Interaction of Vaccinia Virus Complement Control Protein with Human Complement Proteins: Factor I-Mediated Degradation of C3b to iC3b Inactivates the Alternative Complement Pathway

Arvind Sahu, Stuart N. Isaacs, Athena M. Soulika and John D. Lambris

*J Immunol* 1998; 160:5596-5604; ;
http://www.jimmunol.org/content/160/11/5596

**Why The JI?**
- Rapid Reviews! 30 days* from submission to initial decision
- No Triage! Every submission reviewed by practicing scientists
- Speedy Publication! 4 weeks from acceptance to publication

*average

**References**  This article cites 40 articles, 21 of which you can access for free at: http://www.jimmunol.org/content/160/11/5596.full#ref-list-1

**Subscription** Information about subscribing to *The Journal of Immunology* is online at: http://jimmunol.org/subscription

**Permissions** Submit copyright permission requests at: http://www.aai.org/About/Publications/JI/copyright.html

**Email Alerts** Receive free email-alerts when new articles cite this article. Sign up at: http://jimmunol.org/alerts
Interaction of Vaccinia Virus Complement Control Protein with Human Complement Proteins: Factor I-Mediated Degradation of C3b to iC3b1 Inactivates the Alternative Complement Pathway

Arvind Sahu,* Stuart N. Isaacs,† Athena M. Soulika,* and John D. Lambris2*

Vaccinia virus complement control protein (VCP) is a virulence determinant of vaccinia virus that helps protect the virus from the complement attack of the host. To characterize the interaction of VCP with C3 and C4 and understand the mechanism by which VCP inactivates complement, we have expressed VCP in a yeast expression system and compared the biologic activity of the purified protein to that of human factor H and complement receptor 1 (CR1). Recombinant VCP bound to C3 and the proteolytically cleaved form of C3 (C3b), but not to the 135,300-m.w. fragment of C3 generated using elastase (C3c) and the 35,000-m.w. fragment of C3 generated using elastase (C3d) and inhibited both the classical and alternative pathways of complement activation. Although rVCP was less effective at inhibiting the alternative pathway than factor H or CR1, it was more effective than factor H at inhibiting the classical pathway. Unlike factor H, rVCP was unable discriminate between alternative pathway-mediated lysis of rabbit and sheep E. A comparison of the cofactor activity in factor I-mediated cleavage of C3b suggested that in contrast to factor H and CR1, which displayed cofactor activity for the three sites, rVCP displayed cofactor activity primarily for the first site, leading to generation of C3b cleaved by factor I between Arg1281–Ser1282 (iC3b1). Its cofactor activity for C4b cleavages was similar to that of soluble complement receptor type 1. Purification and functional analysis of iC3b1 showed that it was unable to interact with factor B to form the alternative pathway C3 convertase, C3b,Bb. These results suggest that the interaction of VCP with C3 is different from that of factor H and CR1 and that VCP-supported first cleavage of C3b by factor I is sufficient to render C3b nonfunctional. The Journal of Immunology, 1998, 160: 5596–5604.

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

1 Abbreviations used in this paper: C3b, the proteolytically cleaved form of C3; SCR, short consensus repeats; CR1, complement receptor type 1; VCP, vaccinia virus complement control protein; ORF, open reading frame; iC3b1, C3b cleaved by factor I between Arg1281–Ser1282; C3b,Bb, C3b,Bb cleaved by factor I between Arg1281–Ser1282 and Arg1296–Ser1298; C3c, the 115,300-m.w. fragment of C3 generated using elastase; C3d, the 35,000-m.w. fragment of C3 generated using elastase; E, erythrocytes; Ep, rabbit erythrocytes; Es, sheep erythrocytes; iCR1, soluble complement receptor type 1.

Copyright © 1998 by The American Association of Immunologists

0022-1767/98/$20.00

Received for publication November 7, 1997. Accepted for publication February 2, 1998.

