Methods for Producing Optimised Therapeutic Molecules

FIELD OF THE INVENTION

The present invention relates to a method of designing an immunoglobulin library, preferably an antibody library, for target optimisation based on a first lead immunoglobulin. Aspects of the invention further relate to an immunoglobulin library designed by the method, and to immunoglobulins selected from the library.

BACKGROUND TO THE INVENTION

Antibody therapeutics are frequently designed by optimising an initial lead antibody in order to select desired characteristics, such as binding affinity, Kd, or lack of immunogenicity. Frequently human antibodies are generated in animals such as transgenic mice expressing human immunoglobulin genes.

After generation and isolation of a lead candidate antibody, the antibody may be optimised in various ways. Typically the lead antibody is sequenced, and the sequence used to generate an antibody library of variants for further screening. The variants may be constructed using oligonucleotides to introduce degeneracy into the coding regions (for example, the regions coding for one or more of the CDRs). The oligonucleotides may be used for PCR amplification of regions of the nucleic acids coding for the antibody. This will typically generate a large library including many variants, in which each amino acid residue in the lead is replaced with many potential substitutions. The libraries may then be cloned into expression vectors in order to generate the antibodies themselves, Display systems such as ribosome, phage or yeast display systems may be used. The antibodies thereby produced can then be screened for improvements in the desired properties.

A drawback with these known methods is that potentially far more variants are generated than will show desirable properties. This increases the time and resources necessary to generate the library and to select a variant antibody with desired characteristics. Furthermore, optimising both heavy and light chains of a fully human antibody increases the necessary workload, as well as introducing further uncertainty as to the properties of the antibody, particularly for antibodies that have both heavy and light immunoglobulin chains when assembled.

The present invention is intended to address at least some of these disadvantages, and to provide an additional method for generating immunoglobulin libraries. This is achieved in part through the effective pre-selection of certain variants by the immunised animal itself by the process of somatic hypermutation. During generation of native antibodies, proliferation of B cells is accompanied by an extremely high rate of somatic mutation in the B cell receptor locus, which generates the required antibody diversity. The mutations are mainly concentrated at certain somatic hypermutation hotspots. The present invention makes use of this native generation of diversity in order to inform the design of the immunoglobulin library.

SUMMARY OF THE INVENTION

The invention provides a method of designing an immunoglobulin library for optimisation of a biological property of a first lead immunoglobulin, the method comprising:

a) identifying one or more related immunoglobulins, said one or more related immunoglobulins being related to the first lead immunoglobulin, each immunoglobulin having been raised against a target antigen by immunisation of a transgenic non-human mammal comprising human immunoglobulin genes with the target antigen;

b) comparing amino acid sequences of the first lead immunoglobulin and the one or more related immunoglobulins;

c) identifying, based on the sequence comparison, one or more sites at which there are variant amino acid residues between:

(i) the first lead immunoglobulin and the one or more related immunoglobulins, and/or

(ii) where the one or more related immunoglobulins is a plurality of immunoglobulins, between the plurality of immunoglobulins,

wherein the one or more sites at which there are variant amino acid residues comprise potential sites for modification of the first lead immunoglobulin;

d) selecting one or more sites for modification to replace an amino acid of the first lead immunoglobulin with the corresponding variant amino acid of one or more of the related immunoglobulins, based on the sequence comparison; and

e) generating immunoglobulin sequences for the library based on the sequence of the first lead immunoglobulin, modified at one or more of the selected sites for modification.

Preferably the immunoglobulins comprise a CDR3. The immunoglobulins may comprise a set of CDRs: CDR1, CDR2 and CDR3, preferably a set of heavy chain CDRs: HCDR1, HCDR2, and HCDR3. The immunoglobulins may consist of or comprise heavy-chain-only antibodies. The immunoglobulins may consist of or comprise V_H domains.

Preferably the one or more related immunoglobulins are of common lineage and bind the same target antigen as the first lead immunoglobulin, preferably with at least 70%, 80%, 85%, 90%, or at least 95% homology in at least one CDR region when compared to the lead immunoglobulin.

By common lineage it is meant that the immunoglobulins are derived from the same germline sequence, e.g. the immunoglobulins may be obtained by somatic hypermutation of a germline sequence in non-human mammal, in particular following immunisation of the non-human mammal with a target antigen. By aligning a lead immunoglobulin sequence, e.g., a lead V_H sequence, with other immunoglobulin sequences, e.g., V_H sequences, of the same lineage, somatic hypermutation hot spots targeted during the immune response can be identified.

The one or more related immunoglobulins generally have at least 70% homology in CDR3 to the lead immunoglobulin, preferably at least 70%, 80%, 85%, 90%, or at least 95% homology in CDR3 to the lead immunoglobulin.

The one or more related immunoglobulins generally have at least 70% homology in CDR1 and/or CDR2 to the lead immunoglobulin, preferably at least 70%, 80%, 85%, 90%, or at least 95% homology in CDR1 and/or CDR2 to the lead immunoglobulin.

The one or more related immunoglobulins generally have at least 70% homology in the framework regions to the lead immunoglobulin, preferably at least 70%, 80%, 85%, 90%, or at least 95% homology in the framework regions to the lead immunoglobulin

The one or more related immunoglobulins may comprise a plurality of related immunoglobulins comprising at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 immunoglobulins.

Step c) may comprise identifying sites for modification within a CDR of the immunoglobulin sequences, wherein a site within a CDR is considered a site for modification if there is a variant amino acid residue present in at least one, two, three, four, or five of the related immunoglobulins.

Step c) may further comprise identifying sites for modification outside a CDR of the immunoglobulin sequences, wherein a site outside a CDR is considered a site for modification if there is a variant amino acid residue present in at least 20% of the related immunoglobulins.

A potential site for modification, in particular a potential site for modification site outside a CDR which would otherwise be identified as a site for modification is not identified as a site for modification if modifying the site would lead to the introduction of one or more of the following features into the modified immunoglobulin: (i) unpaired cysteines, (ii) oxidation sites (free methionines), (iii) glycosylation sites, (iv) deamidation sites, and (v) isomerisation sites.

The sequences selected in step d) may include variant sequences reflecting each possible combination of modifications at the sites for modification.

Modification at a selected site for modification may include only a conservative amino acid substitution.

The variant immunoglobulins may include no modification outside the selected sites for modification.

Step e) may further comprise generating sequences of additional variant immunoglobulins, wherein the sequences are further modified at one or more of the selected sites for modification to replace an amino acid of the first lead immunoglobulin with a conservative amino acid replacement for the corresponding variant amino acid.

Step e) may further comprise generating sequences of additional variant immunoglobulins, wherein the sequences are further modified at one or more of the selected sites for modification to replace an amino acid of the first lead immunoglobulin with an amino acid not found at the corresponding residue of the related immunoglobulins.

The methods described herein may further comprise step f) generating an immunoglobulin library comprising immunoglobulins having the sequences generated in step e).

Libraries may be generated using various methods conventional in the art.

Method of the invention may further comprise step g) screening the immunoglobulin library to identify one or more immunoglobulins having desired biological properties.

Desired biological properties include, but are not limited to binding affinity, IC_{50}, good expression characteristics, solubility, stability, lack of immunogenicity / potential for generation of anti-drug antibody (ADA).

A method of the invention may comprise prior to step a), the step α) of generating and sequencing a plurality of immunoglobulins, including a first lead immunoglobulin and one or more related immunoglobulins.

The plurality of immunoglobulins may be generated by immunising a non-human mammal, preferably a mouse or rat, preferably a transgenic mouse or rat expressing human immunoglobulin genes, with a target antigen.

A method of the invention may comprise, prior to step a), the step β) of identifying a first lead immunoglobulin.

The first lead immunoglobulin may be selected based on one or more desired biological property including, but not limited to a suitably high binding affinity for the target antigen, specificity for the target antigen, selectivity for the target antigen, ability to neutralise an effect of the target antigen, desired cross reactivity with the

corresponding target antigen from other species, IC_{50}, good expression characteristics, solubility, stability, lack of immunogenicity / potential for ADA.

