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C1 inhibitor: Biologic activities that are independent of protease inhibition

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Abstract

C1 inhibitor therapy improves outcome in several animal models of inflammatory disease. These include sepsis and gram negative endotoxin shock, vascular leak syndromes, hyperacute transplant rejection, and ischemia-reperfusion injury. Furthermore, some data suggest a beneficial effect in human inflammatory disease. In many inflammatory conditions, complement system activation plays a role in pathogenesis. The contact system also very likely is involved in mediation of damage in inflammatory disease. Therefore, the beneficial effect of C1 inhibitor has been assumed to result from inhibition of one or both of these systems. Over the past several years, several other potential anti-inflammatory effects of C1 inhibitor have been described. These effects do not appear to require protease inhibition and depend on non-covalent interactions with other proteins, cell surfaces or lipids. In the first, C1 inhibitor binds to a variety of extracellular matrix components including type IV collagen, laminin, entactin and fibrinogen. The biologic role of these reactions is unclear, but they may serve to concentrate C1 inhibitor at extravascular inflammatory sites. The second is a noncovalent interaction with C3b that results in inhibition of formation of the alternative pathway C3 convertase, a function analogous to that of factor H. The third is an interaction with E and P selectins on endothelial cells that is mediated by the Lewis^x tetrasaccharides that are expressed on C1 inhibitor. These interactions result in suppression of leukocyte rolling and transmigration. The fourth interaction is the binding of C1 inhibitor to gram negative bacterial endotoxin that results in suppression of endotoxin shock by interference with the interaction of endotoxin with its receptor complex on macrophages. Lastly, C1 inhibitor binds directly to gram negative bacteria, which leads to suppression of the development of sepsis, as demonstrated in the cecal ligation and puncture model. These observations suggest that C1 inhibitor is a multi-faceted anti-inflammatory protein that exerts its effects through a variety of mechanisms including both protease inhibition and several different non-covalent interactions that are unrelated to protease inhibition.

Keywords

C1 inhibitor; cecal ligation and puncture model; endotoxin shock; gram negative bacterial sepsis; selectins; serine proteinase inhibitors

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Introduction

Treatment with C1 inhibitor improves outcome in a number of animal models of inflammatory disease including gram negative bacterial sepsis and endotoxin shock, vascular leak syndromes, hyperacute transplant rejection, and ischemia-reperfusion injury (Akita et al., 2003; Buerke et al., 1995; Buerke et al., 1998; Dalmaso and Platt, 1993; De Simoni et al., 2003; De Simoni et al., 2004a; Fiane et al., 1999; Fukuta et al., 2003; Giebler et al., 1999; Guerrero et al., 1993; Hecker et al., 2002; Henze et al., 1997; Horstick et al., 1997; Horstick et al., 2001a; Jansen et al., 1998; Khorram-Sefat et al., 1998; Matsunami et al., 2000; Nielsen et al., 2002; Przemeczek et al., 2002; Radke et al., 2000; Schelzig et al., 2001; Scherer et al., 1996; Schmidt et al., 1999a; Schmidt et al., 1999b)(Table 1). For example, in myocardial ischemia-reperfusion injury, treatment with C1 inhibitor resulted in decreased infarct size, decreased myocardial neutrophil accumulation, decreased plasma levels of creatine kinase, C3a and C5a, and decreased expression of P-selectin and ICAM-1 within the cardiac endothelium (Buerke et al., 1995; Buerke et al., 1998; Horstick et al., 1997; Horstick et al., 2002). Similar effects have been observed in skeletal muscle and middle cerebral artery ischemia-reperfusion injury (Akita et al., 2003; De Simoni et al., 2003; Nielsen et al., 2002). One study suggested that the C1 inhibitor-mediated effect was independent of inhibition of classical pathway activation; a role for inhibition of lectin pathway activation was not examined (De Simoni et al., 2004b). In addition, limited experience in human disease suggests that C1 inhibitor may prove to be a useful addition to therapy of diseases including vascular leak syndromes, sepsis, and shock syndromes (Bauernschmitt et al., 1998; Bauernschmitt et al., 2000; de Zwaan et al., 2002; Hack et al., 1993; Hack et al., 1994; Niederau et al., 1995; Ogilvie et al., 1994; Tassani et al., 2001) (Table 1). Two studies have suggested a beneficial effect in humans with ischemia-reperfusion injury (Bauernschmitt et al., 1998; de Zwaan et al., 2002). Because complement system activation plays a role in the mediation of many of these conditions, these beneficial effects have been thought to be a product of inhibition of activation of the complement system. Protease inhibition clearly is the major biologic role of C1 inhibitor. It is the only protease inhibitor that inactivates C1r and C1s (Sim et al., 1979; Ziccardi, 1981), the initial proteases activated via the classical complement pathway. It also regulates lectin pathway activation via inhibition of MASP2 (Ambrus et al., 2003; Matsushita et al., 2000a; Matsushita et al., 2000b; Matsushita et al., 2001), the initial protease activated in this pathway. However, C1 inhibitor may share this latter role with α_2 macroglobulin (Ambrus et al., 2003). In the contact or kinin system, C1 inhibitor is the primary inhibitor of both plasma kallikrein and factor XIIa (de Agostini et al., 1984; Kaplan et al., 1985; Pixley et al., 1985). In this instance, α_2 macroglobulin clearly plays a lesser role than does C1 inhibitor. It is certain that activation of these pathways have important inflammatory effects, and that their inhibition, whether by C1 inhibitor or other inhibitors, is anti-inflammatory. However, over the past several years, several other interactions of C1 inhibitor with other proteins or cells have come to light. These interactions do not require protease inhibition. Initial data suggest that, in some instances, these reactions may be significant contributors to the anti-inflammatory activity of this important protease inhibitor. These include at least four different binding reactions (Table 2): (1) An interaction with a variety of extracellular matrix components (Patston and Schapira, 1997); (2) inhibition of alternative complement pathway activation via binding of C1 inhibitor to C3b which prevents its interaction with factor B, in a manner analogous to that of factor H (Jiang et al., 2001); (3) an interaction with both E and P selectins on endothelial cells that is mediated by one or more Lewis^x tetrasaccharides expressed on C1 inhibitor, and which results in suppression of leukocyte rolling and transmigration (Cai and Davis III, 2003; Cai et al., 2005); (4) binding to endotoxin from several different gram negative bacteria that results in suppression of endotoxin shock by interference with the interaction of endotoxin with its receptor complex on macrophages (Liu et al., 2003; Liu et al., 2004; Liu et al., 2005a; Liu et al., 2005b); (5) direct binding to gram negative bacteria that results in suppression of the development of sepsis (unpublished data). This review will briefly summarize the limited

