</th>
<th>Tryptic</th>
<th>Chymotryptic</th>
<th>Elastase</th>
<th>Intact bovine light chain</th>
<th>Intact human light chain</th>
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<tr>
<td>$\text{t}_1$</td>
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<td>$D$</td>
<td>$P$</td>
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<tr>
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<td>$E$</td>
<td>$D$</td>
<td>$P$</td>
<td>$E$</td>
<td>$E$</td>
</tr>
<tr>
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<td>$E$</td>
<td>$D$</td>
<td>$P$</td>
<td>$E$</td>
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</tr>
<tr>
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<td>$E$</td>
<td>$D$</td>
<td>$P$</td>
<td>$E$</td>
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</tbody>
</table>

*From Ref. 9.
†From Ref. 18.
‡From Ref. 33.
§Not identified.
¶Not quantitated.
A Phospholipid-binding Domain of Factor Va

DISCUSSION

The protocol described in this paper has permitted us to show that proteolysis of the bovine factor Va light chain bound to phospholipid vesicles lead to protection of two peptide segments which are located in the A3 domain of factor Va. One of the peptide regions is protected from enzymatic digestion in the presence of an acidic lipid bilayer, is capable of binding to membranes which contains acidic phospholipid, and most likely contains a phospholipid-binding site of factor Va.

The proteolysis of the light chain of bovine factor Va bound to PCPS vesicles by trypsin, chymotrypsin, and elastase was studied. In each case, two peptide regions were protected. The amino-terminal sequences of the two peptides derived from the A3 domain of the light chain were obtained and compared with the deduced amino acid sequence of human factor Va (9). Among 20 NH2-terminal amino acids determined for each peptide, an identity of 80% was observed between the human and bovine sequences, indicating that these two portions of the molecule are highly conserved between the two species. These two peptide regions contain a large number of potential cleavage sites for trypsin and chymotrypsin, as shown by the amino acid composition of each peptide. Although some of these sites are inaccessible in the native factor Va light chain structure most of them are exposed and are effectively cleavage by these two enzymes when PCPS is not present. This

Table II

<p>| Amino acid composition of the tryptic and chymotryptic peptides and comparison with the number of residues found in the corresponding region of human factor V |
|-------------------------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|</p>
<table>
<thead>
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<th>#</th>
<th>Amino acid</th>
<th>t1</th>
<th>ct1</th>
<th>1657-1791</th>
<th>1667-1797</th>
<th>t2</th>
<th>ct2</th>
<th>1546-1656</th>
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Fig. 7. Reverse-phase HPLC analysis of the t1-phospholipid complex. The sample was prepared as described under "Experimental Procedures." and the HPLC run was performed as described in the legend of Fig. 4. Three chromatograms are superimposed: short dashed line, base line; long dashed line, PCPS alone; continuous line, PCPS and t1. The vertical arrow indicates a peak which is the only difference between the three chromatograms. The inset shows a 15% silver-stained SDS-PAGE, and the horizontal arrow indicates the position of the molecular weight markers is indicated on the left. Differences in elution profiles between the three chromatograms are attributed to slightly altered chromatographic conditions and/or residual trifluoroacetic acid in the sample.

