TAGGED IGA1 PROTEASES

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ABSTRACT

The present invention discloses the use of bacterial IgA1 proteases to treat IgA1 deposition in tissue and organs. Bacterial IgA1 proteases specifically cleave IgA1 molecules and thus provide a means to specifically cleave and remove IgA1 deposits. Accordingly, therapeutic agents for the treatment of diseases characterized by IgA deposition are provided. In particular, therapeutic agents to treat IgA nephropathy, Dermatitis herpetiformis (DH), and Henoch-Schoenlein purpura (HS) are disclosed.
IgA1 Hinge Region

Amino acids 217-241

1. Clostridium Rasmusum
2. Prevotella species
3. Streptococcus pneumoniae
   Streptococcus saguis
4. Haemophilus Influenzae (1)
   Haemophilus aegyptitus
5. Ureaplasma urealyticum
   Neisseria meningitidis (2)
   Neisseria gonorrhoeae (2)
   Haemophilus Influenzae (2)
6. Neisseria meningitidis (1)
   Neisseria gonorrhoeae (1)

FIG. 1
Pore in bacterial outer membrane

Autocatalytic processing site

IgA protease enzyme active site

Release of active IgA protease by autocatalytic processing

FIG. 2A
Introduction of 6-His stretch into active IgA protease

Autocatalytic processing is normal

Anti-6 His monoclonal antibody (mAb) prepares complex of active enzyme.

This will be infused to target kidney IgA1 deposits in IgA nephropathy.

Amino acid code:
V = valine; S = serine;
P = proline; and H = histidine

FIG. 2B
Schematic diagram showing *H. influenzae* Rd IgA protease precursor contains 4 sections: signal sequence, enzyme domain, α-domain, and β-domain. Active site of the protease is near N-terminus of the enzyme domain (arrow). Top of the diagram shows details of the protein sequence mutation. 6xHis epitope is 2 residues away from the main autocatalytic site, a site.
Haemophilus influenzae Rd protein sequence

MLNKKFKLNFIALTVAYALTPYTEAALVRRDDVYQRIFRDAENKGRFSVGATNVEND
KNNHSLGNVLPQMPFMDSVVDVVKRAITLPQYVYVGVKVSNVSNHSLHFGNLNGN
MNNGNAKSHRDVSVSENRYFSEVKEVTKLNGNVATDQTPKRRBDDYMPRLDKF
VTEVAPIEASTASSDAGTYNDQNKKYPAFVRLGGSGSQQTFIYKKGDNYSLNLNHEVGNNL
KLVPDARYITYIGLAQPTVKVNNENGLGIFNGSKEEBSEHDPSKGLQDSPTLYAVLIGDSP
LFVYDREWKGKWLFLGSGYDWAQYNGKKSQWENITYKPEFAKTVDKDTAGSLTGISTQ
YNWNPQTGKTSVISNNGSNLVNFSDQSSTDKSNHNGKSLTGRTLNLNNIDQGA
GGGLFFEGDYEVKGTSDSTTWTKGAGVSGADTVTWTKVHNPKSRLAKGKGLVSEGK
GENKSGLKVGDGTILKQADDNKNVKAQSFQVGHGRTVLNDKQVDPNSYFGF
RGGLRDLANGNNLTFEHIRNIDDGARLVLVNLNSKSTVTITGSLLTPNTTPYNDAPDE
DNYPARFRJGQDQYLLNLNLYTLYARLKGASTRELPKNSGSSNENLYMGKTSDEA
KRNVMMINHNERMNGFNGYFGEBSGKNNNGLNVYFKGKSEQNRFLLTGTNLNLNGDLK
VEKGTTLFLSGRPITPHARDIASSSTKDDQHFAENVEVeddWINRNFEATNINVTNNATLYSQRN
VANITSNASNADSNKHYGKAGTVRSDYTGYVTCTTDKLSKALNSFN
ATNVSQNVNLGSNGANVFLGLNLFGSTQGNSVRQVLTENSHWHTLDGSNVQNLNLNKDG
GHITLNAQNDANKVTYNTLTNSLNSGNSFYFYLTDLSNKQGDKVVTQSATGNFTLQY
VAKTLTGEPTKNEITLHSDASNATNLNNSLVLGNTDQGWYKLRNVENYGLYNPE
VEKRNQTVDDTNTNPQADVSPSVSNSENSBIEAVETPVPAPAPTSSETETVEANHKS
QKSKTSVEKNDQEDATETQQGEBVQAKPSVKANTQPITBEVAQGSETETQTTBETKAKVE
VEKEAKVEKDEIQEFQPASQMEQAEKPAKVEQSTKDKEETVQVAQQPQTQSTTVAA
EAETSPSNKPAEETQPSKEATQVPTVPVSVKNNQNTENTQDQTERKAKVEKTEKTEＱEPP
QVASQASPKQPSEQSETVQPQALSESENVTPYMSAEVQAOQLQQTSTASATSTKQPAPENSI
NTGSAATAITETAEKSDKPQETETAASTEDASQHKANTVADSNVANNSESSDPSKRSSSIS
QPQBTSAEBTTAASDEETIAADNKRPSKRNSRSVSRSEPVTNSGRSTRVALRDLST
NTNAVISDAMAKAQFVANLVKAPSQHISQLEMNENEGQVNVVWSNTSMNENYSSQY
RREFSKSTQTOGRWDQTEAMQVLFYSVTVRNSRNGKDAKSKNLQAVNFYSKYYAD
NHWYLGDLGYGKFGSOHKLTKHNAKFARHTAOFLTAGKAFLNGNFITPGTVGVRSYLYS
ANFAMALAKDRKYNPSKVTAFAQVDSLSTYHGLGEFSVTQLSARYDNTQGSGKINNNV
QYDFAYVENQQQYNAGLKLKYHNKLSSLJGGLTAKQAEKQTKAELKLSFSF

FIG. 5
FIG. 6A

Haemophilus influenzae Rd nucleotide sequence

atgctaaaa aaaaattcga actcaatatt attgagcctt atggctccta cggcattaacc
cctatacg aagctgggtt atgtgagac gatgtgatg atczaatatt tcgtgatttt
gcagaaaaata aaggggnaat ttcgtgggtt gczaaacaatg tgggaagtgag agataaaaat
aaccactttc taggcaatgt ttaccaatg gccctcgca tgattgtttagtagtgtagt

gatgtgata aacgcctgca cacattgata aactcaacat atgtatgagg tgaanaacac
gttagtaac ccgctgatgta actacatatt ggggaacttta atggcaatat gaaatgtggc
aatgtcata ccacaaatatt gaatggaaag gcagaattc ctgaagcata aactcaaaa

gcgcggtaag actactattt gccacgctctt gataaaatttgg ttaaccaagt tgaccaata
gagccttcaag ctgcaagtag tgaagcgtggc acataataag atcacaataa atatcgtgtc

ttgtaagac taggaaggtgg tagczaatatt atttataaaa aaggggataa ttagcagetta

ttttataaa atataaggtt ggggcaatat ttcgaataat tgggaggggga tgcctataacc
tatggtattt caggcaacaa ttaataagta aaccngaaata ataatggact aatggggtttt
ggcaattcga aagaggaacc aacggataa ccacgataca aaaaagaaa atataacgattccatgattcgtt gaaaccagttt
ggggaggtt gttgtgggtt acggcactt tacgggctta ccacgtggcag tataagttat gaaaaagaaa ataatggcgtttg
ggcaattcga aacgggaacc aacggataa cccatgattc atgagaata tataatcgat ggaatgtttg cccatatattgggagttt

ggagaattt ttaggggca actggtgcctt cccatatattggatag tagtaaaa atatataggac

gagttaaaa tttatatccca gtagcattt cccatatattgggctttt tagtaaaa atatataggac
gagaattt cattcataatc cccatatattgggctttt tagtaaaa atatataggac
gagaattt cattcataatc cccatatattgggctttt tagtaaaa atatataggac
gagaattt cattcataatc cccatatattgggctttt tagtaaaa atatataggac
gagaattt cattcataatc cccatatattgggctttt tagtaaaa atatataggac
FIG. 6B

actttgcata gtaccaacctg gaaaggagct ggcttttctg tttgctatg aaaaaaagacta
gcgtggaaaag tacataaccc gaaatctgat cgtttagct aatactgcc aaagcagactta
tagctagaag gaaagggaga aaataaaggt tgcacaaaag tggcgtagtc actgtttatc
taaaccaac aagctgtgac caataataa gtttaagcct tttaaatagaa aggtataga
tagccgtgct caactgtgct actaatgtg gataacaaag tagatccaa tacctttcct
attggcttta gagggtgctc attagatgc aatggcata atctctactt taacaatcata
cgtaatac agatggtggc aagactagta aatcacaata ccagcaaaaaa ctctactgtc
acaattacgt gggaaggtct aattacagat ccaaatcata ttactccata taataatagac
gcaccagagt agataatacc ttatgcttt cgaacggatta aangatggagc ccagctctat
 ttatatttgg aaaaattcaat ttatattcg ttaagaaag gtgcggagc acgcttcat
taaccaaaa aatggtgccag aagaagctgg aattgctgag tataagaattaa aacagcggcata
gggaattgatt ccacagcaga gataaggtgc cccttacaggt ttaataaggat
ttttgccg aggaagag ggctaaattaa tataatcctc cttaagggca
agtgacccaa atcgcttctt attaacaagc gggaacaacc ttaatggcga ttaaaagggt
gaaaaagcgca cattattct cttggtcaga ccaacacgc acgcaaggga taattgcaggt
atttctgaa caaaaaatca ttaacacttt gtcgaaaaata atgaagttgt agtgaagagat
gactggatta acogcaacc taaagcaaca aatattaatg taaccacata ccgcaaccctt
tatcagggtc gcaatgttgcc aacactactc tcaaatataca cacgtttctg ctaattgcara
gtacatattg gcataaaagc agggcctacc gttggtgtac gttctgacta taccggctat
gtacactgca ctactgcaca gttactccg caagccctta atagcatgaa cgccaccaat
atlacgacg atgaaaatc atcaggttac gcaaaacttgc tcttaggca agctaatcct
ctcgccaa ttaggcgcac gggaaatagc cagagctgt taaacgaaaa atagcacttgg
catttacag cgagtcagca tggtaatcag ttaaatttg gcaagggcca ttcgatcata
aatgcacaaa acgatgcaaataaagactac ccgtgactgt gatagcctta
tcagttactc gttttttctaa ttttttttc attaacaaaa cgccaaagtt
FIG. 6C