information available on the first two reactions and will describe in more detail the data relating to the interactions with selectins and with endotoxin lipopolysaccharide (LPS).

The interaction of C1 inhibitor with extracellular matrix components

C1 inhibitor binds to a number of extracellular matrix components including type IV collagen, laminin, and entactin, as was illustrated by ligand blotting assays and by ELISA (Patston and Schapira, 1997). Half-maximal binding to collagen and laminin was at approximately 8 µg/ml. Digestion of C1 inhibitor with *Crotalus atrox* α -proteinase, which cleaves at Pro³⁶, had no effect on binding. This implies that this binding has quite different requirements than the binding to gram negative endotoxin (Liu et al., 2005a)(see below). Binding had no effect on the rate constant of inhibition of C1s by C1 inhibitor. The interaction with type IV collagen resulted in a slight increase in the stoichiometry of inhibition in the reaction between C1 inhibitor and C1s, but the other proteins had no effect. Neither the biochemical mechanism nor the biologic relevance of these reactions have been defined. Tissue transglutaminase, but not factor XIII, has been shown to cross-link C1 inhibitor to immobilized fibrin via Gln⁴⁵³ (Hauert et al., 2000). Such cross-linked C1 inhibitor retains the ability to inactivate target proteases. The biology of this reaction also remains to be investigated. It seems likely, however, that these reactions with extracellular matrix proteins serve at least to concentrate C1 inhibitor at extravascular sites of inflammation in order to maximize regulation of local complement and contact system activation.

Suppression of alternative complement pathway activation

C1 inhibitor also has been shown to inhibit alternative pathway activation via an incompletely defined mechanism which, however, does not require protease inhibition (Jiang et al., 2001). The data suggested that the findings might be of biologic relevance because removal of C1 inhibitor from plasma resulted in enhanced alternative pathway activation. The mechanism appears to result from inhibition of binding of factor B to C3b via an interaction of C1 inhibitor with C3b. Binding to C3b does not appear to require protease inhibitor activity. This mechanism, if correct, would be quite similar to the mechanism of inhibition of C3 convertase formation by factor H and CR1. The region of the molecule required for this activity remains uninvestigated and it is not known whether the binding to C3b has any effect on protease inhibition by C1 inhibitor. The potential role of this activity *in vivo* has not been determined.