The Journal of Immunology

VCP has been shown to regulate complement activation in vitro. Both partially purified VCP and culture medium containing...
secreted VCP have been shown to inhibit complement-mediated lysis of sheep E (E₈), to bind to C₃b and C₄b, and to accelerate the decay of the classical as well as alternative pathway C₃ conver-
tases (11, 13). VCP shows considerable sequence similarity to other factor I cofactor proteins. Thus, it is important to study its cofactor activity. A previous study has suggested that VCP had cofactor activity in the factor I-mediated cleavage of C₃b and C₄b (13). However, in that study, the C₃b and C₄b cleavage products were not visualized, and conclusions about the nature of cofactor activity could not be obtained.

In the present study, we have characterized the interaction of rVCP with C₃ and C₄ and compared its interaction to that of other known regulators, factor H and CR1. Our results show that the factor I cofactor activity of rVCP for C₄b is similar to soluble complement receptor type 1 (sCR1). However, in contrast to factor H and CR1, which function as a cofactor for inactivation of C₃b by factor I for sites 1 (Arg²¹⁸⁹-Ser²¹⁹⁶), 2 (Arg²¹⁸⁹-Ser²¹⁹⁶), and 3 (Arg⁹³²-Glu⁹³³), VCP primarily functions as a cofactor for the first site. We also present data suggesting that C₃b, when cleaved at site 1 (C₃b cleaved by factor I between Arg²¹⁸⁹-Ser²¹⁹⁶ (iC₃b₁)), is unable to form the alternative pathway C₃ convertase C₃bBb.

These results suggest a mechanism for complement evasion by vaccinia virus and demonstrate that the interaction of VCP with C₃ is different from all the other factor I cofactors characterized to date.

Materials and Methods

Reagents and buffers

Yeast nitrogen base without amino acids was purchased from Difco (Detroit, MI). BSA and n-biotin were obtained from Sigma (St. Louis, MO). Rabbit and sheep blood were purchased from Cocalico Biologicals (Reamstown, PA), and E₈ coated with Abs were prepared by incubating the E₈ with anti-E₈ Abs (Cordis, Miami, FL). Antiserum recognizing rVCP and human C₃b were raised in rabbits. Factor H-depleted serum was prepared by passing human serum containing 20 mM EDTA through an anti-factor H Sepharose column pre-equilibrated in veronal-buffered saline (VBS) containing 0.1% gelatin, GVB2 containing 0.5 mM MgCl₂ and 0.15 mM CaCl₂, and GVBE was GVB with 10 mM EDTA. MgEGTA contained 0.1% gelatin, GVB²⁻ was GVB containing 0.5 mM MgCl₂ and 0.15 mM CaCl₂, and GVBE was GVB with 10 mM EDTA. 

Matrix-assisted laser desorption-ionization mass spectrometry was performed using a VG ToFSpec time-of-flight mass spectrometer (Fisons Instruments, Beverly, MA). The sample was dissolved in 50 μl of 50% acetonitrile containing 0.1% trifluoroacetic acid and diluted before analysis using 2-(4-hydroxyphenylazo)benzoic acid (Aldrich, Milwaukee, WI) as the matrix. Data were analyzed by OPUS software (Fisons Instruments) (21). To determine the N-terminal sequence of rVCP, the sample was applied to a conditioned glass-fiber filter coated with BioBrene Plus cationic polymer (Applied Biosystems, Foster City, CA). Adsorbed protein was subjected to Edman degradation, using an Applied Biosystems 473A Protein Sequencer (19).