In a method of the invention the immunoglobulins may be antibodies, or antigen-binding fragments of an antibody.

The immunoglobulins may comprise or consist of heavy-chain-only antibodies.

The immunoglobulins may comprise or consist of V_H domains of antibodies.

The invention provides a method of optimising a lead immunoglobulin, the method comprising:

a) performing a method of the invention described above; and

b) selecting one or more optimised immunoglobulins from the library based on a desired biological property of the optimised immunoglobulin.

The invention provides a library of polynucleotides encoding a plurality of immunoglobulins, wherein the sequences of the plurality of immunoglobulins are designed in accordance with a method of the invention described above.

The invention provides a library comprising a plurality of immunoglobulins, wherein the sequences of the plurality of immunoglobulins are designed in accordance with the method of the invention described above

The invention provides an isolated immunoglobulin designed or selected in accordance with a method of the invention described above.

The invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding an immunoglobulin of the invention.

The invention provides an isolated polypeptide comprising an amino acid sequence of an immunoglobulin of the invention.

The invention provides a vector comprising a nucleic acid molecule of the invention.

The invention provides a plurality of vectors comprising a polynucleotide library of the invention.

The invention provides a host cell comprising a vector or vectors of the invention.

The host cell may be a bacterium, e.g., *E. coli*; a yeast, an isolated mammalian cell or cell line, *e.g.*, a CHO or NS0 cell line.

The invention provides a method of obtaining an immunoglobulin of the invention, comprising the steps of: providing a host cell according to the invention; allowing the host cell to express the immunoglobulin encoded by the nucleic acid molecule comprised in the vector; and purifying the immunoglobulin.

The method may further comprise preparing a composition, such as a pharmaceutical formulation, comprising an immunoglobulin obtained.

The invention provides a chimeric or fusion polypeptide comprising an immunoglobulin of the invention.

The invention provides a conjugate comprising the immunoglobulin of the invention, or the chimeric or fusion polypeptide of the invention, conjugated or fused to an additional moiety.

The additional moiety may comprise one or more V_H domain, preferably a human V_H domain, specific for the same or a different target antigen, a cytotoxin, a radionuclide, a half-life extending moiety, *e.g.*, a HSA or variant thereof, Fc, PEG or anti-HSA binding molecule, *e.g.*, comprising an anti-HSA V_H domain.

The invention provides a composition, such as a pharmaceutical formulation, comprising an immunoglobulin of the invention, a chimeric polypeptide of the invention or a conjugate of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows an anti-IL-17A clone 1.1 V_H family, with the sequence of the V_H domain of a lead heavy-chain-only antibody candidate, clone 1.1 (top line), together with those of related antibodies. The CDR portions are shaded.

Figure 2 shows BIAcore data showing the binding kinetics of (a) clone 1.1 and (b) clone 2.1 V_H raised against the targets human IL-17A and IL-17RA respectively.

Figure 3 shows agarose gel analysis of PCR products of nucleic acid segments for construction of a variant library based on clone 1.1 run against a marker (M) Fermentas 1K+ ladder.

Figure 4 shows the sequence of the V_H domain of a lead heavy chain only antibody candidate, clone 2.1 (top line), together with those of related antibodies. The CDR portions are shaded.

Figure 5 shows agarose gel analysis of PCR products of nucleic acid segments for construction of a variant library based on clone 2.1 run against a marker (M) generuler 100bp ladder (ThermoSM0243).

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Figure 6 shows BIAcore data showing the binding kinetics of optimised variants of the clone 1.1 and clone 2.1 V_H: (a) parent V_H 1.1, optimised V_H clones 1.10 and 1.6; (b) parent V_H 2.1 and optimised V_H 2.2.

DETAILED DESCRIPTION OF THE INVENTION

The present invention will now be further described, with reference to specific embodiments. It will be understood that these embodiments are merely illustrative of the invention, and that the invention is as defined in the claims. Further, modifications and variations in the described embodiments will occur to the skilled person.

Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, pathology, oncology, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art. The methods and techniques of the present disclosure are generally performed according to conventional methods well-known in the art and as described in various general and more specific references that are cited

and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook *et al.*, Molecular Cloning: A Laboratory Manual (2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclatures used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

The term "antibody" broadly refers to any immunoglobulin (Ig) molecule, or antigen-binding portion thereof, comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains, or any functional fragment, mutant, variant, or derivative thereof, which retains the essential epitope-binding features of an Ig molecule. Such mutant, variant, or derivative antibody formats are known in the art. In a full-length antibody, each heavy chain is comprised of a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. Immunoglobulin molecules can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG 1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass.

Antibodies as described herein may also comprise or consist of a single domain antibody wherein said domain is a V_H immunoglobulin domain. Thus, the antibody may comprise or consist of an immunoglobulin single variable domain antibody (sVD, sdAb or ISV) that has one or more V_H domains, but is devoid of VL domains. Single domain antibodies have been described in the art; they are antibodies whose complementary

determining regions are part of a single domain polypeptide. Preferably, the one or more V_H domain is a human V_H domain.

As used herein, the term VH or "variable heavy domain" refers to immunoglobulin variable heavy domains as defined by Kabat *et al.*, Sequences of Immunological Interest, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The numbering and positioning of CDR amino acid residues within the variable domains is in accordance with the well-known Kabat numbering convention.

Antibodies described herein comprise an amino acid sequence and preferred sequences and/or parts thereof, such as CDRs, are defined herein.

The term "CDR" refers to the complementarity determining regions within antibody variable sequences. There are three CDRs in each of the variable regions of the heavy chain (and the light chain, when present), which are designated CDR1, CDR2 and CDR3, for each of the variable regions. The term "CDR set" refers to a group of three CDRs that occur in a single variable region capable of binding the antigen. The exact boundaries of these CDRs have been defined differently according to different systems. The system described by Kabat is preferred. The terms "Kabat numbering", "Kabat definitions" and "Kabat labeling" are used interchangeably herein. These terms, which are recognized in the art, refer to a system of numbering amino acid residues which are more variable (*i.e.*, hypervariable) than other amino acid residues in the heavy and light chain variable regions of an antibody, or an antigen-binding portion thereof (Kabat *et al.*, (1971) Ann. NY Acad. Sci. 190:382-391 and Kabat, *et al.*, (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242).

"Homology" with respect to comparison of polypeptides or polynucleotides generally refers to the percentage of amino acid (or nucleotide) residues in a first sequence that are identical with the residues of a corresponding second polypeptide (or polynucleotide), after aligning the sequences and, in some embodiments, after introducing gaps, if necessary, to achieve the maximum percent homology, and not considering any conservative substitutions as part of the sequence identity. Neither N- or C-terminal extensions, nor insertions, shall be construed as reducing identity or

homology. Methods and computer programs for the alignment are well known in the art.

"Conservative amino acid substitutions" are those noted in the following table:

Residue	Conservative substitution	Residue	Conservative substitution
Ala	Ser	Leu	Ile; Val
Arg	Lys	Lys	Arg; Gln
Asn	Gln; His	Met	Leu; Ile
Asp	Glu	Phe	Met; Leu; Tyr
Gln	Asn	Ser	Thr; Gly
Cys	Ser	Thr	Ser; Val
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp; Phe
His	Asn; Gln	Val	Ile; Leu
Ile	Leu; Val		

Table 1. Conservative amino acid substitutions

The term "Kd" refers to the "equilibrium dissociation constant" and refers to the value obtained in a titration measurement at equilibrium, or by dividing the dissociation rate constant (Koff) by the association rate constant (Kon). "KA" refers to the affinity constant. The association rate constant, the dissociation rate constant and the equilibrium dissociation constant are used to represent the binding affinity of an antibody to an antigen. Methods for determining association and dissociation rate constants are well known in the art. Using fluorescence-based techniques offers high sensitivity and the ability to examine samples in physiological buffers at equilibrium. Other experimental approaches and instruments such as a BIAcore® (biomolecular interaction analysis) assay can be used.