gttgtaacta aatccgccac aggtaacttt acattacaag tggcagataa aacgggccag
cctcaaaaaa atgaactcag gotttttagct gcgtaaatg ctacaagaaa taattttgat
gtgcattag tgggaattac cgttgatta agtgcgtgga aatataaaat acgtaatttt
aatggaagt tcccattgtga taacccagag gtggaaaaaa aaaaatcaac aagctgatag
acaatataca caaaccctaa taatacaaa gctgatgtgc ctacggtacc aagtaacat
aagaaatatgc ccctgtgtga aacaccagtt ccacacacctg cgcctgtcac accactcagag
acaactgaa cagtggctga aatagtagta caagaaagta aaacagtaga gaanaagag
cagacgcaa cagacacac agctcataa aataaagttt gaaagaagttt cagacgacgacg
taaacatca aactcaagttt aatggaagttg cttcttaaag tttaagagtc gcgctgatag
caccgatcgc ttcagctgag ttcagcagt caggtacgctt cttggtgagtt gcgatgctttg
cggccaagaa aacccctgag aacccctgag aacccctgag aaggtcctct cctcctctttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
FIG. 6D
Saline-treated

Goat IgG

Human IgA

Human IgA

IgA protease-treated

FIG. 7
TAGGED IG A1 PROTEASES

PRIORITY

[0001] This application is a CIP of International Application Number PCT/US04/06615, filed Mar. 5, 2004, which claims priority to U.S. Ser. No. 60/453,055, filed Mar. 7, 2003, the contents of which are incorporated herein in their entirety.

GOVERNMENT SUPPORT

[0002] The invention was supported, in whole or in part, by a grant NIH RO1 DE 09677 from NIH, NIDCR. The U.S. Government has certain rights in the invention.

BACKGROUND

[0003] Immunoglobulin A1 (IgA1) deposition in human tissues and organs is a characteristic of many human diseases including IgA nephropathy, Dermatitis herpetiformis (DH), and Henoch-Schoenlein purpura (HS). IgA1 deposition is responsible for a variety of clinical manifestations such as renal failure, skin blistering, rash, arthritis, gastrointestinal bleeding and abdominal pain.

[0004] There are several available treatment options for patients with abnormal IgA1 deposition. These include administration of corticosteroids that have immunosuppressive and anti-inflammatory properties, dietary fish oil supplements that reduce renal inflammation, and angiotensin converting enzyme inhibitors that reduce the risk of progressive renal disease and renal failure. Such treatments do not directly act on IgA1 deposits in tissue or organs.


[0006] Thus, despite advances in the field, there is a need in the art for therapeutic agents that can be used to treat IgA1 deposition diseases.

SUMMARY OF THE INVENTION

[0007] The present invention discloses the use of bacterial IgA1 proteases to treat IgA1 deposition in tissue and organs. Bacterial IgA1 proteases specifically cleave IgA1 molecules and thus provide a means to specifically cleave and remove IgA1 deposits. Accordingly, therapeutic agents for the treatment of diseases characterized by IgA1 deposition are provided. In particular, therapeutic agents to treat IgA1 nephropathy, Dermatitis herpetiformis (DH), and Henoch-Schoenlein purpura (HS) are disclosed.

[0008] Disclosed herein is a nucleic acid molecule encoding an IgA1 protease that is fused to an amino acid tag located upstream of an IgA1 protease auto-catalytic cleavage site.

[0009] In one embodiment, the tag, which is fused to the IgA1 protease, is a tag that specifically binds to a protein ligand, such as an antibody or peptide. The tag can be e-Myc, HA, VSV-G, HSV, FLAG, V5, or HIS.

[0010] In one aspect, a pharmaceutical composition for the treatment of IgA1 deposition is provided that comprises an IgA1 protease complexed with an antibody, such as an anti-IgA1 protease antibody.

[0011] In another aspect, a pharmaceutical composition for the treatment of IgA1 deposition is provided that comprises a tagged IgA1 protease that is complexed with a ligand of the tag. The tag fused to the IgA1 protease can be c-Myc, HA, VSV-G, HSV, FLAG, V5, or HIS. Accordingly, the ligand can be an anti-tag antibody such as anti-FLAG, anti-MYC, anti-VSV, anti-HA, or anti-V5. Alternatively, the ligand can be a peptide or non-peptide ligand, such as a chelating molecule.

[0012] In another aspect, a method for treatment of a disease characterized by IgA1 deposition is provided. The method involves administering to a patient a therapeutically effective amount of an IgA1 protease.

[0013] In one embodiment, the method for treatment uses an IgA1 protease fused to a tag complexed with a ligand of the tag, such as an anti-tag antibody. The tag fused to the IgA1 protease can be c-Myc, Flag, HA, VSV-G, HSV, FLAG, V5, or HIS. Accordingly, the anti-tag antibody can be anti-FLAG, anti-MYC, anti-VSV, anti-HA, or anti-V5.

[0014] In another embodiment, the disease characterized by IgA1 deposition is IgA nephropathy, Dermatitis herpetiformis, or Henoch-Schoenlein purpura.

BRIEF DESCRIPTION OF THE DRAWINGS

[0015] FIG. 1 shows the hinge region of IgA1 and the cleavage sites for several IgA1 proteases within the hinge region (SEQ ID NO:1).

[0016] FIG. 2a illustrates the IgA1 protease precursor that undergoes auto-catalytic cleavage and releases a soluble mature IgA1 protease by auto-catalytic cleavage.

[0017] FIG. 2b shows an IgA1 protease wherein a His tag has been fused to the IgA1 protease such that the His tag is located near the carboxyl terminus of the mature IgA1 protease. The soluble IgA1 protease can then be complexed with an anti-His antibody for therapeutic purposes.

[0018] FIG. 3 shows a schematic of the Haemophilus influenzae Rd IgA1 protease precursor protein and shows an amino acid sequence that is upstream from the auto-catalytic cleavage site (site a), original sequence (SEQ ID NO:2). The mutated sequence (SEQ ID NO:3) shows where a His tag has been fused in frame to an IgA1 protease, 2 amino acids upstream from the proteolytic cleavage site. The corresponding nucleic acid sequences of the original sequence (SEQ ID NO:25) and mutated sequence (SEQ ID NO:26) are also shown.

[0019] FIG. 4 shows the PCR site directed mutagenesis fragments that were generated for insertion of a HIS tag into H. influenzae Rd IgA1 protease by conventional ligation techniques.

[0020] FIG. 5 shows the protein sequence of Haemophilus influenzae Rd (SEQ ID NO:4).

[0021] FIG. 6 shows the nucleotide sequence of Haemophilus influenzae Rd (SEQ ID NO:5).

[0022] FIG. 7 shows a photomicrograph of mouse kidneys which demonstrates the removal of IC deposition following treatment with IgA1 protease.

DETAILED DESCRIPTION

[0023] The present invention relates to the use of bacterial Immunoglobulin A1 proteases (IgA1 proteases) to treat diseases that are characterized by IgA1 deposition.

DEFINITIONS

[0024] As used herein, the term “IgA1 protease” refers to a bacterial enzyme that specifically cleaves human IgA1 mol-
ecules. By "specifically cleaves" is meant that the protease cleaves in the hinge region of human IgA1 molecules and generally does not cleave human IgA2 molecules. IgA1 proteases are expressed in gram negative and gram positive bacteria as a single-chain precursor that traverses the bacterial membrane. IgA1 proteases are termed "specifically cleaves" to a fragment or portion of a full length IgA1 protease which retains the specific cleavage activity of the full length IgA1 protease.

[0025] As used herein, the term "located upstream" refers to the spatial parameter of a tag wherein the amino acid tag sequence is located at least 2 amino acids, or 1, or none, amino-terminal to, and up to 50 amino acids amino-terminal to, the IgA1 protease site of auto-catalytic cleavage such that the tag is located 2, or 1, or none, to 50 amino acids upstream from the carboxyl terminus of the soluble, secreted, IgA1 protease.

[0026] As used herein, a "tag" refers to a polypeptide sequence 3 to 40 amino acids in length. A tag can possess a specific binding affinity for a peptide, protein ligand, or a non-peptide ligand. The specific binding affinity permits the IgA1 protease to which it is fused to be complexed to a ligand in order that the IgA1 protease can be detected, isolated, or complexed to an antigen or antibody. Non-limiting examples of tags include c-Myc, HA, and VSV-G, H5V, FLAG, V5, and HIS.

