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(54) **Title:**
ANIMAL MODELS AND THERAPEUTIC MOLECULES

(57) **Abstract:**
The invention discloses methods for the generation of chimaeric human –non human antibodies and chimaeric antibody chains, antibodies and antibody chains so produced,and derivatives thereofincluding fully humanised antibodies;compositions comprising said antibodies, antibody chainsand derivatives, as well as cells, non-human mammals and vectors, suitablefor use in said methods.

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(54) **Title**: ANIMAL MODELS AND THERAPEUTIC MOLECULES

(57) **Abstract**: The invention discloses methods for the generation of chimaeric human –non human antibodies and chimaeric antibody chains, antibodies and antibody chains so produced,and derivatives thereofincluding fully humanised antibodies;compositions comprising said antibodies, antibody chainsand derivatives, as well as cells, non-human mammals and vectors, suitablefor use in said methods.

Animal models and therapeutic molecules

Background

The present invention relates inter alia to non-human animals and cells that are engineered to contain exogenous DNA, such as human immunoglobulin gene DNA, their use in medicine and the study of disease, methods for production of non human animals and cells, and antibodies and antibody chains produced by such animals and derivatives thereof.

In order to get around the problems of humanizing antibodies a number of companies set out to generate mice with human immune systems. The strategy used was to knockout the heavy and light chain loci in ES cells and complement these genetic lesions with transgenes designed to express the human heavy and light chain genes. Although fully human antibodies could be generated, these models have several major limitations:

(i) The size of the heavy and light chain loci (each several Mb) made it impossible to introduce the entire loci into these models. As a result the transgenic lines recovered had a very limited repertoire of V-regions, most of the constant regions were missing and important distant enhancer regions were not included in the transgenes.

(ii) The very low efficiency of generating the large insert transgenic lines and the complexity and time required to cross each of these into the heavy and light chain knockout strains and make them homozygous again, restricted the number of transgenic lines which could be analysed for optimal expression.

(iii) Individual antibody affinities rarely reached those which could be obtained from intact (non-transgenic) animals.

WO2007117410 discloses chimaeric constructs for expressing chimaeric antibodies.

WO2010039900 discloses knock in cells and mammals having a genome encoding chimaeric antibodies.

The present invention provides, inter alia, a process for the generation in non-human mammals of antibodies that comprise a human Ig variable region, and further provides non-human animal models for the generation of such antibodies.

Summary of the Invention

In one aspect the invention relates to a non-human mammal whose genome comprises:

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies, or chimaeric light or heavy chains, having a non-human mammal constant region and a human variable region.

In one aspect the invention relates to non-human mammal whose genome comprises

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies, or chimaeric light or heavy chains, having a non-human mammal constant region and a human variable region.

In one aspect the invention relates to non-human mammalian cell whose genome comprises

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region.

In one aspect the invention relates to a non-human mammalian cell whose genome comprises

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region;

In a further aspect the invention relates to a method for producing a non-human cell or mammal comprising inserting into a non-human mammal cell genome, such as an ES cell genome;

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; respectively,

the insertion being such that the non-human cell or mammal is able to produce a repertoire of chimaeric antibodies having a non-human mammal constant region and a human variable region, wherein steps (a) and (b) can be carried out in either order and each of steps (a) and (b) can be carried out in a stepwise manner or as a single step.

Insertion may be by homologous recombination.

In a further aspect the invention relates to a method for producing an antibody or antibody chain specific to a desired antigen the method comprising immunizing a transgenic non-human mammal as disclosed herein with the desired antigen and recovering the antibody or antibody chain.

In a further aspect the invention relates to a method for producing a fully humanised antibody comprising immunizing a transgenic non-human mammal as disclosed herein with the desired antigen, recovering the antibody or cells producing the antibody and then replacing the non-human mammal constant region with a human constant region, for example by protein or DNA engineering.

In a further aspect the invention relates to humanised antibodies and antibody chains produced according to the present invention, both in chimaeric (for example, mouse-human) and fully humanised form, as well as fragments and derivatives of said antibodies and chains, and use of said antibodies, chains and fragments in medicine, including diagnosis.

In a further aspect the invention relates to use of a non-human mammal as described herein as a model for the testing of drugs and vaccines.

Figures

Figures 1 - 8 show an iterative process for insertion of a series of human BACs into a mouse Ig locus.

Figures 9 – 18 show in more detail the process of figures 1-8 for the IgH and kappa locus

Figures 19 and 20 show the principles behind antibody generation in chimaeric mice.

Figure 21 shows a possible insertion site for the human DNA in a mouse chromosome.

Figures 22 – 26 disclose an alternative iterative process for insertion of a series of human BACs into a mouse Ig locus.

Figure 27 – 29 illustrate a mechanism for inversion of the host VDJ region

Figure 30 illustrates proof of principle for insertion of a plasmid using an RMCE approach.

Figure 31 illustrates sequential RMCE – Integration into Landing Pad

Figure 32 illustrates confirmation of Successful Insertion into Landing Pad

Figure 33 illustrates PCR Confirmation of 3' End Curing

Figure 34 illustrates insertion of BAC#1 and PCR Diagnostics

General Description

All nucleotide coordinates for the mouse are from NCBI m37, April 2007 ENSEMBL Release 55.37h for the mouse C57BL/6J strain. Human nucleotides are from GRCh37, Feb 2009 ENSEMBL Release 55.37 and rat from RGSC 3.4 Dec 2004 ENSEMBL release 55.34w.

In the present invention we disclose methods for the construction of chimaeric human heavy and light chain loci in a non-human mammal, for example a mouse. Reference to work in mice herein is by way of example only, and reference to mice is taken to include reference to all non-human mammals unless otherwise apparent from the disclosure, with mice being preferred as the non-human mammal.

In one aspect the invention relates to a non-human mammal whose genome comprises:

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies or antibody chains having a non-human mammal constant region and a human variable region.

In a further aspect the invention relates to a non-human mammal whose genome comprises:

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies having a non-human mammal constant region and a human variable region.

Optionally the non-human mammal genome is modified to prevent expression of fully host-species specific antibodies.

In one aspect the inserted human DNA comprises at least 50% of the human heavy chain variable (V) genes, such as at least 60%, at least 70%, at least 80%, at least 90%, and in one aspect all of the human V genes.

In one aspect the inserted human DNA comprises at least 50% of the human heavy chain diversity (D) genes, such as at least 60%, at least 70%, at least 80%, at least 90%, and in one aspect all of the human D genes.

In one aspect the inserted human DNA comprises at least 50% of the human heavy chain joining (J) genes, such as at least 60%, at least 70%, at least 80%, at least 90%, and in one aspect all of the human J genes.

In one aspect the inserted human DNA comprises at least 50% of the human light chain Variable (V) genes, such as at least 60%, at least 70%, at least 80%, at least 90%, and in one aspect all of the human light chain V genes.

In one aspect the inserted human DNA comprises at least 50% of the human light chain joining (J) genes, such as at least 60%, at least 70%, at least 80%, at least 90%, and in one aspect all of the human light chain J genes.

The inserted human genes may be derived from the same individual or different individuals, or be synthetic or represent human consensus sequences.

Although the number of V D and J regions is variable between human individuals, in one aspect there are considered to be 51 human V genes, 27 D and 6 J genes on the heavy chain, 40 human V genes and 5 J genes on the kappa light chain and 29 human V genes and 4 J genes on the lambda light chain (Janeway and Travers, Immunobiology, Third edition)

In one aspect the human heavy chain locus inserted into the non-human mammal contains the full repertoire of human V, D and J regions, which in the genome is in functional arrangement with the non-human mammal constant regions such that functional chimaeric antibodies can be produced between the human variable and non-human mammal constant regions. This total inserted human heavy chain genetic material is referred to herein as the human IgH VDJ region, and comprises DNA from a human genome that encodes all the exons encoding human V,D and J portions and suitably also the associated introns. Similarly, reference to the human Ig light chain kappa V and J regions herein refers to human DNA comprising all the exons encoding V and J regions and suitably also the associated introns of the human genome. Reference to the human Ig light chain lambda V and J regions herein refers to human DNA comprising all the exons encoding V and J regions and suitably also the associated introns of the human genome.

Human variable regions are suitably inserted upstream of non-human mammal constant region, the latter comprising all of the DNA required to encode the full constant region or a sufficient portion of the constant region to allow the formation of an effective chimaeric antibody capable of specifically recognising an antigen.

In one aspect the chimaeric antibodies or antibody chains have a part of a host constant region sufficient to provide one or more effector functions seen in antibodies occurring naturally in a host mammal, for example that they are able interact with Fc receptors, and/or bind to complement.

Reference to a chimaeric antibody or antibody chain having a host non mammal constant region herein therefore is not limited to the complete constant region but also includes chimaeric antibodies or chains which have all of the host constant region, or a part thereof sufficient to provide one or more effector functions. This also applies to non human mammals and cells and methods of the invention in which human variable region DNA may be inserted into the host genome such that it forms a chimaeric antibody chain with all or part of a host constant region. In one aspect the whole of a host constant region is operably linked to human variable region DNA.

The host non-human mammal constant region herein is preferably the endogenous host wild-type constant region located at the wild type locus, as appropriate for the heavy or light chain. For example, the human heavy chain DNA is suitably inserted on mouse chromosome 12, suitably adjacent the mouse heavy chain constant region.

In one aspect the insertion of the human DNA, such as the human VDJ region is targeted to the region between the J4 exon and the Cμ locus in the mouse genome IgH locus, and in one aspect is inserted between coordinates 114,667,090 and 114,665,190, suitably at coordinate 114,667,091. In one aspect the insertion of the human DNA, such as the human light chain kappa VJ is targeted into mouse chromosome 6 between coordinates 70,673,899 and 70,675,515, suitably at position 70,674,734, or an equivalent position in the lambda mouse locus on chromosome 16.

In one aspect the host non-human mammal constant region for forming the chimaeric antibody may be at a different (non endogenous) chromosomal locus. In this case the inserted human DNA, such as the human variable VDJ or VJ region(s) may then be inserted into the non-human genome at a site which is distinct from that of the naturally occurring heavy or light constant region. The native constant region may be inserted into the genome, or duplicated within the genome, at a different chromosomal locus to the native position, such that it is in a functional arrangement with the human variable region such that chimaeric antibodies of the invention can still be produced.

In one aspect the human DNA is inserted at the endogenous host wild-type constant region located at the wild type locus between the host constant region and the host VDJ region.

Reference to location of the variable region upstream of the non human mammal constant region means that there is a suitable relative location of the two antibody portions, variable and constant, to allow the variable and constant regions to form a chimaeric antibody or antibody chain *in vivo* in the mammal. Thus, the inserted human DNA and host constant region are in functional arrangement with one another for antibody or antibody chain production.