Methods for producing an immunoglobulin, given the amino acid sequence or nucleotide sequence coding for the amino acid sequence, will be known to the skilled person. Certain techniques may be used to facilitate screening of a produced immunoglobulin or immunoglobulin library; for example, a library of amino acid sequences may be displayed on a phage, phagemid, ribosome or suitable micro-organism (such as yeast), such as to facilitate screening. Suitable methods, techniques and host organisms for displaying and screening (a set, collection or library of) amino acid sequences will be clear to the person skilled in the art (see for example Phage

Display of Peptides and Proteins: A Laboratory Manual, Academic Press; 1st edition (October 28, 1996) Brian K. Kay, Jill Winter, John McCafferty).

The immunoglobulins referred to herein can be expressed in a transgenic rodent. The transgenic rodent, for example a mouse, has a reduced capacity to express endogenous antibody genes. In one embodiment, the rodent has a reduced capacity to express endogenous light and/or heavy chain antibody genes. The rodent may therefore comprise additional modifications to disrupt expression of endogenous light and/or heavy chain antibody genes so that no functional endogenous light and/or heavy chains are produced.

The rodent may be a mouse. The mouse may comprise a non-functional lambda light chain locus. Thus, the mouse does not make a functional endogenous lambda light chain. The lambda light chain locus may be deleted in part or completely or rendered non-functional through insertion. For example, at least the constant region genes C1, C2 and C3 may be deleted or rendered non-functional through insertion. The locus may be functionally silenced so that the mouse does not make a functional lambda light chain. Furthermore, the mouse may comprise a non-functional kappa light chain locus. Thus, the mouse does not make a functional endogenous kappa light chain. The kappa light chain locus may be deleted in part or completely or rendered non-functional through insertion.

The mouse having functionally silenced endogenous lambda and kappa L-chain loci may, for example, be made as disclosed in WO 2003/000737, which is hereby incorporated by reference in its entirety.

Furthermore, the mouse may comprise a non-functional heavy chain locus. Thus, the mouse does not make a functional endogenous heavy chain. For example, as described in WO 2004/076618 (hereby incorporated by reference in its entirety), all 8 endogenous heavy chain constant region immunoglobulin genes (μ, δ, γ3, γ1, γ2a, γ2b, ε and α) are absent in the mouse, or partially absent to the extent that they are non-functional, or genes δ, γ3, γ1, γ2a, γ2b and ε are absent and the flanking genes μ and α are partially absent to the extent that they are rendered non-functional, or genes μ, δ, γ3, γ1, γ2a, γ2b and ε are absent and α is partially absent to the extent that it is rendered non-functional, or δ, γ3, γ1, γ2a, γ2b, ε and α are absent and μ is partially

absent to the extent that it is rendered non-functional. By deletion in part is meant that the endogenous locus gene sequence has been deleted or disrupted, for example by an insertion, to the extent that no functional endogenous gene product is encoded by the locus, *i.e.*, that no functional product is expressed from the locus. In another embodiment, the locus is functionally silenced.

In one embodiment, the mouse comprises a non-functional heavy chain locus, a non-functional lambda light chain locus and a non-functional kappa light chain locus. The mouse therefore does not produce any functional endogenous light or heavy chains. Thus, the mouse is a triple knockout (TKO) mouse.

The transgenic mouse comprises a vector encoding and expressing a heterologous heavy chain locus. YACs are vectors that can be employed for the cloning of very large DNA inserts in yeast. As well as comprising all three cis-acting structural elements essential for behaving like natural yeast chromosomes (an autonomously replicating sequence (ARS), a centromere (CEN) and two telomeres (TEL)), their capacity to accept large DNA inserts enables them to reach the minimum size (150 kb) required for chromosome-like stability and for fidelity of transmission in yeast cells. The construction and use of YACs is well known in the art (*e.g.*, Bruschi, C.V. and Gjuracic, K. Yeast Artificial Chromosomes, Encyclopedia of Life Sciences 2002 Macmillan Publishers Ltd, Nature Publishing Group).

Transgenic mice can be created according to standard techniques. The two most characterised routes for creating transgenic mice are via pronuclear microinjection of genetic material into freshly fertilised oocytes, or via the introduction of stably transfected embryonic stem cells into morula or blastocyst stage embryos. Regardless of how the genetic material is introduced, the manipulated embryos are transferred to pseudo-pregnant female recipients where pregnancy continues and candidate transgenic pups are born. The main differences between these broad methods are that ES clones can be screened extensively before their use to create a transgenic animal. In contrast, pronuclear microinjection relies on the genetic material integrating to the host genome after its introduction and, generally speaking, the successful incorporation of the transgene cannot be confirmed until after pups are born.

There are many methods known in the art to both assist with and determine whether successful integration of transgenes occurs. Transgenic animals can be generated by multiple means including random integration of the construct into the genome, site-specific integration, or homologous recombination. There are various tools and techniques that can be used to both drive and select for transgene integration and subsequent modification including the use of drug resistance markers (positive selection), recombinases, recombination-mediated cassette exchange, negative selection techniques, and nucleases to improve the efficiency of recombination. Most of these methods are commonly used in the modification of ES cells. However, some of the techniques may have utility for enhancing transgenesis mediated via pronuclear injection.

Further refinements can be used to give more efficient generation of the transgenic line within the desired background. As described above, in preferred embodiments, the endogenous mouse immunoglobulin expression is silenced to permit sole use of the introduced transgene for the expression of the heavy-chain-only repertoire that can be exploited for drug discovery. Genetically-manipulated mice, for example TKO mice that are silenced for all endogenous immunoglobulin loci (mouse heavy chain, mouse kappa chain and mouse lambda chain) can be used as described above. The transfer of any introduced transgene to this TKO background can be achieved via breeding, (either conventional or with the inclusion of an IVF step to give efficient scaling of the process). However, it is also possible to include the TKO background during the transgenesis procedure. For example, for microinjection, the oocytes may be derived from TKO donors. Similarly, ES cells from TKO embryos can be derived for use in transgenesis.

The immunoglobulins described herein may be conjugated to another moiety. This moiety can be selected from a toxin, enzyme or radioisotope; or a half-life extending moiety such as a HSA or PEG or an anti-HSA Ig, *e.g.*, an anti-HSA V_H. The moiety can be selected from cytotoxic molecules such as chemotherapeutic drugs, bacteria and plant toxins and radionuclides. Tumor cell killing occurs upon binding of the binding molecule to a tumor cell and release and / or activation of the cytotoxic activity of the drug moiety. The selectivity afforded by drug conjugates minimizes toxicity to normal cells, thereby enhancing tolerability of the drug therapy in the patient.

Described herein are compositions, *e.g.*, pharmaceutical compositions comprising immunoglobulins. Pharmaceutical compositions typically comprise one or more active agents (in this case, an immunoglobulin) and a pharmaceutically-acceptable carrier. The composition may be formulated depending on the desired administration route. Examples of administration routes include without limitation topical including dermal administration to or via the skin, subcutaneous or intravenous administration, oral, topical, parenteral, sublingual, rectal, vaginal, ocular, and intranasal administration. Parenteral administration includes subcutaneous injections, intravenous, intramuscular, intrasternal injection or infusion techniques. Compositions can take the form of one or more dosage units. The skilled person will be aware of suitable methods for preparing pharmaceutical formulations.