[0027] By "complexed with a ligand" is meant that the IgA1 protease specifically binds to a binding partner, such as an antibody, or a binding molecule. The specific binding partner can be attached to a matrix, such as a bead. The term "specifically binds" refers to the interaction of two molecules, e.g., an antibody or a protein or peptide or a chelating agent, wherein the interaction is dependent upon the presence of particular structures on the respective molecules. For example, when the two molecules are protein molecules, a structure on the first molecule recognizes and binds to a structure on the second molecule, rather than to proteins in general. "Specific binding", as the term is used herein, means that a molecule binds its specific binding partner with at least 2-fold greater affinity, and preferably at least 10-fold, 20-fold, 50-fold, 100-fold or higher affinity than it binds a non-specific molecule.

[0028] By "detected" is meant a manner of determining the presence or absence of the tag, such as "detection" by western blot with anti-tag monoclonal antibody, detection by immunofluorescence, or detection because the tag itself fluoresces. Non-limiting examples of suitable tags according to the invention include c-Myc, Flag, HA, and VSV-G, H5V, FLAG, V5, and HIS.

[0029] By "isolated" is meant that the IgA1 protease is separated from bacterial cell materials, such as cell membrane and any protein or nucleic acid present in bacterial growth media. Examples of non-limiting methods of isolation include the isolation of an IgA1 protease that has a poly-Histidine tag using a metal-chelate resin or beads, immunoprecipitation, and affinity column purification using anti-tag antibodies.

[0030] As used herein, the term "antibody" refers to an immunoglobulin molecule, or fragment thereof, that is capable of binding antigen, such as a tag or IgA1 protease. The term "antibody" is intended to include whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with a vertebrate, e.g., mammalian, protein. Antibodies can be fragmented using conventional techniques. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a certain protein. Non-limiting examples of such proteolytic and/or recombinant fragments include Fab, Fab', Fv, dAbs and single chain antibodies (scFv) containing a V\textsubscript{L} and V\textsubscript{H} domain joined by a peptide linker. The scFvs may be covalently or non-covalently linked to form antibodies having two or more binding sites. Thus, antibodies include polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies. Herein, the term "anti-tag antibody" refers to an antibody that specifically binds to a tag.

[0031] As used herein, the term "IgA1 deposition" refers to the accumulation of IgA1 immunoglobulin in aggregated or non-aggregated form in human tissue or organs.

[0032] Herein, a "disease characterized by IgA1 deposition" refers to any disease in which IgA1 deposition occurs, such as, but not limited to IgA nephropathy, Dermatitis herpetiformis, and Henoch-Schoenlein purpura.

[0033] As used herein, "IgA nephropathy" refers to a kidney disease characterized by IgA1 deposits within the kidney.

[0034] As used herein, "Dermatitis herpetiformis" refers to a chronic blistering disease associated with deposits of IgA1 in skin and other tissues.

[0035] As used herein, "Henoch-Schoenlein purpura" refers to a skin and kidney disease characterized by deposition of IgA1 in skin tissue and kidney tissue.

[0036] As used herein, a "pharmaceutical composition" comprises a pharmacologically effective amount of an active agent and a pharmaceutically acceptable carrier. As used herein, "pharmacologically effective amount," or simply "effective amount" refers to that amount of an agent effective to produce the intended pharmacological, therapeutic or preventive result. For example, if a given clinical treatment is considered effective when there is at least a 25% reduction in a measurable parameter associated with a disease or disorder.

I. IgA1 Proteases

[0037] Herein, IgA1 proteases are used to treat diseases characterized by IgA1 deposition. IgA1 proteases are bacterial enzymes that specifically cleave human IgA1 molecules. Human IgA2 is resistant to nearly all known IgA1 proteases because IgA2 molecules lack a hinge region that is present in all IgA1 molecules. The hinge region of IgA1 molecules consist of a string of amino acids, that contain cleavage sites for a variety of IgA1 proteases, as illustrated in FIG. 1. IgA1 proteases are expressed in gram-negative bacteria as a single-chain precursor that traverses the inner membrane of bacteria. The precursor protein then inserts itself into the outer bacterial membrane and undergoes auto-catalytic cleavage, releasing a mature soluble IgA1 protease (FIG. 2a). IgA proteases of gram-positive bacteria are also useful in this invention, although they do not have an auto-catalytic secretion mechanism. For such proteases, an epitope tag may be added into the enzyme protein.

[0038] In one embodiment of the present invention a tag sequence is fused in frame to an IgA1 protease, such that the tag sequence is located near the carboxyl terminus of the secreted IgA1 protease (FIG. 2a). FIG. 3 shows a schematic
of the Haemophilus influenzae Rd IgA1 protease precursor protein illustrating that a tag sequence (e.g. His tag) is fused in frame to an IgA1 protease upstream of the auto-catalytic cleavage sites a, b, and c.

[0039] A variety of bacteria produce IgA1 proteases and are useful in the present invention. These include, but are not limited to Haemophilus influenzae type 1 and 2, Neisseria meningitidis type 1 and 2, Neisseria gonorrhoeae, Streptococcus pneumoniae, Streptococcus sanguis, Clostridium ramosum, Prevotella melaninogenicca, and Ureaplasma urealyticum.

[0040] The IgA1 protease nucleotide sequences of the present invention can be obtained from any bacteria where an IgA1 protease is expressed, as long as the IgA1 protease is capable of cleaving human IgA1 molecules. Nucleotide sequences encoding IgA1 proteases from numerous bacterial strains have already been identified and include: Clostridium ramosum (Genebank Accession, NY028440); Ureaplasma urealyticum (Genebank Accession, NC_002162); Haemophilus influenzae (Genebank Accession, X59800) and bacterial strains Rd (Genebank Accession, NC_000907), 7768 (Genebank Accession, AF274862), 6338 (Genebank Accession, AF27486), 2500 (Genebank Accession, AF274859), aegyptius (Genebank Accession, AF369907), 8625 (Genebank Accession, A000714), HK24 (Genebank Accession, X82487), Da66 (Genebank Accession, X82467), HK635 (Genebank Accession, X82488), and other deposited sequences from unidentified strains (Genebank Accession numbers, X59800, X82488, X64357, M87492, M87491, M87490, and M87489); Neisseria meningitidis (Genebank Accession number AF235032) and bacterial strains, Z2491 (Genebank Accession, NC_003316), B40 (Genebank Accession, AF012221), Z4009 (Genebank Accession, AF012210), Z4018 (Genebank Accession, AF012209), Z4400 (Genebank Accession, AF012208), Z3524 (Genebank Accession, AF012207), Z4024 (Genebank Accession, AF012206), Z3910 (Genebank Accession, AF012205), Z3906 (Genebank Accession, AF012204), Z2549 (Genebank Accession, A001740), IHN341 (Genebank Accession, A001739), NL3327 (Genebank Accession, A001738), NL3293 (Genebank Accession, A001737), HK24 (Genebank Accession, X82487), ETTH (Genebank Accession, X82469), NGO93 (Genebank Accession, X82482), NCGB (Genebank Accession, X82479), NGI17 (Genebank Accession, X82483), HI96 (Genebank Accession, X82475), HI54 (Genebank Accession, X82473), HI48 (Genebank Accession, X82480), HI13 (Genebank Accession, X82474), NGC65 (Genebank Accession, X82484), NCGB (Genebank Accession, X82484), SM1894 (Genebank Accession, X82476), EN3771 (Genebank Accession, X82478), NG44/76 (Genebank Accession, X82481), SM1166 (Genebank Accession, X82486), HF159 (Genebank Accession, X82471), 81139 (Genebank Accession, X82477), HF117 (Genebank Accession, X82470), SM1027 (Genebank Accession, X82472) and Genebank Accession number, AF235032; Neisseria gonorrhoeae (Genebank Accession number, A12416) and bacterial strain, MS11 (Genebank Accession, S75490); Streptococcus pneumoniae (Genebank Accession number, X94099) and bacterial strains MGAS315 (Genebank Accession, NC_004070), R6 (Genebank Accession, NC_003098); and Streptococcus sanguis (Genebank Accession, NC_003098) and bacterial strains SK85 (Genebank Accession, Y13461), SK49 (Genebank Accession, Y13460), SK4 (Genebank Accession, Y13459), SK162 (Genebank Accession, Y13458), SK161 (Genebank Accession, Y13457), SK115 (Genebank Accession, Y13456), and SK112 (Genebank Accession, Y13455). IgA1 proteases of the invention may be utilized as described herein either without or with an attached tag as described hereinbelow.

Vector Construction

[0041] In the present invention, sequences encoding IgA1 proteases are cloned into vectors suitable for expression of the protein, such that soluble IgA1 protease can be produced and isolated. The vectors can be constructed using standard methods (Sambrook et al., Molecular Biology: A Laboratory Approach, Cold Spring Harbor, N.Y. 1989; Ausubel, et al., Current protocols in Molecular Biology, Greene Publishing, 1995), guided by the principles discussed below. It is recognized that conventional ligation techniques are used to insert DNA sequences encoding IgA1 protease into a bacterial cloning and/or expression vectors.


[0044] PCR is well known in the art (Mulhis and Falloona, Methods Enzymol., (1987), 155: 335, herein incorporated by reference). In general, oligonucleotide primers useful according to the invention are single-stranded DNA or RNA molecules that hybridize selectively to a nucleic acid template that encodes IgA1 protease to prime enzymatic synthesis of a second nucleic acid strand. The primer is complementary to a portion of a target molecule present in a pool of nucleic acid molecules from the bacterial genome. It is contemplated that primers are prepared by synthetic methods, either chemical or enzymatic. Alternatively, such a molecule or a fragment thereof is naturally occurring, and is isolated from its natural source or purchased from a commercial supplier. Mutagenic oligonucleotide primers are 15 to 100 nucleotides in length, ideally from 20 to 40 nucleotides, although oligonucleotides of different length are of use. Preferably, the primers also comprise a unique restriction enzyme sequence.