In one aspect the inserted human DNA is capable of being expressed with different host constant regions through isotype switching. In one aspect isotype switching does not require or involve trans switching. Insertion of the human variable region DNA on the same chromosome as the relevant host constant region means that there is no need for trans-switching to produce isotype switching.

As explained above, the transgenic loci used for the prior art models were of human origin, thus even in those cases when the transgenes were able to complement the mouse locus so that the mice produced B-cells producing fully human antibodies, individual antibody affinities rarely reached those which could be obtained from intact (non-transgenic) animals. The principal reason for this (in addition to repertoire and expression levels described above) is the fact that the control elements of the locus are human. Thus, the signalling components, for instance to activate hyper-mutation and selection of high affinity antibodies are compromised.

In contrast, in the present invention, host non-human mammal constant regions are maintained and it is preferred that at least one non-human mammal enhancer or other control sequence, such as a switch region, is maintained in functional arrangement with the non-human mammal constant region, such that the effect of the enhancer or other control sequence, as seen in the host mammal, is exerted in whole or in part in the transgenic animal.

This approach above is designed to allow the full diversity of the human locus to be sampled, to allow the same high expression levels that would be achieved by non-human mammal control sequences such as enhancers, and is such that signalling in the B-cell, for example isotype switching using switch recombination sites, would still use non-human mammal sequences.

A mammal having such a genome would produce chimaeric antibodies with human variable and non-human mammal constant regions, but these could be readily humanized, for example in a cloning step. Moreover the *in vivo* efficacy of these chimaeric antibodies could be assessed in these same animals.

In one aspect the inserted human IgH VDJ region comprises, in germline configuration, all of the V, D and J regions and intervening sequences from a human.

In one aspect 800-1000kb of the human IgH VDJ region is inserted into the non-human mammal IgH locus, and in one aspect a 940, 950 or 960 kb fragment is inserted. Suitably this includes bases 105,400,051 to 106,368,585 from human chromosome 14 (all coordinates refer to NCBI36 for the human genome, ENSEMBL Release 54 and NCBIM37 for the mouse genome, relating to mouse strain C57BL/6J).

In one aspect the inserted IgH human fragment consists of bases 105,400,051 to 106,368,585 from chromosome 14. In one aspect the inserted human heavy chain DNA, such as DNA consisting of bases 105,400,051 to 106,368,585 from chromosome 14, is inserted into mouse chromosome 12 between the end of the mouse J4 region and the Eμ region, suitably between coordinates 114,667,091 and 114,665,190, suitably at coordinate 114,667,091.

In one aspect the inserted human kappa VJ region comprises, in germline configuration, all of the V and J regions and intervening sequences from a human.

Suitably this includes bases 88,940,356 to 89,857,000 from human chromosome 2, suitably approximately 917kb. In a further aspect the light chain VJ insert may comprise only the proximal clusters of V segments and J segments. Such an insert would be of approximately 473 kb.

In one aspect the human light chain kappa DNA, such as the human IgK fragment of bases 88,940,356 to 89,857,000 from human chromosome 2, is suitably inserted into mouse chromosome 6 between coordinates 70,673,899 and 70,675,515, suitably at position 70,674,734.

In one aspect the human lambda VJ region comprises, in germline configuration, all of the V and J regions and intervening sequences from a human.

Suitably this includes analogous bases to those selected for the kappa fragment, from human chromosome 2.

All specific human fragments described above may vary in length, and may for example be longer or shorter than defined as above, such as 500 bases, 1KB, 2K, 3K, 4K, 5KB, 10 KB, 20KB, 30KB, 40KB or 50KB or more, which suitably comprise all or part of the human V(D)J region, whilst preferably retaining the requirement for the final insert to comprise human genetic material encoding the complete heavy chain region and light chain region, as appropriate, as described above.

In one aspect the 5' end of the human insert described above is increased in length. Where the insert is generated in a stepwise fashion then the increase in length is generally in respect of the upstream (5') clone.

In one aspect the 3' end of the last inserted human gene, generally the last human J gene to be inserted is less than 2kb, preferably less than 1KB from the human-mouse join region.

In one aspect the non-human mammal comprises some or all of the human light chain kappa VJ region as disclosed herein but not the human light chain lambda VJ region.

In a further aspect the genome comprises an insertion of V, D (heavy chain only) and J genes as described herein at the heavy chain locus and one light chain locus, or at the heavy chain locus and both light chain loci. Preferably the genome is homozygous at one, or both, or all three loci.

In another aspect the genome may be heterozygous at one or more of the loci, such as heterozygous for DNA encoding a chimaeric antibody chain and native (host cell) antibody chain. In one aspect the genome may be heterozygous for DNA capable of encoding 2 different antibody chains of the invention, for example, comprising 2 different chimaeric heavy chains or 2 different chimaeric light chains.

In one aspect the invention relates to a non-human mammal or cell, and methods for producing said mammal or cell, as described herein, wherein the inserted human DNA, such as the human IgH VDJ region and/or light chain V, J regions are found on only one allele and not both alleles in the mammal or cell. In this aspect a mammal or cell has the potential to express both an endogenous host antibody heavy or light chain and a chimaeric heavy or light chain.

In a further aspect of the invention the human VDJ region, or light chain VJ region, is not used in its entirety, but parts of the equivalent human VDJ or VJ region, such as the exons, from other species may be used, such as one or more V, D, or J exons from other species, or regulatory sequences from other species. In one aspect the sequences used in place of the human sequences are not human or mouse. In one aspect the sequences used may be from rodent, or, primate such as chimp. For example, 1, 2, 3, 4, or more, or all of the J regions from a primate other than a human may be used to replace, one, 2, 3, 4, or more or all of the human J exons in the VDJ/VJ region of the cells and animals of the invention.

In a further aspect the inserted human DNA, such as the human IgH VDJ region, and/or light chain VJ regions, may be inserted such that they are operably linked in the genome with a mu constant region from a non-human, non-mouse species, such as a rodent or primate sequence, such as a rat sequence.

Other non-human, non-mouse species from which DNA elements may be used in the present invention include rabbits, lamas, dromedary, alpacas, camels and sharks.

In one aspect the inserted human DNA, such as the human VDJ or VJ region is not operably linked to the endogenous host mu sequence but rather to non-host mu sequence.

Operable linkage suitably allows production of an antibody heavy or light chain comprising the human variable region.

In one aspect the inserted human DNA, such as the human IgH VDJ region (and/or light chain VJ regions) may be inserted into the host chromosome together with mu constant region nucleic acid which is not host mu constant region nucleic acid, and preferably is a mu constant region from a non-mouse, non-human species. Suitably the inserted human DNA, such as the human VDJ region (and/or light chain VJ regions) is operably linked to a non-human, non-mouse mu, and is able to form a chimaeric antibody heavy or light chain. In another aspect a non-mouse, non-human mu may be inserted into the host chromosome on a separate genetic element to that of the human variable region, or at a different location in the genome, suitably operably linked to the variable region such that a chimaeric antibody heavy or light can be formed.

In one aspect the invention relates to a cell, or non-human mammal, the genome of which comprises: one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of all or part of the human kappa constant region.

In another aspect the invention relates to a cell, or non-human mammal, the genome of which comprises: one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of all or part of the human lambda constant region.

Suitably the light chain VJ and C regions are able to form antibody chains in vivo capable of specifically reacting with an antigen.

In one aspect of the invention there is no non-human coding sequence in the inserted light chain region.

In such aspects a human kappa and/or lambda region is inserted into the genome, in combination with insertion of the heavy chain VDJ region or part thereof, upstream of the host heavy chain constant region as disclosed herein.

Thus the cell or non human mammal of the invention may comprise:

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of all or part of the non-human kappa constant region,
wherein the non-human mammal is able to produce a repertoire of antibodies having an antibody chain comprising non human mammal constant region and a human variable region.

The cell or non human mammal of the invention may comprise

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region;
wherein the non-human mammal is able to produce a repertoire of antibodies having an antibody chain comprising a non-human mammal constant region and a human variable region.

Suitably the insertion of the human VJC light chain DNA, or part thereof as disclosed above, is made at the equivalent mouse locus. In one aspect the human light chain kappa VJC DNA, or part thereof, is inserted immediately upstream or downstream of the mouse kappa VJC region. In one aspect, the human light chain lambda VJC region or part thereof is inserted immediately upstream or downstream of the mouse lambda VJC region. In one aspect only the human kappa VJC locus is inserted. Insertions may be made using the techniques disclosed herein, and suitably do not remove the host sequences from the genome. In one aspect the non human mammal host VJC sequences may be inactivated in some way, by mutation, or inversion, or by insertion of the human variable region DNA, or by any other means. In one aspect the cell or non human mammal of the invention may comprise an insertion of the complete VJC human region.

The human kappa variable region DNA might be inserted into the genome in functional arrangement with a lambda constant region, for example inserted upstream of a lambda constant region. Alternatively human lambda region variable DNA might be inserted in functional arrangement with a kappa constant region, for example inserted upstream of a kappa constant region.

In one aspect one or more non-human mammal control sequences such as the enhancer sequence(s) is maintained upstream of the nonhuman mammal Mu constant region, suitably in its native position with respect to the distance from the constant region.

In one aspect one or more non-human mammal control sequences such as an enhancer sequence(s) are maintained downstream of the nonhuman mammal Mu constant region, suitably in its native position with respect to the distance from the constant region.

In one aspect a non-human mammal switch sequence, suitably the endogenous switch sequence, is maintained upstream of the non-human mammal Mu constant region, suitably in its native position with respect to distance from the constant region.

In such location the host enhancer or switch sequences are operative in vivo with the host constant region sequence(s).

In one aspect a switch sequence is neither human, nor native in the non-human mammal, for example in one aspect a non human mammal switch sequence is not a mouse or human switch sequence. The switch sequence may be, for example, a rodent or primate sequence, or a synthetic sequence. In particular the switch sequence may be a rat sequence where the non human mammal is a mouse. By way of example, a mouse or human constant mu sequence may be placed under the control of a switch sequence from a rat, or chimp, or other switch sequence, suitably capable of allowing isotype switching to occur in vivo.

The cell or mammal of the invention may therefore comprise a human or non human mammal switch sequence and a human or non human mammal enhancer region or regions. They may be upstream of a human or non human mammal constant region. Preferably the control sequences are able to direct expression or otherwise control the production of antibodies comprising a constant region with which they are associated. One combination envisaged is a rat switch with mouse enhancer sequences and mouse constant regions in a mouse cell.