vesicles as described under "Experimental Procedures." ct1 was able to interact directly with the phospholipid vesicles as shown by the significant increase in the optical density at 280 nm when comparing the absorbance of the complex PCPS-ct1 with PCPS alone. When t1 was assayed in a similar fashion for the direct binding to PCPS vesicles it showed an interaction as judged by the increase of the optical density at 280 nm compared with the free PCPS peak. The species contained in the phospholipid peak obtained after incubation of t1 with the PCPS vesicles were collected, lyophilized, and submitted to reverse-phase HPLC analysis. Fig. 7 shows the result of three different chromatograms. The base line (short dashed line) indicated a small negative shift at 11 min which is probably the result of a change in the trifluoroacetic acid concentration of the solvent. This shift was consistent and observed in all three chromatograms. The chromatograms obtained with lyophilized phospholipid (long dashed-line) showed a large peak at the beginning of the chromatogram which is a consequence of the buffer components flowing through the column. The other small peaks represented contaminants in the buffer and/or the initial PCPS preparation. When the lyophilized PCPS/t1 mixture was analyzed (Fig. 7, continuous line), the only peak significantly different from the base line or from running lyophilized PCPS alone was detected at about 29.0 min. The components contained within this peak were analyzed by SDS-PAGE (Fig. 7, inset). The gel showed only one band of M. = 18,200 which corresponded to peptide t1. In contrast, when t1 and ct1 were tested for interaction with the PCPS vesicles no significant increase in the absorbance at 280 nm of the phospholipid peak was observed. Further, when the species contained within the lyophilized PCPS peak obtained after incubation of t1 and phospholipid were submitted to reverse-phase HPLC no peak significantly different from the base line was detected.
latter phenomenon occurs whether or not the light chain was in buffer or preincubated with phospholipid vesicles composed of 100% phosphatidylcholine, prior to the addition of the enzymes. In contrast, proteolysis of the light chain bound to PCPS vesicles by TPCK-treated trypsin occurs between amino acids 1556 and 1657, and gives rise to a peptide of \( M_r = 14,000 \) containing the \( \text{NH}_2 \)-terminal part of the light chain and of the A3 domain (9, 18, 33). The other peptide of \( M_r = 18,200 \) contains the central part of the A3 domain of factor Va and shows an interaction with the phospholipid vesicles (Fig. 8).

The results of the enzymatic digestion obtained using trypsin or chymotrypsin and factor Va light chain were obtained as a consequence of proteolysis between residues 1666 and 1667 by both chymotrypsin and elastase. Based upon the deduced human factor V amino acid sequence (9), the relative molecular weight of the two peptides and their amino acid compositions, it is most probable that the enzymatic cleavage which releases these two peptides must occur within the region 1700-1707 of the factor Va light chain. The only potential cleavage site for trypsin within this region as compared with the deduced amino acid sequence of human factor V is located between amino acids 1791-1792 (9) where chymotrypsin and elastase may cleave between residues 1793-1794 or 1797-1798 (Fig. 8). The chymotrypsin-derived peptide containing the central part of the A3 domain of the factor Va light chain binds to the phosphatidylserine-containing phospholipid vesicles in a similar manner to the corresponding trypptic peptide. It is interesting to note that since trypsin cleaves between amino acids 1656-1657 and chymotrypsin at position 1666 and both peptides containing the central part of the A3 domain of the factor Va light chain bound to PCPS vesicles, the 10-residue region between 1657 and 1666 must be exposed to the solvent and probably does not interact with the PCPS vesicles (Fig. 8). The other set of peptides \( t_2 \) (1546-1656) and \( t_3 \) (1546-1666) did not show evidence of direct interaction with the PCPS vesicles. Since \( t_2 \) and \( t_3 \) did not show any affinity for the PCPS vesicles but are protected from enzymatic digestion, it is most likely that these peptide regions are intimately associated by non-covalent interaction with the peptide(s) which bind to the phospholipid vesicles.

The processing of bovine factor Va light chain by factor Xa and/or APC gives rise to a fragment of \( M_r = 30,000 \) (18) containing the amino-terminal portion of the native light chain (residues 1546-1765) and to an insoluble doublet (\( M_r = 46,000/48,000 \)) which is derived from the carboxyl-terminal portion of the molecule (Fig. 8). Krishnaswamy and Mann (21) showed that the fragment of \( M_r = 30,000 \) is involved in the factor Va-PCPS interaction and could quantitatively account for the light chain membrane interaction. These data could not discount participation of the COOH-terminal-derived doublet of \( M_r = 46,000/48,000 \) of the light chain in the interaction of factor Va with the phospholipid vesicles because after HPLC purification of the 46,000/48,000 doublet all attempts to remove acetonitrile from the protein solution resulted in irreversible insolubility; hence, measurement was not possible. The factor Xa-APC cleavage site of the light chain occurs at residue 1765 and the resulting \( A_3 \) domain is a lipid-binding segment of the molecule (Fig. 8). The exact positions of the carboxyl termini of \( t_1 \) and \( t_3 \) are estimated on the basis of their amino acid composition and apparent molecular weights on SDS-PAGE. These peptides include a glycosylation site at position 1675, and the carbohydrate at this site provides for some uncertainty with respect to the molecular weight of the peptides. Therefore, with respect to the considerations reported above (comparison of the \( \text{NH}_2 \)-terminal sequence of the peptides with the corresponding regions within the human factor V sequence, \( M_r \) excluding carbohydrates and amino acid composition of each peptide) the chymotrypsin and trypsin cleavage probably occurs at position Trp1746 and Arg1756 of the light chain respectively (Fig. 8). These cleavage sites may coincide with the cleavage at position 1765 of the factor Va light chain by factor Xa and/or APC (18). Our present data, combined with the competitive binding experiments using the isolated fragment of \( M_r = 30,000 \) from the \( \text{NH}_2 \)-terminal part of the factor Va light chain (21), leads to the conclusion that the lipid-binding region can be narrowed to a 99-amino acid segment corresponding to residues 1667-1765 (Fig. 8). A hydropathy plot in which the lipid-binding segment of 99 amino acids is identified is illustrated in Fig. 9. Within this region are two hydrophobic segments, i.e. residues 1716-1727 and 1741-1748, segments of 12 and 8 amino acids, respectively. It is conceivable that one or both of these two segments are involved in the interaction of the light chain with the phospholipid vesicles.

