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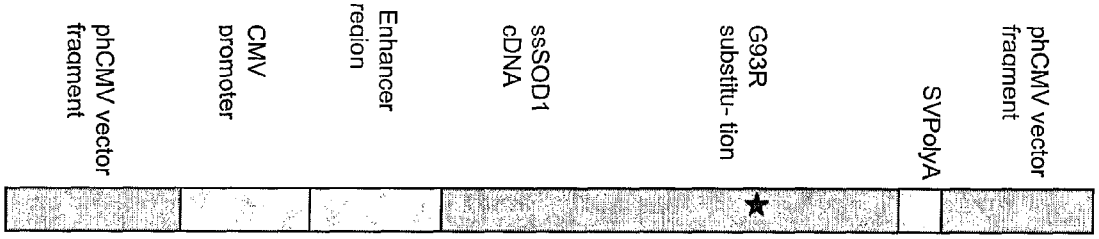
(54) Title: AN ANIMAL MODEL AND A METHOD FOR PRODUCING AN ANIMAL MODEL



(57) Abstract: The present invention discloses a non-human animal model for a hereditary autosomal dominant disease. The non-human animal model expresses at least one phenotype associated with the disease and is obtained by a genetic determinant. The invention also relates to sperm cells and embryos comprising the genetic determinant for an autosomal dominant disease. Furthermore, methods for producing the non-human animal model, sperm cell, and embryos are disclosed.

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An animal model and a method for producing an animal model

All patent and non-patent references cited in the application are hereby incorporated by reference in their entirety.

Field of invention

The present invention relates to a non-human animal model, such as a porcine animal model, and methods for producing a non-human animal model by sperm-mediated gene transfer (SMGT). When a genetic determinant involved in a hereditary disease is used for SMGT, i.e. a genetic determinant which confers a dominant phenotype for said hereditary disease, the non-human animal model can be used for studying such hereditary diseases, such as autosomal dominant hereditary diseases, for example protein conformation diseases, such as Amyotrophic Lateral Sclerosis (ALS), Alzheimer's disease, Parkinson's disease, diseases related to trinucleotide repeats, Huntington's disease but also dyschondroplasia.

Background of invention

Transgenic, non-human animals can be used to understand the action of a single gene in the context of the whole animal and the interrelated phenomena of gene activation, expression, and interaction. The technology has also led to the production of models for various diseases in humans and other animals which contributes significantly to an increased understanding of genetic mechanisms and of genes associated with specific diseases.

While smaller animals, such as mice, have proved to be suitable models for certain diseases, their value as animal models for many human diseases is quite limited. Larger transgenic animals are much more suitable than mice for the study of many of the effects and treatments of most human diseases because of their greater similarity to humans in many aspects.

For the past two decades, pigs have been used in biomedical research with increasing frequency as replacements for dog and primates. This is due to the anatomical and physiological similarity to humans. Pigs and human share anatomical and physiological

characteristics such as heart size, cardiac output, and coronary blood supply which have made pigs widely used in cardiac surgery, pacemaker studies and heart transplantions. Similarly, pig and humans share features in digestive physiology and pigs are therefore widely used in nutritional studies and subjects in relations to this including lipid metabolism, gastric ulceration, diabetes and alcoholism, Furthermore, porcine models are used for the study of disorders of the skin. Organs of porcine origin are also used in organ transplantation research. However, the pig constitutes an evolutionary clade in relation to humans and rodents.

Many human diseases are hereditary. The inheritance of genetic disorders, abnormalities, or traits is a function of both the type of chromosome on which the abnormal gene resides (autosomal or sex chromosome), and of the trait itself, i.e. whether the trait is dominant or recessive. The trait can be due to a single defective gene from one parent (dominant inheritance) or the trait can arise when two copies of the gene (one from each parent) are defective (recessive inheritance).

Dominant inheritance occurs when an abnormal gene from one parent is capable of causing disease even though the matching gene from the other parent is normal. Accordingly, the abnormal gene dominates the outcome of the gene pair and one copy of the mutant gene is sufficient for expression of the abnormal phenotype.

Several distinct characteristics of autosomal dominant inheritance include: Every affected individual has an affected parent (except in cases of new mutations or incomplete penetrance); males and females are equally likely to inherit the allele and be affected (as the genes are located on autosomes, of which each male and female has two copies); and recurrence risk (the probability that a genetic disorder that is present in a patient will recur in another member of the family) for each child of an affected parent is ½ (as only one copy of a gene is necessary for development of the disease). If one parent is a heterozygote for a particular gene, their offspring will either inherit the gene or they will not, with each outcome equally likely. Accordingly, if an affected individual's siblings are not affected, they do not carry the mutation and cannot therefore pass it on to their own offspring.

As many of these autosomal dominant diseases are deleterious, one would expect that over time they would disappear from the population due to natural selection. However,

there are several phenomena, cf. below, that can lead to maintenance of these alleles in the population.

Variable expressivity: the variable severity of a genetic trait. Different individuals with the same mutation will develop different degrees of the disorder due to difference in environment and the modifying effects of other genes. Because of this, a mutation that leads to a relatively mild form of the disease in one individual stands a good chance of being passed on and maintained in the population. The same mutation in another individual may lead to such a severe manifestation that the affected individual is unable to propagate the mutation to the next generation. This demonstrates very well the fact that genetic disease results as combination of genetic and environmental influences.

Late onset: when a disease has an onset later in life, affected individuals may have passed the gene to their offspring before they even knew they carried it themselves. One example of this is Huntington's disease, a late onset neurodegenerative disorder. It is now possible to receive genetic testing for this disorder, a practice that leads to many complex issues for the family undergoing the testing.

High recurrent mutation rate: 85% of cases of achondroplasia, a major cause of dwarfism, are the result of new mutations. Some segments of the genome are subject to higher than normal rates of mutation, which can lead to the maintenance of the disease in the population even if both parents were normal. This is particularly true of diseases that affect fertility. If the disease is invariably lethal at a young age, before reproduction is possible, the only source of the disease would be new mutations.

Incomplete penetrance: phenomena where a portion of individuals with a disease-associated genotype do not develop a disease. If only 30 people out of 50 who have a disease-associated mutation actually develop the disease, it is incompletely penetrant. A disease that is 75% penetrant is one in which 75% of those who carry the disease-associated mutation eventually develop the disease. The rest do not.

Transgenic animals carrying a dominant disease gene which is expressed in the animal makes it possible to study the phenotype associated with said dominant disease gene if the gene when expressed in the animal actually leads to the same disease as in humans. Transgenic animals have traditionally been used for the improvement of

livestock, and for the large scale production of biologically active pharmaceuticals. Historically, transgenic animals have been produced almost exclusively by microinjection of the fertilized egg. The pronuclei of fertilized eggs are microinjected in vitro with foreign, i.e., xenogeneic or allogeneic DNA or hybrid DNA molecules. The microinjected fertilized eggs can then be transferred to the genital tract of a pseudopregnant female.

Only a few examples of success with sperm-mediated gene transfer methods in monkeys and mice have been reported (reviewed e.g. by Vodicka (2005): Ann. N.Y. Acad. Sci.; 1049: 161-171; Chan (2004): Reprod. Biol. Endocrinol.; 2:39; and by Wall (2002): Theriogenology; 57: 189-201).

As noted by Wall (ibid), only few studies convincingly demonstrate transgene expression. Wall (ibid) concludes that the body of evidence is still not sufficient to warrant elevating sperm-mediated gene transfer to the status of other available state of the art methods.

Smith (2004): Int. J. Med. Sci.; 1(2):76-91; notes that sperm-mediated gene transfer has not yet become established as a reliable form of genetic modification and that concerted attempts to utilise sperm-mediated gene transfer often have produced negative results.

WO 2005/038001 is directed to a method for producing transgenic animals.

US 2005/0053910 pertains to cell culture media for sperm-mediated gene transfer methods.

JP 2000-316420 is related to transgene pigs obtained by methods involving micro-injection and not sperm-mediated gene transfer. The pig may carry a gene causing an autosomal, dominant disease.
However, as pigs constitute a distinct evolutionary clade in comparison with humans the introduction of mutations known as disease causing mutations in specific genes in humans cannot be expected to yield a desired phenotype in the pig model.

There is a need for improved animal models for human diseases in order to gain more information of the onset, progression and treatment regimes of hereditary diseases in humans.

Summary of Invention

Until now it has been believed that the phenotypic display of an autosomal dominant disease is caused by the continuous expression of an inherited mutated gene. However, the present invention discloses that a phenotype of an autosomal dominant disease is caused by a sufficiently high expression of the mutated gene in a transient manner. Thus, the present invention discloses that the expression of a gene involved in the development of autosomal dominant diseases primarily has to be expressed in sufficiently high amounts at a specific time point during the development of the embryo of a non-human animal model. The fact that the expression of particular genes associated with autosomal dominant genes is transient also allows for the production of non-human animal models by the addition of gene products to for example embryos or other target cells (seeding effect).

In a first aspect the present invention relates to non-human animal model for a hereditary autosomal dominant disease, wherein the non-human animal model expresses at least one phenotype associated with said hereditary autosomal dominant disease obtained by a genetic determinant.

In a second aspect a non-human animal model for a hereditary autosomal dominant disease, wherein the non-human animal model expresses at least one phenotype associated with said hereditary autosomal dominant disease obtained by sperm-mediated gene transfer.

A third aspect of the present invention pertains to a pig model for a hereditary autosomal dominant disease obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with said hereditary autosomal disease.

A fourth aspect relates to a pig model for a hereditary autosomal dominant disease obtained by a genetic determinant, wherein said disease is a protein conformation disease.

A fifth aspect concerns a pig model for a hereditary neurodegenerative autosomal domainant disease obtained by a genetic determinant.

In further aspects of the invention is disclosed a pig model for amyotrophic lateral sclerosis, Alzheimer's Disease, Parkinson's Disease, diseases related to Trinucleotide Repeats, Huntington's chorea or dyschondroplasia obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with Amyotrophic Lateral Sclerosis, Alzheimer's Disease, Parkinson's Disease, diseases related to Trinucleotide Repeats, Huntington's chorea or dyschondroplasia, respectively.

The present invention also relates to a method for producing the model according to the present invention, said method comprising the steps of
i) providing semen from a male, non-human animal, ii) providing at least one genetic determinant capable of establishing said at least one phenotype associated with said hereditary disease when the at least one genetic determinant is expressed in said non-human animal model, iii) contacting said semen and said at least one genetic determinant, iv) fertilising an oocyte from a female, non-human animal with the semen and the genetic material, and v) incubating said fertilised oocyte under conditions allowing said fertilised oocyte to develop into said non- human animal model.

Furthermore, a method for evaluating the response of a therapeutical treatment of a hereditary disease, said method comprising the steps of a. providing the non-human animal model according to the present invention, b. treating said non-human animal with at least one pharmaceutical composition exerting an effect on said at least one phenotype, and c.evaluating the effect observed, is disclosed.

Yet other aspects concern a non-human sperm cell comprising at least one genetic determinant exerting at least one dominant phenotype for at least one hereditary disease when expressed in a non-human animal host organism, and a method for producing the non-human sperm cell, said method comprising the steps of a. providing a non-human sperm cell, b. providing at least one genetic determinant exerting a dominant phenotype for a hereditary disease when expressed in a non-human animal host organism, c. contacting said non-human sperm cell and said at least one genetic determinant, wherein said contacting results in the uptake of the genetic determinant into the non-human sperm cell.

Moreover, the present invention also relates to a composition comprising a non-human sperm cell in combination with at least one genetic determinant exerting at least one dominant phenotype for at least one hereditary disease when expressed in a non-human animal host organism.

In further aspects the invention pertains to a method for fertilising an oocyte by sperm-mediated gene transfer, said method comprising the steps of providing the non-human sperm cell or the composition as defined above and introducing said non-human sperm cell into the oocyte to be fertilised.

The present invention also relates to an embryo obtained by fertilising an oocyte with the non-human sperm cell or with the composition as defined herein.

Yet a further aspect relates to a method for the cultivation and development of the embryo as described herein, said method comprising the step of cultivating said embryo under conditions allowing the embryo to develop into a non-human animal offspring expressing said genetic determinant and exerting a dominant phenotype for a hereditary disease.

In a final aspect is disclosed a method for screening the efficacy of a pharmaceutical composition, said method comprising the steps of a. providing the non-human animal model of the present invention, b. expressing in said animal model said at least one genetic determinant and exerting said dominant phenotype for said hereditary disease, c. administering to said non-human animal the pharmaceutical composition the efficacy of which is to be evaluated, and d. evaluating the effect, if any, of the pharmaceutical composition on the phenotype exerted by the genetic determinant when expressed in the non-human model.

Description of Figures

Fig. 1: Sequence of porcine SOD1 cDNA.

Fig. 2: Sequence of the mutated porcine SOD1 cDNA.

Fig 3: Comparison of the deduced amino acid sequence of porcine SOD1 (S. scrofa), with human (H. sapiens), mouse (M. musculus) and rat (R. norvegicus). Asterisks indicate amino acid residues that are conserved among the sequences. Dots indicate that the residues are non-conservative among the sequences, and semicolons indicate residues which are conservative. Dashes indicate gaps that have been introduced to optimize the alignment. The amino acid (G) which has shifted is marked in bold.

Fig. 4: Projection of mutations in SOD1 onto the crystal structure of the human SOD1 dimer. The Protein is shown in cartoon mode where helices are red, strands are yellow, and loops are blue. Grey areas represent regions which have been mutated in humans with ALS. The mutations are distributed all over the protein, illustrating that the majority or all of the residues in the protein are important for correct function of the enzyme.

Fig. 5: SOD1 linearised construct used to create transgenic pigs by means of SMGT. The fragment constitutes approximately 2100 bp and includes a CMV promoter, en enhancer region, the porcine SOD1 cDNA, and the SVPolyA (simian virus 40 poly A) fragment. Furthermore, the 5' – and 3' –prime end of the DNA fragment include additional bases derived from the phCMV vector to protect crucial element from being truncated following SMGT.

Fig. 6: PCR evaluation of transgenic offspring. Lane 1: PUC 19 marker, lane 2: piglet 4905, lane 3: piglet 4906, lane 4: piglet 4907, lane 5: piglet 4908, lane 6: piglet 4909, lane 7: piglet 4910, lane 8: piglet 4911, lane 9: minus DNA, lane 10: minus DNA, lane 11: negative control, and lane 12: positive control. All the tested piglets (animal 4905 – 4911) from the litter are positive regarding the transgenic fragment.

Fig. 7: PCR evaluation of DNA from different tissues from animal 4906. Lane 1: PUC 19 marker, lane 2: empty, lane 3: liver, lane 4: lung, lane 5: kidney, lane 6: heart, left ventricle, lane 7: jaw muscle, lane 8: top round, lane 9: shoulder muscle, lane 10: diaphragma, lane 11: cerebellum, lane 12: hippocampus, lane 13: frontal cortex, lane 14: cervical medulla spinallis from 4909, lane 15: minus DNA, lane 16 minus DNA, lane 17 negative control, lane 18: positive control.

Fig. 8. PCR evaluation of DNA from different tissues from animal 4909. Lane 1: PUC 19 marker, lane 2: left shoulder muscle, lane 3: right Spinacea oleracea, lane 4: musculus gloteus, lane 5: musculus pectoralis major, lane 6: facial muscle, lane 7: diaphragma, lane 8: heart, left ventricle, lane 9: lung, upper right part, lane 10 kidney, lane 11: liver, lane 12: hippocampus, lane 13: frontal cortex, lane 14: minus DNA, lane 15: minus DNA, lane 16: negative control, and lane 17: positive control.

Fig. 9: PCR evaluation of DNA purified from sperm cells from boar 4905 and 4908. The DNA is purified both by means of a standard purification procedure and the miniprep purification procedure. Lane 1: marker, lane 2: 4905, standard purification procedure, lane 3: 4905, standard purification procedure, lane 4: 4905, miniprep purification procedure, lane 5: 4905, miniprep purification procedure, lane 6: 4908, standard purification procedure, lane 7: 4908, standard purification procedure, lane 8: 4908, miniprep purification procedure, lane 9: 4908, miniprep purification procedure, lane 10: minus DNA, lane 11: minus DNA, lane 12: negative control, lane 13: empty, lane 14: positive control.

Fig.10: PCR evaluation of transgenic offspring. Lane 1: DNA ladder, lane 2: pig 4905, lane 3: piglet 4908, lane 4: pig 4909, lane 5: pig 4906, lane 6: pig 4907, lane 7: pig 4911, lane 8: pig 4910, lane 9: wild type animal, lane 10: minus DNA, and lane 11: positive control.

Fig. 11: Southern blot. Lane 1-3: genomic DNA from boar 4905, 4908, and wt-pig digested with Pvu II, lane 4-6: genomic DNA from boar 4905, 4908, and wt-pig digested with Pvu II and BAM HI, lane 7-9: undigested genomic DNA from boar 4905, 4908, and wt-pig lane 10: SOD1 fragment used in SMGT digested with Pvu II (1-5 copies), lane 11: SOD1 fragment used in SMGT digested with Pvu II and Bam HI (1-5 copies).

Fig. 12: Analysis of porcine WT SOD1 expression levels in various porcine tissues by quantitative real-time RT-PCR. A) Detection of porcine endogenous SOD1, showing both SOD1 standard dilution and samples from the two affected boars and wild type controls, showing no difference. B) Detection of mutated porcine SOD1. Pink and yellow curves represent amplification of the mutated SOD1 fragment in various dilutions. Blue and green curves shows the lack of amplification of mutated SOD1 in both wild type and affected boars. C) SOD1 endogenous expression analysis. Each

sample was conducted in triplicate. The expression analysis was performed on samples from heart, kidney, liver, lung, spleen, medulla spinalis (M. spinalis), frontal cortex (FCO), parietal cortex (PCO), musculus longissimus dorsi (M. L. dorsi), musculus semitendinosus, left side (M.semit. l.), musculus semitendinosus, right side (M.semit. r.), musculus semibranosus, left side (M.semb. l.), and musculus semibranosus, left side (M.semb. r.) from the two affected boars (4905 and 4908) and two wild type control boars (147 and 3713). SOD1 expression levels were normalized against the 18S ribosomal gene.