Hemolytic assay

Inhibition of the classical and alternative pathway-mediated hemolytic activity was determined as previously described (22). In brief, inhibition of the classical pathway was determined by incubating various concentrations of complement control proteins (rVCP, factor H, and sCR1) with 7 μl of normal human serum (diluted 1:10 in GVB²⁻) and 5 μl of E₈ coated with Abs (1 × 10⁷/ml). The total volume of the reaction mixture was adjusted to 250 μl by adding GVB²⁻ and incubated at 37°C for 1 h. The reaction was stopped by adding the reaction mixture at 0°C followed by centrifugation. The percentage of lysis was determined by measuring the OD of 250 μl of supernatant at 405 nm. To determine the influence of the various complement control proteins on the alternative pathway of complement, 10 μl of rabbit E (E₈) (1 × 10⁷/ml in GVB) were mixed with 8 μl of unidiluted normal human serum and 5 μl of MEGTAs (0.1 M) in the presence of various concentrations of rVCP, factor H, or sCR1. The volume of the reaction mixture was adjusted to 100 μl with GVB. The reaction mixture was incubated at 37°C for 20 min and the reaction was stopped by adding 200 μl of GVBE. After centrifugation, the absorbance of 200 μl of the supernatant from each sample was determined at 405 nm. The percentage of lysis was normalized by setting 100% lysis to be equal to the degree of lysis occurring in the absence of inhibitory proteins. The effect of complement control proteins on the alternative pathway-mediated lysis of E₈ was determined a selectable marker and flanking sequences that permitted homolo-
gous recombination into the yeast genome. Oligonucleotide primers 5′-GCAGCGTCCGATCTGCTGATCTTCCGACGACCC-3′ (the SaI site is underlined) and 5′-CGCGATCCTTACGCTACACTATTTT GAGATTCCG-3′ (the BamHI site is underlined and the stop codon is in boldface), were used to amplify a 735-hp segment of the C3L ORF from a plasmid containing the HindIII-BamHI segment of the HindIII C frag-

The cloned insert and the ligated ends were sequenced to confirm the DNA structure. A recombinant Pichia pastoris was isolated following the manu-

The recombinant yeast cells were grown in 10 ml of sterile BMGY medium (100 mM potassium phosphate, pH 6.0, 10 g/l yeast extract, 20 g/l peptone, 13.4 g/l yeast nitrogen base, 0.4 g/l biotin, and 1% gly-
cerol) on a shaker at 30°C for 18 h. The liquid culture obtained was used as an inoculum for 1 liter of BMGY medium, which was incubated at 30°C with vigorous shaking until the culture reached an OD₆⁰⁰ ≥ 6 (usually at 72 h). The cells were centrifuged at 1500 × g for 5 min, resuspended in 200 ml of BBMMY medium (BBM containing 0.5% methanol, but without 1% glycerol) and incubated with vigorous shaking at 30°C. After 24 h, the liquid culture was centrifuged and the supernatant containing the rVCP was collected.

Expressed rVCP was purified from the culture supernatant as follows. In a typical purification procedure, culture supernatant (250 ml) was first precipitated with 20% ammonium sulfate and the supernatant was then precipitated with 60% ammonium sulfate at 0°C. The resulting pellet con-
taining rVCP was dissolved, dialyzed into PBS, and loaded onto a DEAE-

The molecular mass of the rVCP was determined by mass spectrometry. Matrix-assisted laser desorption-ionization mass spectrometry was performed using a VG ToFSpec time-of-flight mass spectrometer (Fisons Instruments, Beverly, MA). The sample was dissolved in 50 μl of 50% acetonitrile containing 0.1% trifluoroacetic acid and diluted before analysis using 2-(4-hydroxyphenylazo)benzoic acid (Aldrich, Milwaukee, WI) as the matrix. Data were analyzed by OPUS software (Fisons Instruments) (21). To determine the N-terminal sequence of rVCP, the sample was applied to a conditioned glass-fiber filter coated with BioBrene Plus cationic polymer (Applied Biosystems, Foster City, CA). Adsorbed protein was subjected to Edman degradation, using an Applied Biosystems 473A Protein Sequencer (19).
RESULTS

Measurements of factor I cofactor activity of rVCP

A time course of the cleavage of C3b by factor I in the presence of rVCP, factor H, or sCR1 was performed in 10 mM phosphate buffer, pH 7.4, containing 145 mM NaCl. In a typical assay, 33 μg of C3b were mixed with 11 μg of rVCP, factor H, or sCR1 and 0.5 μg of factor I in a total volume of 143 μl and incubated at 37°C. Samples (13 μl) were removed at different time intervals and mixed with sample buffer containing DTT, boiled for 3 min, and subjected to electrophoresis on a 9% SDS-PAGE gel, and analyzed for cleavage products as described above for C3b.