The pharmaceutically-acceptable carrier can be particulate, so that the compositions are, for example, in tablet or powder form, *e.g.*, lyophilised, for reconstitution before use. The carrier(s) can be liquid, with the compositions being, for example, an injectable liquid. In addition, the carrier(s) can be gaseous, so as to provide an aerosol composition useful in, for example, inhalatory administration. The term "carrier" refers to a diluent, adjuvant or excipient, with which the active agent of the composition is administered. Such pharmaceutical carriers can be liquids, water or physiological saline are preferred carriers when the pharmaceutical compositions described herein are administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. The compositions, if desired, can also contain minor amounts of wetting or emulsifying agents, pH buffering agents, or agents that enhance the stability and solubility of the formulation.

The composition can be in the form of a liquid, *e.g.*, a solution, emulsion or suspension. The liquid can be useful for delivery by injection or i.v. infusion. In a composition for administration by topically to the skin or by injection or infusion, one or more of a surfactant, preservative, wetting agent, dispersing agent, suspending agent, buffer, stabilizer and isotonic agent can also be included.

The liquid compositions described herein, whether they are solutions, suspensions or other like form, can also include one or more of the following: sterile diluents such as water for injection, saline solution, preferably physiological saline, Ringer's solution,

isotonic sodium chloride, fixed oils such as synthetic mono or digylcerides, polyethylene glycols, glycerin, or other solvents; antibacterial agents such as benzyl alcohol or methyl paraben; and agents for the adjustment of tonicity such as sodium chloride or dextrose. A parenteral composition can be enclosed in an ampoule, a disposable syringe or a multiple-dose vial made of glass, plastic or other material.

The amount of the immunoglobulin described herein that is effective/active in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays can optionally be employed to help to identify optimal dosage ranges. The precise dose to be employed in the compositions will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. The correct dosage will also vary according to the particular formulation, the mode of application, and its particular site, host and the disease being treated. Other factors like age, body weight, sex, diet, time of administration, rate of excretion, condition of the host, drug combinations, reaction sensitivities and severity of the disease shall be taken into account. Administration can be carried out continuously or periodically within the maximum tolerated dose.

EXAMPLES

Heavy-chain-only antibodies comprising V_H were raised against the antigens IL-17A and IL-17RA in a transgenic triple knockout mouse, which is silenced for endogenous heavy and light chain production, but which expresses exogenous human heavy chains. Two lead antibodies, clone 1.1 and clone 2.1, were obtained and used in subsequent optimisation steps. The following materials and methods section gives brief details of the mouse platform used and the generation of the lead antibodies. The optimisation steps and analysis are described in the examples.

<u>Materials and methods</u>

<u>Tg/TKO mice for immunisation</u>

Mice carrying a heavy-chain antibody transgenic locus in germline configuration within a background that is silenced for endogenous heavy and light chain antibody expression (triple knock-out, or TKO) were created as previously described

(WO2004/076618 and WO2003/000737, Ren *et al.* Genomics, 84, 686, 2004; Zou *et al.*, J. Immunol., 170, 1354, 2003).

Transgenic (Tg) mice were derived following pronuclear microinjection of freshly fertilised oocytes with a yeast artificial chromosome (YAC) comprising a plethora of human V_H, D and J genes in combination with mouse immunoglobulin constant region genes lacking CH1 domains, mouse enhancer and regulatory regions. Yeast artificial chromosomes (YACs) are vectors that can be employed for the cloning of very large DNA inserts in yeast. As well as comprising all three cis-acting structural elements essential for behaving like natural yeast chromosomes (an autonomously replicating sequence (ARS), a centromere (CEN) and two telomeres (TEL)), their capacity to accept large DNA inserts enables them to reach the minimum size (150 kb) required for chromosome-like stability and for fidelity of transmission in yeast cells. The construction and use of YACs is well known in the art (*e.g.*, Bruschi, C.V. and Gjuracic, K. Yeast Artificial Chromosomes, Encyclopedia of Life Sciences, 2002, Macmillan Publishers Ltd., Nature Publishing Group / www.els.net).

The YAC used was about 340kb or 572kb comprising 10 human or 23 heavy chain V genes in their natural configuration, human heavy chain D and J genes, a murine $C\gamma1$ gene and a murine 3' enhancer gene. It lacks the C_H1 exon.

The transgenic founder mice were back crossed with animals that lacked endogenous immunoglobulin expression to create the Tg/TKO lines used in the immunisation studies described.

Antigen for immunisation

The immunisations used recombinant purified protein. Recombinant human IL-17A was purchased from Peprotech (Peprotech, cat# AF-200-17). Recombinant human IL-17A was also used. Other immunogens could also have been employed and include materials such as DNA, crude protein and transfected cells.

Immunisation Protocol

Recombinant protein was administered to the Tg/TKO. Briefly, mice aged 8 – 12 weeks of age each received a total of 10µg of recombinant protein, emulsified in Complete Freund's Adjuvant and delivered subcutaneously, followed by boosts of 1 –

10µg of recombinant protein, emulsified in Incomplete Freund's Adjuvant, also administered subcutaneously, given at various intervals following the initial priming. A final dose of antigen was administered intraperitoneally, in phosphate-buffered saline, in the absence of adjuvant.

Alternative immunisation routes and procedures can also be employed. For example, different adjuvants or immune potentiating procedures may be used instead of Freund's adjuvant. DNA immunisations are often delivered intramuscularly or via a Genegun. Transfected cells or membrane preparations from such cells are often, although not exclusively, administered intraperitoneally.

Generation of Libraries from Immunised Mice and Cloning of Antibody V_H

a) processing tissues, RNA extraction and cDNA manufacture

Spleen, inguinal and brachial lymph nodes were collected into RNAlater™ from each immunised animal. For each animal, 1/3 of the spleen and 4 lymph nodes were processed separately. Initially, the tissues were homogenised; following transfer of tissues to Lysing matrix D bead tubes (MP Bio cat# 116913100), 600µl of RLT buffer containing β-mercaptoethanol (from Qiagen RNeasy kit cat# 74104) was added before homogenisation in a MP Bio Fastprep homogeniser (cat # 116004500) using 6m/s 40 seconds cycles. The tubes containing the homogenised tissues were transferred to ice and debris was pelleted by microcentrifugation at 10g for 5 minutes. A sample of 400µl of the supernatant was removed and used for RT-PCR.

Initially, RNA was extracted using Qiagen RNeasy kit cat# 74104 following the manufacturer's protocol. Each RNA sample was then used to make cDNA using Superscript III RT-PCR high-fidelity kit (Invitrogen cat # 12574-035). For each spleen and LN RNA sample, 5 RT-PCR reactions were performed, each with VH_J/F (long) primer in combination with a primer for V_H1, V_H2, V_H3, V_H4 or VH6 family. Details of the primers are below.

V1a/pelB(long)	**GCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCCATGGCC**CAGG TBCAGCTGGTGCAGTCTGGGGCTGAGG (SEQ ID NO: 14)
V2/pelB(long)	**GCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCCATGGCC**CAGA TCACCTTGAAGGAGTCTGG (SEQ ID NO: 15)
V3/pelB(long)	**GCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCCATGGCC**SAGG TGCAGCTGGTGGAGTCTGGGGGAGG (SEQ ID NO: 16)

V4-4/pelB(long)	**GCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCCATGGCC**CAGG TGCAGCTGCAGGAGTCGGG (SEQ ID NO: 17)
V6/pelB(long)	**GCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCCATGGCC**CAGG TACAGCTGCAGCAGTCAGG (SEQ ID NO: 18)
VH_J/F(long)	**CCGTGGTGATGGTGGTGATGGCTACCGCCACCCTCGAG**TGARGAGA CRGTGACC (SEQ ID NO: 19)

Table 2. Primers. Residues in bold have homology with pUCG3

Mastermixes were prepared for the RT-PCR reactions, based on the following tube reaction components.

12.5µl 2x reaction mix
0.5µl forward primer (10µM)
0.5µl reverse primer (10µM)
0.5µl enzyme mix
500ng - 1µg RNA
Up to 25µl with water

The RT-PCR reactions were carried out in a thermal cycler using the following conditions:

50^{0}C 20min
94^{0}C 2min
35 cycles of 94^{0}C 15sec
58^{0}C 30sec
68^{0}C 30sec
68^{0}C 5min
Hold at 4^{0}C

Products in the range of 370bp were confirmed by gel electrophoresis.