Fig. 13: SOD activity in serum from symptomatic animals (4905 and 4908) and a healthy control (4368).

Fig.14: Investigation of muscle fibers, type I, in affected boars (4905 and 4908) and healthy wild type controls (3713 and 147). The number of type I muscle fibers in each muscle cluster was counted in musculus longissimus dorsi, and the frequency of muscle fibers in each cluster for the four boars are shown in the histograms. The stainings represents typical type I muscle fibers from musculus longissimus dorsi from the four boars.

Fig. 15: Photomicrographs of immunohistochemistry sections from cervical spinal cord showing motorneuron from A) the affected boar (4908) and B) an unaffected wild type control (147) stained with the 100-115 anti-SOD1 peptide antibody.

Fig. 16: The porcine *SNCA* cDNA sequence.

Fig. 17: Alignment of the porcine α-synuclein protein with α-synucleins from other species. Human mutants: A30P, E46K and A53T are indicated by bold and underlined letters. Differences between the human and the porcine sequences are indicated by old blue letters. Asterisks indicate amino acid residues that are conserved among the sequences. The amino acid Ala30 substituted by a Pro in the mutated SNCA sequence is marked by an arrow.

Fig. 18: Phylogenetic tree (unrooted) of porcine alpha-synuclein, and other alpha-synuclein proteins. The tree was constructed using the using the clustal method of DNASTAR Megalign (DNASTAR Inc., Madison, WI) based on amino acid similarities of

the full sequences. The length of each pair of branches represents the distance between sequence pairs, while the units at the bottom of the tree indicate the number of substitution events. The following abbreviations for species acronyms are used along with: Ss = *Sus scrofa*; Hs = *Homo sapiens*; Bt = *Bos taurus*; Mm = *Mus musculus*; Rn = *Rattus norvegicus*; Gg = *Gallus gallus*; Xl = *Xenopus laevis*. The Accession numbers of the sequences used for construction of the phylogenetic tree are: SsSNCA (AY049786); HsSNCA (NM_001037145); BtSNCA (NM_001034041); MmSNCA (AF44672); RnSNCA (NM_019169); GgSNCA (NM_204673); XlSNCA (BC054200).

Fig. 19: The mutated porcine *SNCA* cDNA sequence. The substituted nucleotide is shown as a bold underlined letter.

Fig. 20: *SNCA-phCMV1* linearized construct used to create transgenic pigs by means of SMGT. The fragment constitutes approximately 2100 bp and includes a CMV promoter, en enhancer region, the mutated (A30P) porcine *SNCA* cDNA, and the SVPolyA (simian virus 40 poly(A) fragment. Furthermore, the 5' – and 3' – prime end of the DNA fragment include additional bases derived from the phCMV vector to protect crucial element from being truncated following SMGT.

Fig. 21: PCR evaluation of transgenic offspring. Lane 1: piglet 4363, lane 2: piglet 4364, lane 3: piglet 4365, lane 4: piglet 4366, lane 5: piglet 4367, lane 6: piglet 4368, lane 7: piglet 4369, lane 8: piglet 4370, lane 9: piglet 4371, lanes 10 and 11: positive control, lanes 12 and 13: minus DNA, lane 14: untransformed control. All the tested piglets (animal 4363 – 4371) from the litter are positive regarding the transgenic fragment.

Fig. 22: PCR evaluation of DNA purified from sperm cells from boars 4363-4371. The DNA is purified both by means of a standard purification procedure. Lane 1: DNA marker, lane 2: 4363, lane 3: 4364, lane 4: 4365, lane 5: 4366, lane 6: 4367, lane 7: 4368, lane 8: 4369, lane 9: 4370 lane 10: 4371, lane 11: minus DNA, lanes 12 and 13: negative control, lane 14: positive control.

Fig. 23: Nissl AMG staining of thin-layer sections from substantia nigra of boar # 4363. Neurons in substantia nigra abnormal; presence of cytoplasmatic vacuoles and shrinking of cells. Lewy bodies are not visible and this staining.

Fig. 24: HE staining of thin-layer sections from substantia nigra of boar # 4363. Neurons are shrunken and with numerous lacunae.

Fig. 25: TH staining of thin-layer sections from substantia nigra of boar # 4363 (A) and a minipig control (B). The number of dopaminergic cells are reduced in 4363. Remaining dopaminergic cells and neuropil appear more rough and unordered (lower panels).

Fig. 26: GFAB staining of thin-layer sections from substantia nigra of boar # 4363. Intense GFAB staining is seen in the mesencephalon. Numerous astrocytes are present indicative of active inflammation and reactive gliosis.

Fig. 27: α-synuclein Ab staining of thin-layer sections from substantia nigra of boar # 4363.

Fig. 28: Multiple amino acid sequence alignment of PSEN1. The alignment was performed using Clustal W. The sequences are Sus scrofa (DQ853416), Bos Taurus (NM 174721), Homo sapiens (NM 000021), and Mus musculus (NM 008943). Asterisk (*) indicates amino acids conserved among the sequences; Above the sequence alignments are by (+) indicated the position of pathogenic missense mutations identified in human PSEN1. Also the position of human missense SNPs are indicated above the sequence alignments with the alternative amino acids in bold.

Fig. 29: Multiple amino acid sequence alignment of PSEN2. The alignment was performed using Clustal W. The sequences are Sus scrofa (DQ853415), Bos Taurus (NM 174440), Homo sapiens (NM 000447), and Mus musculus (NM 011183). Asterisk (*) indicates conserved amino acids among the sequences. Above the sequence alignments are by (+) indicated the position of pathogenic missense mutations identified in human PSEN2. Also the position of a human missense SNP is indicated above the sequence alignments with the alternative amino acid in bold.

Fig. 30: Analysis of porcine PSEN1 and PSEN2 expression levels in the developing pig brain by quantitative real-time RT-PCR. Quantitative results are presented as normalized mean (± SD). For quantification and statistical analysis see materials and methods section. Each sample was run both in three biological and three technical triplicates. The expression analysis was performed on samples from frontal cortex, cerebellum, hippocampus, basal ganglia, and brain stem derived from embryonic days 60, 80, 100, and 115 (E60, E80, E100, and E115).

Fig. 31: Immunohistochemical analysis of PSEN1 and PSEN2 expression in embryonic E100 porcine brains. Brain sections were immunohistochemical stained for PSEN1 or PSEN2 and nuclei counterstained by haematoxylin. Sections illustrating PSEN1 and PSEN2 staining patterns in hippocampus (A), cortex (B), and cerebellum (C) are shown for embryonic day E100. Higher magnitude illustrations of neurons representative for each of the three regions are shown in the right part of each panel.

Fig. 32: Sequence alignment of non-coding TNRs from human, pig, and mouse. For the human sequences the most common identified alleles are shown with the variable number of TNRs indicated. Within brackets the most common occurring number of TNRs is shown. Note that human and chimpanzee alleles are highly polymorphic and only one representative sequence is shown. For the porcine sequences the allele frequencies are shown in brackets, furthermore, the identified alleles are revealed. N.P. indicates that a corresponding genomic sequence not was extractable from NCBI. En indicates the number of repeats present minimal in disease causing human alleles.

Fig. 33: Sequence alignment of poly-glutamine encoding TNRs in pig, human, chimpanzee (chimp), dog, opossum, rat, and mouse. For the human sequences the most common alleles are shown with the variable number of TNRs indicated. The most common number of TNRs are shown in brackets. Note that human and chimpanzee alleles are highly polymorphic and only one representative sequence is shown. For the porcine sequences the different alleles are shown and the number in brackets indicates the frequency of each allele. Q indicates the number of glutamines, H the number of histidines, and P the number of prolines. For the *Huntingtin* gene additional alleles with potential to encode 14 or 15 poly-glutamines were identified in a larger Yorkshire and Landrace sample cohort (see table 1). N.P. indicates that a corresponding genomic

sequence not was extractable from NCBI. En indicates the number of repeats present minimal in disease causing human alleles.

Fig. 34: COL10A1 linearised construct used to create transgenic pigs by means of SMGT. The fragment constitutes approximately 3600 bp and includes 5' and 3' prime phCMV vector fragment, a CMV promoter, an enhancer region, the porcine SOD1 cDNA, and the SVPolyA (simian virus 40 polyA).

Fig. 35: Examples of PCR analyses. PCR was performed on genomic DNA extracted from whole blood. Lane 1; PUC19 DNA Ladder, lanes 2-13 indicate the 12 piglets born, lanes 14-15; no DNA added, lane 16; negative control (wild type pig), lane 17; positive control.

Fig. 36: Southern Blot analysis. Lane 1: *Bgl* II digested genomic DNA from the affected pig, lane 2: *Bgl* II digested genomic DNA from wt pig, lane 3: *Bgl* II and *Bam* HI digested genomic DNA from affected pig, lane 4 *Bgl* II and *Bam* HI digested genomic DNA from wt pig. *Bgl* II digestion. *Bgl* II only digested the DNA to a limited degree (lane 1 and 2), lane 3 and for show additional bands in the diseased sow, showing that the transgene is integrated into the genome.

Fig. 37: Analysis of COL10A1 expression in various porcine tissues. Lane 2-11 represents the diseased transgenic pig and lane 12-16 represent a wild type pig. Lane 1; DNA ladder, lane 2; *musculus triceps brachii* (left), lane 3; *musculus triceps brachii* (right), lane 4; ovary, lane 5; kidney, lane 6; skin, lane 7; liver, lane 8; lung, lane 9; *musculus longissmus dorsi*, lane 10; *musculus semimembranosus* (left), lane 11; heart, lane 12; liver, lane 13; spleen, lane 14: kidney, lane 15; lung, lane 16; heart, lane 17-18; - DNA, lane 19; positive control, lane 20; DNA ladder.

Fig. 38: Histopathological investigation of one of the affected forelegs. A) Distal humeral physis. An area of hypertropihic, non-ossified chondrocytes of the growth plate is retained within the metaphysic area. Safranin O, obj. x 1. B) Distal humeral physis. At the margins of the growth plates non-ossified, hypertrophic chondrocytes are localized. Van Gieson, obj. x 2. C) Articular-epiphysial junction from the elbow joint. Within the retained cartilage cavitations with contents of fibrin are present. HE, obj. x

10. D) Articular-epiphysial junction from the elbow joint. Clefts and adjacent fibrosis is present within the chondroid tissue of the articular-epiphysial junction. HE, obj. x 20.

Detailed description of the invention

Definitions

For purposes of the present invention, the following terms are defined below.

The term "sperm" is used to refer to a male gamete cell and includes, without limitation, spermatogonia, primary and secondary permatocytes, spermatids, differentiating spermatids, round spermatids, and spermatozoa.

The term "oocyte" is used to refer to a female gamete cell, and includes primary oocytes, secondary oocytes, and mature, unfertilized ovum.

In some cases the term “embryo” is used to describe a fertilized oocyte after implantation in the uterus until 8 weeks after fertilization at which stage it becomes a foetus. According to this definition the fertilized oocyte is often called a pre-embryo until implantation occurs. However, throughout this patent application we will use a broader definition of the term embryo, which includes the pre-embryo phase. It thus encompasses all developmental stages from the fertilization of the oocyte through morula, blastocyst stages hatching and implantation. An embryo is approximately spherical and is composed of one or more cells (blastomeres) surrounded by a gelatine-like shell, the acellular matrix known as the zona pellucida. The zona pellucida performs a variety of functions until the embryo hatches, and is a good landmark for embryo evaluation. An embryo is formed when an oocyte is fertilized by fusion or injection of a sperm cell (spermatozoa). The feritilised oocyte is traditionally called an embryo for the first 8 weeks. After that (i.e. after eight weeks and when all major organs have been formed) it is called a foetus. However the distinction between embryo and foetus is not generally well defined. During embryonic development, blastomere numbers increase geometrically (1-2-4-8-16- etc.). Synchronous cell division is generally maintained to the 16-cell stage in embryos. After that, cell division becomes asynchronous and finally individual cells possess their own cell cycle. At about the 32-cell stage (morula stage), embryos undergo compaction, as inter-cell adhesion occur when adhesion proteins are expressed.

Accordingly, the term embryo is used in the following to denote each of the stages fertilized oocyte, zygote, 2-cell, 4-cell, 8-cell, 16-cell, morula, blastocyst, expanded blastocyst and hatched blastocyst, as well as all stages in between (e.g. 3 –cell or 5-cell).

The term "non-human animal" can be a non-human primate, e.g., an ape or a monkey; and a farm animal, such as an animal selected from the group consisting of cattle, swine; sheep; goats; horses; and donkeys. Accordingly, the non-human animal can e.g. be a cow, a bull, a bison, a buffalo, a pig, a big-horn sheep, a pony, a mule, a deer, an elk, a lama, and an alpaca. Similarly the non-human animal can be a rodent, such as a mouse or rat.

The term "non-human animal model" refers to any non-human animal in which one or more cells comprise genetic determinants. The non-human animal comprising genetic determinants may for example be the result of introduction of the genetic determinant by sperm-mediated gene transfer. However, the genetic determinant may also be introduced for example by injection into cells or tissues desired.

The term “genetic determinant” of the present invention refers to genes or parts thereof, transcriptional products or parts thereof and/or translational products or part thereof that confer the display of one or more features of phenotypes of autosomal dominant hereditary diseases. Thus, in some embodiments the term "genetic determinant" is used herein to refer to a single-stranded or double-stranded “polynucleotide molecule” or “nucleic acid” comprising a structural gene of interest. The “genetic determinant” encodes a protein not ordinarily made in appreciable amounts in the target cells.

The term genetic determinant is also used to refer to a single-stranded or double stranded ribonucleic acid, RNA expressed from a gene of interest. Thus, “genetic determinants” include nucleic acids which are not ordinarily found in the genome of the target cell. “Genetic determinants” also include nucleic acids which are ordinarily found within the genome of the target cell, but is in a form which allows for the expression of proteins which are not ordinarily expressed in the target cells in appreciable amounts. Alternatively, “genetic determinants” may encode a variant or mutant form of a naturally-occurring protein.

The term genetic determinant is also used herein to refer to a protein or part thereof or a RNA molecule or part thereof of a gene of interest, wherein the gene or polynucleotide encoding said protein or RNA is not present in the target cell. Throughout the description and claims either the three letter code or the one letter code for natural amino acids are used. Where the L or D form has not been specified it is to be understood that the amino acid in question has the natural L form, cf. Pure & Appl. Chem. Vol. (56(5) pp 595-624 (1984) or the D form, so that the peptides formed may be constituted of amino acids of L form, D form, or a sequence of mixed L forms and D forms.

Where nothing is specified it is to be understood that the C-terminal amino acid of a peptide for use according to the invention exists as the free carboxylic acid, this may also be specified as "-OH". However, the C-terminal amino acid of a peptide for use according to the invention may be the amidated derivative, which is indicated as "-NH_2". Where nothing else is stated the N-terminal amino acid of a polypeptide comprises a free amino-group, this may also be specified as "H-".

A peptide, fragment, homologue or variant for use according to the invention can also comprise one or several unnatural amino acids.

Conservative amino acid substitutions: Substitutions within the groups of amino acids, shown below, are considered conservative amino acid substitutions. Substitutions between the different groups of amino acids are considered non-conservative amino acid substitutions.

P, A, G, S, T (neutral, weakly hydrophobic)
Q, N, E, D, B, Z (hydrophilic, acid amine)
H, K, R (hydrophilic, basic)
F, Y, W (hydrophobic, aromatic)
L, I, V, M (hydrophobic)
C (cross-link forming)

In one embodiment the genetic determinant is in the form of microRNAs (miRNA) that are single-stranded RNA molecules of about 21-23 nucleotides in length. miRNAs are typically encoded by genes that are transcribed from DNA but not translated into protein (non-coding RNA); instead they are processed from primary transcripts known

as *pri-miRNA* to short stem-loop structures called *pre-miRNA* and finally to functional miRNA. Mature miRNA molecules are partially complementary to one or more messenger RNA. Thus, protein or RNA may be produced outside the target cell and introduced into a target cell by any method known to the skilled person. For example the genetic determinant is provided from extracts of brains from diseased subjects, such as humans or animals of the present invention. Subsequently, said brain tissue is introduced into a target cell of the present invention.

The target cell may be a sperm cell, an oocyte, a fertilized oocyte, an embryo, which includes the pre-embryo phase encompassing all developmental stages from the fertilization of the oocyte through morula, blastocyst stages hatching and implantation, a fetus, or a cell derived from tissue of the developing fetus. In one embodiment of the present invention the target cell is an adult animal or tissue thereof.
The genetic determinant may be introduced to the target cell by for example injection, virus-mediated transfer or similar methods known to the skilled person.

The genetic determinant may in the form of RNA or protein be introduced into the target cell to yield a non-human animal model for autosomal dominant diseases, such as neurodegenerative diseases as described elsewhere herein, for example protein conformation disorders. In preferred embodiments the genetic determinant is introduced into the target cell to produce a pig model expressing at least one phenotype associated with ALS, Alzheimer's disease, Parkinson's disease, Huntington's chorea, diseases related to trinucleotide repeats. Similarly, in one particular embodiment a pig model is produced expressing at least one phenotype associated with dyschondroplasia.

The genetic determinant may in particular embodiments be introduced by sperm-mediated gene transfer to produce a pig model for autosomal dominant diseases, such as neurodegenerative diseases as described elsewhere herein, for example protein conformation disorders. In preferred embodiments the genetic determinant is introduced by sperm mediated gene transfer to produce a pig model expressing at least one phenotype associated with ALS, Alzheimer's disease, Parkinson's disease, Huntington's chorea, diseases related to trinucleotide repeats. Similarly, in one particular embodiment a pig model is produced expressing at least one phenotype associated with dyschondroplasia.