The interaction of C1 inhibitor with selectins on endothelial cells

The beneficial effect of C1 inhibitor in inflammatory disease is accompanied by a decrease in leukocyte transmigration to the site of inflammation and by decreased selectin expression (Buerke et al., 1998; Horstick et al., 2001b; Lehmann et al., 2000; Lehmann et al., 2004). These effects are probably largely due to a suppression of complement activation; C3a, C5a and C5b-9 all may enhance selectin expression and leukocyte adhesion (Hattori et al., 1989; Jagels et al., 2000; Monsinjon et al., 2003). However, additional potential mechanisms have not been evaluated previously. Selectins are adhesion molecules that are responsible for leukocyte rolling on the endothelium (Butcher and Picker, 1996). E-selectin is expressed on endothelial cells; expression is induced by cytokines (TNF- α , IL-1) and gram negative lipopolysaccharide. P-selectin is expressed on platelets and endothelial cells; it is mobilized to the cell surface from intracellular granules in response to a variety of agents including histamine and thrombin. Selectins bind to fucosylated mucin-like glycoproteins. A number of selectin ligands bind via sialyl Lewis^x, which is a fucose-containing tetrasaccharide expressed on N-linked carbohydrate of a number of cell surface and plasma proteins. All selectins recognize the sialyl Lewis^x moiety (Frenette and Wagner, 1996a; Frenette and Wagner, 1996b; Vestweber and Blanks, 1999). C1 inhibitor previously has been reported to bind to endothelial cells that have been incubated in the cold (Bergamaschini et al., 2001a; Bergamaschini et al., 2001b). Because of these

observations, and because it is heavily glycosylated and is fucosylated (Strecker et al., 1985), we tested the hypothesis that C1 inhibitor might express the sialyl Lewis^x tetrasaccharide and thereby bind to selectins. On immunoblots following separation by SDS-polyacrylamide gel electrophoresis, C1 inhibitor reacted with two different monoclonal antibodies that react with sLewis^x (Cai and Davis III, 2003). Reactivity was lost following removal of N-linked, but not O-linked, carbohydrate.

C1 inhibitor was shown to bind to both E- and P-selectins, as demonstrated by FACS analysis of CHO/K1 cells transfected with either E- or P- selectin and by co-precipitation with soluble E- or P-selectin IgG chimeras (Cai and Davis III, 2003). Furthermore, C1 inhibitor, following incubation with human umbilical vein endothelial cells, co-precipitated with both E- and P-selectin after lysis of the cells and immunoprecipitation with antiserum to C1 inhibitor (unpublished data)(Fig. 1). The interaction with selectins had no discernible effect on the ability of C1 inhibitor to form stable complexes with C1s, although reaction kinetics have not been evaluated. Using the macrophage-like cell line, U937, C1 inhibitor suppressed both adhesion to, and transmigration across, TNF- α -treated endothelial cell monolayers (Cai and Davis III, 2003). Carcinoembryonic antigen (CEA), which expresses the sialyl Lewis^x tetrasaccharide, is an E-selectin ligand. C1 inhibitor suppressed the binding of CEA to E-selectin expressed on the surface of CHO cells in a dose dependent manner (Cai et al., 2005). In addition, reactive center cleaved C1 inhibitor, which retains no protease inhibitor activity, also suppressed the interaction to as great a degree as did active native C1 inhibitor. However, C1 inhibitor with its N-linked carbohydrate removed, lost the ability to interfere with binding.

The effect of C1 inhibitor on leukocyte rolling was analyzed both *in vitro* and *in vivo*. Using a flow chamber in which purified E-selectin was immobilized, C1 inhibitor at concentrations similar to those that occur during acute inflammation (300 μ g/ml) increased rolling velocity two fold (Cai et al., 2005)(Fig. 2). Using P-selectin transfected cells cultured on the chamber, rolling velocity was increase by 2.5 fold. With both E- and P-selectin, reactive center cleaved C1 inhibitor, but not N-deglycosylated C1 inhibitor, increased velocity to the same degree. As visualized by intravital microscopy, C1 inhibitor also was shown to suppress TNF- α induced leukocyte rolling *in vivo* in mice. As with the *in vitro* experiments, reactive center cleaved C1 inhibitor retained full activity. Lastly, in the thioglycollate peritonitis model, C1 inhibitor (300 μ g) suppressed leukocyte infiltration to background levels (Cai et al., 2005). Previous data suggest that leukocyte influx in this model is approximately 50% dependent on the presence of C5 and 50% dependent on leukotriene B(4) (Segal et al., 2002). Therefore, complete suppression of infiltration by C1 inhibitor, together with the effectiveness of inactive C1 inhibitor, suggest that its mechanism is not solely via complement inhibition.

Several plasma proteins, in addition to C1 inhibitor, express sialyl Lewis^x. These include α_1 -acid glycoprotein, α_1 -antichymotrypsin and haptoglobin (Brinkman-van der Linden et al., 1998; De Graaf et al., 1993). All these proteins are acute phase reactants. The normal plasma concentration of C1 inhibitor (80–195 μ g/ml), for example, may increase up to 2.5-fold during an acute inflammatory response (Kirschfink and Nurnberger, 1999; Tietz, 1995). The data discussed here suggest that, at these concentrations, C1 inhibitor, together with these other acute phase reactants, might interfere with the leukocyte-selectin interaction, resulting in the inhibition of migration of cells to inflammatory sites. This may represent a normal physiologic mechanism that participates in down-regulation of the acute inflammatory response.