Gilbert et al. (34) using gel-filtered factor VIII-PCPS complex showed that factor VIII binds to phospholipid vesicles, and the dissociation constant for this binding was found to be close to that obtained using factor V or Va. Data from Foster et al. (35) using synthetic peptides from the C2 domain of factor VIII showed that the region contained within amino acid residues 2304-2322 may be involved in the mediation of factor VIII binding to phosphatidylserine-coated plates. They further observed an identity of 70% when comparing the primary structure in this region to amino acid residues 2170-2196 of the factor V molecule. Nesheim et al. (36), using recombinant factor VIII labeled intrinsically with \(^{125}\)I-methionine, showed that factor VIII binding to thrombin-activated platelets is not displaced by an excess of factor V. Therefore, the authors suggested that factor VIII may bind to a distinct
structure (or receptor) of the platelet membrane which is different from that occupied by factor V. All these results, including ours, imply that the two cofactors may interact with separate components of the activated platelet membrane. However, the possibility that other domains of factors V and VIII are implicated in the phospholipid binding must not be excluded.

The regulation and the formation of the prothrombinase complex includes the interaction of factor Va with prothrombin, factor Xa, and APC on a phospholipid surface in the presence of CaCl₂. The prothrombin-binding site was previously localized to the heavy chain of the factor Va (37). A portion of the factor Xa and the entire APC binding sites are located on the light chain of the cofactor (38, 39). Recent data from Walker et al. (40) using recombinant DNA fragments of factor VIII and synthetic peptides of both factor V and factor VIII suggested that the binding domain for APC is located within the COOH-terminal end of the A3 domain of factor V (between residues 1865-1874). The bulk of information regarding the ability of factor V or factor Va to bind to phospholipid vesicles has been obtained from various studies of the factor Va-PCPS interaction using modified factor Va or modified phospholipid vesicles (20-22, 34). Although these previous studies are not consistent with respect to the dissociation constant for the factor Va-phospholipid interaction, and/or the number of specific sites for factor Va on the phospholipid surface, they all agree with the fact that only the light chain of the active cofactor can account for the interaction of factor Va with the PCPS vesicles.

Our data clearly show that phosphatidylserine is necessary for the binding of the factor Va light chain to phospholipid vesicles. This latter interaction is essential for the protection of part of the light chain from enzymatic degradation. We therefore found that this protected region contains a binding domain of factor Va to phospholipid vesicles. This interactions with the phospholipid vesicles involves a peptide of 99 amino acids (residues 1667-1765) located on the central part of the A3 domain of factor Va (9, 18). It should be interesting to find whether all of the peptide sequence is necessary for the binding of the light chain to PCPS vesicles, and, consequently, if the tertiary structure of this peptide or of the light chain plays a role in the binding of factor Va to the phospholipid bilayer.

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REFERENCES

A Phospholipid-binding Domain of Factor Va

Identification and characterization of a phospholipid-binding site of bovine factor Va.

M Kalafatis, R J Jenny and K G Mann


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