The genetic determinant when present as a gene or DNA construct need not be integrated into the genome of the target cell, fertilised oocyte, embryo, fetus or tissue. In such an example the gene or DNA construct needs to be expressed in an amount sufficient for triggering a cascade that eventually results in the onset and progression of the disease in question. This is in particular the case for autosomal diseases of the neurodegenerative kind, such as protein conformation diseases. Thus, the genetic determinant involved in ALS, Alzheimer´s Disease, Parkinson's disease, diseases related to trinucleotide repeats and Huntington's chorea need not to be integrated in the genome of the pig model. The expression of the gene of interest or DNA construct need not be continuous but has to take place during the development of the embryo to fetus. Similarly, when the genetic determinant is present in the form of protein where the protein is involved in the development of protein conformation diseases the protein need to be present in the embryo or fetus but need not be present continuously in the pig model.

The genetic determinant when present in the form of DNA or cDNA may further comprise regulatory sequences to direct expression of the DNA or cDNA. Such regulatory sequences may be promoters or enhancers. The term promoter will be used here to refer to a group of transcriptional control modules that are clustered around the initiation site for RNA polymerase II. Promoters are composed of discrete functional modules, each consisting of approximately 7-20 bp of DNA, and containing one or more recognition sites for transcriptional activator proteins. At least one module in each promoter functions to position the start site for RNA synthesis. The best known example of this is the TATA box.

Additional promoter elements regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have recently been shown to contain functional elements downstream of the start site as well. The spacing between elements is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. Enhancers were originally detected as genetic elements that increased transcription from a promoter located at a distant position on the same molecule of DNA. The basic distinction between enhancers and promoters is operational. An enhancer region as a whole must be able to stimulate transcription at a distance; this need not be true of a promoter region or its component elements. On the other hand, a

promoter must have one or more elements that direct initiation of RNA synthesis at a particular site and in a particular orientation, whereas enhancers lack these specificities. Aside from this operational distinction, enhancers and promoters are very similar entities. They have the same general function of activating transcription in the cell. They are often overlapping and contiguous, often seeming to have a very similar modular organization.

The terms "polynucleotide" and "nucleic acid" are used interchangeably, and, when used in singular or plural, generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, polynucleotides as defined herein include, without limitation, single- and double-stranded DNA, DNA including single- and double-stranded regions, single- and double-stranded RNA, and RNA including single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or include single- and double-stranded regions. In addition, the term "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. The term "polynucleotide" specifically includes cDNAs. The term includes DNAs (including cDNAs) and RNAs that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritiated bases, are included within the term "polynucleotides" as defined herein. In general, the term "polynucleotide" embraces all chemically, enzymatically and/or metabolically modified forms of unmodified polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells.

"Sperm mediated gene transfer" as used herein refers to any method wherein a non-human animal sperm cell is mixed with a genetic determinant (gene) under conditions resulting in the genetic determinant being 1) taken up by the sperm cell, 2) occurring as extrachromosomal DNA or as stably integrated into the genetic material (genome) harboured by the sperm cell, and 3) optionally expressed in said sperm cell. Once

taken up by the sperm cell, the genetic material (gene) can be transferred to a non-human animal model which allows one to study the expression of the genetic determinant in the chosen genetic background.

"Autosomal diseases" are used herein to refer to diseases which are inherited through the non-sex chromosomes (pairs 1 through 22). The term "autosomal dominant" is used herein to refer to a single, abnormal gene on one of the autosomal chromosomes (one of the first 22 "non-sex" chromosomes) from either parent which can cause certain diseases. One of the parents will usually have the disease (as the gene is dominant) in this mode of inheritance. Only one parent must have an abnormal gene in order for the offspring to inherit the disease.

The present invention relates to animal models for hereditary autosomal dominant diseases. The models of the present invention can be used as model for hereditary autosomal dominant diseases as known from humans. Animal models for human diseases and especially those diseases such as the autosomal dominant diseases which develop over a long period of time, having a late onset in life are very useful in order to gain information on the onset, progression and treatment regime of individuals suffering from such type of diseases. It is appreciated that the animal models are non-human animals. In one aspect of the invention the non-human animal model for a hereditary autosomal dominant disease is a model wherein the non-human animal model expresses at least one phenotype associated with said hereditary autosomal dominant disease obtained by at least one genetic determinant. In another aspect of the invention the non-human animal model for a hereditary autosomal dominant disease is a model wherein the non-human animal model expresses at least one phenotype associated with said hereditary autosomal dominant disease obtained by sperm-mediated gene transfer.

It is appreciated that the non-human animal model may be obtained by the use of at least one, two, three, four, five, six, seven, eight, nine or ten genetic determinants. The genetic determinants of a given autosomal dominant disease whether in the form of DNA, RNA or protein as described herein may be combined in one animal model in order to obtain a strong phenotype of an autosomal dominant disease.

Autosomal dominant diseases are as described elsewhere herein diseases that are normally inherited through the non-sex chromosomes from one of the parents. Autosomal dominant diseases comprise diseases known as protein conformation

diseases, neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Parkinson's disease, diseases related to Trinucleotide Repeats for example huntington's chorea, but also conditions related to dyschondroplasia.

Protein conformation diseases are one type of neurodegenerative diseases in which protein folding disorders occur. The protein misfolding of specific proteins can be observed in affected neuronal tissue. Protein conformation diseases according to the present invention are ALS, Alzheimer's disease, Parkinson's disease, diseases associated with trinucleotide repeats and Huntington's chorea.

ALS

In one embodiment the non- human animal model expresses at least one phenotype associated with ALS. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with ALS.

"Amyotroph lateral sclerosis (ALS)" is used herein to refer to any neurodegenerative disease that usually attacks both upper and lower motor neurons and causes degeneration throughout the brain and spinal cord.

Physicians have limited choices for treating ALS. At this time, Riluzole® is the only drug that has been approved by the FDA for treatment of ALS. In clinical trials, Riluzole® has shown a slight benefit in modestly increasing survival time of patients suffering from ALS.

Amyotrophic lateral Sclerosis (ALS) is the most common motor neurodegenerative disease characterised by a progressive loss of motor neurons in the spinal cord, brain stem, and motor cortex, causing weakness, muscular wasting and paresis, ultimately leading to death. Symptoms of the disease constitute weakness, stiffness, abnormal reflexes, fasciculations, cramps and atrophy. However, especially in the early phases of the disease, ALS can be difficult to diagnose since all symptoms are rarely present at that stage [1].

A common first symptom is a painless weakness in a hand, foot, arm or leg, which occurs in more than half of all cases. Other early symptoms include swallowing or walking difficulty. The biological mechanisms that cause ALS are only partially understood. One known cause of ALS is a mutation of a specific human gene: The SOD1 gene. This mutation is believed to make a defective protein that is toxic to motor

nerve cells. The SOD1 mutation, however, accounts for only 1 or 2 percent of ALS cases, or 20 percent of the familial (inherited) cases. Familial ALS represents between five to 10 percent of all cases - the remaining cases seemingly arise spontaneously and attacks previously healthy adults.

The present invention relates to the production of a non-human animal model for ALS. The below Table 1 shows mutations which are associated with ALS in humans. According to the present invention any of the in table 1 listed mutations and substitutions as known from humans are embodiments of the present invention. Thus, the mutated forms of the porcine homolog of the human SOD1 and/or human SOD1 genes/cDNA, RNA and/or protein or parts thereof may comprise any of the listed mutations in order to produce an non-human animal model for ALS and in particular a pig model for ALS. It is appreciated that at least one or more mutations may be introduced into the porcine homolog of the human SOD1 and/or human SOD1 genes/cDNA, RNA and/or protein or parts thereof. Any number of the listed mutations may be used in combination.

Table 1

Location	Codon	Mutation	Mutation	Mutation	Mutation	Mutation	Mutation
exon 1	4	Ala4Ser	Ala4Thr	Ala4Val			
exon 1	6	Cys6Phe	Cys6Gly				
exon 1	7	Val7Glu					
exon 1	8	Leu8Val	Leu8Gln				
exon 1	10	Gly10Val					
exon 1	12	Gly12Arg					
exon 1	14	Val14Met	Val14Gly				
exon 1	16	Gly16Ser	Gly16Ala				
exon 1	19	Asn19Ser					
exon 1	20	Phe20Cys					
exon 1	21	Glu21Lys	Glu21Gly				
exon 1	22	Gln22Leu					
intron 1		319t>a					
exon 2	37	Gly37Arg					
exon 2	38	Leu38Val	Leu38Arg				
exon 2	40	Glu40Gly					
exon 2	41	Gly41Ser	Gly41Asp				
exon 2	43	His43Arg					
exon 2	45	Phe45Cys					
exon 2	46	His46Arg					

exon 2	47	Val47Phe					
exon 2	48	His48Arg	His48Gln				
exon 2	49	Glu49Lys					
exon 2	54	Thr54Arg					
exon 3	57	Cys57Arg					
exon 3	59	Ser59Ile					
exon 3	65	Asn65Ser					
exon 3	67	Leu67Arg					
exon 3	72	Gly72Cys	Gly72Ser				
exon 3	76	Asp76Tyr	Asp76Val				
exon 4	80	His80Arg					
exon 4	84	Leu84Val	Leu84Phe				
exon 4	85	Gly85Arg					
exon 4	86	Asn86Asp	Asn86Ser				
exon 4	87	Val87Met	Val87Ala				
exon 4	89	Ala89Thr	Ala89Val				
exon 4	90	Asp90Ala	Asp90Val				
exon 4	93	Gly93Cys	Gly93Arg	Gly93Ser	Gly93Asp	Gly93Ala	Gly93Val
exon 4	95	Ala95Thr					
exon 4	96	Asp96Asn					
exon 4	97	Val97Met					
exon 4	100	Glu100Lys	Glu100Gly				
exon 4	101	Asp101His	Asp101Asn	Asp101Gly			
exon 4	104	Ile104Phe					
exon 4	105	Ser105Leu					
exon 4	106	Leu106Val					
exon 4	108	Gly108Val					
exon 4	112	Ile112Thr	Ile112Met				
exon 4	113	Ile113Phe	Ile113Thr				
exon 4	114	Gly114Ala					
exon 4	115	Arg115Gly					
exon 4	116	Thr116Arg					
exon 4	118	Val118Leu (GTG to TTG)	Val118Leu (GTG to CTG)				
intron 4		1415t>g					
exon 5	124	Asp124Va	Asp124Gl				

		I	V				
exon 5	**125**	Asp125His					
exon 5	**126**	Leu126STOP	Leu126Ser				
exon 5	**134**	Ser134Asn					
exon 5	**139**	Asn139His	Asn139Lys				
exon 5	**140**	Ala140Gly					
exon 5	**141**	Gly141STOP	Gly141Glu				
exon 5	**144**	Leu144Ser	Leu144Phe (TTG to TTC)	Leu144Phe (TTG to TTT)			
exon 5	**145**	Ala145Thr	Ala145Gly				
exon 5	**146**	Cys146Arg					
exon 5	**147**	Gly147Arg					
exon 5	**148**	Val148Ile	Val148Gly				
exon 5	**149**	Ile149Thr					
exon 5	**151**	Ile151Thr	Ile151Ser				

Furthermore two mutations in ALS 2 (Ala46delA and Leu623delCT) and three mutations in ALS4, SETX, (Thr3Ile, Leu389Ser, and Arg2136His) are associated with ALS.

Thus, in one aspect of the present invention the non-human animal model expressing at least one phenotype associated with ALS due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human SOD1 gene, mRNA and/or protein (see SEQ ID NO:1, SEQ ID NO:2) comprises at least one mutation yielding the acid mutations as described in table 1, or as described above for ALS 2 (Ala46delA and Leu623delCT) and three mutations in ALS4, SETX, (Thr3Ile, Leu389Ser, and Arg2136His), all associated with ALS.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with ALS due to the introduction of at least one genetic

determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine SOD1 gene, mRNA and/or protein (see SEQ ID NO:3, SEQ ID NO:4 or fragments or parts thereof) comprising at least one mutation yielding the amino acid mutations as described in table 1 or as described above for ALS 2 (Ala46delA and Leu623delCT) and three mutations in ALS4, SETX, (Thr3Ile, Leu389Ser, and Arg2136His), all associated with ALS. It is appreciated that the at least one mutation is present in the gene fragment or DNA fragment, RNA fragment or protein part. In particular the mutated porcine SOD1 cDNA with SEQ ID NO: 5 is used to produce a pig model for ALS.

The non-human animal model for ALS may be generated by introduction of said at least one genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for ALS is generated by sperm mediated gene transfer.

The present invention discloses a pig model for ALS which in one embodiment is produced by sperm mediated gene transfer of the mutated porcine SOD1 (SEQ ID NO:5) as described elsewhere herein. However, the pig model for ALS may also be produced by introducing the mutated procine SOD1 (SEQ ID NO: 5) or protein expressed (SEQ ID NO:6) thereof into a target cell.

It is appreciated that at least one mutation yielding the amino acid mutation of SOD1 in the human SOD1 as listed in table 1 or as described above for ALS 2 (Ala46delA and Leu623delCT) and three mutations in ALS4, SETX, (Thr3Ile, Leu389Ser, and Arg2136His), all associated with ALS are comprised in the human or porcine SOD1 gene or DNA, RNA or proteins of the present invention, such as for example at least two mutations, at least three mutations, at least four mutations, at least five mutations, at least six mutations, at least seven mutations, at least eight mutations, at least ten mutations, at least fifteen mutations yielding the amino acid mutation of SOD1 of table 1 or as described above for ALS 2 (Ala46delA and Leu623delCT) and three mutations in ALS4, SETX, (Thr3Ile, Leu389Ser, and Arg2136His), all associated with ALS.

The non-human animal model for ALS, in particular the pig model for ALS, will typically develop at least one of the symptoms described above such as weakness, stiffness, abnormal reflexes, fasciculations, cramps and atrophy. A common first symptom is a painless weakness in a leg, which occurs in more than half of all cases. Other early symptoms include swallowing or walking difficulty. Furthermore, histopathology performed on a biopsy as described in the examples herein can be used to diagnose the animal model with ALS. The analysis of the motor neurons for the presence aggregates, or even loss of the motor neurons are also characteristics of ALS.

Alzheimer's disease

In another aspect of the present invention the non- human animal model expresses at least one phenotype associated with Alzheimer's disease. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with Alzheimer's disease.

Alzheimer´s disease" is used herein to refer to any neurodegenerative brain disorder characterized by progressive memory loss and severe dementia in advanced cases. Alzheimer's disease is associated with certain abnormalities in brain tissue, involving a particular protein, beta-amyloid. Memory impairment is a necessary feature for the diagnosis of this type of dementia. Change in one of the following areas must also be present: language, decision-making ability, judgment, attention, and other areas of mental function and personality.

The rate of progression is different for each person. If Alzheimer´s disease develops rapidly, it is likely to continue to progress rapidly. If it has been slow to progress, it will likely continue on a slow course. There are two types of Alzheimer´s disease - early onset and late onset. In early onset Alzheimer´s disease, symptoms first appear before age 60. Early onset Alzheimer´s disease is much less common, accounting for only 5-10% of cases. However, it tends to progress rapidly.

Early onset disease can run in families and involves autosomal dominant, inherited mutations that may be the cause of the disease. So far, three early onset genes have been identified. Late onset Alzheimer´s disease, the most common form of the disease, develops in people 60 and older and is thought to be less likely to occur in families. Late onset Alzheimer´s disease may run in some families, but the role of genes is less

direct and definitive. These genes may not cause the problem itself, but simply increase the likelihood of formation of plaques and tangles or other Alzheimer´s disease-related pathologies in the brain.

The cause of Alzheimer´s disease is not entirely known but is thought to include both genetic and environmental factors. A diagnosis of Alzheimer´s disease is made based on characteristic symptoms and by excluding other causes of dementia. The only way to validate a case of Alzheimer´s disease is by microscopic examination of a sample of brain tissue after death.

The brain tissue shows "neurofibrillary tangles" (twisted fragments of protein within nerve cells that clog up the cell), "neuritic plaques" (abnormal clusters of dead and dying nerve cells, other brain cells, and protein), and "senile plaques" (areas where products of dying nerve cells have accumulated around protein). Although these changes occur to some extent in all brains with age, there are many more of them in the brains of people with Alzheimer´s disease.

The destruction of nerve cells (neurons) leads to a decrease in neurotransmitters (substances secreted by a neuron to send a message to another neuron). The correct balance of neurotransmitters is critical to the brain. By causing both structural and chemical problems in the brain, Alzheimer´s disease appears to disconnect areas of the brain that normally work together.

The following human genes are linked to Alzheimer´s disease:
Presenilin 1 (PSEN1, NM_000021),
Presenilin 2 (PSEN2, NM_000447),
Amyloid beta precursor protein (APP, NM_000484)

The below indicated substitutions are believed to be relevant regarding transgenic porcine models for Alzheimer's disease.