In one aspect the invention relates to a cell, preferably a non human cell, or non human mammal comprising an immunoglobulin heavy chain or light chain locus having DNA from 3 or more species. For example, the cell or animal may comprise host cell constant region DNA, one or more human V, D or J coding sequences and one or more non-human, non-host DNA regions that are able to control a region of the immunoglobulin locus, such as a switch sequence, promoter or enhancer which are able to control expression or isotype switching in vivo of the Ig DNA. In one aspect the cell or animal is a mouse and comprises additionally human DNA from the human Ig locus and additionally a non-mouse DNA sequence, such as a rat DNA sequence, capable of regulation of the mouse or human DNA.

In another aspect the invention relates to a cell, preferably non-human cell, or non-human mammal comprising an immunoglobulin heavy chain or light chain locus having DNA from 2 or more different human genomes. For example, it could comprise heavy chain V(D)J sequences from more than one human genome within a heavy or light chain, or heavy chain VDJ DNA from one genome and light chain VJ sequences from a different genome.

In one aspect the invention relates to a DNA fragment or cell or non-human mammal comprising an immunoglobulin heavy chain or light chain locus, or part thereof, having DNA from 2 or more species, where one species contributes a non coding region such as a regulatory region, and the other species coding regions such as V, D, J or constant regions.

In one aspect the human promoter and/or other control elements that are associated with the different human V, D or J regions are maintained in the mouse genome.

In a further aspect one or more of the promoter elements, or other control elements, of the human regions, such as the human V regions, are optimised to interact with the transcriptional machinery of a non-human mammal.

Suitably a human coding sequence may be placed under the control of an appropriate non-human mammal promoter, which allows the human DNA to be transcribed efficiently in the appropriate non-human animal cell. In one aspect the human region is a human V region coding sequence, and a human V region is placed under the control of a non-human mammal promoter.

The functional replacement of human promoter or other control regions by non-human mammal promoter or control regions may be carried out by use of recombineering, or other recombinant DNA technologies, to insert a part of the human Ig region (such as a human V region) into a vector (such as a BAC) containing a non-human Ig region. The recombineering/recombinant technique suitably replaces a portion of the non-human (e.g. mouse) DNA with the human Ig region, and thus places the human Ig region under control of the non-human mammal promoter or other control region. Suitably the human coding region for a human V region replaces a mouse V region coding sequence. Suitably the human coding region for a human D region replaces a mouse D region coding sequence. Suitably the human coding region for a human J region replaces a mouse J region coding sequence. In this way human V, D or J regions may be placed under the control of a non-human mammal promoter, such as a mouse promoter.

In one aspect the only human DNA inserted into the non-human mammalian cell or animal are V, D or J coding regions, and these are placed under control of the host regulatory sequences or other (non-human, non-host) sequences, In one aspect reference to human coding regions includes both human introns and exons, or in another aspect simply exons and no introns, which may be in the form of cDNA.

Alternatively it is possible to use recombineering, or other recombinant DNA technologies, to insert a non human-mammal (e.g. mouse) promoter or other control region, such as a promoter for a V region, into a BAC containing a human Ig region. The recombineering step then places a portion of human DNA under control of the mouse promoter or other control region.

The approaches described herein may also be used to insert some or all of the V, D and J regions from the human heavy chain upstream of a light chain constant region, rather than upstream of the heavy chain constant region. Likewise some or all of the human light chain V and J regions may be inserted upstream of the heavy chain constant region. Insertion may be at the endogenous constant region locus, for example between the endogenous constant and J region, and may be of some, or all, of the V, D or J genes alone, excluding promoter or enhancer sequences, or may be of some, or all, of the V, D or J genes with one or more or all respective promoter or enhancer sequences. In one aspect the full repertoire of V, D or J fragments in germline orientation may be inserted upstream and in functional arrangement with a host constant region.

Thus the present invention allows V and/or D and/or J regions from a human, or any species, to be inserted into a chromosome of a cell from a different species that comprises a constant region, allowing a chimaeric antibody chain to be expressed.

In one aspect the invention requires only that some human variable region DNA is inserted into the genome of a non human mammal in operable arrangement with some, or all, of the human heavy chain constant region at the region of the endogenous heavy chain constant region locus such that an antibody chain can be produced. In this aspect of the invention and where human light chain DNA is additionally inserted, the light chain DNA insertion can be in the form of a completely human construct, having both human variable DNA and human constant region DNA, or have human variable region DNA and constant region DNA from a non-human, non-host species. Other variations are also possible, such as insertion of both of the light chain human variable region and host genome constant region. In addition the insertion of said light chain transgenes need not be at the equivalent endogenous locus, but may be anywhere in the genome. In such a scenario the cell or mammal may produce chimaeric heavy chains (comprising human variable region DNA and mouse constant region DNA) and light chains comprising human variable and human constant region DNA. Thus in one aspect of the invention the lambda and or kappa human variable region DNA can be inserted upstream of the endogenous locus, or downstream, or indeed on a different chromosome to the endogenous locus, and inserted with or without constant region DNA.

As well insertion of human light chain DNA upstream of the host non-human mammal constant region, a further aspect of the invention relates to insertion of one or both light chain human variable regions downstream of the endogenous locus constant region, or elsewhere in the genome.

Generally, insertion of human variable region DNA at or close to the equivalent endogenous locus in the recipient genome is preferred, for example within 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10kb of the boundary (upstream or downstream) of a host immunoglobulin locus.

Thus in one aspect the invention can relate to a cell or non-human mammal whose genome comprises:

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions, and/or , one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies, or chimaeric light or heavy chains, having a non-human mammal constant region and a human variable region.

In one particular aspect the genome of the cell or non human mammal comprises:

a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region;

one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region, and

one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions downstream of the host non-human mammal lambda constant region,

optionally in which the human lambda variable region may be inserted downstream of the endogenous host lambda locus in operable linkage with a human lambda constant region, such that the non human mammal or cell can produce fully human antibody light chains and chimaeric heavy chains.

In a further, different, aspect of the invention, the use of the methods of the invention allows a locus to be built up in a stepwise manner by sequential insertions, and thus allows for the insertion of human variable DNA together with human or non human constant region DNA at any suitable location in the genome of a non-human host cell. For example, methods of the invention can be used to insert human immunoglobulin variable region DNA together with constant region DNA from the host genome anywhere in the genome of a non-human host cell, allowing a chimaeric antibody chain to be produced from a site other than the endogenous heavy region. Any human heavy chain or light chain DNA construct contemplated above can be inserted into any desired position into the genome of a non human host cell using the techniques described herein. The present invention thus also relates to cells and mammals having genomes comprising such insertions.

The invention also relates to a vector, such as a BAC, comprising a human V, D or J region in a functional arrangement with a non-human mammal promoter, or other control sequence, such that the expression of the human V, D or J region is under the control of the non-human mammal promoter in a cell of the non-human mammal, such as an ES cell, in particular once inserted into the genome of that cell.

The invention also relates to cells and non-human mammals containing said cells, which cells or mammals have a human V, D or J region in a functional arrangement with a non-human mammal promoter, or other control sequence, such that the expression of the human V, D or J region is under the control of the non-human mammal promoter in the cells or mammal.

Generally, one aspect of the invention thus relates to a non human mammal host cell capable of expression of a human V, D or J coding sequence under the control of a host promoter or control region, the expression capable of producing a humanised antibody having a human variable domain and non human mammal constant region.

In one aspect the invention relates to a cell, such as a non mammalian cell, such as an ES cell, the genome of which comprises

a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region;

In another aspect the invention relates to a cell, such as a non-human mammal cells, such as ES cells whose genome comprises

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region

In one aspect the cell is an ES cell is capable of developing into a non-human mammal able to produce a repertoire of antibodies which are chimaeric, said chimaeric antibodies having a non-human mammal constant region and a human variable region. Optionally the genome of the cell is modified to prevent expression of fully host-species specific antibodies.

In one aspect the cell is an induced pluripotent stem cell (iPS cell).

In one aspect cells are isolated non human mammalian cells.

In one aspect a cell as disclosed herein is preferably a non human mammalian cell.

The invention also relates to a cell line which is grown from or otherwise derived from cells as described herein, including an immortalised cell line. The cell line may comprise inserted human V, D or J genes as described herein, either in germline configuration or after rearrangement following in vivo maturation. The cell may be immortalised by fusion to a tumour cell to provide an antibody producing cell and cell line, or be made by direct cellular immortalisation.

The present invention also relates to vectors for use in the invention. In one aspect such vectors are BACs (bacterial artificial chromosomes). It will be appreciated that other cloning vectors may be used in the invention, and therefore reference to BACs herein may be taken to refer generally to any suitable vector.

In one aspect BACs used for generation of human DNA to be inserted, such as the VDJ or VJ regions, are trimmed, so that in the final human VDJ or VJ region, or part thereof, in the non-human mammal no sequence is duplicated or lost when compared to the original human genomic sequence.

In one aspect the invention relates to a vector comprising an insert, preferably comprising a region of human DNA from some of the human VDJ or VJ locus, flanked by DNA which is not from that locus. The flanking DNA may comprise one or more selectable markers or one or more site specific recombination sites. In one aspect the vector comprises 2 or more, such as 3, heterospecific and incompatible site specific recombination sites. In one aspect the site specific recombination sites may be loxP sites, or variants thereof, or FRT sites or variants thereof. In one aspect the vector comprises one or more transposon ITR (inverted terminal repeat) sequences.

In one aspect the non-human animals of the invention suitably do not produce any fully humanised antibodies. In one aspect this is because there is no DNA inserted from the human constant region. Alternatively there is no human constant region DNA in the genome capable of forming an antibody in conjunction with the inserted human variable region DNA component, for example due to mutation within any human constant region DNA or distance from any constant region human DNA and human variable region DNA.

In one aspect human light chain constant region DNA may be included in the cell genome, such that a fully human lambda or kappa human antibody chain might be generated, but this would only be able to form an antibody with a chimaeric heavy chain, and not produce a fully human antibody having human variable and constant regions.

In one aspect the non-human mammal genome is modified to prevent expression of fully host-species specific antibodies. Fully host species specific antibodies are antibodies that have both variable and constant regions from the host organism. In this context the term 'specific' is not intended to relate to the binding of the antibodies produced by the cells or animals of the invention but rather to the origin of the DNA which encodes those antibodies.

In one aspect the non-human mammal genome is modified to prevent expression of the native (fully host species specific) antibodies in the mammal by inactivation of all or a part of the host non-human mammal Ig loci. In one aspect this is achieved by inversion of all or part of the non-human mammal VDJ region, or VJ region, optionally by insertion of one or more site specific recombinase sites into the genome and then use of these sites in recombinase-mediated excision or inversion of all or a part of the non-human mammal Ig locus. In one aspect a double inversion, may be employed, the first to move the V(D)Js away from the endogenous locus and then a more local inversion which puts them in the correct orientation. In one aspect a single *lox*P site is used to invert the non-human mammal VDJ region to a centromeric locus or telomeric locus.