The interaction of C1 inhibitor with Gram negative bacterial endotoxin

In a variety of different animal models of Gram negative endotoxin shock and sepsis, survival is significantly improved, together with several physiologic measurements, by treatment with C1 inhibitor (Fischer et al., 1997; Giebler et al., 1999; Guerrero et al., 1993; Jansen et al.,

1998; Liu et al., 2003; Scherer et al., 1996; Schmidt et al., 1999a; Schmidt et al., 1999b). C5a very likely plays a role in the pathogenesis of septic shock (Barton and Warren, 1993; Czermak et al., 1999; Strachan et al., 2000). On the other hand, C3 and C4 deficient mice are quite susceptible to endotoxin shock, which supports the hypothesis that C3 may be required for normal endotoxin clearance (Fischer et al., 1997). Interestingly, survival of C3 deficient mice is improved by treatment with C1 inhibitor, suggesting that the effect of C1 inhibitor is not mediated via inhibition of complement activation (Fischer et al., 1997). The contact system may be involved in the mediation of some aspects of endotoxin shock (Colman, 1999; Jansen et al., 1996; Pixley et al., 1993). Other data suggest that contact system activation does not play an important role (Feletou et al., 1996). Our data indicated that not only did intact, active C1 inhibitor protect from endotoxin shock, but that treatment with inactive, reactive center cleaved C1 inhibitor also was effective (Liu et al., 2003). Both active and inactive C1 inhibitor also prevented both local and systemic vascular permeability changes in response to endotoxin (Liu et al., 2005b). C1 inhibitor prevented the binding of *Salmonella typhimurium* LPS to the murine macrophage cell line, RAW 264.7, and to human blood cells. Direct binding assays showed that C1 inhibitor interacted with LPS, thereby blocking LPS-induced TNF- α expression (Liu et al., 2003). LPS, a component of the outer membrane of Gram negative bacteria, consists of an inner lipid A component, which is responsible for the pathophysiology of endotoxin shock, and an outer polysaccharide component. In blood, LPS binds to LPS-binding protein (LBP), an acute phase plasma protein, that transfers the LPS to CD14 on the surface of monocytes and macrophages (Fenton and Golenbock, 1998; Kitchens, 2000; Poltorak et al., 1998; Schumann and Latz, 2000). The LPS-CD14 complex then initiates intracellular signalling by binding to Toll-like receptor 4 (TLR4) (Aderem and Ulevitch, 2000). At least one other protein, MD-2, is associated with CD14 and TLR4 on the cell surface; together, these make up the LPS receptor (da Silva Correia and Ulevitch, 2002; Juan et al., 1995; Stelter et al., 1997; Stelter et al., 1999; Viriyakosol and Kirkland, 1995; Viriyakosol et al., 2000). The binding of C1 inhibitor to LPS (or lipid A) was inhibited by fetal bovine serum, which contains LBP, and by an LBP peptide that includes the binding site for LBP (Liu et al., 2003).

A recombinant C1 inhibitor from which the amino terminal non-serpin domain was deleted (amino acids 1–97) failed to bind to LPS (Liu et al., 2003). N-deglycosylated C1 inhibitor did not protect mice from endotoxin shock, did not bind to LPS and did not suppress the binding of LPS to RAW 264.7 or to human blood cells (Liu et al., 2004). Therefore, N-linked carbohydrate within the amino terminal domain appears to be required for the interaction with LPS. The lipid A-binding motifs of other LPS-interacting proteins contain positively charged amino acids that interact with the negatively charged phosphate groups within lipid A (Ferguson et al., 2000; Lamping et al., 1996; Mancek et al., 2002; Schumann et al., 1997; Visintin et al., 2003). We, therefore, in addition to analyzing the requirement for N-linked carbohydrate, tested whether the four basic amino acids within the amino terminal domain of C1 inhibitor (Arg¹⁸, Lys²², Lys³⁰, Lys⁵⁵) might be involved in the interaction with lipid A. Using site-directed mutagenesis, single amino acid substitutions and combinations of substitutions were performed in which Ala was introduced at each of the above sites and the three N-linked sites within the amino terminal domain (Asn³, Asn³⁰ and Asn⁵⁵). Substitution of Asn³ resulted in virtually complete loss of the ability to interact with LPS, while little or no effect was observed following replacement of the other Asn residues (Liu et al., 2005a)(Fig. 3). However, the effect of the substitution of the individual positively charged residues was additive; replacement of any single residue reduced binding to 75–80% of that of the wild type control protein, replacement of 2, 3 and 4 residues reduced binding progressively to 10–12% of the control with replacement of all four (Fig. 4). These results were confirmed by the observations that the mutants that lost the ability to bind also lost the abilities to inhibit binding of LPS to RAW264.7 cells and to inhibit LPS-induced TNF- α mRNA expression. A likely explanation of these findings is that the binding site for LPS consists of