For each mouse, the V_H products amplified for a given family from the 1/3 spleen and each of the 4 lymph nodes were then pooled for purification using Thermo/Fermentas GeneJet PCR purification kit (cat #K0702) which was used according to the Manufacturer's instructions, with the products eluted in 50ul of water.

b. Cloning into phagemid vector

The phagemid vector, pUCG3, was employed in these studies. As indicated, V_H may be cloned into pUCG3, using conventional methods involving restriction enzyme digestions with NcoI and XhoI, ligation and transformation. Alternatively, a PCR based method may be used to construct the V_H phagemid libraries. Both of these procedures were used to generate libraries from the amplified V_H sequences. The former method is widely used in the art and details can be found. For the PCR based method, the following procedure was used:

A linearised version of pUCG3 was created using PCR;

Primers:

pUCG3-F3 CTCGAGGGTGGCGGTAGCCATCACCACCATC (SEQ ID NO: 65)

pUCG3-R3 TCCATGGCCATCGCCGGCTGGGCCGCGAG (SEQ ID NO: 66)

Phusion High fidelity PCR master mix with GC buffer (cat # F532L, NEB) was used for the PCR reactions which comprised the following reagents;

Phusion GC 2x mix	25µl
pUCG3	5-10ng
Primers (10µM)	1.25µl of each
DMSO	1.5µl
Nuclease-free H_2O	to final volume of 50µl

The cycling conditions used were

98°C 30 seconds

10 cycles of

98 °C 10 seconds

58 °C 20 seconds

68 °C 2 minutes, 30 seconds

20 cycles of

98 °C 10 seconds

58 °C 20 seconds

68 °C 3 minutes

68 °C 5 minutes

4 °C hold

The PCR product (3152bp) was gel purified using Fermentas GeneJet Gel purification kit (cat # K0691), according to the manufacturer's instructions, with final elution in 40µl of elution buffer.

The purified V_H RT-PCR products were employed as megaprimers with the linearised pUCG3 to give phagemid products for transformation and library creation, based on the following reactions:

Phusion GC 2x mix	25µl
Linearised pUCG3	700ng
VH PCR product	250ng
DMSO	1.5µl
Nuclease-free H2O	to 50µl final volume

PCR was performed as follows;

	98°C 30sec
10 cycles of:	98°C 10sec
	58°C 20sec
	72°C 2min
	72°C 5min
	Hold at 10°C

The products of PCR were analysed on a 1% agarose gel.

The various family V_H/phagemid products were purified using Fermentas PCR purification kit (cat #K0702) according to the manufacturer's instructions with the final elution being in 25µl H_2O and used for transformations of TG1 *E. coli* (Lucigen, Cat: 60502-2) by electroporation using BioRad 10 x 1 mm cuvettes (BioRad cat # 165-2089), an Eppendorf Eporator and pre-warmed recovery medium (Lucigen, proprietary mix). 2µl of the purified products were added to 25µl of cells for the electroporation, with up to 10 electroporations being performed for each V_H/phagemid product at 1800v. Electroporated cells were pooled and recovered in 50ml Falcon tubes incubated for 1 hour at 37°C with shaking at 150rpm. A 10-fold dilution series of an aliquot of the transformations was performed and plated in petri dishes containing 2xTY agar

supplemented with 2% (w/v) glucose and 100µg/ml ampicillin. Resulting colonies on these dishes were used to estimate the library size. The remainder of the transformation was plated on large format Bioassay dishes containing 2xTY agar supplemented with 2% (w/v) glucose and 100µg/ml ampicillin. All agar plates were incubated overnight at 30°C. 10ml of 2xTY broth was added to the large format bioassay dishes and colonies were scraped and OD_{600} measured (OD of 1.0 = 5 x 10^8 cells/ml). Aliquots were stored at -80°C in cryovials after addition of 50% v/v glycerol solution (50%) or used directly in a phage selection process.

Selection of antibodies

Several heavy-chain-only antibodies were obtained from the immunised mice, and screened for binding affinity to the immunogen (IL-17A or IL-17RA), ability to inhibit IL-17A / IL-17RA interaction, and binding kinetics, by a combination of binding ELISA, biochemical inhibition assay, cell based inhibition assay, and BIAcore® assay, using standard techniques. From these screens, two antibodies were selected as lead antibodies – clone 1.1, raised against IL-17A, and clone 2.1, raised against IL-17RA.

BIAcore assays.

Binding kinetics of V_H antibodies were measured on a BIAcore T200 instrument. Target (either recombinant IL-17A or IL-17RA) was diluted to 1µg/ml in acetate buffer, pH 5.5 (BIAcore, cat# BR-100-52) and coupled to a CM5 Series S chip (cat # BR-1006-68) using amine-coupling chemistry (NHS-EDC amine-coupling kit, cat # BR-1000-50) and the BIAcore immobilization Wizard software. In this way 100RU of target was immobilised plus a blank surface (no target) was also prepared for reference subtraction.

Binding kinetics of V_H antibodies were determined by single-cycle kinetics. V_H antibodies were prepared in dilution series (typically 1:3 dilution series starting with 100nM V_H at the highest concentration), and then injected over the antigen-coated surfaces and also a blank surface, starting with the lowest concentration of V_H and then working progressively up to the highest concentration. V_H binding kinetics were then determined from the (blank subtracted) sensorgram traces using 1:1 binding models and BIAevaluation software.

EXAMPLE 1. Generation of Mutagenized V_H containing combinations of somatic hypermutations

a. Generation of clone 1.1 V_H (anti-IL-17A V_H) variants containing combinations of somatic hypermutations

A novel optimisation strategy was used to increase binding affinities of V_H isolated from immunised mice. Lead V_H were aligned with other members of the same lineage to identify somatic hypermutation hot spots targeted during the immune response (Figure 1). The choice of amino acids at these positions formed the basis of a new recombination library approach, and led to the design of new libraries aimed at selecting higher affinity V_H with optimal amino acids at each mutation hot spot.

As an example for IL-17A, clone 1.1 was isolated directly from an immunised Tg/TKO mouse as described above. This V_H was shown to bind IL-17A with high affinity (Figure 2). Alignment of V_H clone 1.1 with other members of the same lineage identified a number of amino acid positions that had been mutated during the immune response, and both V_H -CDRs and V_H -framework regions were affected (Figure 1). This information was then utilised to design a new clone 1.1 recombination library with the aim of identifying a higher affinity variant of V_H clone 1.1.

PCR	Primer	Sequence	Amino acid changes (Kabat position)	PCR product size
1	V3/pelB(long)	GCCGCTGGATTGTTATTACTCGCG GCCCAGCCGGCCATGGCCSAGGT GCAGCTGGTGGAGTCTGGGGGAG G (SEQ ID NO: 20)	none	160bp
	clone 1.1-33S-R	TGGCGGACCCAGTACATNYBATAA CTACTAAAGGTG (SEQ ID NO: 21)	S33 to S, G, E, R	
2	clone 1.1-33S-F	CACCTTTAGTAGTTATVRNATGTA CTGGGTCCGCCA (SEQ ID NO: 22)	S33 to S, G, E, R	100bp
	clone 1.1-57K-R	CACATAGTATTBCTCACTTCCATCT TGNTYTATSYYGGCCACCCACTCC AG (SEQ ID NO: 23)	N50 to N, S, D, K K52 to K, E, N K57 to K, Q, E	
3	clone 1.1-57K-F	CAAGATGGAAGTGAGVAATACTAT GTGGACTCTGTGA (SEQ ID NO: 24)	K57 to K, Q, E	100bp
	clone 1.1-76/79-R	AGGCTATTCATTTGCAGAWACAGT GASTTCTTGGCGTTGTCTCTG (SEQ ID NO: 25)	N76 to N, K F79 to F, Y	
4	clone 1.1-76/79-F	CAGAGACAACGCCAAGAASTCACT GTWTCTGCAAATGAATAGCCT	N76 to N, K F79 to F, Y	90bp