Table 2: Mutations causing Alzheimer´s disease in APP (NM_000484)

Mutation #	Mutation
1	Duplication of APP
2	LysMet670/671AsnLeu

3	Ala673Thr
4	Asp678Asn
5	Ala692Gly
6	Glu693Lys
7	Glu693Gln
8	Glu693Gly
9	Asp694Asn
10	Leu705Val
11	Ala713Thr
12	Ala713val
13	Thr714Ala
14	Thr714Ile
15	Val715Ala
16	Ile716Thr
17	Val717Ile
18	Val717Leu
19	Val 717Phe
20	Val717Gly
21	Leu723Pro

Table 3: Mutations causing Alzheimer´s disease in PSEN2 (NM_000447)

Mutation #	Mutation
1	Arg62His
2	Thr122Pro
3	Ser130Leu
4	Asn141Ile
5	Val148Ile
6	Gln228Leu
7	Met239Ile
8	Met239Val
9	Thr430Met
10	Asp439Ala

Table 4: Mutations causing Alzheimer´s disease in PSEN1 (NM_000021)

Mutation #	Mutation
1	Ala79Val
2	Val82Leu
3	delIle83/Met84
4	Leu85Pro
5	Val89Leu
6	Cys92Ser
7	Val94Met
8	Val96Phe
9	Phe105Ile
10	Phe105Leu

11	Leu113Gln
12	Leu113Pro
13	Intron4;InsTAC
14	Tyr115Asp
15	Tyr115Cys
16	Tyr115Asp
17	Thr116Asn
18	Thr116Ile
19	Pro117Ser
20	Pro117Arg
21	Pro117Leu
22	Glu120Lys
23	Glu120Asp
24	Glu123Lys
25	Asn135Asp
26	Asn135Ser
27	Met139Val
28	Met139Lys
29	Met139Thr
30	Met139Ile
31	Ile143Phe
32	Ile143Asn
33	Ile143The
34	Ile143Met
35	Met146Leu
36	Met146Val
37	Met146Leu
38	Met146Ile
39	Thr147Ile
40	Leu153Val
41	Tyr154Asn
42	Tyr154Cys
43	InsPhe/Ile
44	His163Tyr
45	His163Arg
46	Trp165Gly
47	Trp165Cys
48	Leu166Pro
49	Leu166Arg
50	Del_Ile197
51	Ser169Pro
52	Ser170Phe
53	Leu171Pro
54	Leu173Trp
55	Leu174Met
56	Leu174Arg
57	Phe177Leu
58	Phe177Ser
59	Ser178Pro
60	Gly183Val

61	Glu184Asp
62	Gly206Ser
63	Gly206Asp
64	Gly206Ala
65	Gly206Val
66	Gly209Val
67	Gly209Arg
68	Gly209Glu
69	Ile213Leu
70	Ile213Phe
71	Ile213Thr
72	His214Tyr
73	Gly217Asp
74	Leu219Phe
75	Leu219Pro
76	Gln222Arg
77	Gln222His
78	Leu226Arg
79	Ile229Phe
80	Ala231Thr
81	Ala231Val
82	Met233Leu
83	Met233Val
84	Met233Thr
85	Leu235Val
86	Leu235Pro
87	Phe237Leu
88	Ala246Glu
89	Leu250Val
90	Leu250Ser
91	Tyr256Ser
92	Ala260Val
93	Val261Phe
94	Leu262Phe
95	Cys263Arg
96	Cys263Phe
97	Pro264Leu
98	Pro267Ser
99	Pro267Leu
100	Arg269Gly
101	Arg269His
102	Leu271Val
103	Val272Ala
104	Glu273Ala
105	Thr274Arg
106	Arg278Lys
107	Arg278Thr
108	Glu280Ala
109	Glu280Gly
110	Leu282Val

111	Leu282Arg
112	Pro284Leu
113	Ala285Val
114	Leu286Val
115	Deletions in intron 8
116	InsArg(g63786_63787)
117	Thr354Ile
118	Arg358Gln
119	Ser365Tyr
120	Arg377Met
121	Gly378Glu
122	Gly378Val
123	Leu381Val
124	Gly384Ala
125	Phe386Ser
126	Ser390Ile
127	Val391Phe
128	Leu392Val
129	Leu392Pro
130	Gly394Val
131	Asn405Ser
132	Ala409The
133	Cys410Tyr
134	Leu418Phe
135	Leu424His
136	Leu424Arg
137	Ala426Pro
138	Ala431Glu
139	Ala431Val
140	Ala434Cys
141	Leu435Phe
142	Pro436Ser
143	Pro436Gln
144	Ile439Val
145	DelThr440

Thus, in one embodiment the non-human animal model expressing at least one phenotype associated with Alzheimer's disease due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human PSEN1 gene, mRNA and/or protein (see SEQ ID NO:7, SEQ ID NO:8), comprises at least one mutation yielding the amino acid mutations as described in table 4.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with Alzheimer's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine PSEN1 gene, mRNA and/or protein (see SEQ ID NO:9, SEQ ID NO:10) or fragments or parts thereof, respectively) comprising at least one mutation yielding the amino acid mutations as described in table 4 It is appreciated that the at least one mutation is present in the gene fragment or DNA fragment, RNA fragment or protein part. In particular the mutated porcine PSEN1 protein with SEQ ID NO: 11 is used to produce a pig model for Alzheimer's disease.

The non-human animal model for ALS may be generated by introduction of said at least one genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for Alzheimer's disease is generated by sperm mediated gene transfer.

According to the present invention a pig model for Alzheimer's disease is in one embodiment produced by sperm mediated gene transfer of the mutated porcine PSEN1 as described elsewhere herein. However, the pig model for Alzheimer's disease may also be produced by introducing the mutated PSEN1 or protein expressed thereof ((SEQ ID NO: 11) into a target cell.

Moreover, in one embodiment the non-human animal model expressing at least one phenotype associated with Alzheimer's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human PSEN2 gene, mRNA and/or protein (see SEQ ID NO:12, SEQ ID NO:13) comprises at least one mutation yielding the amino acid mutations as described in table 3.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with Alzheimer's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment

thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine PSEN2 gene, mRNA and/or protein corresponding to SEQ ID NO:14, SEQ ID NO:15, or fragments or parts thereof, respectively) fitted with at least one mutation yielding the amino acid mutations as described in table 3. It is appreciated that the at least one mutation is present in the gene fragment or DNA fragment, RNA fragment or protein part. In particular the mutated porcine PSEN2 DNA with SEQ ID NO: 16 is used to produce a pig model for Alzheimer's disease.

The non-human animal model for ALS may be generated by introduction of said at least one genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for Alzheimer's disease is generated by sperm mediated gene transfer.

According to the present invention a pig model for Alzheimer's disease is in one embodiment produced by sperm mediated gene transfer of the mutated porcine PSEN1 as described elsewhere herein. However, the pig model for Alzheimer's disease may also be produced by introducing the mutated PSEN1 or protein expressed thereof into a target cell (SEQ ID NO: 16).

Furthermore, in yet another embodiment the non-human animal model expressing at least one phenotype associated with Alzheimer's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human APP gene, mRNA and/or protein (SEQ ID NO:17, SEQ ID NO:18) comprises at least one mutation yielding the amino acid mutations as described in table 2. Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with Alzheimer's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine APP gene, mRNA and/or protein corresponding to SEQ ID NO:19, SEQ ID NO:20, or fragments or parts thereof,)comprising at least one mutation yielding the amino acid mutations as described in table 2. It is appreciated that the at least one mutation is

present in the gene fragment or cDNA fragment, RNA fragment or protein part. In particular the mutated porcine APP DNA is used to produce a pig model for Alzheimer's disease.

The non-human animal model for Alzheimer's disease may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell.

In one particular embodiment the non-human animal model for Alzheimer's disease is generated by sperm mediated gene transfer.

According to the present invention a pig model for Alzheimer's disease is in one embodiment produced by sperm mediated gene transfer of the mutated porcine APP as described elsewhere herein. However, the pig model for Alzheimer's disease may also be produced by introducing the mutated APP or protein expressed thereof into a target cell (SEQ ID NO: 21).

It is within the scope of the present invention that at least one mutation yielding the amino acid mutation homologous to the human PSEN1, PSEN2 and/or APP as listed in table 4, 3, and/or 2 is comprised in the human or porcine PSEN1, PSEN2 and/or APP gene or DNA, RNA or proteins of the present invention, such as for example at least two mutations, at least three mutations, at least four mutations, at least five mutations, at least six mutations, at least seven mutations, at least eight mutations, at least ten mutations, at least fifteen mutations yielding the amino acid mutation homologous to the human PSEN1, PSEN2 and/or APP as listed in table 4, 3, and/or 2. It is appreciated that one or more of the genes and mutations thereof may be combined in an animal model for example a pig model for Alzheimer's disease.

The non-human animal model for Alzheimer's disease, in particular the pig model for Alzheimer's disease, will typically develop at least one of the symptoms described above such as progressive memory loss and severe dementia in advanced cases which can be monitored by behavioural studies. Evidence also exists for the impairment of olfactoric sense which can be monitored by behavioural changes. Furthermore, scannings of the brain of the animal models by magnetic resonance

and/or positron emission tomography can also be employed to determine whether the animal model is indicative for Alzheimer's disease.

Parkinson's disease

In one embodiment of the present invention the non- human animal model expresses at least one phenotype associated with Parkinson's disease. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with Parkinson's disease.

"Parkinson´s disease" is used herein to refer to an inherited condition usually associated with the following symptoms - all of which result from the loss of dopamine-producing brain cells: tremor or trembling of the arms, jaw, legs, and face; stiffness or rigidity of the limbs and trunk; bradykinesia - slowness of movement; postural instability, or impaired balance and coordination.

Parkinson's disease (PD) is a common progressive neurodegenerative disease affecting 1-2% of the population over 60 years of age. The number of PD affected individuals reaches a maximum value between 70 and 79 years of age with a mean age of onset between 60 and 65 years (1). The cardinal clinical symptoms of PD are resting tremor, bradykinesia, rigidity and postural instability. The pathological manifestations of PD are characterized by degeneration of dopaminergic neurons in the substantia nigra pars compacta and the presence of so called Lewy bodies in degenerating neurons. Lewy bodies are cytoplasmic protein inclusions and the main constituent is the protein α-synuclein. Lewy bodies are required for a pathological diagnosis of PD but can also be observed in other neurodegenerative diseases. Degeneration of dopaminergic neurons results in decreased production of dopamine and the lack of this signal substance is responsible for bradykinesia and rigidity. The etiology of PD is largely unknown but is probably due to both genetic and environmental factors. Impaired mitochondrial function, changes in protein sorting by the ubiquitin-proteasome pathway and facilitated apoptosis may all represent factors associated with development of PD (2). Environmental factors suggested are exposure to pesticides and heavy metals (3).
Most cases of PD are sporadic but 5-10% of cases are caused by genetic mutations.

Several transgenic animal models of PD have been established including nematodes (C. elegans), Drosophila, mice and rats and different PD associated genes. Several limitations to the mice models have been observed, including the absence of loss of nigrostriatal dopaminergic neurons in some of the models suggesting that a better animal model would be of advantage regarding the study of the factors involved in PD pathology and underlying mechanisms.

The following genes are linked to Parkinson´s disease:
Alpha synuclein (SNCA, NM_000345),
Ubiquitin C-terminal hydrolase (UCHL1, NM_004181),
Leucine rich repeat kinase (LRRK2, NM_198578).

The below indicated substitutions are believed to be relevant regarding transgenic porcine models for Parkinsons's disease.

Table 5: Mutations causing Parkinson´s disease in SNCA (NM_000345)

Mutation #	Mutation
1	Ala30Pro
2	Glu46Lys
3	Ala53Thr

Table 6: Mutations causing Parkinson´s disease in UCHL1 (NM_004181)

Mutation #	Mutation
1	Ser18Tyr
2	Ile93Met

Table 7: Putative pathogenic mutations causing Parkinson´s disease in LRRK2 (NM_198578)

Mutation #	Mutation
1	Arg793Met
2	Gln930Arg
3	Arg1067Gln
4	Ser1096Cys
5	Ser1228Thr

6	Ile1371Val
7	Arg1441His
8	Arg11514Gln
9	Met1869Thr
10	Arg1941His
11	Thr2356Ile
12	Gly2385Arg

One aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with Parkinson's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human SNCA gene, mRNA and/or protein (SEQ ID NO:22, SEQ ID NO:23) comprises at least one mutation yielding the amino acid mutations as described in table 5.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with Parkinson's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine SNCA gene, mRNA and/or protein corresponding to SEQ ID NO:24, SEQ ID NO:25 or fragments or parts thereof, respectively) comprising at least one mutation yielding the amino acid mutations as described in table 5. It is appreciated that the at least one mutation is present in the gene fragment or DNA fragment, RNA fragment or protein part. In particular the mutated porcine SNCA cDNA with SEQ ID NO: 26 is used to produce a pig model for Parkinson's disease.

The non-human animal model for ALS may be generated by introduction of said at least one genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for Parkinson's disease is generated by sperm mediated gene transfer.

According to the present invention a pig model for Parkinson's disease is in one embodiment produced by sperm mediated gene transfer of the mutated porcine SNCA (SEQ ID NO:26) as described elsewhere herein. However, the pig model for Parkinson's disease may also be produced by introducing the mutated SNCA DNA (SEQ ID NO: 26) or protein expressed thereof into a target cell SEQ ID NO: 27).

Moreover, in one embodiment the non-human animal model expressing at least one phenotype associated with Parkinson's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human UCHL1 gene, mRNA and/or protein (SEQ ID NO:28, SEQ ID NO:29) comprises at least one mutation yielding the amino acid mutations as described in table 6.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with Parkinson's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine UCHL1 gene, mRNA and/or protein or fragments or parts thereof comprising at least one mutation yielding the amino acid mutations as described in table 6. It is appreciated that the at least one mutation is present in the gene fragment or DNA fragment, RNA fragment or protein part. In particular the mutated porcine UCHL1 DNA is used to produce a pig model for Parkinson's disease.

The non-human animal model for Parkinson's disease may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell.

In one particular embodiment the non-human animal model for Parkinson's disease is generated by sperm mediated gene transfer.

According to the present invention a pig model for Parkinson's disease is in one embodiment produced by sperm mediated gene transfer of the mutated porcine UCHL1 as described elsewhere herein. However, the pig model for Parkinson's disease may also be produced by introducing the mutated UCHL1 or protein expressed thereof into a target cell.

Furthermore, in yet another embodiment the non-human animal model expressing at least one phenotype associated with Parkinson's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human LRRK2 gene, mRNA and/or protein (SEQ ID NO:30, SEQ ID NO:31) comprises at least one mutation yielding the amino acid mutations as described in table 7.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with Parkinson's disease due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine LRRK2 gene, mRNA and/or protein or fragments or parts thereof, respectively) fitted with at least one mutation yielding the amino acid mutations as described in table 7. It is appreciated that the at least one mutation is present in the gene fragment or DNA fragment, RNA fragment or protein part. In particular the mutated porcine LRRK2 DNA is used to produce a pig model for Parkinson's disease.

The non-human animal model for Parkinson's disease may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell.

In one particular embodiment the non-human animal model for Parkinson's disease is generated by sperm mediated gene transfer.

According to the present invention a pig model for Parkinson's disease is in one embodiment produced by sperm mediated gene transfer of the mutated porcine LRRK2 as described elsewhere herein. However, the pig model for Alzheimer's disease may also be produced by introducing the mutated LRRK2 or protein expressed thereof into a target cell.

It is within the scope of the present invention that at least one mutation yielding the amino acid mutation homologous to the human SNCA, UCHL1 and/or LRRK2 as listed in table 5, 6 and/or 7 is comprised in the human or porcine SNCA, UCHL1 and/or LRRK2 gene or DNA, RNA or proteins of the present invention, such as for example at

least two mutations, at least three mutations, at least four mutations, at least five mutations, at least six mutations, at least seven mutations, at least eight mutations, at least ten mutations, at least fifteen mutations yielding the amino acid mutation homologous to the human SNCA, UCHL1 and/or LRRK2 as listed in table 5, 6 and/or 7. It is appreciated that one or more of the genes and mutations thereof may be combined in an animal model for example a pig model for Parkinson's disease.

The non-human animal model for Parkinson's disease, in particular the pig model for Parkinson's disease, will typically develop at least one of the symptoms described above such as symptoms - all of which result from the loss of dopamine-producing brain cells: tremor or trembling of the jaw, legs, and face, stiffness or rigidity of the limbs and trunk, bradykinesia - slowness of movement; postural instability, or impaired balance and coordination.

Trinucleotide repeat (TNR) disorders

In one embodiment of the present invention the non- human animal model expresses at least one phenotype associated with diseases related to trinucleotide repeat disorders. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with diseases related to trinucleotide repeat disorders.

Trinucleotide repeat disorders or expansion disorders are caused by stretches of DNA in a gene that contain the same trinucleotide sequence repeated many times. Unstable microsatellite repeats are found throughout all genomic sequences and TNRs constitute a subset of such unstable repeats.

Nucleotide repeat instability is associated with more than 40 inherited neurodegenerative, neuromuscular, and mental retardation disorders in humans [2,3]. The nucleotide repeat instability process is a dynamic process, where mutations continue to recur during meiosis and in mitotic tissue [3]. Long stretches of repeats are more likely to expand than short stretches of repeats and the length is correlated with age of onset and the severity of disease, a phenomen called anticipitation [3]. Diseases caused by trinucleotide repeat (TNR) instability can be divided into two groups. In the first group the TNRs reside in the untranslated part of the affected genes. The untranslated TNR expansions, constituting either CTGs, CAGs, GAAs, or CGGs, result

in an RNA gain-of-function that may alter the gene expression control of the affected genes or have *cis* and *trans* effects on splicing and gene regulation at the chromatin level [4-7]. Expanded noncoding TNRs have been identified as causative mutations in disorders including Friedreich ataxia, spinocerebellar ataxia 8 (SCA-8), SCA-12, myotonic dystrophy, and fragile–X syndromes [3].

In the second group the TNRs are located in the coding region of the transcript. This type of TNRs are translated in frame of the coding region and expansions include GAC encoding poly-aspargine, GCG encoding poly-alanine, and the most commonly identified CAG TNRs encoding poly-glutamine [3]. Expanded CAG TNRs, are identified as causative mutations in disorders, including SCA-1, SCA-2, SCA-3, SCA-6, SCA-7, SCA17, Huntington's disease, spinal and bulbar muscular atrophy (SBMA), and dentatorubral pallidoluysian atrophy (DRPLA). In these disorders cytoskeletal and vesicular functions are affected as well as the regulation of cellular gene expression due to the sequestering of transcriptional regulatory proteins.