[0045] Typically, selective hybridization occurs when two nucleic acid sequences are substantially complementary (at least about 65% complementary over a stretch of at least 14 to
25 nucleotides, preferably at least about 75%, more preferably at least about 90% complementary). See Kanelhisa, Nucleic Acids Res., (1984), 12: 203, incorporated herein by reference. As a result, it is expected that a certain degree of mismatch at the priming site is tolerated. Such mismatch may be small, such as a mono-, di- or tri-nucleotide. Alternatively, it may comprise nucleotide loops, which we define as regions in which mismatch encompasses an uninterrupted series of four or more nucleotides.

Overall, five factors influence the efficiency and selectivity of hybridization of the primer to a second nucleic acid molecule. These factors, which are (i) primer length, (ii) the nucleotide sequence and/or composition, (iii) hybridization temperature, (iv) buffer chemistry and (v) the potential for steric hindrance in the region to which the primer is required to hybridize, are important considerations when non-random priming sequences are designed.

There is a positive correlation between primer length and both the efficiency and accuracy with which a primer will anneal to a target sequence: longer sequences have a higher melting temperature (TM) than do shorter ones, and are less likely to be repeated within a given target sequence, thereby minimizing promiscuous hybridization. Primer sequences with a high G-C content or that comprise palindromic sequences tend to self-hybridise, as do their intended target sites, since unimolecular, rather than bimolecular, hybridization kinetics are generally favored in solution: at the same time, it is important to design a primer containing sufficient numbers of G-C nucleotide pairings to bind the target sequence tightly, since each such pair is bound by three hydrogen bonds, rather than the two that are found when A and T bases pair. Hybridization temperature varies inversely with primer annealing efficiency, as does the concentration of organic solvents, e.g. formamide, that might be included in a hybridization mixture, while increases in salt concentration facilitate binding. Under stringent hybridization conditions, longer probes hybridize more efficiently than do shorter ones, which are sufficient under more permissive conditions. Stringent hybridization conditions typically include salt concentrations of less than about 1M, more usually less than about 500 mM and preferably less than about 200 mM. Hybridization temperatures range from as low as 0°C to greater than 22°C, greater than about 30°C, and (most often) in excess of about 37°C. Longer fragments may require higher hybridization temperatures for specific hybridization.

As several factors affect the stringency of hybridization, the combination of parameters is more important than the absolute measure of any one alone.

Primers preferably are designed using computer programs that assist in the generation and optimization of primer sequences. Examples of such programs are “PrimerSelect” of the DNASTar™ software package (DNASTar, Inc.; Madison, Wis.) and Oligo 4.0 (National Biosciences, Inc.). Once designed, suitable oligonucleotides are prepared by a suitable method, e.g. the phosphoramidite method described by Beaucage and Caruthers (1981 Tetrahedron Lett., 22: 1859) or the triester method according to Matteucci and Caruthers (1981) J. Am. Chem. Soc., 103: 3185, both incorporated herein by reference, or by other chemical methods using either a commercial automated oligonucleotide synthesizer or VLSIPS™ technology.

PCR is performed using template bacterial DNA (at least 1 pg: more usefully, 1-1000 ng) and at least 25 pmol of oligonucleotide primers: it may be advantageous to use a larger amount of primer when the primer pool is heavily heterogeneous, as each sequence is represented by only a small fraction of the molecules of the pool, and amounts become limiting in the later amplification cycles. A typical reaction mixture includes: 2 μl of DNA, 25 pmol of oligonucleotide primer, 2.5 μl of 10X PCR buffer 1 (Perkin-Elmer, Foster City, Calif.), 0.4 μl of 1.25 mM dNTP, 0.15 μl (or 2.5 units) of Taq DNA polymerase (Perkin Elmer, Foster City, Calif.) and deionized water to a total volume of 25 μl. Mineral oil is overlaid and the PCR is performed using a programmable thermal cycler.

The length and temperature of each step of a PCR cycle, as well as the number of cycles, is adjusted in accordance to the stringency requirements in effect. Annealing temperature and timing are determined both by the efficiency with which a primer is expected to anneal to a template and the degree of mismatch that is to be tolerated; obviously, when nucleic acid molecules are simultaneously amplified and mutagenised, mismatch is required, at least in the first round of synthesis. An annealing temperature of between 30°C and 72°C is used. Initial denaturation of the template molecules normally occurs at between 92°C and 99°C for 4 minutes, followed by 20-40 cycles consisting of denaturation (94-99°C for 15 seconds to 1 minute), annealing (temperature determined as discussed above: 1-2 minutes), and extension (72°C for 1-5 minutes, depending on the length of the amplified product). Final extension is generally for 4 minutes at 72°C, and may be followed by an indefinite (0-24 hour) step at 4°C.

Subsequent to PCR amplification, the DNA can be isolated by standard means, such as gel electrophoresis, or column purification. The DNA encoding the bacterial IgAI protease can then be digested with appropriate restriction enzymes and ligated into a suitable cloning and/or expression vector.

Vectors and Host Cells

Any vector can be used in the present invention. As used herein, vector refers to a discrete element that is used to introduce heterologous DNA into bacterial cells for the expression and/or replication thereof. Numerous vectors suitable for the present invention are publicly available, including bacterial plasmids and bacteriophage. Each vector contains various functional components, which generally include a cloning (or “polylinker”) site, an origin of replication and at least one selectable marker gene. If given vector is an expression vector, it additionally possesses one or more of the following: enhancer element, promoter, transcription termination and signal sequences, each positioned in the vicinity of the cloning site, such that they are operatively linked to the gene encoding an IgAI protease according to the invention.

Both cloning and expression vectors generally contain nucleic acid sequences that enable the vector to replicate in one or more selected host cells. Typically in cloning vectors, this sequence is one that enables the vector to replicate independently of the host chromosomal DNA and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria. For example, the origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria.

Advantageously, a cloning or expression vector may contain a selection gene also referred to as a selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective
culture medium. Host cells not transformed with the vector containing the selection gene will therefore not survive in the culture medium. Typical selection genes encode proteins that confer resistance to antibiotics and other toxins, e.g. ampicillin, neomycin, methotrexate or tetracycline, complement auxotrophic deficiencies, or supply critical nutrients not available in the growth media.

Since the replication of vectors according to the present invention is most conveniently performed in E. coli, an E. coli-selectable marker, for example, the β-lactamase gene that confers resistance to the antibiotic ampicillin, is of use. These can be obtained from E. coli plasmids, such as pBR322 or a pUC plasmid such as pUC18 or pUC19.

Expression vectors usually contain a promoter that is recognized by the host organism and is operably linked to the coding sequence of interest. Such a promoter may be inducible or constitutive. The term “operably linked” refers to a juxtaposition wherein the components described are in a relationship permitting them to function in their intended manner. A control sequence “operably linked” to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences.

Promoters suitable for use with prokaryotic hosts include, for example, the β-lactamase and lactose promoter systems, alkaline phosphatase, the tryptophan (trp) promoter system and hybrid promoters such as the tac promoter. Promoters for use in bacterial systems will also generally contain a Shine-Dalgarno sequence operably linked to the coding sequence. A preferred promoters of the present invention are the isopropylthiogalactoside (IPTG)-regulatable promoters.

Any bacterial strain is considered a suitable host cell for expression of and cloning of the IgA1 proteases of the present invention. An exemplary host is E. coli.

Introduction of Vectors to Host Cells.

Vectors can be introduced to selected host cells by any of a number of suitable methods known to those skilled in the art. For example, vector constructs may be introduced to appropriate bacterial cells by infection using bacteriophage vector particles such as lambda or M13, or by any of a number of transformation methods for plasmid vectors or for bacteriophage DNA. For example, standard calcium-chloride-mediated bacterial transformation is still commonly used to introduce naked DNA to bacteria (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.), but electroporation may also be used (Ausubel et al., Current Protocols in Molecular Biology, (1988), (John Wiley & Sons, Inc., NY, N.Y.)).

Purification of Soluble IgA1 Protease

After introduction of an expression vector encoding IgA1 protease into a suitable bacterial host cell, the bacteria are propagated for the overproduction of soluble IgA1 protease by standard means (Sambrook et al., Molecular Biology: A laboratory Approach, Cold Spring Harbor, N.Y. (1989) and Ausubel et al., Current protocols in Molecular Biology, Greene Publishing, (1995), herein incorporated by reference). Briefly, bacteria, such as E. coli, which harbor an expression vector that encodes IgA1 protease, or bacteria that have DNA encoding IgA1 protease integrated into the bacterial genome, are grown in bacterial growth media at 37°C. When the bacterial cultures reach log phase, soluble IgA1 protease is purified from the growth media by means well known in the art.