Separation of C3b, iC3b, and C3b cleaved by factor I between Arg<sup>281</sup>-Ser<sup>282</sup> and Arg<sup>298</sup>-Ser<sup>299</sup> (iC3b<sub>2</sub>) by anion-exchange chromatography

C3b and its inactivated forms, iC3b<sub>1</sub> and iC3b<sub>2</sub>, were separated by anion-exchange chromatography using a Mono Q HR 5/5 column (Pharmacia). C3b (1 mg) was mixed with 300 μg of rVCP and 16 μg of factor I in a total volume of 1.3 ml and incubated at 37°C for 10 h. This resulted in degradation of C3b into iC3b<sub>1</sub> and iC3b<sub>2</sub>. To better indicate all three species on the chromatogram, 0.6 mg of C3b was added to the mixture. The reaction mixture containing all the three fragments of C3 was diluted in buffer A (10 mM sodium phosphate, pH 7.9) and passed over the column, which had been preequilibrated in buffer A. The column was washed with 5 ml of 20% buffer B (10 mM sodium phosphate, 500 mM NaCl, pH 7.9) to wash the rVCP off the column (rVCP elutes between 10 and 20% of buffer B). Bound proteins were then eluted with a linear gradient of 55 ml from 20 to 60% of buffer B. All the protein-containing fractions were analyzed by SDS-PAGE.

Detection of C3 convertase formation

The ability of C3b, iC3b<sub>1</sub>, and iC3b<sub>2</sub> to interact with factor B to form C3 convertase, C3bBb, was analyzed as follows: C3b or its inactivated forms, iC3b<sub>1</sub> and iC3b<sub>2</sub> (0.5 μg each), were mixed with factor B (0.6 μg) and factor D (4 ng) in 25 μl of PBS, pH 7.4, containing 5 mM MgEGTA. The reaction mixture was incubated at 37°C for 30 min and run on a 7.5% SDS-PAGE gel under reducing conditions. The gel was stained with silver stain to visualize the proteins. The presence of Bb and Ba fragments indicated the formation of C3 convertase. Controls were incubated in GVBE to inhibit the factor B cleavage.

RESULTS

Expression, purification, and characterization of rVCP

In the present study, we have expressed a functionally active rVCP using the yeast expression system (Fig. 1). This expression system produced a high yield of rVCP; the recombinant protein was secreted into the medium at a level of 50 to 150 μg/ml, as determined by SDS-PAGE and Western blot analysis. The culture supernatant containing the expressed protein was subjected to electrophoresis on a 9% SDS-PAGE gel, and analyzed for cleavage products as described above for C3b.
precipitated by ammonium sulfate and further purified by anion-exchange chromatography on a DEAE-Sephacel column. These two methods concentrated the protein and removed most of the yeast proteins, in particular the yeast metal-binding proteins, which impart yellow and green colors to the culture supernatant. Following these steps, the sample was passed over the Mono Q anion-exchange column and eluted with a linear salt gradient. The eluted protein was homogeneous and >95% pure as determined by SDS-PAGE analysis (Fig. 2).