		(SEQ ID NO: 26)		
	clone 1.1-89V-R	AGTATTTCCCCTTTCGCACAGTAA TACACAGCCGTG (SEQ ID NO: 27)	none	
5	clone 1.1-89V-F(long)	CACGGCTGTGTATTACTGTGCGAA AGGGGAAATACTACCCCTCYASTT TGACYACTGGGGCCAGGGA (SEQ ID NO: 28)	H100A to H, Y, Q Y100D to Y, H	130bp
	VH_J/F(long)	CCGTGGTGATGGTGGTGATGGCT ACCGCCACCCTCGAGTGARGAGA CRGTGACC (SEQ ID NO: 29)	none	

Table 3. Primers

Phusion High fidelity PCR master mix with HF buffer (cat # F531L, Thermo) was used for the PCR reactions which were set up for each primer pairing as follows:

Phusion HF 2x mix	25µl
Primers (10µM)	1.25µl each (pairings as in table)
clone 1.1 plasmid DNA (34ng/µl)	0.5µl
Nuclease-free H_2O	to 50µl final volume

PCR was performed as follows;

98°C 30sec

31 cycles: 98°C 10sec

58°C 20sec

72°C 20sec

72°C 10min

Hold at 10°C

The products of each PCR were analysed on a 1% agarose gel (Figure 3 (a)). Each product was then purified using Fermentas PCR purification kit (K0701) into 40µl elution buffer. Assembly PCRs were then set up to rebuild the full V_H sequence:

Phusion HF 2x mix	25µl
Purified PCR product 1	5µl
Purified PCR product 2	5µl
Purified PCR product 3	5µl
Purified PCR product 4	5µl

Purified PCR product 5 5µl

PCR was performed as follows;

98°C 30sec

5 cycles: 98°C 10sec

58°C 20sec

72°C 20sec

0.5µl of primers V3/pelB(long) and V_H _J/F(long) (both 10µM) were added to the reaction and then continued for a further 10 PCR cycles at the above conditions. The PCR product was analysed on a 1% agarose gel (Figure 3 (b)) and purified using Fermentas PCR purification kit into 40µl elution buffer. The PCR product was then used as a megaprimer for library construction as described in Example 2.

b. Generation of clone 2.1 V_H (anti-IL-17RA) variants containing combinations of somatic hypermutations

A similar recombination library approach was also used for the anti-IL-17RA lineage headed up by V_H clone 2.1. This V_H was shown to bind IL-17RA with high affinity (Figure 2). Alignment of clone 2.1 with other members of the same lineage identified a number of amino acid positions that had been mutated during the immune response (Figure 4). This information was then utilised to design a new clone 2.1 recombination library with the aim of identifying a higher affinity variant of clone 2.1.

PCR	Primer	Sequence	Amino acid changes (Kabat position)	PCR product size
1	pUCG3-VH-F	GGATTGTTATTACTCGCGGCCCAG (SEQ ID NO: 1)	none	100bp
	B clone 2.1	CTGGTGAAGGNGTATCCAGAAGCC TTGC (SEQ ID NO: 2)	P28 to S, P, T, A	
2	C clone 2.1	GCAAGGCTTCTGGATACNCCTTCA CCASTTWTGATATCAATTGGGTGC GACAGGCCACAGGACRAAGCCTTG AGTGGATGGGATGGATGAACC (SEQ ID NO: 3)	P28 to S, P, T, A S30 to S or T Y31 to Y or F Q43 to Q or R	150bp
	D clone 2.1	CCTGGTCATGGTGACTCTGYCCTG GAATTTCTGTGCATAGACTGTGTHA CCAYTBBYAGGGTTCATCCATCCCA TCCAC (SEQ ID NO: 4)	N54 to T, S, E, D, K, N S55 to S or N D57 to Y, N, D G66 to G or D	
3	G clone 2.1	GGCAGAGTCACCATGACCAGGAA (SEQ ID NO: 5)	none	120bp
	F clone 2.1	GTTCTTCCAGTYATCCCTTMTGCCT	R100 to R or I	

		CTCGCAC (SEQ ID NO: 6)	D104 to N or D	
4	E clone 2.1	GTGCGAGAGGCAKAAGGGATRACT GGAAGAAC (SEQ ID NO: 7)	R100 to R or I D104 to N or D	100bp
	pUCG3-VH-R	CCGTGGTGATGGTGGTGATG (SEQ ID NO: 8)	none	

Table 4. Primers

Phusion High fidelity DNA polymerase (cat # F518, Thermo) was used for the PCR reactions which were set up for each primer pairing as follows:

Phusion HF 5x buffer	10µl
25mM dNTPs (cat # R0182, Thermo)	1µl
Primers (10µM)	1µl each (pairings as in table)
clone 2.1 plasmid DNA	20ng
Nuclease-free H_2O	to 50µl final volume

PCR was performed as follows;

	94^0C 60sec
30 cycles:	94^0C 30sec
	58^0C 30sec
	72^0C 30sec
	72^0C 5min
	Hold at 10^0C

The products of each PCR were analysed on a 1% agarose gel (Figure 5 (a)). Each product was then purified using Fermentas PCR purification kit (K0701). Assembly PCRs were then set up to rebuild the full VH sequence:

Phusion HF 5x buffer	10µl
25mM dNTPs (cat # R0182, Thermo)	1µl
pUCG3-VH-F primer (10µM)	1µl
pUCG3-VH-R primer (10µM)	1µl
Purified PCR product 1	5µl
Purified PCR product 2	5µl
Purified PCR product 3	5µl

Purified PCR product 4	5µl
Nuclease-free H_2O	to 50µl final volume

94°C 60sec
30 cycles: 94°C 30sec
58°C 30sec
72°C 30sec
72°C 5min
Hold at 10°C

The PCR product was analysed on a 1% agarose gel (Figure 5 (b)) and purified using Fermentas PCR purification kit into 40µl elution buffer. The PCR product was then used as a megaprimer for library construction as described in Example 2.

EXAMPLE 2. Generation of Phage Display Libraries of Mutagenised Clone 1.1 and Clone 2.1 V_H

A PCR-based method was used to construct V_H phagemid libraries containing clone 1.1 and clone 2.1 mutagenised sequences. The purified V_H assembly PCR products (from Example 1) were employed as megaprimers with linearised pUCG3 phagemid vector to give products for transformation and library creation, based on the following reactions;

Phusion GC 2x mix	25µl
Linearised pUCG3	700ng
V_H PCR product	250ng
DMSO	1.5µl
Nuclease-free H_2O	to 50µl final volume

PCR was performed as follows;

98°C 30sec
10 cycles: 98°C 10sec
58°C 20sec
72°C 2min
72°C 5min
Hold at 10°C

The V_H/phagemid PCR products were purified using Fermentas PCR purification kit (cat #K0702) according to the manufacturer's instructions with the final elution being in 25µl H_2O. The purified V_H/phagemid PCR products were used for transformations of TG1 *E. coli* (Lucigen, Cat: 60502-2) by electroporation using BioRad 10 x 1 mm cuvettes (BioRad cat # 165-2089), an Eppendorf Eporator and pre-warmed recovery medium (Lucigen, proprietary mix). 2µl of the purified products were added to 25µl of cells for the electroporation, with up to 10 electroporations being performed for each V_H/phagemid product at 1800v. Electroporated cells were pooled and recovered in 50ml Falcon tubes incubated for 1 hour at 37°C with shaking at 150rpm. A 10-fold dilution series of an aliquot of the transformations was performed and plated in petri dishes containing 2xTY agar supplemented with 2% (w/v) glucose and 100µg/ml ampicillin. Resulting colonies on these dishes were used to estimate the library size. The remainder of the transformation was plated on large format Bioassay dishes containing 2xTY agar supplemented with 2% (w/v) glucose and 100µg/ml ampicillin. All agar plates were incubated overnight at 30°C. 10ml of 2xTY broth was added to the large format bioassay dishes, colonies were scraped and OD_{600} measured (OD of 1.0 = 5 x 10^8 cells/ml). Aliquots were stored at -80°C in cryovials after addition of 50% v/v glycerol solution (50%) or used directly in phage display selections.