Arg¹⁸, Lys²², Lys³⁰, and Lys⁵⁵, while the carbohydrate at Asn³ is required to maintain a conformation of the amino terminal domain in which the binding site is exposed.

More recently, experiments have been initiated to analyze the effect of C1 inhibitor in the mouse cecal ligation and puncture (CLP) model of peritonitis and sepsis. These experiments demonstrate that C1 inhibitor also improves survival in this model. A single dose (600 µg) increased survival from approximately 15% to 45%, while three doses at 0, 12 and 24 hours increased survival to 65% (unpublished data). In agreement with the findings in LPS-induced shock, treatment of CLP mice with reactive center cleaved C1 inhibitor was at least as beneficial as was intact, active C1 inhibitor. Fewer bacteria could be recovered from the peritoneal fluid and blood of treated than from untreated mice. C1 inhibitor did not have a direct effect on bacterial growth *in vitro*, but it did enhance bacterial phagocytosis and/or killing by both neutrophils and macrophages. Furthermore, C1 inhibitor treatment enhanced H₂O₂ release by neutrophils and macrophages from CLP mice. Although C1 inhibitor does interact with the bacteria from CLP mice, it has not yet been determined whether the binding site is the LPS or if it is some other site on the bacterial surface. Furthermore, the mechanism of the enhanced phagocytosis/killing remains to be defined.

Conclusions

The data discussed here suggest that C1 inhibitor is a multi-faceted anti-inflammatory protein. Protection from inflammatory diseases, sepsis and septic shock very likely is a result of multiple mechanisms. These obviously include inhibition of both complement and contact system activation. In the complement system, the most important effect of C1 inhibitor in inflammatory disease very likely reflects decreased generation of C5a, while in the contact system, decreased generation of bradykinin is probably the most important effect. In addition to protease inhibition, direct effects of C1 inhibitor via interactions with endotoxin, with selectins and possibly with extracellular matrix components very likely also are important.

Abbreviations

CEA	carcinoembryonic antigen
CLP	cecal ligation and puncture
LBP	LPS-binding protein
LPS	lipopolysaccharide
TLR4	Toll-like receptor 4

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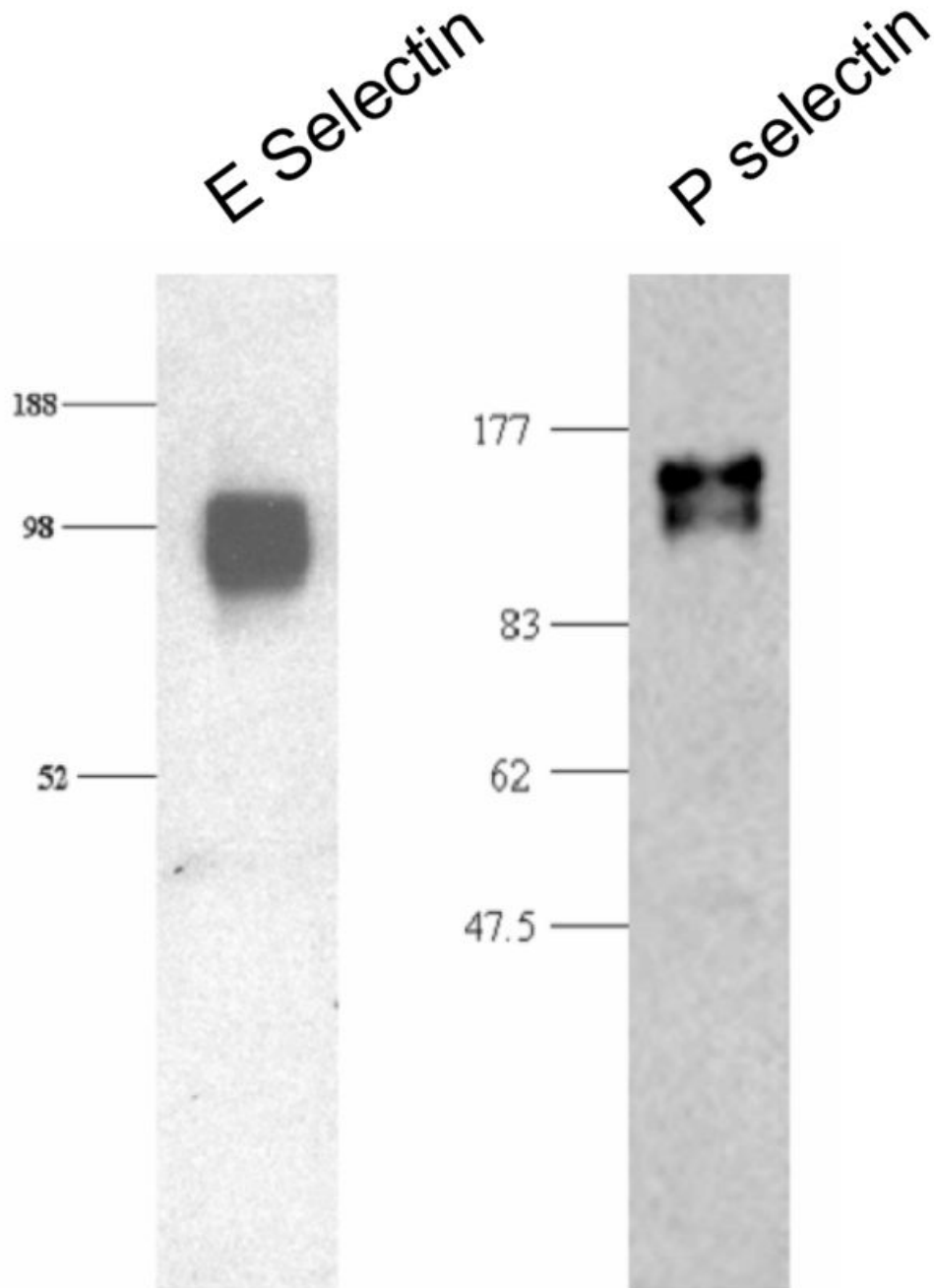