To confirm the identity of rVCP, the purified protein was subjected to automated Edman degradation. The predicted N-terminal sequence of the first 10 residues of the expressed VCP is R-L-C-C-T-I-P-S-R-P. The amino acid sequence of rVCP corresponded to the predicted sequence (Table I). The sequencing data also confirmed that the signal peptide was cleaved in the mature protein. The first two amino acids, RL, are the result of cloning VCP into the Pichia vector. The size of the expressed protein was analyzed by SDS-PAGE (Fig. 2) and mass spectrometry (Table I). The calculated molecular mass of rVCP was 26,906 Da, but the protein migrated as a single band of 30,000 Da. However, this apparent overestimation by SDS-PAGE is not due to glycosylation, because the primary sequence lacks glycosylation sites (10). Thus, mass spectrometry was used to determine the accurate mass of the protein. The mass 27,164 Da was closer to the calculated mass of the predicted sequence (Table I). The sequencing data also confirmed that the N-terminal sequence lacks glycosylation sites at positions 3 and 4. The primary sequence contains cysteines at these positions.

Table I. Molecular mass and N-terminal analysis of rVCP

<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Molecular mass (Da) as determined by</td>
<td></td>
</tr>
<tr>
<td>Formula</td>
<td>26,906</td>
</tr>
<tr>
<td>SDS-PAGE</td>
<td>30,000</td>
</tr>
<tr>
<td>Mass spectrometry</td>
<td>27,164</td>
</tr>
<tr>
<td>N-terminal sequence</td>
<td>R-L-X-X-T-I-P-S-R-P</td>
</tr>
</tbody>
</table>

* Based on the primary sequence (10).
* Calculated from Figure 1.
* Determined as described in Materials and Methods.
* Amino acids were not detected at positions 3 and 4. The primary sequence contains cysteines at these positions.

Binding of rVCP to C3 fragments

A previous study (13) had shown that VCP secreted by vaccinia virus-infected cells binds to C3b. To test whether rVCP is biologically active and has retained its ligand binding activity, we performed a direct ELISA binding assay. Our results showed that rVCP, like virally secreted VCP, bound to C3b (Fig. 3). In this study, we also characterized the binding of rVCP to various physiologic fragments of C3. When we measured its binding to C3, iC3b2, C3c, and C3d, we found that unlike C3b, the expressed rVCP did not bind to C3c and C3d. Surprisingly, rVCP did bind to C3 and weakly to iC3b2. It is likely that the observed binding to C3 was due to the presence of C3(H2O), since this preparation contained 61% native C3 and 39% C3(H2O), but we cannot rule out the possibility that VCP binds to native C3. Additional experiments described below suggest that the binding we observed to iC3b2 is not physiologically significant.

Inhibition of complement activation by rVCP, CR1, and factor H

We compared the effects of rVCP, factor H, and sCR1 on the classical and alternative pathways of complement by evaluating their ability to inhibit the complement-mediated lysis of E (Fig. 4). We chose to use hemolytic assays because these assays have been used in the past to quantitate the effect of complement control proteins and inhibitors. Therefore, the IC50 values we obtained would be useful for comparison purposes. In our assays, rVCP inhibited lysis of E R and E S by the alternative and classical pathways with IC50 values of 3.4 μM and 0.1 μM, respectively (Fig. 4). The concentrations of factor H and sCR1 required to inhibit the alternative pathway-mediated lysis of E R were 0.54 μM and 2.7 nM, respectively (Fig. 4A). The concentrations of factor H and sCR1 required to inhibit the classical pathway were 0.42 μM and 0.21 nM, respectively (Fig. 4C). On a molar basis, rVCP was four times more active in inhibiting the classical pathway than was factor H. These results suggest that although rVCP is a poor inhibitor of the alternative pathway when compared with factor H, it is more potent than factor H in inhibiting the classical pathway.