In one aspect the non human mammal genome into which human DNA is inserted comprises endogenous V, (D) and J regions, and the endogenous sequences have not been deleted.

The invention comprises a method for insertion of multiple DNA fragments into a DNA target, suitably to form a contiguous insertion in which the inserted fragments are joined together directly without intervening sequences. The method is especially applicable to the insertion of a large DNA fragment into a host chromosome which can be carried out in a stepwise fashion.

In one aspect the method comprises insertion of a first DNA sequence into a target, the sequence having a DNA vector portion and a first sequence of interest (X1); insertion of a second DNA sequence into the vector portion of the first sequence, the second DNA sequence having a second sequence of interest (X2) and a second vector portion; and then excising any vector sequence DNA separating X1 and X2 to provide a contiguous X1X2, or X2X1 sequence within the target. There is optionally insertion of a further one or more DNA sequences, each DNA sequence having a further sequence of interest (X3,...) and a further vector portion, into the vector portion of the preceding DNA sequence, to build up a contiguous DNA fragment in the target.

The DNA target for insertion of the first DNA sequence may be a specific site or any point in the genome of a particular cell.

The general method is described herein in relation to the insertion of elements of the human VDJ region, but is applicable to insertion of any DNA region, from any organism, and in particular insertion of large DNA fragments of > 100kB, such as 100 – 250kb, or even larger, such as that of the TCR or HLA. Features and approaches described herein in respect of the VDJ insertion may be equally applied to the any of the methods disclosed

In one aspect the inserted DNA is human DNA, such as the human VDJ or VJ region, is built up in the genome of a cell, such as an ES cell, in a stepwise manner using 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20 or more separate insertions for each heavy chain or light chain region. Fragments are suitably inserted at the same or substantially the same cell locus, e.g. ES cell locus, one after another, to form the complete VDJ or VJ region, or part thereof. The present invention also relates to cells and non-human animals comprising intermediates in the process whose genomes may comprise only a partial VDJ region, such as only human variable region DNA.

In a further aspect the method for producing a transgenic non-human mammal comprises the insertion of human VDJ or VJ regions upstream of the host non-human mammal constant region by step-wise insertion of multiple fragments by homologous recombination, preferably using an iterative process. Suitably fragments of approximately 100KB from the human VDJ and VJ locus are inserted, suitably to form part of, or a complete, VDJ or VJ region after the final iteration of the insertion process, as disclosed herein.

In one aspect the insertion process commences at a site where an initiation cassette has been inserted into the genome of a cell, such as an ES cell, providing a unique targeting region. In one aspect the initiation cassette is inserted in the non human mammal heavy chain locus, for use in insertion of human heavy chain DNA. Similarly an initiation cassette is inserted in the non human mammal light chain locus, for use in insertion of human light chain VJ DNA The initiation cassette suitably comprises a vector backbone sequence with which a vector having a human DNA fragment in the same backbone sequence can recombine to insert the human DNA into the cell (e.g. ES) cell genome, and suitably a selection marker, such as a negative selection marker. Suitably the vector backbone sequence is that of a BAC library, to allow BACs to be used in the construction of the ES cells and mammals. The vector backbone sequence may however be any sequence which serves as a target site into which a homologous sequence can insert, for example by homologous recombination and RMCE, and is preferably not DNA encoding any of the VDJ or constant region.

In one aspect the insertion of the first DNA fragment into an initiation cassette is followed by insertion of a second DNA fragment into a portion of the first DNA fragment, suitably a part of the vector backbone of the second DNA fragment. In one aspect an inserted DNA fragment comprises a part of the human VDJ region flanked by 5' and/or 3' sequences that are not from the human VDJ region. In one aspect the 5' and/or 3' flanking sequences may each contain one or more selectable markers, or be capable of creating a selectable system once inserted into the genome. In one aspect one or both flanking sequences may be removed from the genome in vitro, or in vivo, following insertion. In one aspect the method comprises insertion of a DNA fragment followed by selection of both 5' and 3' ends of the inserted fragment flanking the human VDJ DNA. In one aspect the iterative insertion is made by insertion of DNA fragments at the 5' end of the previous inserted fragment, and in this aspect there may be deletion in vivo of the vector DNA which separates the inserted human DNA sequences, to provide a contiguous human DNA sequence.

In one aspect insertion of human VDJ DNA into a genome may be achieved without leaving any flanking DNA in the genome, for example by transposase mediate DNA excision. One suitable transposase is the Piggybac transposase.

In one aspect the first human variable region fragment is inserted by homologous recombination at the initiation cassette backbone sequence and then the DNA of any negative selection marker and initiation cassette are subsequently removed by recombination between recombinase target sequences, such as FRT using in this example, FLPase expression. Generally repeated targeted insertions at the (e.g. BAC) backbone initiation sequence and subsequent removal by rearrangement between recombinase target sequences are repeated to build up the entire human VDJ region upstream of the host non-mammal constant region.

In one aspect a selectable marker or system may be used in the method. The marker may be generated upon insertion of a DNA fragment into a genome, for example forming a selectable marker in conjunction with a DNA element already present in the genome.

In one aspect the cell (e.g. ES) cell genome does not contain 2 identical selectable markers at the same time during the process. It can be seen that the iterative process of insertion and selection can be carried out using only 2 different selection markers, as disclosed in the examples herein, and for example the third selectable marker may be identical to the first marker, as by the time of insertion of the third vector fragment the first vector fragment and the first marker has been removed.

In one aspect a correct insertion event, is confirmed before moving to the next step of any multistep cloning process, for example by confirmation of BAC structure using high density genomic arrays to screen ES cells to identify those with intact BAC insertions, sequencing and PCR verification.

In one aspect the method uses site specific recombination for insertion of one or more vectors into the genome of a cell, such as an ES cell. Site specific recombinase systems are well known in the art and may include Cre-lox, and FLP/FRT or combinations thereof, in which recombination occurs between 2 sites having sequence homology.

Suitable BACs are available form the Sanger centre, see "A genome-wide, end-sequenced 129Sv BAC library resource for targeting vector construction". Adams DJ, Quail MA, Cox T, van der Weyden L, Gorick BD, Su Q, Chan WI, Davies R, Bonfield JK, Law F, Humphray S, Plumb B, Liu P, Rogers J, Bradley A. Genomics. 2005 Dec;86(6):753-8. Epub 2005 Oct 27. The Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire CB10 1SA, UK. BACs containing human DNA are also available from, for example, Invitrogen. A suitable library is described in Osoegawa K *et al*, Genome Research 2001. 11: 483-496.

In one aspect a method of the invention specifically comprises:

(1) insertion of a first DNA fragment into a non-human ES cell, the fragment containing a first portion of human VDJ or VJ region DNA and a first vector portion containing a first selectable marker;

(2) optionally deletion of the a part of the first vector portion;

(3) insertion of a second DNA fragment into a non-human ES cell containing the first DNA fragment, the insertion occurring within the first vector portion, the second DNA fragment containing a second portion of the human VDJ or VJ region and a second vector portion containing a second selectable marker,

(4) deletion of the first selectable marker and first vector portion, preferably by a recombinase enzyme action;

(5) insertion of a third DNA fragment into a non-human ES cell containing the second DNA fragment, the insertion occurring within the second vector portion, the third DNA fragment containing a third portion of the human VDJ or VJ region and a third vector portion containing third selectable marker,

(6) deletion of the second selectable marker and second vector portion; and

(7) iteration of the steps of insertion and deletion, as necessary, for fourth and further fragments of the human VDJ or VJ human regions, as necessary, to produce an ES cell with a part or all of

the human VDJ or VJ region inserted as disclosed herein, and suitably to remove all the vector portions within the ES cell genome.

In another aspect the invention comprises

1 insertion of DNA forming an initiation cassette into the genome of a cell;

2 insertion of a first DNA fragment into the initiation cassette, the first DNA fragment comprising a first portion of a human DNA and a first vector portion containing a first selectable marker or generating a selectable marker upon insertion;

3 optionally removal of part of the vector DNA

4 insertion of a second DNA fragment into the vector portion of the first DNA fragment, the second DNA fragment containing a second portion of human DNA and a second vector portion, the second vector portion containing a second selectable marker, or generating a second selectable marker upon insertion;

5 optionally, removal of any vector DNA to allow the first and second human DNA fragments to form a contiguous sequence; and

6 iteration of the steps of insertion of human VDJ DNA and vector DNA removal, as necessary, to produce a cell with all or part of the human VDJ or VJ region sufficient to be capable of generating a chimaeric antibody in conjunction with a host constant region,

wherein the insertion of one, or more, or all of the DNA fragments uses site specific recombination.

In one aspect the non-human mammal is able to generate a diversity of at least 1×10^6 different functional chimaeric immunoglobulin sequence combinations.

In one aspect the targeting is carried out in ES cells derived from the mouse C57BL/6N, C57BL/6J, 129S5 or 129Sv strain.

In one aspect non-human animals, such as mice, are generated in a RAG-1-deficient background, or other suitable genetic background which prevents the production of mature host B and T lymphocytes.

In one aspect the non-human mammal is a rodent, suitably a mouse, and cells of the invention, are rodent cells or ES cells, suitably mouse ES cells.

The ES cells of the present invention can be used to generate animals using techniques well known in the art, which comprise injection of the ES cell into a blastocyst followed by implantation of chimaeric blastocystys into females to produce offspring which can be bred and selected for homozygous recombinants having the required insertion. In one aspect the invention relates to a chimeric animal comprised of ES cell-derived tissue and host embryo derived tissue. In one aspect the invention relates to genetically-altered subsequent generation animals, which include animals having a homozygous recombinants for the VDJ and/or VJ regions.

In a further aspect the invention relates to a method for producing an antibody specific to a desired antigen the method comprising immunizing a transgenic non-human mammal as above with the desired antigen and recovering the antibody (see e.g. Harlow, E. & Lane, D. 1998, 5th edition, Antibodies: A Laboratory Manual, Cold Spring Harbor Lab. Press, Plainview, NY; and Pasqualini and Arap, Proceedings of the National Academy of Sciences (2004) 101:257-259). Suitably an immunogenic amount of the antigen is delivered. The invention also relates to a method for detecting a target antigen comprising detecting an antibody produced as above with a secondary detection agent which recognises a portion of that antibody.

In a further aspect the invention relates to a method for producing a fully humanised antibody comprising immunizing a transgenic non-human mammal as above with the desired antigen, recovering the antibody or cells expressing the antibody, and then replacing the non-human mammal constant region with a human constant region. This can be done by standard cloning techniques at the DNA level to replace the non-human mammal constant region with an appropriate human constant region DNA sequence – see e.g. Sambrook, J and Russell, D. (2001, 3'd edition) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Lab. Press, Plainview, NY).