Fig. 1. Endothelial cell E- and P-selectin co-immunoprecipitate with C1 inhibitor. Human umbilical vein endothelial cells were treated with TNF- α and H₂O₂ and were then incubated with C1 inhibitor. The cells then were lysed and immunoprecipitated with rabbit anti-C1 inhibitor antiserum, following which SDS-polyacrylamide gel electrophoresis was performed and blots were probed with antiserum to E-selectin or P-selectin.

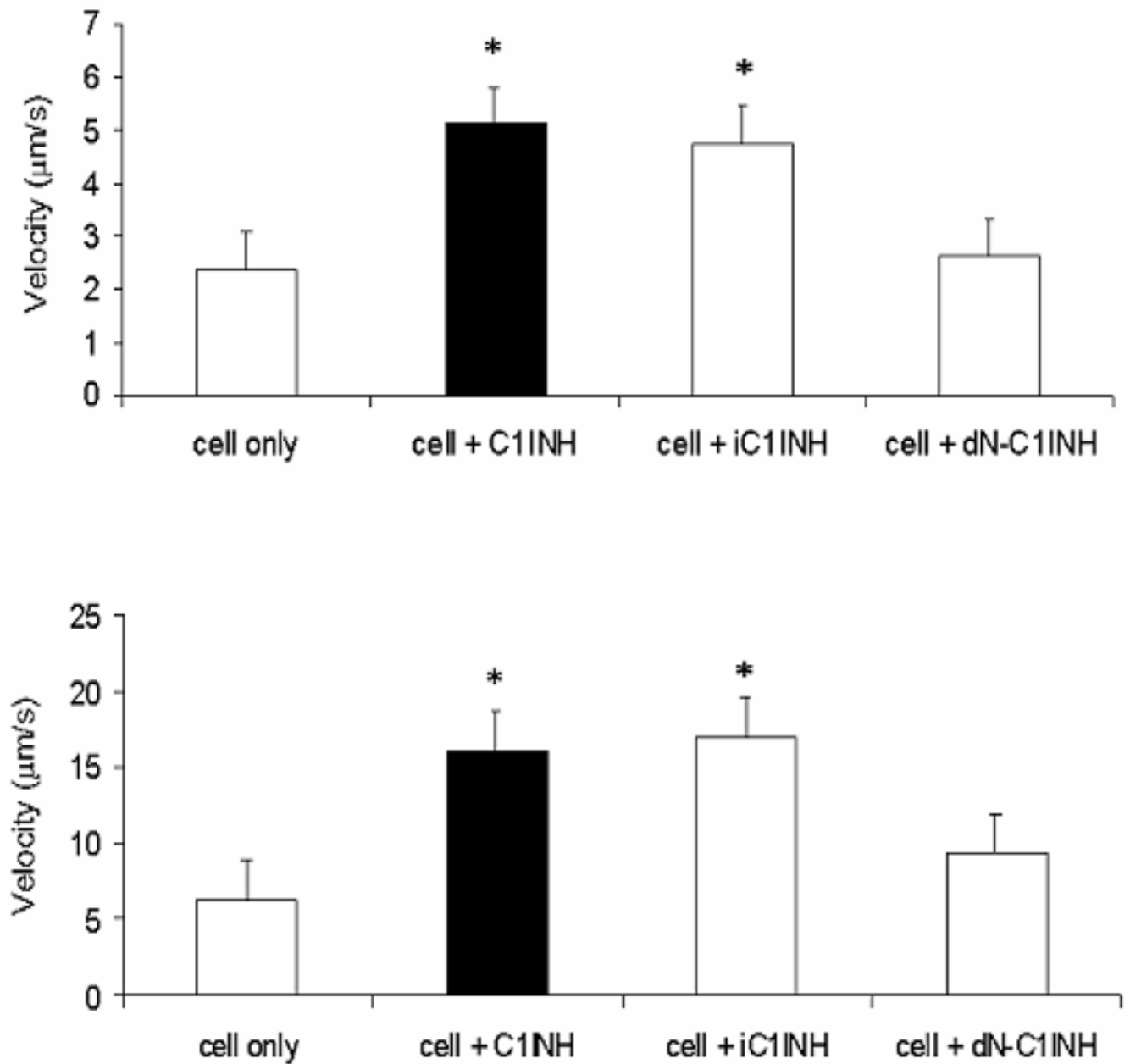


Fig. 2.

C1 inhibitor blocks the rolling of HL-60 cells on E- and P-selectin under flow conditions *in vitro*. Human E-selectin (top) was immobilized and CHO cells that express recombinant P-selectin (bottom) were grown to a monolayer on a plate. HL-60 cells ($1 \times 10^6/\text{ml}$) were perfused for a 15 min period in the absence or presence of various forms of C1 inhibitor (300 $\mu\text{g}/\text{ml}$). The velocity of 30 rolling cells was determined.