The molecular mechanisms responsible for TNR instability are not completely elucidated. The degree of tissue-specific and inherited TNR instability is determined by both the specific *cis*-sequences within the affected genes and *trans*-functioning metabolic proteins as for example DNA repair proteins [3]. TNR instability probably involves the formation of specific DNA structures during DNA replication, repair and recombination [8]. Slippage during DNA replication is the best characterized mechanism. The direction of DNA replication through the TNR tract also affects the stability [9-11]. In addition to the TNR itself, the sequence environment of the repeat contributes to the mechanism of instability, and, for example, similar CAG tract lengths show different stability depending on the genomic context [3, 12]. In the human population the length of TNR repeat tracts is polymorphic but stably transmitted [13]. Beyond a certain TNR length, which appears to be gene specific, the TNR tract becomes unstable [3]. An unstable TNR tract that has not yet expanded to a size sufficient for the full disease phenotype is called a premutation [2]. However, TNR expansions of the premutation size in for example *FMR1* have been shown to result in a specific disease phenotype of late onset. The genetic instability of TNRs is related to the repeat tract length and expanded tracts have increased risk of being affected by a subsequent expanding mutation than the original tract [2, 3, 14]. Also TNR interruptions, as for example CAA triplets in CAG TNRs, play an important role

conferring TNR stability and their absence predisposes alleles towards instability and pathological expansions [15]. A large level of somatic and transmitted instability is observed for premutation and fully expanded TNR tracts [2, 3]. The fully expanded and disease causing TNR tracts can be composed of approximately twenty TNRs as observed in *SCA-6* to several thousands as observed in for example myotonic dystrophy [2, 3]. Interestingly, it was recently shown that an induced level of transcription promotes contraction of TNR tracts in human cells [16]. Furthermore, transgenic animal models of TNR instability also points out the importance for specific TNR flanking sequences to create TNR instability [9, 17, 18].

One embodiment of the present invention relates to a non-human animal model expressing at least one phenotype associated with myotonic dystrophy. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with myotonic dystrophy.

Myotonic dystrophy is caused by TNR in the 3´-UTR of the human myotonic dystrophy protein kinase gene, DMPK, where a CTG TNR is located [19-23]. The normal size of this TNR varies between 5 and 37. Expansions from above 50 to several thousand CTG repeats result in myotonic dystrophy.

One aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with myotonic dystrophy due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human myotonic dystrophy protein kinase gene, DMPK gene, mRNA and/or protein (SEQ ID NO:32, SEQ ID NO:33), wherein the number of CTG repeats is at least 40, 45, 50 or at least 60.

Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with myotonic dystrophy due to the introduction of a genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human DMPK gene, mRNA and/or protein or fragments or parts thereof, respectively), wherein the number of CTG repeats in the DNA is at least 40, 45, 50 or at least 60.

The non-human animal model for myotonic dystrophy may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for myotonic dystrophy is generated by sperm mediated gene transfer.
According to the present invention a pig model for myotonic dystrophy is in one embodiment produced by sperm mediated gene transfer of the human or porcine DMPK gene, mRNA and/or protein, wherein the number of CTG repeats in the DNA is at least 40, 45, 50 or at least 60. However, the pig model for myotonic dystrophy may also be produced by introducing the human or porcine DMPK gene, mRNA and/or protein, wherein the number of CTG repeats in the DNA is at least 40, 45, 50 or at least 60, or protein expressed thereof into a target cell.

The non-human animal model for myotonic dystrophy, in particular the pig model for myotonic dystrophy, will typically develop at least one of the symptoms such as generalized weakness and muscular wasting that affects the face and neck; difficulty with the feet that spreads to the legs, shoulders and hips. Other symptoms include a wasting of the muscles (muscular dystrophy), opacity of the lens of the eyes (cataracts), heart conduction defects and myotonia (difficulty in relaxing muscles).

Fragile X syndrome
One embodiment of the present invention relates to a non-human animal model expressing at least one phenotype associated with fragile X syndrome. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with fragile X syndrome.

Fragile X syndrome is caused by repeats in the promoter region of the human FMR1 gene, 6 to 52 CGG repeats are normally present [24, 25]. Expansions in the range of 55 to 200 repeats result in the pre- mutation while the full mutation ranges from 200 to several thousand repeats resulting in fragile X syndrome. Fragile X syndrome may also be by caused by CCG repeats in the TNR of the 5´end of the human FMR2 gene, wherein the number of repeats varies from 6 to 35 [26]. Expansions containing from 61

to 200 repeats result in the pre-mutation and expansions above 200 repeats result in the full mutation and the fragile X syndrome.

One aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with Fragile X syndrome due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human FMR1 gene/cDNA, mRNA and/or protein (SEQ ID NO:34, SEQ ID NO:35) wherein the number of CGG repeats is at least 55, 60, 70 or at least 200, and/or of the human FMR2 gene/cDNA, mRNA and/or protein (SEQ ID NO:36, SEQ ID NO:37) wherein the number of CCG repeats is at least 61, 65, 70, 80 or at least 200,

Similarly, one embodiment relates to the non-human animal model expressing at least one phenotype associated with fragile X syndrome due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human FMR1 gene/cDNA, mRNA and/or protein , wherein the number of CGG repeats is at least 55, 60, 70 or at least 200, and/or of the porcine homolog of the human FMR2 gene/cDNA, mRNA and/or protein, wherein the number of CCG repeats is at least 61, 65, 70, 80 or at least 200,

The non-human animal model for fragile X syndrome may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell.

In one particular embodiment the non-human animal model for fragile X syndrome is generated by sperm mediated gene transfer.
According to the present invention a pig model for fragile X syndrome is in one embodiment produced by sperm mediated gene transfer of the human or the porcine homolog of the human FMR1 gene/cDNA, mRNA and/or protein, fragments or part thereof, wherein the number of CGG repeats is at least 55, 60, 70 or at least 200, and/or the human or the porcine homolog of the human FMR2 gene/cDNA, mRNA and/or protein, fragment or part thereof, wherein the number of CCG repeats is at least 61, 65, 70, 80 or at least 200, However, the pig model for myotonic dystrophy may also

be produced by introducing the human or porcine FMR1 gene/cDNA, mRNA and/or protein, fragments or part thereof, wherein the number of CGG repeats is at least 55, 60, 70 or at least 200, and/or the human or the porcine homolog of the human FMR2 gene/cDNA, mRNA and/or protein, fragment or part thereof, wherein the number of CCG repeats is at least 61, 65, 70, 80 or at least 200, or protein expressed thereof into a target cell.

The non-human animal model for fragile X syndrome, in particular the pig model for fragile X syndrome, will typically develop at least one of the symptoms associated with autism. Non-limiting examples of symptoms of autism is for example repetitive behaviour and impairment in social interaction.

Spinocerebellar ataxia

One embodiment of the present invention relates to a non-human animal model expressing at least one phenotype associated with spinocerebellar ataxia. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with spinocerebellar ataxia.

Spinocerebellar ataxia (SCA12) is caused by repeats in the within the 5´-UTR of the human PPP2R2B gene and the number of CAG repeats normally varies in size from 7 to 28 and in the expanded form from above 65 to 78 TNRs [27].

Spinocerebellar ataxia (SCA 1) is caused by CAG repeats in the ATX1 protein. The human SCA1 TNR region is characterized by the presence of 12 CAG repeats followed by two CAT repeats flanking a CAG triplet [28]. The CAG TNR prone to expand is normally composed of between 6 and 39 repeats and the expanded version consists of 41 to 81 repeats.

Spinocerebellar ataxia (SCA 2) is caused by TNR expansions affecting the ATX2 protein. This TNR normally consists of 15 to 30 CAG repeats and the expanded form ranges from 35 to 59 triplets [29].

Spinocerebellar ataxia (SCA 3) is caused by a CAG TNR expansion in the human ataxin-3 gene, wherein the presence of above 54 repeats results in ataxia whereas the normal number of CAG repeats varies between 12 and 36 [30-32].

Spinocerebellar ataxia (SCA6) is caused by TNR expansion in the CACNA1A voltage dependent calcium channel results in ataxia [33]. The normal number of TNRs is between 4 and 18 and expansions from 21 to 27 TNRs are disease causative.

Spinocerebellar ataxia (SCA7) is caused by TNR of the human SCA7 locus in the N-terminal end of the ataxin-7 protein, which is normally composed of 7 to 35 CAG repeats [34]. Disease causing expansions range from 37 to 200 repeats.

Spinocerebellar ataxia (SCA17) is caused by a CAG expansion in the TATA box binding protein (TBP) gene and results in the SCA17 phenotype resulting in ataxia [35]. The human TNR region is composed of two groups of CAG repeats separated by multiple CAA and CAG triplets. Expansions normally progress from the larger of the two CAG groups. The normal stretch of encoded poly-glutamines varies between 29 and 42 whereas poly-glutamine stretches from 47 to 55 have been identified in SCA17 patients.

One aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with Spinocerebellar ataxia due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human PPP2R2B gene/cDNA, mRNA and/or protein (SEQ ID NO:38, SEQ ID NO:39), wherein the number of CAG repeats is at least 65, 70 or at least 75, and/or of the human ATX1 gene/cDNA, mRNA and/or protein (SEQ ID NO:40 SEQ ID NO:41), wherein the number of 12 CAG repeats followed by two CAT repeats flanking a CAG triplet is at least 41, 45, 50, 60, 70 or at least 80. The at least one genetic determinant may also be a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human ATX2 gene/cDNA, mRNA and/or protein (SEQ ID NO:42, SEQ ID NO:43), wherein the number of CAG repeats is at least 35, 40, 45, 50 or at least 55, and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human ataxin- 3 gene/cDNA, mRNA and/or protein (SEQ ID NO:44, SEQ ID NO:45), wherein the number of CAG repeats is at least 54 and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human CACNA1A gene/cDNA, mRNA and/or protein (SEQ ID NO:46, SEQ ID NO:47),

wherein the number of TNR expansions is at least 21, 22, 23, 24, 25, 26 or at least 27, or in the range of 21 to 27 repeats; and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human N-terminal end of the ataxin-7 protein encoding gene/cDNA, mRNA and/or protein (SEQ ID NO:48, SEQ ID NO:49), wherein the number of CAG expansions is at least 37, 45, 55, 65, or at least 100; and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human TATA box binding protein (TBP) gene/cDNA, mRNA and/or protein (SEQ ID NO:50, SEQ ID NO:51), wherein the number of poly-glutamine stretches as defined above is in the range of from 47 to 55 repeats.

Similarly, one embodiment relates to the non-human animal model expressing at least one phenotype associated with spinocerebellar ataxia due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human PPP2R2B gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 65, 70 or at least 75, and/or of the porcine homolog of the human ATX1 gene/cDNA, mRNA and/or protein, wherein the number of 12 CAG repeats followed by two CAT repeats flanking a CAG triplet is at least 41, 45, 50, 60, 70 or at least 80. The at least one genetic determinant may also be a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human ATX2 gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 35, 40, 45, 50 or at least 55, and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human ataxin- 3 gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 54 and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human CACNA1A gene/cDNA, mRNA and/or protein, wherein the number of TNR expansions is at least 21, 22, 23, 24, 25, 26 or at least 27, or in the range of 21 to 27 repeats; and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human N-terminal end of the ataxin-7 protein encoding gene/cDNA, mRNA and/or protein, wherein the number of CAG expansions is at least

37, 45, 55, 65, or at least 100; and/or the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human TATA box binding protein (TBP) gene/cDNA, mRNA and/or protein, wherein the number of poly-glutamine stretches as defined above is in the range of from 47 to 55 repeats.

The non-human animal model for spinocerebellar ataxia may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for spinocerebellar ataxia is generated by sperm mediated gene transfer.

According to the present invention a pig model for spinocerebellar ataxia is in one embodiment produced by sperm mediated gene transfer of the human or the porcine homolog of the human PPP2R2B gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 65, 70 or at least 75, and/or the porcine homolog of the human or the human ATX1 gene/cDNA, mRNA and/or protein, wherein the number of 12 CAG repeats followed by two CAT repeats flanking a CAG triplet is at least 41, 45, 50, 60, 70 or at least 80, and/or the human or the porcine homolog of the human ATX2 gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 35, 40, 45, 50 or at least 55, and/or the human or the porcine homolog of the human ataxin- 3 gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 54 and/or the human or the porcine homolog of the human CACNA1A gene/cDNA, mRNA and/or protein, wherein the number of TNR expansions is at least 21, 22, 23, 24, 25, 26 or at least 27, or in the range of 21 to 27 repeats; and/or the human or the porcine homolog of the human N-terminal end of the ataxin-7 protein encoding gene/cDNA, mRNA and/or protein, wherein the number of CAG expansions is at least 37, 45, 55, 65, or at least 100; and/or the human or porcine homolog of the human TATA box binding protein (TBP) gene/cDNA, mRNA and/or), wherein the number of poly-glutamine stretches as defined above is in the range of from 47 to 55 repeats.

However, the pig model for spinocerebellar ataxia may also be produced by introducing the human or porcine homolog of PPP2R2B, ATX1, ATX2, ataxin- 3, CACNA1A, ataxin-7 and/or TATA box binding protein (TBP) in any combination.

The non-human animal model for spinocerebellar ataxia, in particular the pig model for spinocerebellar ataxia, will typically develop at least one of the symptoms such as atrophy of the cerebellum which can be seen by magnetic resonance imaging and/or poor coordination of movement.

Dentatorubral-pallidoluysian atrophy (DRPLA)

One embodiment of the present invention relates to a non-human animal model expressing at least one phenotype associated with DRPLA. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with DRPLA.

DRPLA is caused by CAG expansions within the human atrophin-1 gene results in dentatorubral-pallidoluysian atrophy (DRPLA) [36]. The normal range of repetitive CAG repeats is from 3 to 25, and in patients with DRPLA allele sizes have expanded to 49 to 88 CAG repeats. The most common natural occurring human allele encodes a stretch of 17 poly-glutamines.

Thus, one aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with DRPLA due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human atrophin-1 /cDNA, mRNA and/or protein (SEQ ID NO:52, SEQ ID NO:53), wherein the number of CAG repeats is at least 49, 55, 60, 70 or at least 80 repeats.

Similarly, one embodiment relates to the non-human animal model expressing at least one phenotype associated with DRPLA due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the human atrophin-1 gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 49, 55, 60, 70 or at least 80 repeats.

The non-human animal model for DRPLA may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for

example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for DRPLA is generated by sperm mediated gene transfer.
According to the present invention a pig model for DRPLA is in one embodiment produced by sperm mediated gene transfer of the human or the porcine homolog of the human atrophin-1 gene/cDNA, mRNA and/or protein, fragments or part thereof), wherein the number of CAG repeats is at least 49, 55, 60, 70 or at least 80 repeats.

However, the pig model for DRPLA may also be produced by introducing the human or porcine homolog of the human atrophin-1 gene/cDNA, mRNA and/or protein, fragments or part thereof, wherein the number of CAG repeats is at least 49, 55, 60, 70 or at least 80 repeats, or protein expressed thereof into a target cell.

The non-human animal model for DRPLA, in particular the pig model for ALS, will typically develop at least one of the symptoms epileptic seizures, myoclonus, ataxia, and dementia.

Spinal and bulbar muscular atrophy (SBMA)
One embodiment of the present invention relates to a non-human animal model expressing at least one phenotype associated with SBMA. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with SBMA.

SBMA is caused by CAG repeat expansions in exon 1 of the androgen receptor (AR) gene on the X-chromosome results in spinal and bulbar muscular atrophy (Kennedy's disease) [37]. The normal length of the human CAG TNR is between 11 and 33 CAG copies and in diseased individuals the expansion ranges from 38 to 62.

Thus, one aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with SBMA due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human AR gene/cDNA, mRNA and/or protein (SEQ ID NO:54, SEQ ID

NO:55), wherein the number of CAG repeats is at least 38, 45, 50, 55 or at least 60, or in the range of 38 to 62 repeats.

Similarly, one embodiment relates to the non-human animal model expressing at least one phenotype associated with SBMA due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the the human AR gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 38, 45, 50, 55 or at least 60, or in the range of 38 to 62 repeats.

The non-human animal model for SBMA may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for SBMA is generated by sperm mediated gene transfer.
According to the present invention a pig model for SBMA is in one embodiment produced by sperm mediated gene transfer of the human or the porcine homolog of the human human AR gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 38, 45, 50, 55 or at least 60, or in the range of 38 to 62 repeats.

However, the pig model for SBMA may also be produced by introducing the human or porcine homolog of the human human AR gene/cDNA, mRNA and/or, wherein the number of CAG repeats is at least 38, 45, 50, 55 or at least 60, or in the range of 38 to 62 repeats, or protein expressed thereof into a target cell.

The non-human animal model for SBMA, in particular the pig model for SBMA, will typically develop at least one of the symptoms: uncontrollable twitching (fasciculations) followed by weakness and wasting of the muscles becomes apparent sometime after the age of fifteen. The muscles of the face, lips, tongue, mouth, throat, vocal chords, trunk and limbs may be affected.

Huntington's disease (HD)

One embodiment of the present invention relates to a non-human animal model expressing at least one phenotype associated with HD. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with HD.

"Huntington's disease" (also known as Huntington chorea) is used herein to refer to any inherited condition characterized by abnormal and/or uncontolled body movements, mental and emotional problems, and loss of thinking ability (cognition).

Adult-onset Huntington disease, the most common form of this disorder, usually begins in middle age. Signs and symptoms can include irritability, depression, small involuntary movements, poor coordination, and trouble learning new information or making decisions. As the disease progresses, involuntary jerking movements (chorea) become more pronounced. Affected individuals may have trouble walking, speaking, and swallowing. People with the disorder also typically experience changes in personality and a decline in thinking and reasoning abilities. Individuals with this form of Huntington disease generally survive about 15 to 25 years after onset.

There is also an early-onset form of Huntington disease that begins in childhood or adolescence. Some of the clinical features of this disease differ from those of the adult-onset form. Signs and symptoms can include slowness, clumsiness, rigidity, loss of developmental milestones (such as motor skills), slow speech, and drooling. Seizures occur in 30 percent to 50 percent of individuals with this condition. The course of early-onset Huntington disease may be shorter than adult-onset Huntington disease; affected individuals generally survive 10 to 15 years after onset.

Huntington´s disease in humans is linked to the Huntingtin gene (HD gene, accession number: NM_002111). The function of the corresponding protein is not yet known, but it likely plays an important role in nerve cells. The disease causing mutation in Huntington´s disease is an extension of a CAG repeat, to a length above 35 CAG units. The number of repeats can to a certain extent be correlated with disease onset.