It is well known that E R spontaneously activate the alternative pathway because the C3b attached to E R have a relatively low...
the appearance of a 43-kDa fragment indicated the second cleavage between Arg^{1281} - Ser^{1282} and generation of iC3b_{ii}; and the appearance of 25-kDa and C3dg fragments indicated the third cleavage between Arg^{932} - Glu^{933} and generation of C3c and C3dg. The first and second cleavages occurred immediately (within the first 5 min) in the presence of both factor H and sCR1 (Fig. 5). The third cleavage was slow in the presence of sCR1 and did not occur in the presence of factor H under these conditions. The third cleavage was observed in the presence of factors H and I only when the reaction was performed overnight in half-ionic-strength buffer (data not shown). These results suggest that factor H is as efficient as sCR1 in inactivating fluid-phase C3b to iC3b_{ii}. However, this similarity did not hold true for activator-bound C3b, since 200-fold higher concentrations of factor H than of sCR1 were needed to inhibit E lytic when C3b was bound to E_R (Fig. 5A).

Our data indicated that rVCP also acts as a cofactor in factor I-mediated cleavage of C3b (Fig. 5). However, it behaved differently from factor H and sCR1 in two ways. 1) The cleavage pattern of C3b was different from that obtained in the presence of factor H and sCR1, and 2) the rate of C3b cleavage was slower than that observed in the presence of factor H and sCR1. It is clear that in the presence of rVCP, C3b was predominantly cleaved at the first site, leading to the generation of iC3b_{i}. The second cleavage was much slower, occurring only after 4 h instead of 5 min. Furthermore, rVCP failed to support the third cleavage, even when the reaction mixture was incubated overnight at 37°C in half-ionic-strength buffer (data not shown). Cofactors incubated with C3b in the absence of factor I showed no cleavage products (data not shown). Whether the predominant species generated (iC3b_{ii}) is inactive or is able to participate in the formation of C3 convertase was not clear from these experiments. Additional experiments (described below) were performed to determine the role of iC3b_{ii} in complement activation.

The factor I cofactor activity of rVCP for C4b was also determined in a fluid phase assay and compared with that of sCR1 (Fig. 6). The α’ chain of C4b is cleaved by factor I between Arg^{1318} - Asn^{1319} (first cleavage) and Arg^{937} - Thr^{938} (second cleavage) (23). In this assay, generation of 71-kDa and 16-kDa fragments would indicate the first cleavage and formation of iC4b. However, the 71-kDa and 16-kDa fragments comigrate with the β-chain and the dye front, respectively, and thus were not seen in the gel. The appearance of 25-kDa and C4d fragments indicated the second cleavage and generation of C4c and C4d. The results depicted in Figure 6 show that similar to sCR1, both of the cleavages of the α’ chain of C4b also occurred in the presence of rVCP, resulting in the generation of C4d. These data suggest that rVCP acts as a factor I cofactor for inactivation of C4b.

**Does iC3b_{ii} form C3 convertase?**

The ability of rVCP to act as a cofactor in the factor I-mediated cleavage of C3b to iC3b_{ii} allowed us to isolate and determine the role of this C3b species in complement activation. rVCP was incubated for 10 h with C3b and factor I, the products of the reaction were mixed with C3b and separated on a Mono Q HR 5/5 column. The three C3 forms (C3b, iC3b_{i}, and iC3b_{ii}) bound to the union-exchange column and eluted according to the number of cleavages in the molecule (Fig. 7). The identity of each C3 form was confirmed by analyzing the samples on SDS-PAGE under reducing conditions.

The ability of iC3b_{ii} to form C3 convertase was examined in a fluid-phase assay. C3 fragments generated and purified as described above were incubated with factors B and D in the presence of MgEGTA at 37°C for 30 min (Fig. 8). The generation of Bb and Ba fragments indicated the formation of C3 convertase, C3b,Ba. As expected, C3b participated in the formation of C3 convertase (Fig. 8, **Comparison of the cofactor activity of rVCP, factor H, and sCR1**