In a further aspect the invention relates to humanised antibodies and antibody chains produced according to the present invention, both in chimaeric and fully humanised form, and use of said antibodies in medicine. The invention also relates to a pharmaceutical composition comprising such an antibodies and a pharmaceutically acceptable carrier or other excipient.

Antibody chains containing human sequences, such as chimaeric human–non human antibody chains, are considered humanised herein by virtue of the presence of the human protein coding regions region. Fully humanised antibodies may be produced starting from DNA encoding a chimaeric antibody chain of the invention using standard techniques.

Methods for the generation of both monoclonal and polyclonal antibodies are well known in the art, and the present invention relates to both polyclonal and monoclonal antibodies of chimaeric or fully humanised antibodies produced in response to antigen challenge in non human mammals of the present invention.

In a yet further aspect, chimaeric antibodies or antibody chains generated in the present invention may be manipulated, suitably at the DNA level, to generate molecules with antibody-like properties or structure, such as a human variable region from a heavy or light chain absent a constant region, for example a domain antibody; or a human variable region with any constant region from either heavy or light chain from the same or different species; or a human variable region with a non-naturally occurring constant region; or human variable region together with any other fusion partner. The invention relates to all such chimaeric antibody derivatives derived from chimaeric antibodies identified according to the present invention.

In a further aspect, the invention relates to use of animals of the present invention in the analysis of the likely effects of drugs and vaccines in the context of a quasi-human antibody repertoire.

The invention also relates to a method for identification or validation of a drug or vaccine, the method comprising delivering the vaccine or drug to a mammal of the invention and monitoring one or more of: the immune response, the safety profile; the effect on disease.

The invention also relates to a kit comprising an antibody or antibody derivative as disclosed herein and either instructions for use of such antibody or a suitable laboratory reagent, such as a buffer, antibody detection reagent.

In certain aspects the invention relates to:

A non-human mammal whose genome comprises:

(a) the human IgH VDJ region upstream of the host non-human mammal constant region; and

(b) the human Ig light chain kappa V and J regions upstream of the host non-human mammal kappa constant region and/or the human Ig light chain lambda V and J regions upstream of the host non-human mammal lambda constant region;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies having a non-human mammal constant region and a human variable region,

and optionally wherein the non-human mammal genome is modified to prevent expression of fully host-species specific antibodies.

A non-human mammal ES cell whose genome comprises:

(a) the human IgH V, D and J region upstream of a non-human mammal constant region; and

(b) the human Ig locus light chain kappa V and J regions upstream of the host non-human mammal kappa constant region, and /or the human Ig locus light chain lambda V and J regions upstream of the host non-human mammal lambda constant region

wherein the ES cell is capable of developing into a non-human mammal, being able to produce a repertoire of antibodies which are chimaeric, having a non-human mammal constant region and a human variable region.

A method for producing a transgenic non-human mammal able to produce a repertoire of chimaeric antibodies, the antibodies having a non-human mammal constant region and a human variable region, the method comprising inserting by homologous recombination into a non-human mammal ES cell genome

(a) the human IgH VDJ region upstream of the host non-human mammal heavy chain constant region, and

(b) the human IgL VJ region for lambda or kappa chains upstream of the host non-human mammal lambda or kappa chain constant region, respectively

such that the non-human mammal is able to produce a repertoire of chimaeric antibodies having a non-human mammal constant region and a human variable region, wherein steps (a) and (b) can be carried out in either order and each of steps (a) and (b) can be carried out in a stepwise manner or as a single step.

In one aspect the insertion of human VDJ or VJ regions upstream of the host non-human mammal constant region is accomplished by step-wise insertion of multiple fragments by homologous recombination.

In one aspect the step-wise insertions commence at a site where an initiation cassette has been inserted into the genome of an ES cell providing a unique targeting region consisting of a BAC backbone sequence and a negative selection marker.

In one aspect the first human variable region fragment is inserted by homologous recombination at the initiation cassette BAC backbone sequence and said negative selection marker and initiation cassette are subsequently removed by recombination between recombinase target sequences.

In one aspect repeated targeted insertions at the BAC backbone initiation sequence and subsequent removal of the backbone by rearrangement between recombinase target sequences is repeated to build up the entire human VDJ region upstream of the host non-mammal constant region.

Other aspects include:

A method for producing an antibody specific to a desired antigen the method comprising immunizing a non-human mammal as disclosed herein with the desired antigen and recovering the antibody or a cell producing the antibody.

A method for producing a fully humanised antibody comprising immunizing a non-human mammal as disclosed herein and then replacing the non-human mammal constant region of an antibody specifically reactive with the antigen with a human constant region, suitably by engineering of the nucleic acid encoding the antibody.

A method, cell or mammal as disclosed herein wherein a human coding region DNA sequence is in a functional arrangement with a non-human mammal control sequence, such that transcription of the DNA is controlled by the non-human mammal control sequence. In one aspect the human coding region V, D or J region is in a functional arrangement with a mouse promoter sequence.

The invention also relates to a humanised antibody produced according to any methods disclosed herein and use of a humanised antibody so produced in medicine.

It will be understood that particular embodiments described herein are shown by way of illustration and not as limitations of the invention. The principal features of this invention can be employed in various embodiments without departing from the scope of the invention. Those skilled in the art will recognize, or be able to ascertain using no more than routine study, numerous equivalents to the specific procedures described herein. Such equivalents are considered to be within the scope of this invention and are covered by the claims. All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference. The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one," but it is also consistent with the meaning of "one or more," "at least one," and "one or more than one." The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or." Throughout this application, the term "about" is used to indicate that a value includes the inherent variation of error for the device, the method being employed to determine the value, or the variation that exists among the study subjects.

As used in this specification and claim(s), the words "comprising" (and any form of comprising, such as "comprise" and "comprises"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including, such as "includes" and "include") or "containing" (and any form of containing, such as "contains" and "contain") are inclusive or open-ended and do not exclude additional, unrecited elements or method steps

The term "or combinations thereof" as used herein refers to all permutations and combinations of the listed items preceding the term. For example, "A, B, C, or combinations thereof is intended to include at least one of: A, B, C, AB, AC, BC, or ABC, and if order is important in a particular context, also BA, CA, CB, CBA, BCA, ACB, BAC, or CAB. Continuing with this example, expressly included are combinations that contain repeats of one or more item or term, such as BB, AAA, MB, BBC, AAABCCCC, CBBAAA, CABABB, and so forth. The skilled artisan will understand that typically there is no limit on the number of items or terms in any combination, unless otherwise apparent from the context.

Any part of this disclosure may be read in combination with any other part of the disclosure, unless otherwise apparent from the context.

All of the compositions and/or methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and/or methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

The present invention is described in more detail in the following non limiting Examples. Example 3 discloses experimental data that has been obtained which supports the proof of concept of certain aspects of the invention, while Example 1 and 2 provide detailed guidance for the person skilled in the art in carrying out the claimed invention.

Example 1

Overall strategy

A mouse model of the invention can be achieved by inserting ~960kb of the human heavy chain locus containing all the V, D and J-regions upstream of the mouse constant region and 473kb of the human kappa region upstream of the mouse constant region. Alternatively, or in tandem, the human lambda region is inserted upstream of the mouse constant region. This insertion is achieved by gene targeting in ES cells using techniques well known in the art.

High fidelity insertion of intact V-D-J regions into each locus in their native (wild-type) configuration is suitably achieved by insertion of human bacterial artificial chromosomes (BACs) into the locus. Suitably the BACs are trimmed so that in the final locus no sequence is duplicated or lost compared to the original. Such trimming can be carried out by recombineering.

The relevant human BACs, suitably trimmed covering these loci are on average 90kb in size.

In one approach the full complement of human D and J-elements as well as seven or eight human V-regions are covered by the first BACs to be inserted in the experimental insertion scheme described below. The first BACs to be inserted in the IgH and IgK loci may contain the following V-regions. IgH :V6-1, VII-1-1, V1-2, VIII-2-1, V1-3, V4-4, V2-5 and IgK: V4-1, V5-2, V7-3, V2-4, V1-5, V1-6, V3-7, V1-8.

Suitably the performance of each locus is assessed after the first BAC insertion using chimaeric mice and also after each subsequent BAC addition. See below for detailed description of this performance test.

Nine additional BAC insertions will be required for the *IgH* locus and five for *IgK* to provide the full complement of human V-regions covering all 0.96Mb and 0.473Mb of the *IgH* and *IgK* loci, respectively.

Not all BACs retain their wild-type configuration when inserted into the ES cell genome. Thus we deploy high density genomic arrays to screen ES cells to identify those with intact BAC insertions (Barrett, M.T., Scheffer, A., Ben-Dor, A., Sampas, N., Lipson, D., Kincaid, R., Tsang, P., Curry, B., Baird, K., Meltzer, P.S., *et al.* (2004). Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA. Proceedings of the National Academy of Sciences of the United States of America *101*, 17765-17770.).This screen also enables one to identify and select against ES clones in which the ES cell genome is compromised and thus not able to populate the germ line of chimeric animals. Other suitable genomic tools to facilitate this assessment include sequencing and PCR verification.

Thus in one aspect the correct BAC structure is confirmed before moving to the next step.

It is implicit from the description above that in order to completely engineer the loci with 90kb BACs, it is necessary to perform a minimum of 10 targeting steps for *IgH* and 5 steps for the *IgK*. Mice with an IgL locus can be generated in a similar manner to the IgK locus. Additional steps are required to remove the selection markers required to support gene targeting. Since these manipulations are being performed in ES cells in a step-wise manner, in one aspect germ line transmission capacity is retained throughout this process.

Maintaining the performance of the ES cell clones through multiple rounds of manipulation without the need to test the germ line potential of the ES cell line at every step may be important in the present invention. The cell lines currently in use for the KOMP and EUCOMM global knockout projects have been modified twice prior to their use for this project and their germ line transmission rates are unchanged from the parental cells (these lines are publicly available, see www.komp.org and www.eucomm.org). This cell line, called JM8, can generate 100% ES cell-derived mice under published culture conditions (Pettitt, S.J., Liang, Q., Rairdan, X.Y., Moran, J.L., Prosser, H.M., Beier, D.R., Lloyd, K.C., Bradley, A., and Skarnes, W.C. (2009). Agouti C57BL/6N embryonic stem cells for mouse genetic resources. Nature Methods.). These cells have demonstrated ability to reproducibly contribute to somatic and germ line tissue of chimaeric animals using standard mouse ES cell culture conditions. This capability can be found with cells cultured on a standard feeder cell line (SNL) and even feeder-free, grown only on gelatine-coated tissue culture plates. One particular sub-line, JM8A3, maintained the ability to populate the germ line of chimeras after several serial rounds of sub-cloning. Extensive genetic manipulation via, for example, homologous recombination – as would be the case in the present invention – cannot compromise the pluripotency of the cells. The ability to generate chimeras with such high percentage of ES cell-derived tissue has other advantages. First, high levels of chimerism correlates with germ line transmission potential and provide a surrogate assay for germ line transmission while only taking 5 to 6 weeks. Second, since these mice are 100% ES cell derived the engineered loci can be directly tested, removing the delay caused by breeding. Testing the integrity of the new Ig loci is possible in the chimera since the host embryo will be derived from animals that are mutant for the RAG-1 gene as described in the next section.