The expanded repeat leads to the production of a huntingtin protein that contains a long stretch of the amino acid glutamine. The elongated protein disrupts the normal function of nerve cells in certain parts of the brain, and ultimately leads to the death of

those cells. The dysfunction and loss of nerve cells cause the signs and symptoms of Huntington disease.

Thus, one aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with HD due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human Huntingtin gene/cDNA, mRNA and/or protein (SEQ ID NO:56, SEQ ID NO:57), wherein the number of CAG repeats is at least 35, 45, 50, 55 or at least 60.

Similarly, one embodiment relates to the non-human animal model expressing at least one phenotype associated with HD due to the introduction of at least one genetic determinant, wherein the at least one genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine homolog of the the human Huntingtin gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 35, 45, 50, 55 or at least 60.

The non-human animal model for HD may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for HD is generated by sperm mediated gene transfer.
According to the present invention a pig model for HD is in one embodiment produced by sperm mediated gene transfer of the human or the porcine homolog of the human human Huntingtin gene/cDNA, mRNA and/or protein, wherein the number of CAG repeats is at least 35, 45, 50, 55 or at least 60.

However, the pig model for HD may also be produced by introducing the human or porcine homolog of the human human huntingtin gene/cDNA, mRNA and/or, wherein the number of CAG repeats is at least 35, 45, 50, 55 or at least 60; or protein expressed thereof into a target cell.

The non-human animal model for HD, in particular the pig model for HD, will typically develop at least one of the symptoms described above such as slowness, clumsiness, rigidity, loss of developmental milestones (such as motor skills), slow speech, and drooling or seizures.

Dyschondroplasia (Collagen X type)

In one embodiment of the present invention the non- human animal model expresses at least one phenotype associated with dyschondroplasia. In a particular aspect the non-human animal model is a pig model expressing at least one phenotype associated with dyschondroplasia.

Chondrodysplasias are a group of disorders affecting the skeleton and are often associated with proteins of the collagen superfamily constituting at least 19 different types of collagen, these being major components of cartilages throughout the mammalian organism implicating roles in the processes of calcification and ossification [38]. One third of the collagens (types I, II, III, V, and IX) are denoted fibrillar collagens due to their tissual status as long, highly organised fibers. The remaining two thirds of the collagens are nonfibrillar and are further divided into two groups; the fibril associated with interrupted helices and the network forming collagens [39]. Collagen X belongs to the group of network forming collagens and has been reported to be expressed mainly in the hypertrophic region of growth plate cartilage [40], and has only rarely been detected in calcifying region of articular cartilage [41].

Type X collagen has been suggested to be structurally important in the extracellular matrix by offering the molecular milieu essential for endochondral bone formation [40]. Furthermore, it has been shown that type X collagen exists in ostechondrotic and osteoarthritic porcine articular cartilage and it may be a product of the cell population trying to repair the breakdown [41]. However, in osteochondrosis the endochondral ossification is impaired regardless of the unaltered collagen X levels in the growth plate and the increase of said collagen in articular cartilage. This could indicate that type X collagen alone is not able to cause ossification of cartilage [41]. Moreover, it has previously been shown, in a naturally occurring porcine model, that a mutation in the porcine noncollagenous domain 1 (NC1) of collagen X causes a phenotype similar to the human dwarfism Schmid metaphyseal chondrodysplasia (SCMD) [42]. Said cartilage disorder is an autosomal dominant disease which characteristics are short

stature, coxa vara, and a waddling gait, and histopathological examinations show an extremely irregular organisation of the growth plate in long bones [43,44].

Transgenic animals are important tools as model organisms in basic research as well as in applied scientific areas and they have now been used for several years to study for instance gene function and human diseases. In relation to transgenesis, collagen X offers a unique opportunity regarding the detection of transgene expression, since wild type collagen X is almost selectively expressed in chondrocytes, making the detection of transgene expression in other tissues uncomplicated and hence easy to ascribe to the transgenic procedure.

One aspect of the present invention thus relates to a non-human animal model expressing at least one phenotype associated with dyschondroplasia due to the introduction of at least one genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the human COL10 A1 gene, mRNA and/or protein (SEQ ID NO:58, SEQ ID NO:59) being present in at least a transient manner.
Similarly, in one embodiment the non-human animal model expressing at least one phenotype associated with dyschondroplasia due to the introduction of a genetic determinant, wherein the genetic determinant is a gene or DNA or fragment thereof, and/or RNA or fragment thereof and/or protein or part thereof of the porcine COL10A1 gene, mRNA and/or protein corresponding to SEQ ID NO:60, SEQ ID NO:61 or fragments or parts thereof, being present in at least a transient manner.

The non-human animal model for dyschondroplasia may be generated by introduction of said genetic determinant into a target cell by any method available to the skilled person, for example by injection into the target cell, or by virus-mediated transfer or any method suitable as known by the skilled person.

In one particular embodiment the non-human animal model for dyschondroplasia is generated by sperm mediated gene transfer.

According to the present invention a pig model for dyschondroplasia is in one embodiment produced by sperm mediated gene transfer of the constitutively expressed porcine COL10A1 of porcine or human origin as described elsewhere herein. However,

the pig model for dyschondroplasia may also be produced by introducing the COL10A1 DNA or protein expressed thereof into a target cell.

The non-human animal model for dyschondroplasia, in particular the pig model for dyschondroplasia, will typically develop at least one of the symptoms described above such as disorders involving tubular bones, and characterized by a neoplasmlike proliferation of cartilage in the metaphyses that cause distorted growth in length or pathological fractures.

Non-human animals

The present invention relates to a non-human animal serving as a disease model for autosomal dominant disorders, for example neurodegenerative diseases such as protein conformation diseases such as listed elsewhere herein.

In one embodiment the non-human animal model may be any model with the proviso that the animal is not a rodent such as rat, mouse or hamster. The non-human animal is selected from the group consisting of ape, monkey, cattle, pig, sheep, goat, horse, donkey.

In a special embodiment of the present invention the non-human animal model is a pig. In one embodiment the pig presenting the pig model is a wild pig. In another embodiment the pig is the domestic pig, Sus scrofa, such as S. domesticus. In yet another embodiment the invention relates to mini pigs, as well as to inbred pigs. The pig can be selected e.g. from the group consisting of Landrace, Yorkshire, Hampshire, Duroc, Chinese Meishan, Berkshire and Piêtrain, such as the group consisting of Landrace, Yorkshire, Hampshire and Duroc, for example the group consisting of Landrace, Duroc and Chinese Meishan, such as the group consisting of Berkshire, Pietrain, Landrace and Chinese Meishan, for example the group consisting of Landrace and Chinese Meishan. In one embodiment, the pig is not a mini-pig.

In another embodiment of the present invention the pig is a mini-pig and the mini-pig is preferably selected from the group consisting of Goettingen, Yucatan, Bama Xiang Zhu, Wuzhishan and Xi Shuang Banna.

One aspect of the present invention relates to a non-human animal model produced by sperm-mediated gene transfer. The method of sperm mediated gene transfer of the

present invention for the production of a non-human animal model for studying a hereditary autosomal dominant disease and/or for the production of a pig model for studying amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, diseases associated with trinucleotide repeats, Huntington's chorea and/or dyschondroplasia comprises the steps of i) providing semen from a male, non-human animal ii) providing a genetic determinant capable of establishing said hereditary disease when the genetic determinant is expressed in said non-human animal model iii) contacting said semen and said genetic determinant iv) fertilising an oocyte from a female, non-human animal with the semen and the genetic determinant and v) incubating said fertilised oocyte under conditions allowing said fertilised oocyte to develop into said non-human animal model.

The semen for the method is provided from a male, non-human animal, in particular a boar. The selection of the sperm donor boars is crucial for the outcome of the procedure. The boars of choice are selected so that the initial sperm motility is ≥90 %. Preferably the semen is fresh and collected in sterile 10 mL tubes and transported undiluted at a temperature not below 15°C as this will cause damage to the sperm cells. The quality of the sperm cell and thus the efficiency of the sperm-mediated gene transfer procedure is affected by numerous factors such as season of year, collection frequency, breed and age of the donor. In order to choose the correct donor cells, the sperm cells from the different boars are examined under a light microscope. The sperm cells originating from the boar having the highest sperm cell motility after the washing procedure are chosen. Next, the sperm cells from the boar of choice are counted. It is important for the present invention that the sperm cell motility is maintained following the removal of seminal fluid.

In one embodiment the boar has abstained for 1 to 10 days, 2-8 days, 1-2 days or in a particular embodiment of the invention the donor boar has abstained for 2 days prior to collecting the semen to be employed in the procedure.

The mechanism of internalization of foreign DNA involves specific proteins capable of binding DNA in a CD4-like manner to sperm heads. The proteins of 30-35 kDa have been identified in a variety of species such as mice, cattle, pig and humans. However, under normal conditions the seminal fluid strongly protects the sperm cells from foreign DNA by antagonizing the binding of the DNA to be internalized. The main antagonist is

inhibitory factor 1 (IF-1). Accordingly, the antagonist has to be removed or neutralised before the sperm is used in sperm-mediated gene transfer procedures. Therefore, in one embodiment of the present invention the seminal fluid is removed from the spermatozoa for example by washing.

Ejaculated spermatozoa will under normal conditions capacitate which means that the spermatozoa undergo physiological changes rendering the cells able to fertilise. Therefore, in one embodiment of the present invention the sperm-mediated gene transfer method the initiation of the sperm – DNA interaction should be started shortly after removal of the seminal fluid (for example during the washing step of the procedure). In another embodiment, in order to facilitate capacitation and correct sperm-DNA incubation time, the applied buffer is calcium free as calcium under normal conditions promotes capacitation. Additionally, the absence of calcium prevents endonucleases from acting on the foreign DNA. Thus, in a particular embodiment of the invention the sperm is washed in a buffer devoid of calcium. In a further particular embodiment the washing buffer comprises the following components are 56.1 g Glucose, 3.5 g EDTA ($2H_20$), 3.5 g Sodium citrate, 1.1 g Sodium bicarbonate (for 1 liter of buffer) dissolved in water and the solution is sterilized through a filter. Before the buffer is added to the sperm cells, 6 mg/ml BSA (Bovine Serum Albumine, Fraction V, Sigma) is added.

One preferred washing procedure according to the present invention is accomplished as fast as possible as follows: 5 mL sperm is transferred to a 50 mL tube and 5 mL washing buffer preheated to 37°C is added, mix by inverting the tubes. The solution is incubated for 5 min at room temperature (approximately 22 °C) and 40 mL buffer (room temperature) is added. Upon centrifugation at 800 g, for 10 min at 25°C the supernatant is removed and the pellet resuspended in 50 mL buffer (room temperature). The mixture is subjected to centrifugation at 800 g, for 10 min at 17°C and the supernatant is removed. The pellet is carefully resuspended in the remaining buffer in the tube.

When the genetic determinant has been provided the semen is contacted with the genetic determinant. Sperm cells are diluted in buffer as described above for the washing of sperm cells. In one embodiment the buffer temperature is in the range of 15°C to 25°C, and in particular the temperature is 17°C. The genetic determinant in the

form of DNA is added to the diluted sperm cells. The concentration of the genetic determinant is in the range of 0.1µg to 1 µg per 10^6 sperm cells. In a particular embodiment the genetic determinant is linearised DNA added in a concentration of 0.4 µg linearised DNA/10^6 sperm cells.

In one particular embodiment the following procedure is used:
10^9 sperm cells are diluted into 120 mL 17°C buffer
0.4 µg linearised DNA/10^6 sperm cells is added (that is, a total of 400 µg linearised DNA)
Incubate 100 min at 17°C
To avoid sedimentation of the cells, invert the tube every 20 min
Transfer the tube to room temperature, and transport it (at room temperature) to animal houses or stable facilities (approx. 10 minutes.)

The incubated sperm cells are now ready to be applied in artificial insemination methods.

The non-human animal model and in particular the pig models of the present invention may be produced by methods other than sperm mediated gene transfer, for example by pronuclear microinjection, somatic cell nuclear transfer, or retrovirus mediated gene transfer.

A further aspect of the present invention pertains to a non-human sperm cell comprising at least one genetic determinant exerting at least one dominant phenotype for at least one hereditary disease when expressed in a non-human animal host organism. The non-human sperm cell may originate from any of the animals listed elsewhere herein. As described in detail elsewhere herein the genetic determinant is of mammalian origin, for example of human and/or porcine origin. The non-human sperm cell may be a non-human sperm cell exerting an autosomal dominant phenotype for a hereditary disease such as any of the diseases according to the present invention. The non-human host organism is any of the animals presented herein, and in particular a pig.
The non-human sperm cell according to the present invention may be produced by a method comprising the steps of a) providing a non-human sperm cell, b) providing at least one genetic determinant exerting a dominant phenotype for a hereditary disease

when expressed in a non-human animal host organism, c) contacting said non-human sperm cell and said at least one genetic determinant, wherein said contacting results in the uptake of the genetic determinant into the non-human sperm cell.

A further aspect of the invention relates to a composition comprising a non-human sperm cell in combination with at least ond genetic determinant exerting at least one dominant phenotype for at least one hereditary disease when expressed in a non-human animal host organism. In preferred embodiments the genetic determinant is of human and/or porcine origin.

The present invention also discloses a method for fertilising an oocyte by sperm-mediated gene transfer. The method comprises the steps of providing the non-human sperm cell as carrying the at least one genetic determinant for a phenotype associated with autosomal dominant diseases as defined herein and introducing the non-human sperm cell into the oocyte to be fertilised. Consequently, another aspect of the invention relates to a method for fertilising an oocyte by sperm-mediated gene transfer, wherein the method comprises the steps of providing the composition as described herein and introducing the composition into the oocyte to be fertilised.

Therefore, the present invention also pertains to an embryo obtained by fertilising an oocyte with the non-human sperm cell comprising at least one genetic determinant exerting at least one dominant phenotype for at least one hereditary disease of the present invention when expressed in a non-human animal host organism. Similarly an embryo obtained by fertilising an oocyte with the composition as disclosed herein is within the scope of the present invention. Furthermore, as an embryo has been established the present invention offers a method for the cultivation and development of the embryo comprising the step of cultivating the embryo under conditions allowing the embryo to develop into a non-human animal offspring expressing said genetic determinant and exerting a dominant phenotype for a hereditary disease.

The presence of a non-human animal model of autosomal dominant diseases provides the opportunity of evaluating whether a given pharmaceutical composisiton, compound, treatment and/or drug has an effect on the phenotype of the given non-human animal. Therefore, it is within the scope of the present invention to provide for a method for evaluating the response of a therapeutical treatment of a hereditary disease, said

method comprising the steps of a) providing the non-human animal model according to the invention b) treating said non-human animal with at least one pharmaceutical composition exerting an effect on said at least one phenotype, and c) evaluating the effect observed. Additionally, the method also allows for a further step of advising on medical treatment of for example a human being suffering from an autosomal dominant disease such as a neurodegenarative diseases, protein conformation diseases such as ALS, Alzheimer's disease, HD, PD, trinucleotide repeat-associated diseases but also dyschondroplasia based on the effects observed during the method of evaluation .

In addition the availability of a non-human animal model expressing a particular phenotype associated with autosomal dominant diseases offers the ability of providing a method for screening the efficacy of a pharmaceutical composition, wherein the method comprises the steps of a) providing the non-human animal model of the present invention, b) expressing in said animal model said at least one genetic determinant and exerting said dominant phenotype for said hereditary disease, c) administering to said non-human animal the pharmaceutical composition the efficacy of which is to be evaluated, and d) evaluating the effect, if any, of the pharmaceutical composition on the phenotype exerted by the genetic determinant when expressed in the non-human model.

Furthermore, the present invention also relates to a method for treatment of a human being suffering from an autosomal dominant disease, wherein the method comprisies the initial steps of a) providing the non-human animal model of the present invention, b) expressing in said animal model said genetic determinant and exerting said dominant phenotype for said hereditary disease, c) treating said non-human animal with a pharmaceutical composition exerting an effect on said phenotype, d) evaluating the effect observed, and e) treating said human being suffering from said hereditary disease based on the effects observed in the non-human animal model.

Moreover, a method for linking a genetic determinant with the occurrence of a hereditary disease in a human being is also disclosed, said method comprising the steps of a) cultivating and developing an embryo obtained by fertilising an oocyte with a non-human sperm cell and a genetic determinant potentially constituting an autosomal dominant disease gene, for example a porcine gene exerting a dominant phenotype for a disease, such as a neurodegenerative disease when expressed in a non-human

animal host organism, wherein said cultivation and development result in the generation of an non-human animal offspring, and b) observing whether said genetic determinant confers said autosomal dominant disease in said non-human animal offspring.

Examples

Example 1

Transgenic Porcine Model of Amyotrophic Lateral Sclerosis (ALS)

In order to establish transgenic pigs which could serve as potential animal models for the human neurodegenerative disease ALS, a mutation, Gly93Arg, was introduced into the gene encoding porcine SOD1 by means of site directed mutagenesis. The choice of mutation was based on protein structural speculations, since the crystal structure of human SOD1 reveals an extremely condensed structure, showing that a substitution of the small relatively flexible glycine at position with the large charged arginine is likely to cause severe alteration in the protein. Furthermore, several different substitutions at this position cause ALS in humans including the G93R mutation [45,46]. In order to impede possible truncation of important elements in the DNA construct following the SMGT procedure the DNA fragment containing the porcine SOD1 cDNA contains additional nucleotides 5' – and 3' –prime to the CMV promoter and SVpolyA fragment. Totally, as shown in fig 1, the fragment used to make transgenic animals constitutes approximately 2100 bp.