For example, H. influenzae Rd bacteria that express 6xHis-IgA1 protease are cultured as 20 L (two 10 L) in a fermentor charged with brain-heart infusion broth supplemented with NAD and hemin. The cells are grown at 37°C until they reach stationary phase, 16-20 h. The bacterial mass is then removed with a Pellicon system, and each 10 L of culture supernatant containing the active enzyme is concentrated to 400 ml. The buffers are adjusted to have the protein in 25 mM Tris/HCl buffer, pH 7.5, with 0.05% NaN3. To remove unwanted protein, 80 ml batches of this concentrate are applied to a 40 ml bed-volume DE-52 anion-exchange column equilibrated in 25 mM Tris buffer. IgA protease does not bind to this column, and is collected as flow through using 500 ml Tris buffer. Yield of recovery is typically 85-90% based on assay using human IgA substrate. Ammonium sulfate is then used to precipitate the enzyme (60% saturation ammonium sulfate; 390 gm per L). The precipitate is dissolved with the following buffer: 50 mM sodium phosphate, 12.5 mM Tris/HCl, 0.3 M NaCl and 0.025% sodium azide, adjusted to pH 7.5, and the enzyme is then dialyzed against this buffer for several days. The final volume of enzyme solution is approximately 200 ml for each 10 L of starting culture.

For affinity purification, 40 ml aliquots of the enzyme solution is applied to Ni-NTA-agarose in a column with bed volume of 40 ml. The bound enzyme is washed three times with volumes of 500 ml of buffers containing 50 mM sodium phosphate, 12.5 mM Tris/HCl, 0.3 M NaCl and 0.025% sodium azide. pH of these buffer washes is reduced in stepwise fashion, beginning with pH 7.5, then 6.6, then 6.0, intended to remove weakly adherent, non-enzyme proteins from the nickel ligand. The final wash again uses buffer at pH 7.5, now 200 ml. The 6xHis-IgA protease is then eluted from Ni-NTA agarose using 50 ml 0.1 M imidazole in 50 mM Tris/HCl, pH 7.5. The recovered enzyme is concentrated by positive pressure filtration using a 100 kDa cut-off Centricron membrane, washed three times with 25 mM Hepes, pH 7.15, and then stored in Hepes buffer.

Assay for IgA1 Protease Activity

The IgA1 protease is tested for enzyme activity by standard means as described in Plant, AG and Bachovchin WW, IgA-specific prolyl endopeptidases: serine type. Methods Enzymol. 1994; 244:137-51, herein incorporated by reference. The assay can be performed with purified protease or IgA1 protease present in bacterial growth media. An IgA1 protease has sufficient activity to be useful according to the invention if it has one Unit activity, with Unit equal to one microgram human IgA1 cleaved per minute at 37°C.

II. Tagged IgA1 Protease

In one embodiment, the IgA1 protease is fused to a tag, although the invention may be practiced in the absence of a tag and/or ligand complexed thereto. Fusion a tag to the IgA1 proteases of the present invention aids in purification and detection of the protease, as well as provides a means in which the IgA1 protease can form a complex with a ligand, such as an anti-tag antibody, for therapeutic purposes.

To generate an IgA1 protease comprising a tag, a sequence encoding a tag can be ligated in frame to a sequence encoding an IgA1 protease using conventional molecular
biology techniques. The tag sequence is ligated upstream of the DNA sequence encoding the IgA1 protease auto-cataytic cleavage site such that, upon cleavage of the IgA1 protease precursor protein, a soluble IgA1 protease comprising a tag is secreted into bacterial growth media.

[0066] Alternatively, an IgA1 protease comprising a tag is generated by PCR-based site directed mutagenesis. There are a number of site-directed mutagenesis methods known in the art which allow one to mutate specific regions within a protein. These methods are embodied in a number of kits available commercially for the performance of site-directed mutagenesis, including both conventional and PCR-based methods. Examples include the EXSITE™ PCR-based site-directed mutagenesis kit available from Stratagene (Catalog No. 200502; PCR based) and the QUIKCHANGE™ site-directed mutagenesis kit from Stratagene (Catalog No. 200518; PCR based), and the CHAMELEON® double-stranded site-directed mutagenesis kit, also from Stratagene (Catalog No. 200509). Briefly, a tag sequence is introduced into a PCR fragment by inclusion of a sequence encoding the tag near the 5’ or 3’ end of one of the PCR primers. The PCR fragment is generated in a manner to provide appropriate restriction sites such that the fragment can be digested then ligated into parental vector for replacement of specific amino acid codons.

[0067] In one embodiment, the tag of the present invention has a specific binding affinity for an antibody, so that the protease forms an immuno-complex upon binding ligand. For example, the tag may comprise a unique epitope for which antibodies are readily available. Alternatively, the tag can comprise metal-chelating amino acids (e.g. His) so that the IgA proteases can complex with a metal-chelating resin or bead, for example nickel-NTA beads.

[0068] In another embodiment, the tag comprises a detectable marker, such as an enzyme, or comprises an amino acid that can be labeled with a detectable marker. Detectable markers include, for example, radioisotopes, fluorescent molecules, chromogenic molecules, luminescent molecules, and enzymes. Useful detectable markers in the present invention include biotin for staining with labeled streptavidin conjugate, fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., H, 125I, 35S, 32P), reagents (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold. Particular examples include the EXSITE™ PCR-based site-directed mutagenesis kit available from Stratagene (Catalog No. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241, the entireties of which are incorporated by reference herein.

[0069] Non-limiting examples of suitable tags according to the invention include c-Myc, HA, and VSV-G, HSV, FLAG, V5, and HIS. The amino acid and nucleic acid sequence for each tag is shown below.

<table>
<thead>
<tr>
<th>Tag</th>
<th>Peptide and Nucleic Acid Sequences</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIS</td>
<td>Protein: His-His-His-His-His-His</td>
</tr>
<tr>
<td>DNA</td>
<td>CAC CAT CAC CAT CAC CAT</td>
</tr>
<tr>
<td>c-Myc</td>
<td>Protein: SQKLIHSEEDL</td>
</tr>
<tr>
<td>DNA</td>
<td>GAG CAA AAG CTC ATT TCT GAA GAC GAG GAC TTG</td>
</tr>
<tr>
<td>HA</td>
<td>Protein: TPYYTFPDY</td>
</tr>
<tr>
<td>DNA</td>
<td>TAC CCT TAT GAT GTG CCA GAT TAT GCC</td>
</tr>
<tr>
<td>VSV-G</td>
<td>Protein: YDILHNLIRK</td>
</tr>
<tr>
<td>DNA</td>
<td>TAT ACA GAC ATA GAG ATG AAC CCA TCT GGA AAG</td>
</tr>
<tr>
<td>HSV</td>
<td>Protein: QPFLAEPDP</td>
</tr>
<tr>
<td>DNA</td>
<td>CAC CCA GAA CTC GCC CCG GAA GAG CCC GAG GAT</td>
</tr>
<tr>
<td>V5</td>
<td>Protein: GHPDPNZLGLGDST</td>
</tr>
<tr>
<td>DNA</td>
<td>GGC AAA CCA ATC CCA AAG CCA CTG GAG CTG GAT ACT</td>
</tr>
<tr>
<td>FLAG</td>
<td>Protein: DYKDDDDK</td>
</tr>
<tr>
<td>DNA</td>
<td>GAT TAC AAA GAC GAT GAC GAT AAA GGA</td>
</tr>
</tbody>
</table>

[0070] Placing a tag on an IgA1 protease has the benefit of enabling easy detection of the IgA1 protease both in vivo and in vitro. A tag that comprises an epitope for an antibody can be detected either using anti-tag antibodies or antibodies that are conjugated to a detectable marker. The detectable marker can be a naturally occurring or non-naturally occurring amino acid that bears, for example, radioisotopes (e.g., 125I, 35S), fluorescent or luminescent groups, biotin, hapten, antigens and enzymes. There are many commercially available Abs to tags, such as c-myc, HIA, VSV-G, HSV, V5, HIS, and FLAG. In addition, antibodies to tags used in the invention can be generated using standard methods to produce antibodies, for example, by monoclonal antibody production (Campbell, A. M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, the Netherlands (1984); St. Groth et al., J. Immunology, (1990) 35: 1-21; and Kozbor et al., Immunology Today (1983) 4:72). The anti-tag antibodies can then be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, etc.) using methods well known in the art, such as described in international application WO 00/70023 and (Harlow and Lane (1989) Antibodies, Cold Spring Harbor Laboratory, pp. 1-726), herein incorporated by reference.

[0071] Assays for detecting tags include, but are not limited to, Western Blot analysis, Immunohistochemistry, Elisa,
FACS analysis, enzymatic assays, and autoradiography. Means for performing these assays are well known to those of skill in the art. For example, radioisotope labels may be detected using photographic film or scintillation counters and fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate. Means for performing these assays are well known in the art.

[0072] The tag can be further used to isolate the IgA1 protease away from other cellular material. For example, by immunoprecipitation, or by using anti-tag antibody affinity columns or anti-tag antibody conjugated beads. When a HIS tag is used, isolation can be performed using a metal-chelate column (See Hochuli in Genetic Engineering: Principles and Methods ed. JK Setlow, Plenum Press, NY, chp 18, pp87-96). Means for performing these types of purifications are also well known in the art.

[0073] In a preferred embodiment, an anti-tag antibody is used to isolate the IgA1 protease immuno-complex such that the IgA1 protease retains enzymatic activity once complexed. Such an immuno-complex can be used in pharmaceutical preparations for the treatment of IgA1 deposition diseases. For example, an IgA1 immuno-complex, when administered to a patient, is believed to be trapped in the glomerulon of the kidney, a site of IgA1 deposition in IgA nephropathy and Henoch-Schoenlein purpura disease.

III. Treatment of IgA1 Deposition Diseases

[0074] Herein, IgA1 proteases are used as therapeutic agents to treat IgA1 deposition diseases. The abnormal deposition of IgA1 molecules is known to cause renal failure, skin blistering, rash, arthritis, gastrointestinal bleeding and abdominal pain.