Another cell line that may be used is an HPRT-ve cell line, such as AB2.1, as disclosed in "Chromosome engineering in mice, Ramírez-Solis R, Liu P and Bradley A, Nature 1995;378;6558;720-4.

RAG-1 complementation

While many clones will generate 100% ES derived mice some will not. Thus, at every step mice are generated in a RAG-1-deficient background. This provides mice with 100% ES-derived B- and T-cells which can be used directly for immunization and antibody production. Cells having a RAG-2 deficient background, or a combined RAG-1/RAG-2 deficient background may be used, or equivalent mutations in which mice produce only ES cell-derived B cells and/or T cells.

In order that only the human-mouse *IgH* or *IgK* loci are active in these mice, the human-mouse *IgH* and *IgK* loci can be engineered in a cell line in which one allele of the *IgH* or *IgK* locus has already been inactivated. Alternatively the inactivation of the host Ig locus, such as the IgH or IgK locus, can be carried out after insertion.

Mouse strains that have the RAG-1 gene mutated are immunodeficient as they have no mature B- or T-lymphocytes (US 5,859,307). T- and B-lymphocytes only differentiate if proper V(D)J recombination occurs. Since RAG-1 is an enzyme that is crucial for this recombination, mice lacking RAG-1 are immunodeficient. If host embryos are genetically RAG-1 homozygous mutant, a chimera produced by injecting such an embryo will not be able to produce antibodies if the animal's lymphoid tissues are derived from the host embryo. However, JM8 cells and AB2.1 cells, for example, generally contribute in excess of 80% of the somatic tissues of the chimeric animal and would therefore usually populate the lymphoid tissue. JM8 cells have wild-type RAG-1 activity and therefore antibodies produced in the chimeric animal would be encoded by the engineered JM8 ES cell genome only. Therefore, the chimeric animal can be challenged with an antigen by immunization and subsequently produce antibodies to that antigen. This allows one skilled in the art to test the performance of the engineered human/mouse IgH and IgK loci as described in the present invention. See figures 19 and 20.

One skilled in the art would use the chimeric animal as described to determine the extent of antibody diversity (see e.g. Harlow, E. & Lane, D. 1998, 5th edition, Antibodies: A Laboratory Manual, Cold Spring Harbor Lab. Press, Plainview, NY). For example, the existence in the chimeric animal's serum of certain antibody epitopes could be ascertained by binding to specific anti-idiotype antiserum, for example, in an ELISA assay. One skilled in the art could also sequence the genomes of B-cell clones derived from the chimeric animal and compare said sequence to wild-type sequence to ascertain the level of hypermutation, such hypermutation indicative of normal antibody maturation.

One skilled in the art would also use said chimeric animal to examine antibody function wherein said antibodies are encoded from the engineered Ig loci (see e.g. Harlow, E. & Lane, D. 1998, 5th edition, Antibodies: A Laboratory Manual, Cold Spring Harbor Lab. Press, Plainview, NY). For example, antisera could be tested for binding an antigen, said antigen used to immunize the chimeric animal. Such a measurement could be made by an ELISA assay. Alternatively, one skilled in the art could test for neutralization of the antigen by addition of the antisera collected from the appropriately immunized chimeric animal.

It is well known to those skilled in the art that positive outcomes for any of these tests demonstrate the ability of the engineered Ig loci, the subject of the instant invention, to encode antibodies with human variable regions and mouse constant regions, said antibodies capable of functioning in the manner of wild-type antibodies.

Experimental Techniques

Recombineering for the production of vectors for use in homologous recombination in ES cells is disclosed in, for example, WO9929837 and WO0104288, and the techniques are well known in the art. In one aspect the recombineering of the human DNA takes place using BACs as a source of said human DNA. Human BAC DNA will be isolated using Qiagen BAC purification kit. The backbone of each human BAC will be modified using recombineering to the exact same or similar configuration as the BAC already inserted into the mouse IgH region. The genomic insert of each human BAC will be trimmed using recombineering so that once the BACs are inserted, a seamless contiguous part of the human V(D)J genomic region will form at the mouse IgH or IgK locus. BAC DNA transfection by electroporation and genotyping will be performed accordingly to standard protocols (Prosser, H.M., Rzadzinska, A.K., Steel, K.P., and Bradley, A. (2008). Mosaic complementation demonstrates a regulatory role for myosin VIIa in actin dynamics of stereocilia. Molecular and Cellular Biology *28*, 1702-1712; Ramirez-Solis, R., Davis, A.C., and Bradley, A. (1993). Gene targeting in embryonic stem cells. Methods in Enzymology *225*, 855-878.). Recombineering will be performed using the procedures and reagents developed by Pentao Liu and Don Court's laboratories (Chan, W., Costantino, N., Li, R., Lee, S.C., Su, Q., Melvin, D., Court, D.L., and Liu, P. (2007). A recombineering based approach for high-throughput conditional knockout targeting vector construction. Nucleic Acids Research *35*, e64).

These and other techniques for gene targeting and recombination of BAC-derived chromosomal fragments into a non-human mammal genome, such as a mouse are disclosed in, for example, in http://www.eucomm.org/information/targeting/ and http://www.eucomm.org/information/publications.

Cell culture of C57BL/6N-derived cell lines, such as the JM8 male ES cells will follow standard techniques. The JM8 ES cells have been shown to be competent in extensively contributing to somatic tissues and to the germline, and are being used for large mouse mutagenesis programs at the Sanger Institute such as EUCOMM and KOMP (Pettitt, S.J., Liang, Q., Rairdan, X.Y., Moran, J.L., Prosser, H.M., Beier, D.R., Lloyd, K.C., Bradley, A., and Skarnes, W.C. (2009). Agouti C57BL/6N embryonic stem cells for mouse genetic resources. Nature Methods.). JM8 ES cells ($1.0X10^7$) will be electroporated (500µF, 230V; BioRad) with 10µg I-SceI linearized human BAC DNA. The transfectants will be selected with either Puromycin (3µg/ml) or G418 (150µg/ml). The selection will begin either 24 hours (with G418) or 48 hours (with Puromycin) post electroporation and proceed for 5 days. 10µg linearized human BAC DNA can yield up to 500 Puromycin or G418 resistant ES cell colonies. The antibiotic resistant ES cell colonies will be picked into 96-well cell culture plates for genotyping to identify the targeted clones.

Once targeted mouse ES cell clones are identified, they will be analyzed by array Comparative Genomic Hybridization (CGH) for total genome integrity (Chung, Y.J., Jonkers, J., Kitson, H., Fiegler, H., Humphray, S., Scott, C., Hunt, S., Yu, Y., Nishijima, I., Velds, A.*, et al.* (2004). A whole-genome mouse BAC microarray with 1-Mb resolution for analysis of DNA copy number changes by array comparative genomic hybridization. Genome research *14*, 188-196.and Liang, Q., Conte, N., Skarnes, W.C., and Bradley, A. (2008). Extensive genomic copy number variation in embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America *105*, 17453-17456.). ES cells that have abnormal genomes do not contribute to the germline of the chimeric mice efficiently. BAC integrity will be examined by PCR-amplifying each known functional V gene in the BAC. For example, in one approach the first human BAC chosen for the IgH locus has 6 functional V genes. To confirm the integrity of this BAC for the presence of these 6 IGH V genes, at least 14 pairs of PCR primers will be designed and used to PCR-amplify genomic DNA from the targeted ES cells. The human wild-type size and sequence of these fragments will ensure that the inserted BAC has not been rearranged.

More detailed CGH will also confirm the integrity of the inserted BACs. For example, one skilled in the art could use an oligo aCGH platform, which is developed by Agilent Technologies, Inc. This platform not only enables one to study genome-wide DNA copy number variation at high resolution (Barrett, M.T., Scheffer, A., Ben-Dor, A., Sampas, N., Lipson, D., Kincaid, R., Tsang, P., Curry, B., Baird, K., Meltzer, P.S.*, et al.* (2004). Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA. Proceedings of the National Academy of Sciences of the United States of America *101*, 17765-17770.), but permit examination of a specific genome region using custom designed arrays. Comparing the traditional aCGH techniques which rely on cDNA probes or whole BAC probes, the 60-mer oligonucleotides probes can ensure specific hybridization and high sensitivity and precision that is needed in order to detect the engineered chromosome alterations that we have made. For example, oligos designed to hybridize at regular intervals along the entire length of the inserted BAC would detect even quite short deletions, insertions or other rearrangements. Also, this platform provides the greatest flexibility for customized microarray designs. The targeted ES cell genomic DNA and normal human individual genomic DNA will be labelled separately with dyes and hybridized to the array. Arrays slides will be scanned using an Aglient Technologies DNA microarray scanner. Reciprocal fluorescence intensities of dye Cy5 and dye Cy3 on each array image and the log2 ratio values will be extracted by using Bluefuse software (Bluegnome). Spots with inconsistent fluorescence patterns (“confidence” < 0.29 or “quality” = 0) will be excluded before normalizing all log2 ratio values. Within an experiment, Log2 ratio between -0.29 and +0.29 for the signal from any oligo probe are regarded as no copy number change. The log2 ratio threshold for “Duplication” is usually >0.29999, and for deletion is <0.29999.

Once the first human BAC is inserted into the mouse IgH locus and confirmed to be in its intact, native configuration, the FRT-flanked BAC backbone will be excised by using Flp site-specific recombinase. If regular Flp-catalyzed FRT recombination is not high enough, one can use Flo, an improved version of Flpo recombinase which in certain tests is 3-4 times more efficient than the original Flp in ES cells. After the BAC backbone is excised, ES cells will become sensitive to Puromycin (or G418) and resistant to FIAU (for loss of the TK cassette). The excision events will be further characterized by PCR amplification of the junction fragment using human genomic DNA primers. These FRT-flanked BAC backbone-free ES cells will be used for the next round of human BAC insertion and for blastocyst injection.

Targeting of the genome of an ES cell to produce a transgenic mouse may be carried out using a protocol as explained by reference to the attached figures 1- 18.