RNA isolation and cDNA synthesis

Various porcine tissues were dissected from slaughtered pigs (Duroc boars and Landrace-Yorkshire sows (D X LY) and immediately frozen in liquid nitrogen and stored at -80°C. 100 mg of the tissue of choice was used for RNA isolation. RNA was isolated using the Nucleospin, Midi Kit from Macherey-Nagel.

cDNA synthesis was accomplished by mixing 1 µg of total RNA with 1 µL of oligo (dT)12-18 (500 µg/mL), and DEPC treated H20 to a final volume of 12 µL. The mixture was incubated at 70°C for 10 min, after which 4 µL of 5 x first-strand buffer, 2 µL of 0.1 mM DTT, 1µL of 10 mM dNTP mix and 1 µL (200 U/µL) of Superscript II (Invitrogen) was added and the sample was further incubated at 42°C for 1 hour followed by an inactivation step at 70°C for 15 min.

Sequencing genes of interest, including porcine SOD1

Based on homology search between the human SOD1 gene and an "in house" porcine EST database, 2 primers (SOD1_CDF and SOD1_CDR) were designed for amplification of the cDNA for the porcine SOD1 gene.The PCR reaction was performed in a total volume of 25 µL consisting of 2.5 µL of 10 x reaction buffer, 4 µL of dNTP (2.5 mM), 1 µL of both forward and reverse primer (10 pmol each), 1 µL 1 U/µL Dynazyme polymerase (Finnzymes), 2 µL cDNA template, and 13.5 µL H20.

The touchdown PCR reaction was performed in a GeneAmp® PCR System 9700 (Applied Biosystems) under the following conditions: Initial denaturation at 95°C for 3 min, denaturation at 95°C for 30 sec, touchdown from 63°C to 58°C with a decrement of 0.5°C for 30°C, followed by 1 min of elongation at 72°C per cycle. Furthermore 35 cycles of 30 sec denaturation at 95°C, 30 sec of annealing at 58°C, and 1 min of elongation at 72°C was included together with a final elongation step at 72°C for 7 min.

The primers used to amplify the SOD1 cDNA were:
SOD1_CDF: 5' –ATGGCGACGAAGGCCGTGT-3' (SEQ ID NO:62)
SOD1_CDR: 5' –TTACTGGGTGATCCCAATTACACCAC-3' (SEQ ID NO:63)

The PCR product was purified using QIAEX® II Gel Extraction Kit (Qiagen) from a 1 % Seakem agarose gel.

Amplicons were cloned into the pCR®2.1-TOPO vector (Invitrogen, CA) using manufactures recommendations and, applying standard procedures, clones were subsequently sequenced to ensure that they contained the SOD1 amplicon.

The porcine SOD1 cDNA sequence is shown in Fig. 1

Cycle sequencing reactions were accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) where an initial denaturation step at 95°C for 2 min, 99 cycles of 10 sec denaturation and 4 min elongation at 60°C, was applied to the sample mixture consisting of: 1.5 µL of Big Dye Terminator mix version 3.1, 1 µL of primer (5 pmol), 2 µL of a 5 x reaction buffer, 2 µL of the purified PCR product and 3.5 µL H20. Sequencing product were precipitated with 2.5 volumes of ethanol and 1/10 volume of 3 M NaAc, air dried and resuspended in 10 µL formamide (sequencing grade). The samples were run on a 3730xl DNA Analyzer (Applied Biosystems).

Site directed mutagenesis of porcine SOD1

In order to introduce the Gly93Arg mutation into SOD1 site directed mutagenesis was performed using the QuickChange® XL Site-Directed Mutagenesis Kit (Stratagene) and accomplished in accordance with the manufacturer's recommendations as described herein. The PCR reaction was performed in a total volume of 50 µL consisting of 5 µL of 10 x reaction buffer, 2 µL of both forward and reverse primer (10 pmol each), 1 µL dNTP mix, 3 µL QuickSolution, 1 µL PfuTurbo® DNA polymerase (2.5 U/µL), 1µL TOPO -SOD1 template (10 ng), and 35 µL H20.

Forward and reverse primers used for the above PCR procedure were:
SOD1G93R_F:
5'-GACTGCTGGCAAAGATCGTGTGGCCACTGTGTACATC-3' (SEQ ID NO:64)
SOD1G93R_R:
5'-GATGTACACAGTGGCCACACGATCTTTGCCAGCAGTC-3' (SEQ ID NO:65)

The PCR reaction was accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) under the following conditions: Initial denaturation at 95°C for 1 min, 18 cycles of 50 sec denaturation at 95°C, 50 sec of annealing at 60°C, and 6 min of elongation at 68°C and a final elongation step at 68°C for 7 min.

Subsequently 1 µL of Dpn I (10 U/µL) was added to the sample mixture in order to digest the nonmutated parental DNA template. The reaction was incubated for 1 hour at 37°C. After digestion of the parental DNA template XL10-Gold® Ultracompetent Cells (Invitrogen, CA) were transformed with the Dpn I treated DNA in the following manner: XL10-Gold® Ultracompetent Cells were thawn on ice and 45 µL were aliquoted to a prechilled Eppendorf tube and 2 µL of β-mercaptoethanol was added followed by a gentle swirling of the tube. The tube was now left on ice for 10 min. After incubation, 2 µL of the Dpn I treated DNA was added, the sample was swirled and incubated on ice for another 30 min and then exposed to a heat pulse of 42°C for 30 sec. Subsequently, the sample was put on ice for 2 min followed by an addition of 0.5 mL 42°C NZY+ broth. The mix was plated onto LB-amp plates and incubated overnight at 37°C.To ensure that the mutation of interest was integrated in the porcine SOD1 gene, 16 colonies were picked and grown overnight in liquid LB-Amp media and plasmids were purified using the QIAprep® Spin Miniprep kit (Qiagen) according to

manufactures recommendations. Cycle sequencing reactions were accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) where an initial denaturation step at 95°C for 2 min, 99 cycles of 10 sec denaturation and 4 min elongation at 60°C, was applied to the sample mixture consisting of: 1.5 µL of Big Dye Terminator mix version 3.1, 1 µL of either T7 or SP6 primer (5 pmol), 2 µL of a 5 x reaction buffer, 1 µL of the purified plasmid and 4.5 µL H20. Sequencing product were precipitated with 2.5 volumes of ethanol and 1/10 volume of 3 M NaAc, air dried and resuspended in 10 µL formamide (sequencing grade). The samples were run on a 3730xl DNA Analyzer (Applied Biosystems). Sequences were checked and a plasmid containing the mutation was chosen as template for the subsequent procedures. The sequence of the mutated porcine SOD1 cDNA is shown in Fig. 2.

Cloning of gene(s) of interest - SOD1 into the expression vector, phCMV1

To facilitate a continuous high expression of the transgene of interest, the gene was cloned into the phCMV1 vector (Gene Therapy Systems). For release of the mutated SOD1 DNA 6 µL plasmid DNA was digested with 1.5 µL EcoRI (20 U/µL) in a total volume of 30 µL in addition of 3 µL EcoRI 10 x reaction buffer. The reaction was incubated at 37°C for 90 min and run on a 1 % Seakem GTG agarose gel. The correctly sized band was isolated from the agarose gel employing a QIAEX® II Gel Extraction Kit (Qiagen) and dissolved in 30 µL H_2O. Likewise, phCMV1 was EcoRI digested and isolated from a 0.8 % Seakem GTG agarose gel and dissolved in 30 µL H_2O. Furthermore, in order to avoid self-ligation of the vector, 6 µL of the digested phCMV1 vector was dephosphorylated in a total volume of 25 µL applying 1.5 µL CIP (10 U/µL) and 2.5 µL 10 x CIP reaction buffer. The sample was incubated 60 min at 37°C. Enzyme inactivation occurred at 80°C for 15 min.

Ligation of mutagenised SOD1 into the EcoRI digested and dephosphorylated phCMV1 was performed in a total volume of 15 µL in the addition of 3 µL dephosphorylated phCMV1, 8 µL EcoRI linked mutagenised SOD1, 1.5 µL T4 DNA ligase (400 U/µL), 1.5 µL 10 x T4 DNA ligase buffer, and 1 µL H_2O. The reaction was incubated at 16°C overnight. XL10-Gold® Ultracompetent Cells were thawn on ice and 45 µL were aliquoted to a prechilled ependorf tube and 2 µL of β-mercaptoethanol was added followed by a gentle swirling of the tube. The sample was now left on ice for 10 min. After incubation, 3 µL of the ligation mix was added, the sample was swirled and incubated on ice for another 30 min and then exposed to a heat pulse of 42°C for 30

sec. Subsequently, the sample was put on ice for 2 min followed by an addition of 0.5 mL 42°C NZY+ broth. The mix was plated onto LB-amp plates and incubated overnight at 37°C.

To ensure that the insert had integrated correctly into the phCMV1 vector 16 colonies were picked and grown overnight in liquid LB-Amp media and plasmids were purified using the QIAprep® Spin Miniprep kit (Qiagen) in accordance with manufactures recommendations. Cycle sequencing reactions were accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) where an initial denaturation step at 95°C for 2 min, 99 cycles of 10 sec denaturation and 4 min elongation at 60°C, was applied to the sample mixture consisting of: 1.5 µL of Big Dye Terminator mix version 3.1, 1 µL of either T7 or SP6 primer (5 pmol), 2 µL of a 5 x reaction buffer, 1 µL of the purified plasmid and 4.5 µL H_2O. Sequencing product was precipitated with 2.5 volumes of ethanol and 1/10 volume of 3 M NaAc, air dried and resuspended in 10 µL formamide (sequencing grade). The samples were run on a 3730xl DNA Analyzer (Applied Biosystems). Sequences were checked and a plasmid containing the SOD1 construct in the correct direction was chosen.

Large scale preparation of DNA

In order to create DNA for incubation of sperm cells both PCR and large scale plasmid preparations have been employed.

The PCR reaction was performed in a GeneAmp® PCR System 9700 (Applied Biosystems) in a final volume of 25 µL consisting of 5 µL 5 x Phusion HF buffer, 2 µL dNTP (2.5 mM each) 0.63 µL forward and reverse primer 5 pmol, 0.1 µL Phusion DNA Polymerase (2 U/µL), 1 µL SOD1-phCMV1 template, and 15.6 µL H_2O. The PCR reaction consisted of an initial denaturation at 98°C for 30 sec followed by 30 cycles of denaturation for 10 sec at 98°C, annealing at 74°C for 30 sec and elongation for 95 sec at 72°C followed by a final elongation step at 72°C for 7 min.

The following primers were used to amplify the mutagenised SOD1 construct plus the flanking (før var termen matching) CMV promoter, intron sequence, and SVpolyA, generating a fragment of 1643 bp + the mutagenised SOD1 fragment, generating a fragment of approximately 2100 bp:

phCMVF: 5'-GTCGGAACAGGAGAGCGCACGAGGG-3' (SEQ ID NO:66)
phCMVR: 5'-GGGTGATGGTTCACGTAGTGGGC-3' (SEQ ID NO:67)

In order to purify the generated PCR product a "High Pure PCR Product Purification Kit" (Roche) was applied. The suppliers' instructions were followed throughout the purification procedure. The PCR purified fragments were sequenced to check for errors in the sequence as described below.

Large scale plasmid preparation was accomplished from ½ liter E. coli cell cultures. Purification of plasmids was performed using a Plasmid Mega Kit (Qiagen). In order to linearise and release the desired fragment from the vector, the vector was digested with BssS I and Dra III in the following way: 1.5 µL BssSI (4 U/µL), 1.5 µL DraIII (20 U/µL), 3 µL 10 x BSA, 3 µL 10 x Ne buffer 3, and 2 µL plasmid DNA was added to 19 µL H_2O to yield a total volume of 30 µL and was left overnight at 37°C. The digested fragments were separated on a 0.8 % GTG Seakem agarose gel and the correctly sized band were isolated and extracted from the gel using QIAquick Gel Extraction Kit Protocol (Qiagen), according to manufactures recommendations.

Both the PCR purified fragments and the plasmid prepared fragments were sequenced to check for errors in the sequence. Cycle sequencing reactions were accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) where an initial denaturation step at 95°C for 2 min, 99 cycles of 10 sec denaturation and 4 min elongation at 60°C, was applied to the sample mixture consisting of: 1.5 µL of Big Dye Terminator mix version 3.1, 1 µL of either T7 or SP6 primer (5 pmol), 2 µL of a 5 x reaction buffer, 1 µL of the purified plasmid and 4.5 µL H_2O. Sequencing product were precipitated with 2.5 volumes of ethanol and 1/10 volume of 3 M NaAc, air dried and resuspended in 10 µL formamide (sequencing grade). The samples were run on a 3730xl DNA Analyzer (Applied Biosystems).

Fig. 3 illustrates a comparison of the deduced amino acid sequence of porcine SOD1 with human, mouse and rat. The amino acid (G) which is mutated is marked in bold.

Fig. 4 shows projection of mutations in SOD1 onto the crystal structure of the human SOD1 dimer. The mutations are distributed all over the protein, illustrating that all residues of the protein are important for correct function of the enzyme.

Preparation of sperm and DNA uptake

Selection of Sperm Donor Boars

The selection of the sperm donor boars are crucial for the outcome of the procedure. A boar station (Hatting KS Viborg), have therefore been contacted and the boars of choice are selected so that the initial sperm motility is ≥90 %. The sperm is collected in sterile 10 mL tubes and transported undiluted at a temperature not below 15°C as this will cause damage to the sperm cells.

First and second semen ejaculate, were collected from 8 different boars yielding 16 semen fractions in total. All fractions of spermatozoa had an initial motility of 90 prior to the washing procedure. Seminal fluid was quickly removed by centrifugation and washing the sperm in Fertilization Buffer (FB) consisting of 56.1 g Glucose, 3.5 g EDTA ($2H_2O$), 3.5 g Sodium Citrate (2 H_2O), and 1.1 g sodium bicarbonate dissolved in 1 liter of sterilized water. Furthermore 6 mg/ml BSA (Fraction V, Sigma) was added. Briefly, 5 mL of FB/BSA prewarmed to 37°C was added to 5 mL of undiluted semen, mixed by inverting the tube, and left for 5 minutes at room temperature (approximately 22°C). Next, FB/BSA at room temperature was added to 50 ml and centrifuged for 10 minutes at room temperature at 500g, or alternatively at 800g for 10 min at 25°C. The supernatant was removed and semen was resuspended in 50 mL FB/BSA at room temperature and further centrifuged at 500g at 17 °C, after which, the supernatant was removed again and the spermatozoa was resuspended in 15 mL of FB/BSA. Next, in order to choose the optimal donor cells, the spermatozoa from the different boars and the two separate ejaculates were quickly examined under a light microscope. The sperm cells originating from the two boars having the highest sperm cell motility after the washing procedure were chosen as vehicles for the subsequent transgenic procedures. Furthermore, the spermatozoa were counted.

Generation of Transgene Pigs

1×10^9 sperm cells washed spermatozoa from each of the two chosen donor boars were incubated for 100 minutes at 17 °C with the linearized SOD1 DNA fragment (Fig. 5) in a concentration of 0.4 µg DNA/106 spermatozoa in a suspension of 120 mL FB/BSA. Containers were inverted every 20 minutes to prevent sedimentation of spermatozoa. Finally, the mixture was incubated 10 minutes at room temperature and employed in artificial insemination of two sows in natural heat.

Animals

Two recipient sows (Danish Landrace x Yorkshire) at approximately 140 kg were selected due to their natural heating period and used for artificial insemination (1×10^9 DNA treated sperm(spermatozoa)/sow) meeting standard insemination procedures. Insemination was accomplished in the local stable areas at DIAS. Semen was collected from trained Danish Landrace boars that have abstained for 2 days. Semen was treated according to aforementioned procedures. Both sows were examined for pregnancy 24 and 42 days after insemination, showing that only one of the sows was pregnant. After ended gestation period, 2 boars and 5 sow piglets were born naturally. Animal care and experimental procedures met local, national and European Union Guidelines.

Analysis of piglets

Test for the transgene

After 115 days (20.06.2005) 7 normal looking piglets were born, 2 of these were boar piglets and 5 were sow piglets. Blood samples were collected from the piglets in 6 mL EDTA blood collection tubes. Furthermore, blood from a wild type animal was collected as well and handled together with the 7 aforementioned animals. DNA was purified according to standard blood purification procedures in special clean laboratories, in order to avoid any possible contamination.

The PCR reaction was performed in a total volume of 10 µL consisting of 1 µL 10 x MgCl2 free reaction buffer, 0.4 µL 50 mM MgCl2, 1 µL of both forward and reverse primer (10 pmol each), 0.5 µL dNTP mix, 0.5 µL DyNazyme EXT DNA polymerase (1U/µL), 0.5 µL DNA template (50 ng), and 5.1 µL H_2O.

Forward and reverse primer used for the above PCR procedure:
PhCMV_430F: 5'-GTCTCCACCCCATTGACGTC-3' (SEQ ID NO:68)
PhCMV_646R: 5'-GGATCGGTCCCGGTGTCTTC-3' (SEQ ID NO:69)

The touchdown PCR reaction was accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) under the following conditions: Initial denaturation at 95 °C for 3 min, denaturation at 95 °C for 30 sec, touchdown from 62 °C to 57 °C with a decrement of 0.5 °C for 20 sec, followed by 1 min of elongation at 72 °C pr cycle. Furthermore 35

cycles of 30 sec denaturation at 95 °C, 20 sec of annealing at 57 °C, and 1 min of elongation at 72 °C was included together with a final elongation step at 72 °C for 7 min.

This created PCR fragments of 218 bp and the result is shown in fig. 6.

Fig. 6 shows that all animals (4905-4911) are positive regarding the transgenic DNA fragment. However, mosaicsm can not be ruled out neither the possibility of the various animals having different copy numbers. Therefore 2 animals were sacrificed (pig 4906 and pig 4909) and various tissues were sampled and snap frozen in liquid nitrogen and subsequently stored at -80°C. DNA was purified from the different tissues and the same PCR as above was performed, the only difference being that the amount of DNA was not normalized.

The result of the PCR for animal 4906 and 4909 is shown in figure 7 and 8, respectively.