In some instances, clones were picked directly and sequence was determined to give an estimate of the diversity of the library. For both clone 1.1 and clone 2.1, phage display libraries with greater than 1e8 (1x10^8) recombinants were constructed to fully capture the V_H diversity generated by the mutagenic PCR reactions.

EXAMPLE 3. Phage Display Selections of Mutagenised Clone 1.1 and Clone 2.1 V_H libraries

Preparation of library phage stocks and phage display selections were performed according to published methods (Antibody Engineering, edited by Benny Lo, chapter 8, p161-176, 2004). In most cases, phage display combined with a panning approach was used to isolate binding V_H domains. However, a variety of different selection methods are well described in the art, including soluble selections, selections performed under stress (e.g. heat) and competitive selections, where excess antigen or antigen-reactive V_H domains are added as competition to encourage the recovery of high affinity V_H domains or to skew selections away from a particular epitope.

For both clone 1.1 and clone 2.1 recombination libraries, one round of panning selection was performed (antigen immobilised onto maxisorb plates (Nunc 443404) in 50µl volumes at 10ug/ml in PBS), followed by 2-3 rounds of soluble selection using reducing amounts of antigen at successive rounds of selection (1nm down to 100pM of biotinylated antigen).

EXAMPLE 4. Identification of V_H with Improved Binding Affinities

V_H from the different selections were screened using a BIAcore T200 instrument to identify V_H with improved binding affinities.

Recombinant IL-17A (Peprotech AF-200-17) was diluted to 1µg/ml in acetate buffer, pH 5.5 (BIAcore, cat# BR-100-52) and coupled to a CM5 Series S chip (cat # BR-1006-68) using amine-coupling chemistry (NHS-EDC amine-coupling kit, cat # BR-1000-50) and the BIAcore immobilization Wizard software. In this way 100RU of IL-17A was immobilised plus a blank surface (no IL-17A) was also prepared for reference subtraction. For IL-17RA, first a protein G chip was prepared by diluting protein G to 20µg/ml in acetate buffer, pH 4 (BIAcore, cat# BR-100-49) and then coupled 1200 RU to a CM5 Series S chip using amine coupling chemistry. This surface was then used to capture IL-17RA Fc fusion protein from solution: IL-17RA at 10µg/ml in HBS injected for 10 seconds at 30µl/min flow rate would capture approximately 100-150RU of IL-17RA onto the protein G surface.

Binding kinetics of optimised clone 1.1 (anti-IL-17A) and clone 2.1 (anti-IL-17RA) V_H were determined by single-cycle kinetics. V_H were prepared in dilution series (typically 1:3 dilution series starting with 100nM V_H at the highest concentration), and then injected over the antigen -coated surfaces and also a blank surface, starting with the lowest concentration of V_H and then working progressively up to the highest concentration. V_H binding kinetics were then determined from the (blank subtracted) sensorgram traces using 1:1 binding models and BIAevaluation software.

Following BIAcore analysis, variants of clone 1.1 were isolated from the recombination libraries with up to 10-fold improved affinities for IL-17A (*e.g.*, clones clone 1.10 and clone 1.6, Figure 6 (a)). Similarly, for clone 2.1 a new variant was isolated (clone 2.2) that was improved in affinity for IL-17RA by 5-fold (Figure 6 (b)).

Sequence Listing Information

V_H Nucleic acid sequences

1.1

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCT
GAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGTTATTCGATGTACTGGG
TCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATG
GAAGTGAGAAATACTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGA
CAACGCCAAGAACTCACTGTTTCTGCAAATGAATAGCCTGAGAGCCGAGGACACG
GCTGTGTATTACTGTGCGAAAGGGGAAATACTACCCCTCCACTTTGACTACTGGG
GCCAGGGAACCCTGGTCACTGTCTCCTCA (SEQ ID NO: 9)

1.6

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCT
GAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGTTATAGCATGTACTGGG
TCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCGAGATAAAGCAAGAT
GGAAGTGAGCAATACTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAG
ACAACGCCAAGAACTCACTGTATCTGCAAATGAATAGCCTGAGAGCCGAGGACAC
GGCTGTGTATTACTGTGCGAAAGGGGAAATACTACCCCTCTACTTTGACTACTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO: 10)

1.10

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCT
GAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGTTATCGCATGTACTGG
GTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAGCATAGAACAAGA
TGGAAGTGAGGAATACTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGA
GACAACGCCAAGAAGTCACTGTTTCTGCAAATGAATAGCCTGAGAGCCGAGGACA
CGGCTGTGTATTACTGTGCGAAAGGGGAAATACTACCCCTCTACTTTGACTACTG
GGGCCAGGGAACCCTGGTCACTGTCTCTTCA (SEQ ID NO: 11)

2.1

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGT
GAAGGTCTCCTGCAAGGCTTCTGGATACCCCTTCACCAGTTATGATATCAATTGG

GTGCGACAGGCCACAGGACAAAGCCTTGAGTGGATGGGATGGATGAACCCTAAC
AGTGGTGACACAGTCTATGCACAGAAATTCCAGGGCAGAGTCACCATGACCAGGA
ATACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC
GGCCGTGTATTTTTGTGCGAGAGGCAGAAGGGATGACTGGAAGAACAATTATTGG
GGCCAGGGAACCCTGGTCACTGTCTCCTCA (SEQ ID NO: 12)

2.2
CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGT
GAAGGTCTCCTGCAAGGCTTCTGGATACCCCTTCACCAGTTATGATATCAATTGG
GTGCGACAGGCCACAGGACGAAGCCTTGAGTGGATGGGATGGATGAACCCTACC
AATGGTAACACAGTCTATGCACAGAAATTCCAGGACAGAGTCACCATGACCAGGA
ATACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC
GGCCGTGTATTTTTGTGCGAGAGGCAGAAGGGATGACTGGAAGAACAATTATTGG
GGCCAGGGAACCCTGGTCACTGTCTCCTCA (SEQ ID NO: 13)

Table 5. V_H amino acid sequences

Clone	FR1	**CDR1**	FR2	**CDR2**	FR3	**CDR3**	FR4
1.1	EVQLVESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO: 30)	**SYSMY** (SEQ ID NO: 31)	WVRQAPGKGLEWVA (SEQ ID NO: 32)	**NIKQDGSEKYYVDSVKG** (SEQ ID NO: 33)	RFTISRDNAKNSLFLQMNSLRAEDTAVYYCAK (SEQ ID NO: 34)	**GEILPLHFDY** (SEQ ID NO: 35)	WGQGTLVTVSS (SEQ ID NO: 36)
1.6	EVQLVESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO: 37)	**SYSMY** (SEQ ID NO: 38)	WVRQAPGKGLEWVA (SEQ ID NO: 39)	**EIKQDGSEQYYVDSVKG** (SEQ ID NO: 40)	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAK (SEQ ID NO: 41)	**GEILPLYFDY** (SEQ ID NO: 42)	WGQGTLVTVSS (SEQ ID NO: 43)
1.10	EVQLVESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO: 44)	**SYRMY** (SEQ ID NO: 45)	WVRQAPGKGLEWVA (SEQ ID NO: 46)	**SIEQDGSEEYYVDSVKG** (SEQ ID NO: 47)	RFTISRDNAKKSLFLQMNSLRAEDTAVYYCAK (SEQ ID NO: 48)	**GEILPLYFDY** (SEQ ID NO: 49)	WGQGTLVTVSS (SEQ ID NO: 50)
Clone	FR1	**CDR1**	FR2	**CDR2**	FR3	**CDR3**	FR4
2.1	QVQLVQSGAEVKKPGASVKVSCKASGYPFT (SEQ ID NO: 51)	**SYDIN** (SEQ ID NO: 52)	WVRQATGQSLEWMG (SEQ ID NO: 53)	**WMNPNSGDTVYAQKFQG** (SEQ ID NO: 54)	RVTMTRNTSISTAYMELSSLRSEDTAVYFCAR (SEQ ID NO: 55)	**GRRDDWKNNY** (SEQ ID NO: 56)	WGQGTLVTVSS (SEQ ID NO: 57)
2.2	QVQLVQSGAEVKKPGASVKVSCKASGYPFT (SEQ ID NO: 58)	**SYDIN** (SEQ ID NO: 59)	WVRQATGRSLEWMG (SEQ ID NO: 60)	**WMNPTNGNTVYAQKFQD** (SEQ ID NO: 61)	RVTMTRNTSISTAYMELSSLRSEDTAVYFCAR (SEQ ID NO: 62)	**GRRDDWKNNY** (SEQ ID NO: 63)	WGQGTLVTVSS (SEQ ID NO: 64)