IgA Nephropathy

[0075] In one embodiment, the invention provides a method for treating IgA nephropathy by administering to a patient in need of such treatment an IgA1 protease. IgA nephropathy is a disease of the kidney. The disease is considered to be an immune-complex-mediated glomerulonephritis, which is characterized by granular deposition of IgA1 in the glomerular mesangial areas. Nephropathy results and is defined by proliferative changes in the glomerular mesangial cells.

[0076] IgA nephropathy is one of the most common types of chronic glomerulonephritis and a frequent cause of end-stage renal disease.

Dermatitis Herpetiformis

[0077] The invention further provides a method for treating Dermatitis herpetiformis (DH) by administering to a patient in need of such treatment an IgA1 protease. Dermatitis herpetiformis is a chronic blistering skin disease associated with deposits of IgA1 at the dermal-epidermal junction (Hall, RP & T. J. Lawley, J. Immunol. (1985) 135(3): 1760-5). DH patients have granular IgA1 deposits and have an associated gluten-sensitive enteropathy (GSE).

Henoch-Schoenlein Purpura

[0078] In another embodiment, the invention provides a method for treating Henoch-Schoenlein purpura (HS) by administering to a patient in need of such treatment an IgA1 protease. Henoch-Schoenlein purpura is a skin and kidney disease. HSP is characterized by deposition of IgA1-containing immune complexes in tissue. The disease is diagnosed by observing evidence of IgA1 deposition in the skin tissue or kidney via immunofluorescence microscopy. The clinical manifestations typically include rash; arthralgias; abdominal pain; and renal disease.

Animal Models

[0079] The therapeutic effect of IgA1 proteases of the present invention can be tested in any suitable animal model known to those skilled in the art. Some exemplary animal models are described below.

[0080] 1. IgA nephropathy

[0081] A number of rat and mice animal models of IgA nephropathy are available and are useful in the present invention. These models are described in Kacavipr, S. N. et al., (1987) Animal models of IgA nephropathy in IgA nephropathy. A. R. Clarkson, editor. Martinus Nijhoff Publishing, Boston. 188-203, herein incorporated by reference in its entirety. An exemplary model is described in Gesualdo, L. et al., (1990) J. Clin. Invest. 86: 715-722, also herein incorporated in its entirety. Briefly, an IgA antibody/dextran sulfate complex is injected into mice. The immune-complex lodges in the kidney and the mice present with glomerulonephritis that resembles typical cases of human IgA nephropathy. It is preferred that in the above models, human IgA1 is introduced and expressed in the model as described further in the Examples. How the model is made and used for testing therapeutic agents is described in more detail below.

[0082] Soluble immune complexes of dextran sulfate (500 kD, Sigma Chemical Co., St. Louis, Mo.) and monoclonal IgA anti-I-6 glycoside (J558: Litton Bionetics, Kensington, Md.) are prepared at threefold excess (26.5 µg dextran/mg J558 (Nephropathy model); 22.0µg dextran/mg MOPC 104E (normal control)). Complexes containing 3 mg antibody are injected into Swiss-Webster mice via tail vein injection. After 1 hour, the point of maximal deposition of IgA1 complexes in the kidney, mice are injected intraperitonially with multiple doses of either saline or therapeutic agent at given intervals, such as 10 minute intervals. The mice are killed 1 hour after the last injection.

[0083] Kidneys are then isolated from each mouse to look at IgA1 deposition and morphology by light, immunofluorescence, and electron microscopy.


Normal mesangial matrix is scored as 0. Expansion of mesangial matrix is scored as +1 when widened mesangial stalks are observed, +2 when matrix encroachment on capillary lumens is observed, and +3 when conspicuous widening of mesangial stalk is observed along with a decrease in capillary lumen. A therapeutic agent is regarded as effective agent when the expansion of mesangial matrix is reduced towards the morphology of the matrix observed in a normal kidney, for example to a score of +2, or +1, or 0.

Normal mesangial cellularity is scored as 0 and is defined as 3 or fewer cell nuclei per mesangial area. Hypercellularity is scored as +1 when 4 to 6 cell nuclei per mesangial area are observed, +2 when 4 to 6 cell nuclei per mesangial area are observed in most areas but some areas have 7 or more nuclei, and +3 when 7 or more cell nuclei per mesangial area are observed in most areas. A therapeutic agent is regarded as effective agent when the mesangial hypercellularity is reduced towards that observed in a normal kidney, for example to a score of +2, or +1, or 0.

Total glomerular area, matrix area, and glomerular cellularity are also quantified in randomly selected glomeruli from each mouse by computer morphometry (Cue image analysis system, Olympus Corp., Columbia, Md.) (Gesualdo L. et al., 1990) J. Clin. Invest. 86: 715-722). Briefly, cubes of cortex are fixed in 2.5% glutaraldehyde in 0.1 M sodium cacodylate, post fixed in 1% OsO₄, and embedded in Spurr's epoxy (Polysciences, Inc. Warrington, Pa.). 50-70 nm sections are stained with uranyl acetate and lead hydroxide. Coded grids are examined in a JEOL JEM 100 EX microscope and matrix, cellularity, and immune deposits are semi-quantified as described in Nakazawa, M. et al., 1986) J. Exp. Med. 164:1973-1987, herein incorporated by reference in its entirety.

Hematuria (the presence of red blood cells in urine) and proteinuria (the presence of protein in urine) are also a suitable measure of IgA Nephropathy. Briefly, mice are placed in metabolic cages and urine is collected for 24 hours. The urine is then centrifuged and assayed for protein by turbidimetry in 3% sulfosalicylic acid and hematuria by microscopy, as described in Nakazawa, M. et al., 1986) J. Exp. Med. 164:1973-1987, herein incorporated by reference in its entirety. Typically, a normal mouse without IgA nephropathy will have less than 3 red blood cells per high power field (40x), while mice with IgA nephropathy will have greater than 10 red blood cells per high power field. A reduction in the number of red blood cells per high power field is indicative that the therapeutic agent is effective for IgA nephropathy. Mice are tested for hematuria and proteinuria before treatment to determine the reference value indicative of disease. A reduction in the reference value, as compared to the value for hematuria and proteinuria obtained before treatment, of 5%, 10%, 30%, 40% preferably 50%, and more preferably greater than 50% after treatment with the therapeutic agent is indicative that the agent is effective for treatment of IgA1 Nephropathy.

IV Dosage, Formulation and Administration

Herein, bacterial IgA proteases are used to treat IgA deposition diseases. The IgA1 protease of the present invention can be used in a composition that is combined with a pharmaceutically acceptable carrier. Such a composition may also contain diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. In one aspect, the IgA1 protease is complexed with an antibody to form a therapeutic immuno-complex. Such a therapeutic immuno-complex is particularly useful for treatment of diseases characterized by IgA1 deposition in the kidney since the large immuno-complex is believed to lodge in the renal glomerulus upon administration.

In an alternate embodiment, the pharmaceutical formulation may include two or more different IgA proteases, administered together or sequentially, providing a synergistic effect. For example, an IgA protease of H. influenzae, a serine-type protease, may be administered with an IgA protease of Streptococcus sanguis, an entirely different metal-dependent protease. Such combined or sequential administration of different proteases may be useful because the enzymes may interact with (e.g., bind to) the IgA1 substrate in different ways, thus providing an advantage over single protease administration.

The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. For drugs administered orally, pharmaceutically acceptable carriers include, but are not limited to pharmaceutically acceptable excipients such as inert diluents, disintegrating agents, binding agents, lubricating agents, sweetening agents, flavoring agents, coloring agents and preservatives. Suitable inert diluents include sodium and calcium carbonate, sodium and calcium phosphate, and lactose, while corn starch and alginic acid are suitable disintegrating agents. Binding agents may include starch and gelatin, while the lubricating agent, if present, will generally be magnesium stearate, stearic acid or talc. If desired, tablets may be coated with a material such as glyceryl monostearate or glyceryl distearate, to delay absorption in the gastrointestinal tract.

Pharmaceutically acceptable salts can be formed with inorganic acids such as acetate, adipate, alginate, aspartate, benzoate, benzenesulfonate, bisulfate butyrate, citrate, camphorate, camphorsulfonate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptanoate, glycerophosphate, hemisulfate heptanoate, hexanoate, hydrochloride hydrobromide, hydroiodide, 2-hydroxyethanesulfonate, lactate, maleate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, oxalate, thioycionate, tosylate and undecanoate. Base salts include ammonium salts, alkali metal salts such as sodium and potassium salts, alkaline earth metal salts such as calcium and magnesium salts, salt with organic bases such as dicyclohexylamine salts, N-methyl-D-glucamine, and salts with amino acids such as arginine, lysine, and so forth. Also, the basic nitrogen-containing groups can be quaternized with such agents as lower alkyl halides, such as methyl, ethyl, propyl, and butyl chloride, bromides and iodides; dialkyl sulfates like dimethyl, diethyl, dibutyl and dimethyl sulfates, long chain halides such as decyl, lauryl, myristyl and stearyl chlorides, bromides and iodides, aralkyl halides like benzyl and phenethyl bromides and others. Water or oil-soluble or dispersible products are thereby obtained.

The composition may also contain other agents, which either enhance the activity of the composition, or complement its activity or use in treatment, or maintain the activity...
of the therapeutic agent in storage. Such additional factors and/or agents may be included in the composition to produce a synergistic effect or to minimize side effects. Additionally, administration of the composition of the present invention may be administered concurrently with other therapies.