Figure 1 illustrates three basic backbone vectors; an initiating cassette and 2 large insert vectors 1 and 2 respectively. The initiating cassette comprises sequences homologous to the desired site of insertion into the mouse genome, those sites flanking a selectable marker and stuffer primer sequence for PCR based genotyping to confirm correct insertion of BACs. The Stuffer-primer sequence provides the basis for genotyping each BAC addition step. This sequence is considered to provide a robust well validated sequence template for PCR primer and may be located at the ISceI site, ideally ~1kb from the BAC insert.

The large insert vectors comprise human DNA on plasmids with selectable markers and a unique restriction site for linearisation of the plasmid to aid in homologous recombination into the genome of the ES cell.

Figure 2 illustrates insertion of an initiating cassette into the mouse genome by Homologous recombination between the mouse J4 and C alpha exons. Puromycin selection allows identification of ES cells with insertion of the cassette. pu(Delta)tk is a bifunctional fusion protein between puromycin N-acetyltransferase (Puro) and a truncated version of herpes simplex virus type 1 thymidine kinase (DeltaTk). Murine embryonic stem (ES) cells transfected with pu(Delta)tk become resistant to puromycin and sensitive to 1-(-2-deoxy-2-fluoro-1-beta-D-arabino-furanosyl)-5-iodouracil (FIAU). Unlike other HSV1 tk transgenes, puDeltatk is readily transmitted through the male germ line. Thus pu(Delta)tk is a convenient positive/negative selectable marker that can be widely used in many ES cell applications.

Figure 3 illustrates targeting of the large insert vector 1 to the mouse ES cell genome. Linearisation of the vector is made at the same position as the stuffer primer sequence which allows for a gap repair genotyping strategy, well known in the art – see Zheng et al NAR 1999, Vol 27, 11, 2354 - 2360. In essence, random insertion of the targeting vector into the genome will not 'repair' the gap whereas a homologous recombination event will repair the gap. Juxtaposition of appropriate PCR primer sequences allows colonies to be screened individually for a positive PCR fragment indicating proper insertion. Positive selection using G418 allows for identification of mouse ES cells containing the neo selection marker. PCR verification can be made of all critical V, D and J regions. Array comparative genomic hybridization can be used to validate the BAC structure.

Figure 4 illustrates the *puro-delta-tk* cassette and the BAC plasmid backbone is deleted using Flpe and select in FIAU. Since Flpe works inefficiently in mouse ES cells (5% deletion with transient Flpe expression), it is expected that in most cases, the recombination occurs between the two FRT sites flanking the BAC backbone. Flpo can also be tested to find out the recombination efficiency between two FRT sites that are 10kb away.

Given that the FRT deletion step is selectable it is possible to pool FIAU resistant clones and proceed immediately to the next step in parallel with clonal analysis. Alternatively it may be desirable to show by short range PCR that the human sequences are now adjacent to those of the mouse as shown (Hu-primer 1 and Mo-primer)

At this stage a 200kb human locus will have been inserted

Figure 5 illustrates a second large insert vector is targeted into the ES cell chromosome. The human BAC is targeted to the mouse IgH locus using the same initiation cassette insertion followed by *ISce1* BAC linearization, BAC targeting to the initiation cassette and gap-repair genotyping strategy. Verification of the BAC insertion is carried out as before.

Figure 6 illustrates the FRTY flanked BAC backbone of large insert vector 2 and the neo marker are deleted via *Flpo*. Note that this is not selectable, thus it will be necessary for clonal analysis at this point. This will enable confirmation of the juxtaposition of the human 2 insert with human 1 and other validation efforts.

At this stage a ~ 200kb human locus will have been inserted.

Figure 7 illustrates the next large insert vector targeted to the mouse IgH locus. The pu-delta TK cassette is then removed, as for figure 4. The process can be repeated to incorporate other BACs.

Figure 8 illustrates the final predicted ES cell construct.

Figures 9 – 18 provide a further level of detail of this process.

Example 2

In a further method of the invention site specific recombination can also be employed. Site-specific recombination (SSR) has been widely used in the last 20-years for the integration of transgenes into defined chromosomal loci. SSR involves recombination between homologous DNA sequences.

The first generation of SSR-based chromosomal targeting involved recombination between (i) a single recombination target site (RT) such as loxP or FRT in a transfected plasmid with (ii) a chromosomal RT site provided by a previous integration. A major problem with this approach is that insertion events are rare since excision is always more efficient than insertion. A second generation of SSR called RMCE (recombinase-mediated cassette exchange) was introduced by Schlake and Bode in 1994 (Schlake, T.; J. Bode (1994). "Use of mutated FLP-recognition-target-(FRT-)sites for the exchange of expression cassettes at defined chromosomal loci". *Biochemistry* **33**: 12746–12751). Their method is based on using two heterospecific and incompatible RTs in the transfected plasmid which can recombine with compatible RT sites on the chromosome resulting in the swap of one piece of DNA for another – or a cassette exchange. This approach has been successfully exploited in a variety of efficient chromosomal targeting, including integration of BAC inserts of greater than 50 kb (Wallace, H.A.C. et al. (2007). “Manipulating the mouse genome to engineering precise functional syntenic replacements with human sequence”. Cell 128: 197-209; Prosser, H.M. et al. (2008). “Mosaic complementation demonstrates a regulatory role for myosin VIIa in actin dynamics of Stereocilia”. Mol. Cell. Biol. 28: 1702-12).

The largest insert size of a BAC is about 300-kb and therefore this places an upper limit on cassette size for RMCE.

In the present invention we utilise a new SSR-based technique called sequential RMCE (SRMCE), which allows continuous insertion of BAC inserts into the same locus.

The method comprises the steps of

1 insertion of DNA forming an initiation cassette (also called a landing pad herein) into the genome of a cell;

2 insertion of a first DNA fragment into the insertion site, the first DNA fragment comprising a first portion of a human DNA and a first vector portion containing a first selectable marker or generating a selectable marker upon insertion;

3 removal of part of the vector DNA;

4 insertion of a second DNA fragment into the vector portion of the first DNA fragment, the second DNA fragment containing a second portion of human DNA and a second vector portion, the second vector portion containing a second selectable marker, or generating a second selectable marker upon insertion;

5 removal of any vector DNA to allow the first and second human DNA fragments to form a contiguous sequence; and

6 iteration of the steps of insertion of a part of the human V(D)J DNA and vector DNA removal, as necessary, to produce a cell with all or part of the human VDJ or VJ region sufficient to be capable of generating a chimaeric antibody in conjunction with a host constant region,

wherein the insertion of at least one DNA fragment uses site specific recombination.

In one specific aspect the approach utilizes three heterospecific and incompatible loxP sites. The method is comprised of the steps as follows, and illustrated in Figures 22 – 26:

1. Targeting a landing pad into the defined locus. An entry vector containing an HPRT mini-gene flanked by inverted piggyBac (PB) ITRs is targeted into defined region (for example: a region between IGHJ and Eμ or IGKJ and Eκ or IGLC1 and Eλ3-1) to serve as a landing pad for BAC targeting. The HPRT mini-gene is comprised of two synthetic exons and associated intron. The 5' HPRT exon is flanked by two heterospecific and incompatible loxP sites (one wild-type and the other a mutated site, lox5171) in inverted orientation to each other (Fig. 22). These two loxP sites provide recombination sites for the BAC insertion through RMCE.

2. Insertion of the 1st modified BAC into the targeted landing pad. The 1st BAC has a length of DNA to be inserted into the genome flanked by engineered modifications. The 5' modification (loxP - neo gene - lox2272 - PGK promoter – PB 5'LTR) and 3' modification (PB3'LTR - puroΔTK gene – lox5171) is depicted in Fig 23 along with the relative orientations of the lox sites and PB LTRs. With transient CRE expression from a co-electroporated vector, the DNA sequence would be inserted into the defined locus through RMCE. The cells in which a correct insertion has occurred can be selected as follows: (i) Puromycin-resistance (the puroΔTK gene has acquired a promoter – "PGK" – from the landing pad), (ii) 6TG-resistance (the HPRT mini-gene has been disrupted), and (iii) G418-resistance (selects for any insertion via the 5' region PGK-neo arrangement). Any combination of these selection regimes can be used. G418- and 6TG-resistance select for correct events on the 5' end while puro-resistance selects for correct events on the 3' end.

3. Curing (removing) the 3' modification of the 1st insertion. A properly inserted 1st BAC results the 3' end having a puroΔTK gene flanked by inverted PB LTRs (Fig. 24) – essentially a proper transposon structure. This transposon can then be removed by the transient expression of the piggyBac transposase (from an electroporated vector). Cells with the correct excision event can be selected by FIAU resistance – ie, no thymidine kinase activity from the puroΔTK gene. This completely removes the 3' modification leaving no trace nucleotides.

4. Insertion of a 2nd modified BAC into the 5' end of 1st insertion. The 2nd BAC has a length of DNA to be inserted into the genome (usually intended to be contiguous with the DNA inserted with the 1st BAC) flanked by engineered modifications. The 5' modification (loxP – HPRT mini gene 5' portion – lox5171 – PGK promoter – PB5'LTR) and 3' modification (PB3'LTR – puroΔTK – lox2272) is depicted in Fig 25 along with the relative orientations of the lox sites and PB LTRs. With transient CRE expression from a co-electroporated vector, the DNA sequence would be inserted into the defined locus through RMCE. The cells in which a correct insertion has occurred can be selected as follows: (i) HAT-resistance (the HPRT mini-gene is reconstituted by a correct insertion event, ie: the 5' and 3' exon structures are brought together), and (ii) puromycin-resistance (puroΔTK gene has acquired a promoter – "PGK" – from the landing pad).

5. Curing (removing) the 3' modification of the 2nd insertion. A properly inserted 2nd BAC results the 3' end having a puroΔTK gene flanked by inverted PB LTRs (Fig. 26) – essentially a proper transposon structure, exactly analogous to the consequence of a successful 1st BAC insertion. And therefore this transposon can likewise be removed by the transient expression of the piggyBac transposase (from an electroporated vector). Cells with the correct excision event can be selected by FIAU resistance – ie, no thymidine kinase activity from the puroΔTK gene. This completely removes the 3' modification leaving no trace nucleotides.

6. After curing of the 3' modification of the 2nd BAC insertion, the landing pad becomes identical to the original. This entire process, steps 2 through 5, can be repeated multiple times to build up a large insertion into the genome. When complete, there are no residual nucleotides remaining other than the desired insertion.

With the insertion of an odd number of BACs into the Ig loci, the endogenous VDJ or VJ sequences can be inactivated through an inversion via chromosomal engineering as follows (see figures 27 – 29):

1. Targeting a "flip-over" cassette into a 5' region 10 to 40 megabases away from the endogenous VDJ or VJ. The flip-over vector (PB3'LTR – PGK promoter – HPRT mini gene 5' portion – loxP – puroΔTK – CAGGS promoter – PB3'LTR) is depicted in Fig 27 along with the relative orientations of the lox sites and PB LTRs.