Complement control proteins inhibit complement activation by supporting the proteolytic inactivation of C3b and/or C4b by factor I. We further analyzed the interaction of rVCP with C3b and C4b by assessing its ability to act as a cofactor in factor I-mediated cleavage of C3b and C4b. The cofactor activity of rVCP for C3b was compared with that of two physiologic regulators of complement, factor H and CR1. These assays allowed us to analyze the complete time course of C3b inactivation by the three proteins. While previous studies have compared the interaction of factor H or CR1 with C3b, a comparative time course of C3b inactivation has not been reported to date. In this assay, the appearance of 68-kDa and 46-kDa fragments indicated the first factor I-mediated cleavage of C3b between Arg^{1281} - Ser^{1282} and generation of iC3b_{i};
lane 2), while iC3b2 failed to do so (Fig. 8, lanes 4 and 5). It is important to note that iC3b1 was unable to participate in the formation of C3 convertase (Fig. 8, lane 3), suggesting that the single cleavage in the C3b molecule converts the molecule into an inactive species that no longer supports complement activation.

**Discussion**

Previous in vivo studies have established that VCP, a major secretory product from vaccinia virus-infected cells, is a virulence factor. It has been shown that vaccinia virus mutants that do not express VCP are...
The expressed VCP was functionally active, as judged by its binding to C3b (Fig. 3) and inhibition of complement-mediated E lysis (Fig. 4). To characterize the ligand-binding properties of rVCP, we studied its interaction with various C3 fragments (Fig. 3). Binding was observed with C3 and C3b but not with C3c or C3d. A weak binding was also observed with iC3b2. These results suggest that the affinity of the binding site for small C3 fragments (C3c or C3d) is very low and was therefore below the detection limit of our assay system. Another possibility is that the binding site on C3 is conformational and is lost after the cleavage of C3b to C3c and C3d. Further studies are needed to address this issue and to localize the binding site of VCP on C3.

Recently, Subramanian et al. (29) have demonstrated that tyrosine and aspartic acid at positions 37 and 79 determine the binding specificity of SCRs 1 to 3 of CR1 to C3b/C4b. Because VCP binds to both C3b and C4b (13), we aligned its sequence with SCRs 1 to 3 of CR1 to determine whether VCP contains tyrosine and aspartic acid at comparable positions. We found that VCP contains arginine and glycine instead of tyrosine and aspartic acid. Thus, the presence of tyrosine and aspartic acid at positions 37 and 79 does not, by itself, always dictate the binding specificity for C3b/C4b.

VCP has previously been shown to inhibit the classical pathway-mediated lysis of Eᵦ (11); however, it was not clear whether it also inhibits the alternative pathway in whole human serum. In the present study, we show that rVCP inhibits the classical as well as alternative pathway-mediated lysis of E in normal human serum (Fig. 4). It is clear from the data that the concentration of rVCP required to inhibit the classical pathway (Fig. 4 C) is about 34-fold lower than that required to inhibit the alternative pathway-mediated lysis Eᵦ (Fig. 4 A). It is possible that the higher concentrations of rVCP required to inhibit Eᵦ lysis are due to reduced affinity of rVCP for the C3b bound to Eᵦ. This phenomenon is well documented for factor H activity on C3b bound to Eᵦ vs Eᵦs (30, 31). However, this seems unlikely for rVCP, as its alternative pathway regulatory activity is nearly same for Eᵦ and Eᵦs (Fig. 4, A and B).

The ammonium sulfate precipitation step followed by anion-exchange chromatography on a DEAE-Sephacel column removed most of the yeast proteins. Thus, these two steps should be useful in purifying other yeast-expressed proteins, since yeast proteins bind tightly to the DEAE-Sephacel column and elute only at high salt concentration (2 M) or low pH (pH 2.3).

FIGURE 7. Separation of C3b, iC3b₁, and iC3b₂ by anion exchange chromatography. The sample containing a mixture of C3b, iC3b₁, and iC3b₂ was diluted in Mono Q buffer A and loaded onto the column. The column was washed and proteins were eluted with a linear salt gradient. Fractions containing protein were analyzed on 9% SDS-PAGE gels under reducing conditions. The gels were visualized by silver stain and subjected to image analysis to obtain data points for graphical representation of the results. The amount of C3b, iC3b₁, and iC3b₂ was determined by measuring the intensity of the α’, 46-kDa, and 43-kDa bands, respectively.
These results suggest that, unlike factor H, rVCP does not discriminate between activator (Eg)- and nonactivator (Eg)-bound C3b. Thus, based on the present and previous (13) observations, the greater effect of VCP on the classical pathway could be attributed to its effect on C3 as well as C4. This dual effect of VCP on C3 as well as C4 could benefit the virus by preventing its damage by host complement in the absence as well as the presence of a specific Ab response.