[0095] Administration of the therapeutic agent of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection.

[0096] The compositions containing the therapeutic agent of the present invention can be administered intravenously, as by injection of a unit dose, for example. The term “unit dose” when used in reference to a therapeutic composition of the present invention refers to physically discrete units suitable as unitary dosage for the subject, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent, i.e., carrier or vehicle.

[0097] Modes of administration of the therapeutic agent of the present invention include intravenous, intramuscular, intraperitoneal, intraskeletal, subcutaneous and intra-articular injection and infusion; preferably intravenous injection. Pharmaceutical compositions for parenteral injection comprise pharmaceutically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions as well as sterile powders for reconstitution into sterile injectable solutions or dispersions just prior to use. Examples of suitable aqueous and nonaqueous carriers, diluents, solvents or vehicles include water, ethanol, polyols (e.g., glycerol, propylene glycol, polyethylene glycol and the like), carboxymethylcellulose and suitable mixtures thereof, vegetable oils (e.g., olive oil) and injectable organic esters such as ethyl oleate. Proper fluidity may be maintained, for example, by the use of coating materials such as lecithin, by the maintenance of the required particle size in the case of dispersions and by the use of surfactants. These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents, and/or compounds to shield the immunogenic determinant of the therapeutic agent. Prevention of the action of microorganisms may be improved by the inclusion of various antibacterial and antifungal agents such as paraben, chlorobutanol, phenol sorbic acid and the like. It may also be desirable to include isotonic agents such as sugars, sodium chloride and the like. Prolonged absorption of an injectable pharmaceutical form may be brought about by the inclusion of agents, such as aluminum monostearate and gelatin, which delay absorption. Injectable depot forms are made by forming microencapsulate matrices of the therapeutic agent in biodegradable polymers such as polylactic-polycaproamide, poly(orthoesters) and poly(anhydrides). Depending upon the ratio of therapeutic agent to polymer and the nature of the particular polymer employed, the rate of therapeutic agent release can be controlled. Depot injectable formulations are also prepared by entrapping the therapeutic agent in liposomes or microemulsions which are compatible with body tissues. The injectable formulations may be sterilized, for example, by filtration through a bacterial-retaining filter or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable media just prior to use.

[0098] The formulations include those suitable for oral, rectal, ophthalmic (including intravitreal or intracameral), nasal, topical (including buccal and sublingual), intraterine, vaginal or parenteral (including subcutaneous, intraperitoneal, intramuscular, intravenous, intradermal, intracranial, intratracheal, and epidural) administration. The formulations may conveniently be presented in unit dosage form and may be prepared by conventional pharmaceutical techniques. Such techniques include the step of bringing into association the active ingredient and the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

[0099] Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose vials or multi-dose containers. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described.

[0100] As used herein, a “therapeutically effective amount” means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously. Generally, a composition will be administered in a single dose in the range of 100 µg-10 mg/kg body weight, preferably in the range of 1 µg-100 µg/kg body weight. This dosage may be repeated daily, weekly, monthly, or as considered appropriate by the treating physician.

[0101] When a therapeutically effective amount of the therapeutic agent of the present invention is administered orally, the composition of the present invention can be in the form of a liquid or a solid composition. The compositions can be formulated to contain from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

[0102] When a therapeutically effective amount of the therapeutic agent of the present invention is administered by intravenous, cutaneous or subcutaneous injection, the protein will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill of the art. A preferred composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer’s Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer’s Injection, or other vehicle as known in the art. The composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

[0103] Topical administration, in which the composition is brought in contact with tissue(s), may be suitable for Derma-
tis herpetiformis. By “contacting” is meant not only topical application, but also those modes of delivery that introduce the composition into the tissues, or into the cells of the tissues.

[0104] Use of timed release or sustained release delivery systems are also included in the invention. Such systems are highly desirable in situations where surgery is difficult or impossible, e.g., patients debilitated by age or the disease course itself, or where the risk-benefit analysis dictates control over cure.

[0105] A sustained-release matrix, as used herein, is a matrix made of materials, usually polymers, which are degradable by enzymatic or acid/base hydrolysis or by dissolution. Once inserted into the body, the matrix is acted upon by enzymes and body fluids. The sustained-release matrix desirably is chosen from biocompatible materials such as liposomes, polyalkylacids (polylactic acid), polylactide, polyglycolide (polymer of glycolic acid), polylactide-co-glycolide (co-polymers of lactic acid and glycolic acid) polyalkylacids, poly(ortho)esters, polyproplys, polyoctamethylene, hyaluronic acid, collagen, chondroitin sulfate, carboxylic acids, fatty acids, phospholipids, polyaspartic acids, nucleic acids, polyamino acids, amino acids such as phenylalanine, tyrosine, isoleucine, polynucleotides, polyvinyl pyrrolidone and silicone. A preferred biodegradable matrix is a matrix of one of either polyalkylacids, polylactide, or polylactide-co-glycolide (co-polymers of lactic acid and glycolic acid).

[0106] The amount of the therapeutic agent of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments, which the patient has undergone. Ultimately, the attending physician will decide the amount of the therapeutic agent of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of the therapeutic agent of the present invention and observe the patient’s response. Larger doses of may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further.

[0107] The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the therapeutic agent of the present invention will be in the range of 12 to 72 hours of continuous intravenous administration, at a rate of approximately 30 mg/hour. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

EXAMPLES

Example 1

Construction of Tagged IgA1 Protease

[0108] A His tag has been fused in frame into Haemophilus influenzae IgA1 protease by PCR-based site directed mutagenesis using plasmid pFG26 that contains the DNA sequence encoding Haemophilus influenzae IgA1 protease. Two PCR fragments were generated from pFG26 as illustrated in FIG. 4. The first fragment, Xba I and pm1 I fragment, containing the newly inserted HIS tag and pm1 I site was generated using oligonucleotide primers “HFD6His1” (primer 1) and “HFD6His2” (primer 2) shown below. The second fragment, pmL I and Acc I fragment, was generated using primer 3 and primer 4 also shown below.

Primer 1: HFD-5 XbaI: 5' GATCCGCTTACCAATTATGC 3' (SEQ ID NO:20)
Primer 2: HFD6His1: 5' CTTGTCACGCTTACCAATTATGC (SEQ ID NO:21)
Primer 3: HFD6His2: 5' CTTGTCACGCTTACCAATTATGC (SEQ ID NO:22)
Primer 4: HFD-P-ACCI: 5' TCTGCCAGCTTACCAATTATGC (SEQ ID NO:23)

[0109] After amplification of the two fragments by PCR, the fragments were digested with either Xba I and Pml I or Pml I and Acc I and ligated into the Xba I and Acc I sites of the parental pFG26 plasmid using conventional techniques. The mutation was confirmed by DNA sequence and the new plasmid designated pQ/Rd6His. The fragments were designed such that DNA codons for six Histidines replaced the original codons at position 1007-1012 of the IgA1 protease; asn-asn-ile-gln-ala-asp (SEQ ID NO:24).

Example 2

Generation of a Bacterial Strain that Expresses Tagged IgA1 Protease

[0110] A Haemophilus influenzae bacterial strain that expresses only a tagged IgA1 protease that is enzymatically active was generated by standard recombination techniques. Briefly, the plasmid pQ/Rd6His that was generated in Example 1 was cut with restriction enzymes Cla I and Nde I. The gene was isolated and transformed into a Haemophilus influenzae bacterial Rd strain (Rd 3-13) that produces an IgA1 protease without enzyme activity (Plant A G, Qiu, J, Grundy, F. and Wright, A. J Infect Dis. (1992) July 1 66(1): 43-52) to allow for insertion of the His tagged IgA1 protease into the bacterial genome by recombination. The bacteria were then screened for restoration of enzyme activity by testing bacterial growth media of selected colonies for the presence of active protease using human IgA1 as a substrate.

[0111] Introduction of the 6-His mutation into the active enzyme was confirmed by verifying the presence of a Pml I site using PCR fragment of the genomic DNA. This strain was designated Rd 6His.

[0112] The Rd 6His strain had identical growth rate and colony morphology as did wild type strain Rd. IgA protease activity yield and the size of the enzyme were indistinguishable from wild type. Although the 6 His mutation was introduced just two amino acids away from the auto-proteolytic site, there was no detectable problem with either the enzyme secretion from the bacterial cell, nor its self-processing.

[0113] A monoclonal anti-5His antibody (Qiagen, Inc) bound to the protease as determined by Western blot analysis. When combined with the monoclonal antibody in solution, Rd 6His IgA protease retained full activity.

Example 3

[0114] The therapeutic effect of IgA1 protease for the treatment of IgA nephropathy can be tested in a mouse model for IgA nephropathy.

Mouse Model of IgA Nephropathy

[0115] In this model, human IgA1 immunoglobulin is deposited in the mouse glomerular mesangium, and is
detected by immunofluorescent analysis using standard immunopathologic methods and three defined antisera. This model shows that injecting these animals with IgA protease decreases IgA deposits.