CLAIMS:

1. A method of designing an immunoglobulin library for optimisation of a biological property of a first lead immunoglobulin, the method comprising:

a) identifying one or more related immunoglobulins, said one or more related immunoglobulins being related to the first lead immunoglobulin, each immunoglobulin having been raised against a target antigen by immunisation of a transgenic non-human mammal comprising human immunoglobulin genes with the target antigen;

b) comparing amino acid sequences of the first lead immunoglobulin and the one or more related immunoglobulins;

c) identifying, based on the sequence comparison, one or more sites at which there are variant amino acid residues between:

(i) the first lead immunoglobulin and the one or more related immunoglobulins, and/or

(ii) where the one or more related immunoglobulins is a plurality of immunoglobulins, between the plurality of immunoglobulins,

wherein the one or more sites at which there are variant amino acid residues comprise potential sites for modification of the first lead immunoglobulin;

d) selecting one or more sites for modification to replace an amino acid of the first lead immunoglobulin with the corresponding variant amino acid of one or more of the related immunoglobulins, based on the sequence comparison; and

e) generating immunoglobulin sequences for the library based on the sequence of the first lead immunoglobulin, modified at one or more of the selected sites for modification.

2. The method of claim 1, wherein the one or more related immunoglobulins are of common lineage and bind the same target antigen as the first lead immunoglobulin, preferably with at least 70%, 80%, 85%, 90%, 95% homology in at least one CDR region to the lead immunoglobulin.

3. The method of claim 1 or claim 2, wherein the one or more related immunoglobulins have at least 70% homology in CDR3 to the lead immunoglobulin.

4. The method of any preceding claim, wherein the one or more related immunoglobulins have at least 70% homology in CDR1 and/or CDR2 to the lead immunoglobulin.

5. The method of any preceding claim, wherein the one or more related immunoglobulins have at least 70% homology in the framework regions to the lead immunoglobulin.

6. The method of any preceding claim wherein the plurality of related immunoglobulins comprises at least 2 ,3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 immunoglobulins.

7. The method of any preceding claim wherein step c) comprises identifying sites for modification within the CDRs of the immunoglobulin sequences, wherein a site within the CDRs is considered a site for modification if there is a variant amino acid residue present in at least one, two, three, four, or five of the related immunoglobulins.

8. The method of any preceding claim wherein step c) further comprises identifying sites for modification outside the CDRs of the immunoglobulin sequences, wherein a site outside the CDRs is considered a site for modification if there is a variant amino acid residue present in at least 20% of the related immunoglobulins.

9. The method of claim 8 wherein a site outside the CDRs which would otherwise be identified as a site for modification is not identified as a site for modification if modifying the site would lead to the introduction of one or more of the following features into the modified immunoglobulin: (i) unpaired cysteines, (ii) oxidation sites (free methionines), (iii) glycosylation sites, (iv) deamidation sites, and (v) isomerisation sites.

10. The method of any preceding claim wherein the sequences selected in step d) include variant sequences reflecting each possible combination of modifications at the sites for modification.

11. The method of any preceding claim wherein the modifications at the sites for modification include only conservative amino acid substitutions.

12. The method of any preceding claim wherein the variant immunoglobulins include no modifications outside the sites for modification.

13. The method of any preceding claim, wherein step e) further comprises generating sequences of additional variant immunoglobulins, wherein the sequences are further

modified at one or more of the selected sites for modification to replace an amino acid of the first lead immunoglobulin with a conservative amino acid replacement for the corresponding variant amino acid.

14. The method of any preceding claim, wherein step e) further comprises generating sequences of additional variant immunoglobulins, wherein the sequences are further modified at one or more of the selected sites for modification to replace an amino acid of the first lead immunoglobulin with an amino acid not found at the corresponding residue of the related immunoglobulins.

15. The method of any preceding claim, further comprising step f) generating an immunoglobulin library comprising immunoglobulins having the sequences generated in step e).

16. The method of claim 15, further comprising step g) screening the immunoglobulin library to identify one or more immunoglobulins having desired biological properties.

17. The method of any preceding claim, comprising, prior to step a), the step α) of generating and sequencing a plurality of immunoglobulins, including a first lead immunoglobulin and one or more related immunoglobulins.

18. The method of claim 17 wherein the plurality of immunoglobulins is generated by immunising a non-human mammal, preferably a mouse or rat, preferably a transgenic mouse or rat expressing human immunoglobulin genes, with a target antigen.

19. The method of any preceding claim, comprising, prior to step a), the step β) of identifying a first lead immunoglobulin.

20. The method of any preceding claim wherein the immunoglobulins are antibodies, or antigen-binding fragments of an antibody.

21. The method of claim 20 wherein the immunoglobulins comprise or consist of heavy chain only antibodies.

22. The method of claim 20 wherein the immunoglobulins comprise or consist of V_H domains of antibodies.

23. A method of optimising a lead immunoglobulin, the method comprising:

A) performing the method of any preceding claim; and

B) selecting one or more optimised immunoglobulins from the library based on a desired property of the optimised immunoglobulin.

24. A library of synthetic polynucleotides encoding a plurality of immunoglobulins, wherein the sequences of the plurality of immunoglobulins are designed in accordance with the method of any of claims 1 to 22.

25. A library comprising a plurality of immunoglobulins, wherein the sequences of the plurality of immunoglobulins are designed in accordance with the method of any of claims 1 to 22.

26. An isolated immunoglobulin designed in accordance with the method of any of claims 1 to 22; or selected in accordance with the method of claim 23.

27. An isolated nucleic acid molecule comprising a nucleotide sequence encoding an immunoglobulin according to claim 26.

28. An isolated polypeptide comprising an amino acid sequence of an immunoglobulin according to claim 26.

29. A vector comprising a nucleic acid molecule according to claim 27.

30. A plurality of vectors comprising the polynucleotide library according to claim 24.

31. A host cell comprising the vector or vectors of claim 29 or 30.

32. A method of obtaining an immunoglobulin of claim 26, comprising the steps of: providing a host cell according to claim 31; allowing the host cell to express the immunoglobulin encoded by the nucleic acid molecule comprised in the vector; and purifying the immunoglobulin.

33. The method of claim 32, further comprising preparing a pharmaceutical formulation comprising the immunoglobulin.

34. A chimeric polypeptide comprising the immunoglobulin of claim 26.

35. A conjugate comprising the immunoglobulin of claim 26, or the chimeric polypeptide of claim 34, conjugated to an additional moiety.

36. A pharmaceutical formulation comprising the immunoglobulin of claim 26, the chimeric polypeptide of claim 34, or the conjugate of claim 35.