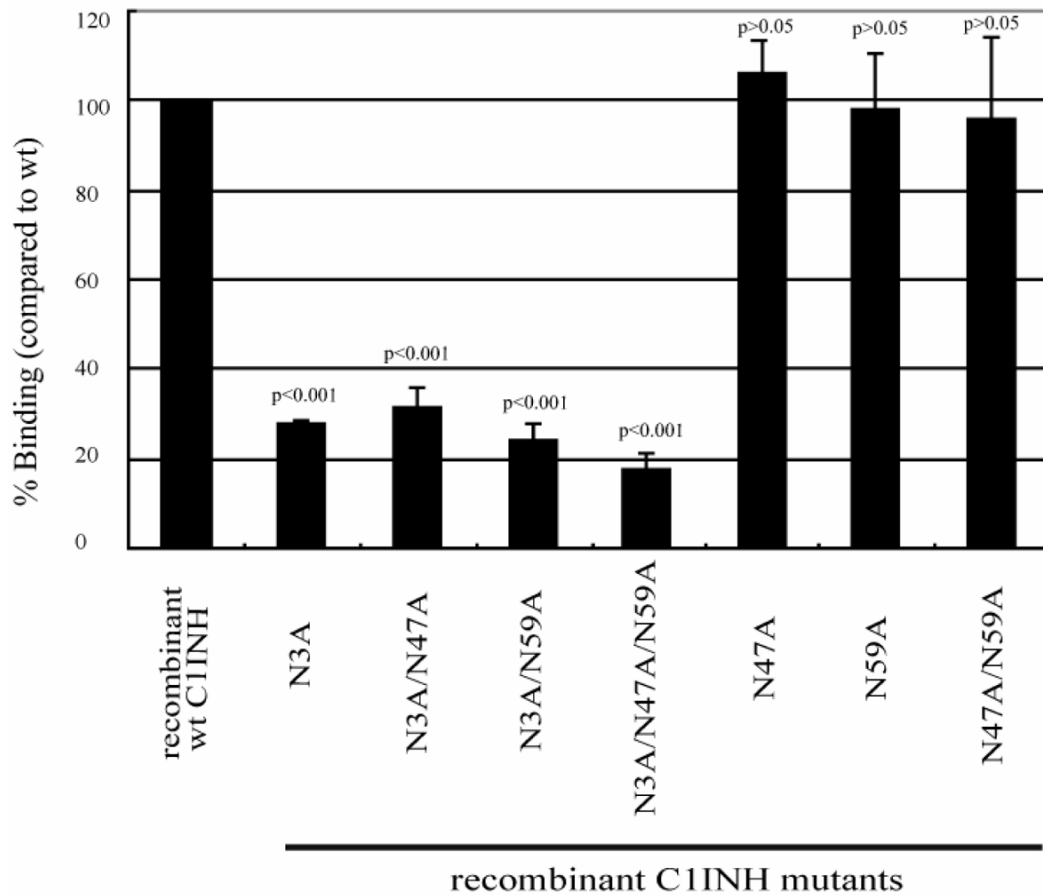


Fig. 3. Binding of C1 inhibitor Asn substitution mutants to immobilized LPS. LPS was immobilized on the surfaces of polyvinyl chloride plates as described in Materials and Methods. Binding was detected using an anti-human C1 inhibitor antibody followed by goat anti-rabbit IgG conjugated with horseradish peroxidase, with absorbance measured at 490 nm. Results (level of binding as a percentage of the binding of recombinant wild type C1 inhibitor [wt C1INH]) were expressed as the means \pm SD from at least three independent experiments.

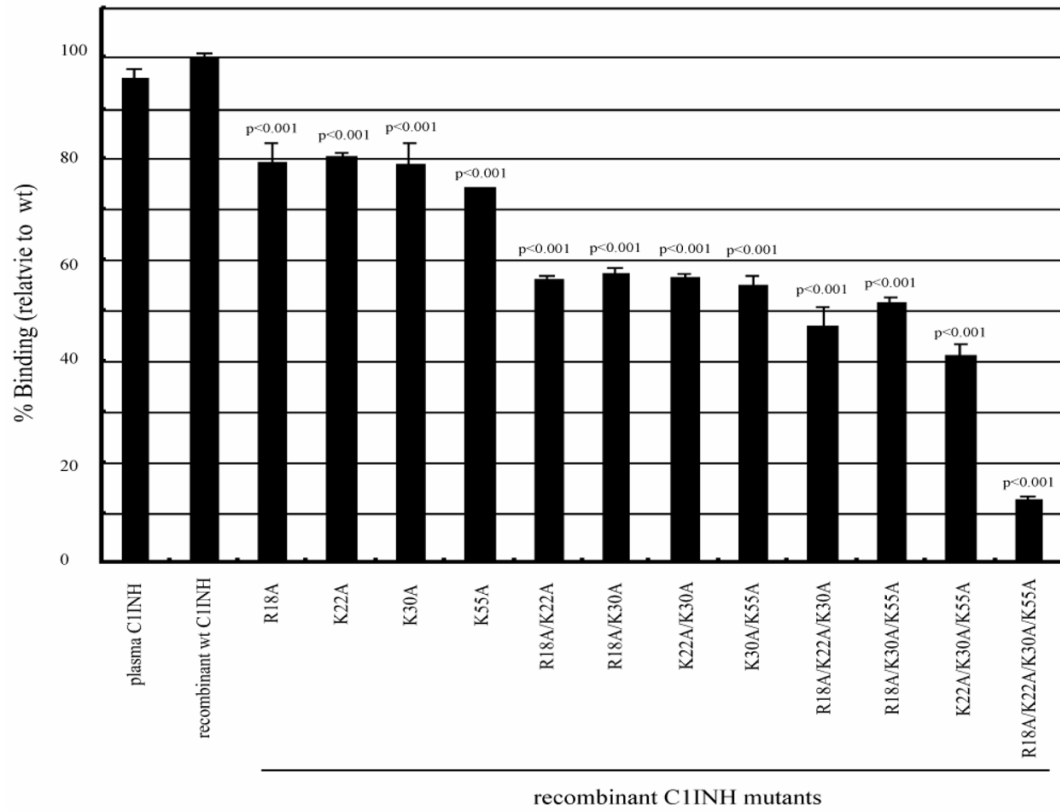


Fig. 4. Binding of C1 inhibitor Arg and Lys substitution mutants to immobilized LPS. Assays were performed and results expressed as described in Fig. 3.

Table 1

C1 inhibitor-mediated modulation of inflammatory disease.

Animal Models	Human Disease
Ischemia-reperfusion injury (myocardial, brain, skeletal muscle)	Myocardial infarction
Vascular leak associated with thermal injury	Capillary leak associated with IL-2 therapy
Gram negative bacterial sepsis and endotoxin shock	Sepsis
Hyperacute transplant rejection	Cardiopulmonary bypass Traumatic and hemorrhagic shock

Table 2

C1 inhibitor: interactions unrelated to protease inhibition.

Component	Potential Biologic Function
Extracellular matrix proteins (type IV collagen, laminin, entactin, fibrin)	Retain C1 inhibitor at inflammatory sites
C3b	Alternative pathway regulation
E and P selectins	Inhibition of leukocyte rolling and transmigration
Gram negative bacteria and endotoxin	Protection from sepsis and endotoxin shock