[0116] Description of the Model:

Purification of Polycyclic Human Dimeric IgA1 (dlgA1):

[0117] Outdated, pooled blood bank plasma was clotted, and the resulting serum was rendered 50% saturated at room temperature by the addition of solid (NH₄)₂SO₄ with stirring. The suspension was kept at 4°C for 1 h followed by centrifugation at 3000 g for 30 min. The washed precipitate was dissolved in PBS, pH 7.2, dialyzed against this buffer, and then passed through a Sephacryl 300 column. Fractions containing dlgA1 were pooled. To separate IgA1 from IgA2, this pool was applied to a column of immobilized jacobin in PBS, and dlgA1 was eluted with 0.25M D-galactose in PBS. The dlgA1 was dialyzed against PBS, concentrated, and stored at 4°C. The purity of the dlgA1 was confirmed by SDS-PAGE, reduced and un-reduced, and by double diffusion (Ouchterlony) analysis with IgA subclass-specific antisera.

Precipitin Curves to Determine Equilibrium:

[0118] Goat F(ab)₂ anti-human F(ab)₂ antibody was purchased from The Jackson Laboratory. Tubes were set up with varying amounts of dlgA1, 0.01 mg-0.4 mg per tube. Each tube received 0.1 mg of goat F(ab)₂ anti-human F(ab)₂ and then incubated 37°C, for 1 h, and at 4°C, overnight. To obtain the immune precipitates the tubes were centrifuged at 3000 rpm. The precipitates were washed three times in buffer, and after the last wash the wash buffer was removed and the tubes inverted and allowed to dry. Precipitates were dissolved in 0.1M NaOH and OD₂₉₅, estimated to determine the point of maximum precipitation, the equilibrium point.

Immune Complexes (IC) for Injection:

[0119] After preliminary animal experiments to decide dosage and time of sacrifice, it was decided to prepare soluble IC at 2-times antigen excess (in our model system IgA1 is the antigen), and to inject complexes containing 800 μg of dlgA1 and 400 μg of goat F(ab)₂ anti-human F(ab)₂ per mouse. Control preparations contained IgA1 plus F(ab)₂ of normal goat IgG.

Injection of Mice:

[0120] Six-seven week old Balb/c females obtained from the Charles River VAF facility, were injected intravenously (IV) with IC. After T₂₀min half the animals received an IV injection of 20 μg of IgA1 protease followed by intraperitoneal (IP) injections of 20 μg of protein at T₆₀min and T₁₂₀min. The other animals, controls, received IV saline instead of enzyme at the same time intervals. All animals were sacrificed at T₁₂₀min. Kidneys were removed and frozen for cryostat sectioning.

[0121] The IgA protease in these initial experiments was a recombinant type 1 enzyme that had been cloned into Rd, the parent strain of H. influenzae to produce an enzyme we designated 6HiIgA protease. Approximately 2-3 μg of pure protein was expressed and isolated from this expression system for the preliminary experiments.

Staining of Kidney Sections:

[0122] Four μm-thick kidney sections were made in a cryostat and adhered to silane-coated slides. After sections were air-dried they were fixed in acetone for one minute and then frozen at −20°C. until stained. Sections on slides were rehydrated with three-10 min soaks in PBS. Fluorescent antibodies were diluted in PBS containing 1% BSA, and all antibody dilutions were microfiltered at 10,000 rpm for 5 min before applying to sections. Dilutions of fluorescein or rhodamine conjugates were applied to rehydrated sections, and the slides were incubated for 90 min in a covered humid chamber. Slides were then washed in PBS, mounted, and randomly numbered. Two readers examined each slide, and independently scored the level of fluorescence. The antibodies used were FITC F(ab)₂, rabbit anti-human IgA (a chain specific), FITC F(ab)₂ rabbit anti-human F(ab)₂, and rhodamine F(ab)₂, rabbit anti-goat F(ab)₂, all purchased from The Jackson Laboratory.

Results:

Fluorescent antibody staining of mesangial IgA1 IC

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<th></th>
<th>FITC</th>
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<td>saline</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>2</td>
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<tr>
<td>Group avg.</td>
<td>3.6</td>
<td>2.2</td>
<td>2.8</td>
<td>2.7</td>
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</table>
| Group median | 1.9
| (n = 5/group) | 4.0   | 3.0  | 3.0        | 2.0          |
| Exact p-value | .0238 | .0476| .0397      |

*p = .0238
p = .0476
p = .0397

*p value comparing saline treated and enzyme treated

Six week old Balb/c female mice were injected IV with dlgA1 IC containing polycyclic human IgA1 and goat F(ab)₂ anti-human F(ab)₂. Beginning one hour later the mice were injected with either IgA1 protease or saline. After another hour kidneys were removed and 4 cm fresh frozen sections cut, fixed, and stained with fluorescein antibodies. Slides were scored in blinded fashion on a scale of 0-4. Five mice received IgA1 protease and 5 mice (controls) received saline.

[0124] Representative photomicrographs of kidney sections are shown in FIG. 7. FIG. 7 shows a photomicrograph of kidneys of mice injected IV 2 hours prior to sacrifice with IC composed of human IgA1 and goat anti-human F(ab)₂ and 1 hour prior to sacrifice with IgA1 protease or saline. The right column are from IgA1 protease-treated mice and the left column are from saline-treated mice. The top row (rhodamine fluorescence) shows the IgA component of the IC. The middle and bottom rows (fluorescein fluorescence) show the human IgA component. The IgA is detected with anti-human F(ab)₂ and anti-human Fc alpha in the middle and bottom rows respectively. As can be seen in the figure, the enzyme has removed most of the deposited IC, both the IgA antigen and the IgG antibody.

Example 4

[0125] The therapeutic effect of IgA1 protease for the treatment of Dermatitis herpetiformis can be tested in a mouse model for Dermatitis herpetiformis.

Example 5

[0126] The therapeutic effect of IgA1 protease for the treatment of Henoch-Schoenlein purpura can be tested in a mouse model for Henoch-Schoenlein purpura.
All patents, patent applications, and published references cited herein are hereby incorporated by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

SEQUENCE LISTING

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Arg Arg Glu Asp Tyr Tyr Met Pro Arg Leu Asp Lys Phe Val Thr Glu
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Asn Asp Gln Asn Lys Tyr Pro Ala Phe Val Arg Leu Gly Ser Gly Ser
195   200   205
Gln Phe Ile Tyr Lys Gly Asp Asn Tyr Ser Leu Ile Leu Asn Asn
210   215
His Glu Val Gly Gly Asn Asn Leu Lys Leu Val Gly Asp Ala Tyr Thr
225   230   235   240
Tyr Gly Ile Ala Gly Thr Pro Tyr Lys Val Asn His Glu Asn Asn Gly
245   250   255
Leu Ile Gly Phe Gly Asn Ser Lys Glu His Ser Asp Pro Lys Gly
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Val Asp Leu Phe Asp Ser Ser Gin Asp Thr Asp Ser Lys Asn Asn
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FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide for site directed mutagenesis
SEQUENCE: 22
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SEQ ID NO 23
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide for site directed mutagenesis
SEQUENCE: 23
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SEQ ID NO 24
LENGTH: 6
TYPE: PRT
ORGANISM: Haemophilus influenzae
SEQUENCE: 24
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SEQ ID NO 25
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide encoding heterologous peptide tag sequence
SEQUENCE: 25
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SEQ ID NO 26
LENGTH: 39
TYPE: DNA
ORGANISM: Haemophilus influenzae
SEQUENCE: 26
atcacaacac ctctatctca tctcatcatc gttgctagc

SEQ ID NO 27
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
SEQUENCE: 27
the tagged IgA1 protease is encoded by a nucleotide sequence comprising an IgA1 protease sequence covalently linked to a tag sequence, wherein the IgA1 protease sequence encodes an IgA1 protease selected from the group consisting of *Streptococcus pneumoniae* IgA1 protease sequence, *Streptococcus sanguis* IgA1 protease sequence, *Clostridium ramosum* IgA1 protease sequence, *Haemophilus influenzae* IgA1 protease sequence, *Haemophilus aegyptius* IgA1 protease sequence, *Neisseria meningitidis* IgA1 protease sequence, and *Neisseria gonorrhoeae* IgA1 protease sequence, and wherein each of which includes an enzyme domain sequence, and wherein the tag sequence encodes a tag and is linked with the protease sequence.

19. The tagged IgA1 protease of claim 18, wherein the protease sequence further comprises a cleavage site and a helper domain sequence, wherein the cleavage site is located between the helper domain sequence and enzyme domain sequence, wherein the tag is located fewer than three amino acid residues from the cleavage site, and wherein the tag remains linked to the enzyme domain sequence after cleavage at the cleavage site.

20. The tagged IgA1 protease of claim 18, wherein the tag sequence encodes a polypeptide comprising a tag selected from the group consisting of c-Myc, HA, VSV-G, HSV, FLAG, V5, and His.

21. The tagged IgA1 protease of claim 20, wherein the tag comprises a poly-His epitope.

22. A pharmaceutical composition comprising a tagged protease wherein:

23. The pharmaceutical composition of claim 22, wherein the protease sequence further comprises a cleavage site and a helper domain sequence, wherein the cleavage site is located between the helper domain sequence and enzyme domain sequence, wherein the tag is located fewer than three amino acid residues from the cleavage site, and wherein the tag remains linked to the enzyme domain sequence after cleavage at the cleavage site.

24. The pharmaceutical composition of claim 22, wherein the tag sequence encodes a polypeptide comprising a tag selected from the group consisting of c-Myc, HA, VSV-G, HSV, FLAG, V5, and His.

25. The pharmaceutical composition of claim 24, wherein the tag comprises a poly-His epitope.

26. The pharmaceutical composition of claim 22, further comprising a pharmaceutically acceptable carrier.

27. The pharmaceutical composition of claim 22, wherein the pharmaceutical composition contains a unit dose of a therapeutically effective amount of the tagged IgA1 protease.

* * * * *