2. Transient CRE expression will result in recombination between the loxP site in the "flip-over" cassette and the loxP site in the 5' modification. This 5' modification is as described in Steps 2 and 3 above – essentially the modification resulting from insertion of an odd number of BACs, after the 3' modification has been cured. The loxP sites are inverted relative to one another and therefore the described recombination event results in an inversion as depicted in Fig 28. Cells with the correct inversion will be HAT-resistance since the HPRT mini-gene is reconstituted by a correct inversion.

3. A correct inversion also leaves two transposon structures flanking the "flip-over" cassette and the 5' modification. Both can be excised with transient piggyBAC transposase expression, leaving no remnant of either modification (Fig 29). Cells with the correct excisions can be selected as follows: (i) 6TG-resistance (the HPRT mini-gene is deleted) and (ii) FIAU-resistance (the puroΔTK gene is deleted). An inversion as described in the Ig loci would move the endogenous IGH-VDJ or IGK-VJ region away from the Eμ or Eκ enhancer region, respectively, and lead to inactivation of the endogenous IGH-VDJ or IGK-VJ regions.

The methods of insertion of the invention suitably provide one or more of:

Selection at both 5' and 3' ends of the inserted DNA fragment;

Efficient curing of the 3' modification, preferably by transposase mediated DNA excision;

Inactivation of endogenous IGH or IGK activity through an inversion; and

Excision of modifications, leaving no nucleotide traces remaining in the chromosome.

Example 3

Proof of concept of the approach is disclosed in Figure 30. In Figure 30 a landing pad as shown in figure 22 was inserted into the genome of a mouse by homologous recombination, followed by insertion of the R21 plasmid into that landing pad via cre-mediated site specific recombination. The insertion event generated a number of general insertion events, 360 G418 resistant colonies, of which ~220 were inserted into the desired locus, as demonstrated by disruption of the HRPT minilocus.

The R21 vector mimicks the 1st BAC insertion vector at the 5' and 3' ends, including all selection elements and recombinase target sites. In place of BAC sequences, there is a small 'stuffer' sequence. This vector will both test all the principals designed in the invention and allow easy testing of the results in that PCR across the stuffer is feasible and therefore allows both ends of the insertion to be easily tested. R21 was co-electroporated with a cre-expressing vector into the ES cells harbouring the landing pad in the IGH locus. Four sets of transformed cells were transfected in parallel and then placed under different selection regimes as indicated in Figure 30. G418 selection (neo gene expression) resulted in the largest number of colonies due to there being no requirement for specific landing-pad integration. Any integration of R21 into the genome will provide neo expression leading to G418-resistance. Puro selection resulted in a similar colony number to Puro + 6TG or G418 + 6TG, suggesting that the stringency of Puro selection is due to the PuroΔTK lacking a promoter in the vector. Puro expression is only acquired when an integration occurs near a promoter element – in this design most likely specifically in the landing pad. These conclusions are supported by the results from junction PCR which is shown in Figure 31.

The next step in the invention is to 'cure' the 3' end of the integrated BAC vector, leaving a seamless transition between the insertion and the flanking genome. We demonstrated this curing by expanding an individual clone from above (R21 inserted into the landing pad) and expressing piggyBac recombinase in this clone via transfection of an expressing plasmid. FIAU was used to select colonies in which the 3' modification was excised – ie, through loss of the 'PGK-puroΔTK' element between the piggyBac terminal repeats. Fifty such clones resulted from a transfection of 10^6 cells; of these we tested 6 for the expected genomic structure. Successful curing resulted in positive PCR between the primer set labelled "3" in Figure 32. Of the 6 clones, 4 had correct excisions, 1 clone remained in the original configuration and 1 other had a deletion.

These data demonstrate iterative insertion of DNA into a landing pad at a defined genomic locus using the approaches outlined above.

Example 4

Example 3 demonstrated that the design of the claimed invention was capable of providing for the insertion of a test vector into the genome at a defined location, in this case the R21 vector into the mouse IGH locus. The use of the appropriate selection media and the expression of cre-recombinase resulted in a genomic alteration with the predicted structure.

The same design elements described in this invention were built into the 5' and 3' ends of a BAC insert. Said insert comprised human sequences from the IGH locus and was approximately 166-kb. This engineered BAC was electroporated along with a cre-expressing plasmid DNA into mouse ES cells harbouring the landing pad at the mouse IGH locus. The transfected cell population was grown in puro-containing media to select for appropriate insertion events.

Seven resulting clones were isolated and further analysed. The expected recombination event and resulting structure are depicted in Figure 33. Based upon data from the R21 experiment outlined in Example 3, a stringent selection for correct clones was expected when the transfected population was selected in puro-containing media. This is because the puro-coding region requires a promoter element and this is preferentially supplied by the landing pad after recombination. Accordingly, the majority of the 7 isolated clones had inserted correctly into the genome at the landing pad as determined by the diagnostic PCR. The primers for diagnosing a correct insertion are depicted in Figure 33. Correct junctions are present in the genome if a 610-bp fragment is amplified between primers 'A' and 'X' and a 478-bp fragment is amplified between primers 'Y' and 'B' (Figures 33 and 34). Note that there are amplified fragments between 'A' and '1' primers and '2' and 'B' primers indicating the presence of parental genome (that is, the landing pad alone). These result from parental cells present internally in the cell colonies under puro-selection that escape the selection due to the geometry of a colony. After passaging the colony through puro-containing media, these parental junction fragments disappear indicating that the parental cells are removed from the population. In addition, all the clones were shown to be resistant to 6-TG as expected if the HPRT gene is inactivated by the correct insertion event.

These data indicate that the disclosed strategy for inserting large parts of the human IG loci into defined positions in the mouse genome will enable the construction of a mouse with a plurality of the variable regions of human IG regions upstream of the mouse constant regions as described.

Claims

1 A non-human mammal whose genome comprises:

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies, or chimaeric light or heavy chains, having a non-human mammal constant region and a human variable region.

2 A non-human mammal whose genome comprises

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant;

wherein the non-human mammal is able to produce a repertoire of chimaeric antibodies, or chimaeric light or heavy chains, having a non-human mammal constant region and a human variable region.

3 A non-human mammal cell whose genome comprises

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region.

4 A non-human mammal cell whose genome comprises

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region.

5 A cell according to claim 3 or 4 which is an ES cell, hematopoietic stem cell or other cell capable of developing into a non-human mammal able to produce a repertoire of antibodies or antibody chains which are chimaeric, said chimaeric antibodies or chains having a non-human mammal constant region and a human variable region.

6. A cell according to claim 3 or 4 which is an ES cell, hematopoietic stem cell or other cell capable of contributing to tissues and organs of a non-human mammal which is able to produce a repertoire of antibodies or antibody chains which are chimaeric, said chimaeric antibodies or chains having a non-human mammal constant region and a human variable region.

7 A cell or mammal according to claim 1-6 wherein the cell or mammal genome is modified to prevent or reduce expression of fully host-species specific antibodies.

8 A cell or mammal according to claims 1-7 comprising inserted human variable region DNA from at least a human heavy and human light chain.

9 A cell or mammal according to claim 8 wherein the cell or mammal is homozygous at one, two or all three immunoglobulin loci for DNA encoding a chimaeric antibody chain.

10 A cell or mammal according to claim 8 wherein the cell or mammal is heterozygous at one, two or all three immunoglobulin loci for DNA encoding a chimaeric heavy or light chain.

11 A cell or mammal according to any of claims 1-10 wherein the insertion of the human heavy chain DNA is located upstream of the non human mammal heavy chain constant region, and/or the insertion of the human light chain DNA is upstream of a non-human mammal light chain constant region, such that a chimaeric heavy or light chain may be produced in the cell or mammal.

12 A cell or mammal according to claim 11 wherein the insertion of the human DNA is made between the non-human mammal constant region and the last, 3', non-human mammal J region.

13 A cell or mammal according to any preceding claim wherein the genome of the cell does not comprise constant region DNA from another cell or organism.

14 A cell according to claims 2-13 which is immortalised.

15 A method for producing a non-human mammal or cell, the method comprising inserting into a non-human mammal cell genome;

(a) a plurality of human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant region; and

(b) optionally one or more human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or one or more human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; respectively,

the insertion being such that the non-human mammal is able to produce a repertoire of chimaeric antibodies or heavy or light antibody chains having a non-human mammal constant region and a human variable region, wherein steps (a) and (b) can be carried out in either order and each of steps (a) and (b) can be carried out in a stepwise manner or as a single step.

16 A method for producing a non-human mammal or cell, the method comprising inserting into a non-human mammal cell genome;

(a) a plurality of human Ig light chain kappa V regions and one or more human Ig light chain kappa J regions upstream of the host non-human mammal kappa constant region and/or a plurality of human Ig light chain lambda V regions and one or more human Ig light chain lambda J regions upstream of the host non-human mammal lambda constant region; and

(b) optionally one or more human IgH V regions, one or more human D regions and one or more human J regions upstream of the host non-human mammal constant;

the insertion being such that the non-human mammal is able to produce a repertoire of chimaeric antibodies or heavy or light antibody chains having a non-human mammal constant region and a human variable region, wherein steps (a) and (b) can be carried out in either order and each of steps (a) and (b) can be carried out in a stepwise manner or as a single step.

17 A method according to claim 15 or 16 wherein the cell is an ES cell.

18 A method according to claim 15-17 wherein the insertion of human VDJ or VJ regions upstream of the host non-human mammal constant region is accomplished by step-wise insertion of multiple fragments by homologous recombination.

19 A method according to claims 15-18 wherein one or more insertion events utilises site specific recombination.

20 A method for producing an antibody or antibody heavy or light chain specific to a desired antigen, the method comprising immunizing a non-human mammal as claimed in claim 1 or 2 with the desired antigen and recovering the antibody or antibody chain or recovering a cell producing the antibody or heavy or light chain.

21 A method for producing a fully humanised antibody or antibody chain comprising immunizing a non-human mammal according to claim 20 and then replacing the non-human mammal constant region of an antibody specifically reactive with the antigen with a human constant region, suitably by engineering of the nucleic acid encoding the antibody.

22 A method, cell or mammal as claimed in claims 1-21 wherein a human coding region DNA sequence is in a functional arrangement with a non-human mammal control sequence, such that transcription of the human DNA is controlled by the non-human mammal control sequence.

23 A humanised antibody or antibody chain produced according to claim 20 or 21.

24 Use of a humanised antibody or chain produced according to claim 20 or 21 in medicine.

25 A humanised antibody or antibody chain produced according to claim 20 or 21 for use in medicine.