VCP is composed entirely of four SCR domains and is much smaller in size than factor H (composed of 20 SCR) or CR1 (composed of 30 SCRs). This difference led us to ask: Is VCP as effective as other physiologic regulators of complement in inhibiting complement activation? The data shown in Figure 4 demonstrate that it is less effective than CR1 in inhibiting both pathways of complement and than factor H in inhibiting the alternative pathway. However, it is noteworthy that rVCP was four times more effective than factor H in inhibiting the classical pathway, due to its dual action on C3 and C4. Thus, it seems that the virus encodes a small protein that reflects the limited size of its genome, but at the same time this protein is able to regulate multiple components of the complement system, a situation that produces a cumulative effect on the classical pathway activation that results in a higher inhibitory effect than that of factor H. This phenomenon could be essential for the survival of the virus. Recently it has become clear that this strategy of complement evasion is not unique to the vaccinia virus and that other viruses also encode proteins similar to human complement control proteins (8).

While prior work (13) suggested that VCP had factor I cofactor activity, this activity was not conclusively established, as the resulting C3b/C4b cleavage products had not been identified. To characterize the cofactor activity of VCP, we have studied the factor I-mediated cleavages of C3b and C4b in the presence of VCP. Although no differences in the cleavage pattern of C4b was observed (Fig. 6), to our surprise, we found that rVCP primarily supports the cleavage of C3b to iC3b1 (Fig. 5); before this study, it had not been clear whether iC3b1 could participate in the formation of C3 convertase, C3b,Bb. While iC3b1 is also generated in the presence of other cofactors (factor H, CR1, and MCP), the second cleavage occurs immediately after the first, and therefore it had been difficult in the past to isolate and purify this cleavage product. Generation and accumulation of iC3b1 in the presence of VCP allowed us to study this second form. We used anion exchange chromatography to separate iC3b1 from C3b and iC3b2 (Fig. 7). This method provided sufficient resolution to yield monodisperse populations of each of the C3 cleavage products. Incubation of C3b with factors B and D in the presence of MgEGTA showed that iC3b1 is unable to form the alternative pathway of C3 activation and is biologically inactive (Fig. 8). These data suggest that the first cleavage by itself is sufficient to inactivate C3b, and second cleavage is not necessary, as has been previously thought. Our data also reinforce the belief that accessibility to different cleavage sites by factor I is dependent upon the cofactor involved (4).

The data obtained in the present and previous studies make it clear that VCP effectively regulates complement by inactivating C3 and C4 and helps the vaccinia virus to evade the host immune response. It is reasonable to assume that at the site of infection, VCP effectively inhibits complement activation and the generation of C3a and C5a. As a result, it would protect the virus from complement-mediated damage and also reduce the specific inflammatory response against the virus. However, it would be advantageous for the virus to encode a membrane-bound complement regulatory protein, which could inhibit the complement activation focused on the viral surface and the surface of infected cells. Vaccinia virus encodes a second protein (the gene product of B5R) (32), which is present on the outer envelope of the virus (33–36) and shows sequence similarity to complement control proteins (32–34). The role of this protein in complement inactivation, however, remains unknown. Further characterization of this protein would provide valuable insight into other essential aspects of viral pathogenesis.

Acknowledgments

We thank Zhege Lao and Jeannie Chu for their excellent technical work, J. Nicoloudis and Yvonne H. Shahain for mass spectrometric analysis and N-terminal sequencing, respectively, and Dr. Deborah McClellan for editorial assistance.

References