Figs. 7 and 8 show that nearly all tissues applied in the PCR control harbor the transgenic fragment. Furthermore, it should be noted that the genomic template DNA is not normalized regarding concentration. Still, the lack of DNA fragments in lane 9 in fig. 6 and in lanes 3 and 5 in fig. 8 could well be explained by a mosaic nature of the animals regarding the transgene. However, for pigs 4906 and 4909 the transgene is present in a large variety of tissues.

Transgene in the germ cells

In order to transfer the transgene to next generation it is important to ensure that the transgene is present in the germ cells. Therefore, DNA has been extracted from sperm cells from the two boars (4905 and 4908). The purification of DNA was accomplished using two different procedures, standard purification procedure and miniprep purification procedure:

Standard purification procedure

300 µL of semen was washed in 1 mL 0.9 % NaCl, followed by centrifugation for 5 min at 3000 rpm where after the supernatant was discarded. This step was repeated twice and 20 µL Pronase (20 mg/mL), 20 µL 1 M DTT, and 300 µL buffer S was added to

each sample, where after these were left to incubate at room temperature overnight. Subsequently, 180 µL 6 M NaCl was added to each sample and shaken vigorously for approximately 20 seconds. The samples were now centrifuged for 15 min. at 10000 rpm and the supernatant was then carefully transferred to a new eppendorf tube where the DNA was precipitated adding twice the volume of supernatant and centrifuged at 10000 rpm for 10 min. Subsequently the ethanol was removed and the DNA was air dried and resuspended in 300 µL of nuclease free water.

Miniprep purification procedure

300 µL of semen was washed in 1 mL 0.9 % NaCl, followed by centrifugation for 5 min at 3000 rpm where after the supernatant was discarded. This step was repeated twice and 20 µL Pronase (20 mg/mL), 20 µL 1 M DTT, and 300 µL buffer S was added to each sample, where after these were left to incubate at room temperature overnight. In order to enrich each sample regarding low molecular DNA and obtain a more pure DNA product the miniprep procedure from Qiagen was applied. The DNA was eluted in 200 µL of nuclease free water.

Buffer S composition: 10 mM Tris HCl (pH 8.0); 100 mM NaCl; 10 mM EDTA (pH 8.0); 0.5 % SDS; H_2O.

DNA from both procedures was employed in the same PCR test as already mentioned and the result is shown in fig. 9.

Fig. 9 shows that the transgene is present in the sperm cells, however DNA purified with the miniprep purification procedure clearly shows much more distinct bands that the DNA purified with the standard procedure. This is probably due either the DNA being more pure or to the DNA being present as extra chromosomal fragments. Still, as the two boars harbor the transgene, these will used in the production of the next transgene SOD1 generation.

Veterinary declaration

Extracts from Veterinary Declarations dated 9th of February 2006 and 9th of March 2006, respectively, concerning transgenic animals are disclosed below.

"The boar 4905 has a bent back and very straight hocks. It raises and lays down with difficulty and stands with uneasiness in the back portion, seems slightly ataxic. A significant deterioration has ocurred as compared to last month. No direct signs of soreness in the limbs.
It is unclear if the cause is in the big joints at the back and pelvis region or the nerve system. Neurological symptoms of ataxia in the back portion of pigs are normally assumed to be caused by damages in the bone marrow and not the brain. Ataxia can be due to a lacking propioception, i.e. feeling of the positioning of the limbs.
The remaining pigs in the experiment move freely around."

The above section is a translation of an extract of a Veterinary Declaration dated 9th of February 2006.

"White 4905: Boar in normal condition and without signs of external damages. It stands on both front and rear legs, but is a little insecure when having to move and if pushed. This is clear from slight ataxic movements: Crosses front legs and have cocked angles from time to time and stands with rear legs widely to the side. Strong itching reflex can be released by touching the backside. Eats and drinks normally. No signs of limping.

White 4908: Boar in normal condition and without signs of external damages. It stands with underpositioned ("understillede") rear legs. It is slightly ataxic when turning and pushes from the side. No signs of limping.

White 4907, 4911, 4910: 3 sows move freely. They show some signs of slight ataxic movements which can be provoked when pushing them around."

The above section is a translation of an extract of a Veterinary Declaration dated 9th of March 2006.

Analysis of transgenic piglets

Biological Samples

Blood samples were withdrawn 3 days after birth and when the piglets reached 115 days blood samples were withdrawn every third week in 6 mL EDTA tubes and 6 mL serum tubes. Two sows were sacrificed at the age of 5 month, and before any phenotypic changes could be observed. One 1 boar, 4908 was sacrificed at the age of

14 month and another boar, 4905, was sacrificed at the age of 15 month. Both boars had severe phenotypic changes. For all sacrificed animals various tissues have been snap frozen in liquid nitrogen and subsequently stored at -80 °C. Furthermore, various tissues, including porcine brains have been fixed in formalin.

DNA and RNA Studies of transgenic pigs

DNA was prepared from EDTA stabilized blood samples and from snap frozen tails. RNA was prepared from snap frozen tissues from heart, kidney, liver, lung, spleen, medulla spinalis (M. spinalis), frontal cortex (FCO), parietal cortex (PCO), musculus longissimus dorsi (M. L. dorsi), musculus semitendinosus, left side (M.semit. l.), musculus semitendinosus, right side (M.semit. r.), musculus semibranosus, left side (M.semb. l.), and musculus semibranosus. All DNA and RNA samples were extracted in special clean laboratory facilities under highly stringent experimental conditions using standard protocols.

PCR Evaluation

50 ng of genomic DNA isolated from blood samples from each of the seven pigs were amplified using the following primers: SOD1Exon3F: 5'-GCTGTACCAGTGCAGGTCCTC-3' (SEQ ID NO:70) and SOD1Exon4R: 5'-CCATTGTGCGGCCAATGATG-3' (SEQ ID NO:71) yielding a fragment of approximately 800 bp when amplifying the endogenous genomic SOD1 and approximately 200 bp when amplifying the exon 3 to exon 4 cDNA fragment. The following sample mix was employed 1 µL 10 x MgCl2 free reaction buffer, 0.4 µL 50 mM MgCl2, 10 pmol of each primer, 5 mM dNTP-mix, and 0.5 U Dynazyme Ext DNA polymerase. The reaction was performed in a total volume of 10 µL and accomplished as a touchdown PCR in a GeneAmp® PCR system 9700 (Applied Biosystems) under the following conditions: Initial denaturation at 95 °C for 3 min, denaturation at 95 °C for 30 sec, touchdown from 62 °C to 57 °C with a decrement of 0.5 °C for sec, followed by 1 min of elongation at 72 °C pr cycle. Furthermore, 35 cycles of 30 sec denaturation at 95 °C, 20 sec of annealing at 57 °C, and 1 min of elongation at 72 °C was included together with a final elongation step at 72 °C for 7 min.

Expression Analysis

Of the total RNA, 2 µg was reverse transcribed from the various tissues, employing a SuperScript III kit (Invitrogen, USA) according to manufactures recommendation using

random hexamer primers. RT-PCR experiments were conducted in triplicate. The risk of amplifying genomic DNA was apart from primer designed to span exon-exon junctions ruled out by running the PCR prior to reverse transcription. Quantitative real time PCR was performed using the TaqMan® assay and PCR amplification in an ABI-PE prism 7900 sequence detection system (PE Applied Biosystems). Primers, ssSOD1_EX4F 5' -GGATCAAGAGAGGCACGTTGG-3' (SEQ ID NO:72) and ssSOD1_EX4R 5'-GGCGATCACAGAATCTTCGATG-3' (SEQ ID NO:73), and MGB probes were designed using the Primer Express Software 2.0 (PE Applied Biosystems), and the MGB probes, designed to match the endogenous and mutated porcine SOD1, were designed with VIC and FAM as reporter dyes (SS_SOD1_WT: VIC-5'-CAAAGATGGTGTGGCCAC-3' (SEQ ID NO:74) and SS_SOD1_Mut: FAM-5' -CAAAGATCGTGTGGCCAC-3') (SEQ ID NO:75). Furthermore the 18S ribosomal RNA gene was chosen as the endogenous control using the following primers and probes: 18S-F: 5'-CGCTCCACCAACTAAGAACG -3' (SEQ ID NO:76), 18S-R: 5'-CTCAACACGGGAAACCTCAC-3' (SEQ ID NO:77), and 18S-probe: SYBR-5'-GGTGGTGG-3' (SEQ ID NO:78). Separate mixtures for mutated SOD1, wild type SOD1, and 18S were prepared and consisted of 5µL 2x TagMan® Universal PCR Master Mix, 0.3 µL of each primer (10 µM), 0.25 µL probe (5 µM), 2 µL of a 10 fold diluted cDNA template, or in the case of 18s, 2 µL of a 10,000 fold diluted cDNA template, and H_2O to a final volume of 10 µL. Real-time PCR was accomplished under the following conditions: 2 min at 50 °C, 10 min at 95 °C, 40 cycles of 95 °C for 15 sec and 60 °C for 1 min. All PCRs were performed in triplicate. The cycle threshold (Ct) values corresponding to the PCR cycle number at which fluorescence emission in real time reaches a threshold above baseline emission were determined in the software SDS 2.2 (PE Applied Biosystems). To compare expression levels of wild type SOD1 in the various tissues relative mRNA template concentrations were calculated using the standard curve method.

Southern Blot Analysis

Transgene integration was determined by Southern blot analysis of DNA from musculus longissimus dorsi from the two affected boars. 15 µg of genomic DNA, undigested, Pvu II –digested, and double digested with Pvu II and Bam HI were separated on a 0.9% agarose gel, blotted to a nylon membrane and probed with [32P]-labelled SOD1 cDNA fragment constituting approximately 450 bp spanning the entire porcine SOD1 coding region derived from PCR amplification followed by nick

translation. Genomic DNA from a healthy wild type pig was subjected to the same treatment as DNA from the two boars and has been included as control. Hybridization was accomplished in a hybridization buffer containing 5 x Denhardt's solution and 6 x SSC at 68 °C for 16 hours.

SOD analysis

The SOD activity was determined with the Superoxide Dismutase assay kit (Cayman Chemicals, Ann Arbor, MI), based on the ability of SOD1 to inhibit the reduction of tetrazolium salt induced by xanthine-xanthine oxidase as described [47], and was accomplished according to manufactures recommendations using serum from the two diseased pigs and one control. One unit of SOD is defined as the amount of enzyme needed to exhibit 50% dismutation of the superoxide radical, O2•-, and a solution of bovine erythrocyte SOD (Cu/Zn was used as standard. Serum samples have been extracted on regular basis for 9 month yielding a total 19 samples from boar 4905, 17 from 4908, and 19 from the control pig, which all were included in the assay. The absorbance was read at 450 nm using a plate reader. The serum protein content was determined with a standard protein assay based on bicinchoninic acid (BCA) using manufactures recommendations (Pierce, Rockford, IL) employing bovine serum albumin as a reference and measuring the absorbance at 562 nm.

Histopathology

For examination of muscle tissue samples were taken from the center of longissimus dorsi above the curvature of the last rib from the two affected boars (4905 and 4908) and two wild type controls (147 and 3713). The size of the sample was app. 5 X 5 X1 cm. At excision the samples were frozen in isopentane cooled in liquid nitrogen to minimize internal freeze artefacts. Transverse serial sections (10 µm) were cut in a cryostat at -20 °C and collected on lysine coated cover slips. The sections were immunohistochemically stained for slow myosin heavy chain (MHC) isoform (Catalogue no. CRL-2043, American Type Culture Collection) to identify type I fibres. A description of the methods used for the immunohistochemical stainings is given in Pedersen et al. (2001) [48]. The architecture of fibre types in pig muscles is unique as type I and IIA fibres are located in clusters. For the analysis we have counted the number of fibres within clusters as this is less affected by growth or differences in size of animals and compared the distributional characteristics of fibres within clusters. In the analysis clusters of type I fibres have been included.

For histopathological investigation of medulla spinalis both affected boars, 4905 and 4908, as well as two wild type boars, 147 and 3713, at approximately the same age were employed. After immersion fixation of cervical medulla spinalis in 4 % paraformaldehyde, the tissues were embedded in paraffin was and sectioned into slices of 5 µm. Sections were stained with 7 anti-SOD1 peptide antibodies. However, only the 100-115 anti SOD1 peptide antibody were specific for the porcine SOD1, and is therefore, the one used in this work. The immunohistochemistry was performed using the Ventana immunohistochemistry system.

Statistics

Variation in number of type I muscle fibers in musculus longissimus dorsi between the two affected boars (4905 and 4908) and controls (3713 and 147) were tested with respect to statistical significance employing students t-test considering unequal variances ($\alpha = 0.05$), since data approaches the underlying assumption of normality.

Description of the Porcine Phenotype

Initially, the first signs of phenotypic alterations were appearing in one of the boars, 4905, at the age of seven months. The boar was slightly ataxic and showed reduced propioception and it preferred to lie down. The symptoms became gradually worse and at the age of ten months the boar showed fasciculation when getting up and laying down. Furthermore, the boar had pronounced, abnormal itching reflexes and at the age of 15 months the boar was sacrificed since it was nearly unable to get up without help. The other boar, 4908 got slightly symptomatic at the age of approximately 8 months, where it like the other boar, was slightly ataxic and showed reduced propioception. One month later it showed fasciculations, which turned gradually worse and at the age of 12 month, these fasciculations was very severe and continuously present when the boar was standing in an upright position. Furthermore, this boar showed abnormal tongue movements. At the age of 14 months the boar was sacrificed. Both of the boars were all the time able to accomplish basic necessities of life such as eating, drinking, and urinating without any help.

Southern Blot Analysis

To establish whether integration of the transgene had occurred Southern blot analysis was performed on tissue from musculus logissimus dorsi from the two affected boars

and on wild type control. The used probe spans the entire SOD1 coding region, constituting approximately 450 bp. However, no detectable bands can be seen in any of the samples constituting undigested, Pvu II digested and Pvu II and BAM HI double digested DNA from boar 4905 and 4908 and the wild type pig showing that genomic integration has not occurred. Furthermore, under the same conditions the ~five copy fragment control harboring the SOD1 cDNA, were clearly detected (lane 11 and 12, in fig. 10), suggesting that the SOD1 cDNA is markedly underrepresented in the genome (<1 copy per genome).

PCR Analysis

To further establish if the transgene could be present, for instance as an extrachromosomal entity, which has been demonstrated in a recent study [49], both the two affected boars and the five littermates were checked for the presence of transgene using DNA purified from blood as a template. Primers enabling both the amplification of the wild type genomic SOD1 fragment spanning exon 3 to exon 4, yielding approximately 800 bp, and the mutated SOD1 DNA fragment, yielding approximately 200 bp were employed. Fig. 11 shows that apart from the positive control only the 800 bp DNA fragment arising from the endogenous SOD1 was amplified. This indicates that none of the seven animals harbour the fragment used during the SMGT procedure. Furthermore, also DNA extracted from the tails of the seven animals has been subjected to PCR analysis, yielding also negative results regarding the occurrence of the mutated SOD1.

Still, it can not be ruled out that a minor fraction of the cells harbours the construct, applied in the SMGT procedure, possibly stored as an extrachromosomal fragment; however this is beyond our detection limit. Furthermore, the presence of transgene in other tissues in a minor fraction of the cells ruled out either; however since PCR amplification in various tissues of the sacrificed pigs did not give rise to any consistent amplification of the DNA fragment used in the SMGT procedure only a minor fraction of the total number of cells include said fragment.

SOD1 Expression Analysis

Expression of the SOD1 construct harbouring the Gly93Arg substitution was accomplished by quantitative RT-PCR using TaqMan probes spanning the DNA region harbouring the substitution, and hence separate RT-PCR's were conducted regarding

the wild type SOD1 mRNA and the mutagenised SOD1 mRNA from heart, kidney, liver, lung, spleen, medulla spinalis, frontal cortex, parietal cortex, musculus longissimus dorsi, musculus semitendinosus left side, musculus semitendinosus right side, musculus semibranosus left side, and musculus semibranosus from the two affected boars and from the two wild type controls and assayed for the presence of the mutagenised SOD1 transcript or alternatively altered endogenous SOD1 levels. Furthermore, the mutagenised SOD1 fragment was included in the expression analysis to ensure that the SOD1 probe matching the mutagenised fragment was perfectly suited to detect any transcript. Fig. 12B shows amplification of the mutagenised fragment in various concentrations emphasizing, that the probe is suitable for detection of mutagenised transcripts. However, since no difference is seen between the amplification curves, representing of the affected boars and the controls in any of the 12 tissues it is concluded that mutagenised transcripts are not present in the affected boars, Fig. 12. Although a wide variety of tissues have been included, it can not be ruled out that expression of the transgene could possibly be present in other tissues or at very low levels which could not be detected in this assay.

Fig. 12A shows the amplification curves using the probe detecting the SOD1 wild type transcript. This reveals that the SOD1 probe detects the SOD1 transcript, even though some background amplification would be present in case of possible SOD1 mutant transcript, since an amplification curve is present using the SOD1 mutagenised fragment (pink curve in Fig 12A). However, since no mutagenised transcript could be detected, this is not considered in the real time analysis in Fig 12C. The real time analysis reveals no differences in the endogenous SOD1 expression levels between the two wild type boars and the two affected boars in any of the analysed tissues. However, large inter tissue variations are present, which is also the case between tissues. The highest expression levels are seen in liver and kidney, which is also in agreement with studies performed on human tissues [50].

SOD Analysis in Serum

SOD1 activity was detected spectrophotometrically in serum as a measurement for the SOD1 to inhibit the reduction of tetrazolium salt induced by xanthine-xanthine oxidase [47] and was not corrected for Mn-SOD, meaning that the activities in Fig.13 represent the total SOD activity in serum. However, since Mn-SOD accounts for a minor fraction of the total SOD activity in serum [51] it is not likely that it would mask possible

differences between affected boars and the control. The SOD activity levels in serum of the two transgenic affected boars was approximately at the same level as the control boar during the time course recorded, and no significant variation across time (from Oct 2005 - Aug 2006) has been revealed, Fig. 13.

Furthermore, proteome analysis employing protein extracts from liver and musculus longissimus dorsi failed to detect any mutagenised SOD1 protein in the two transgenic boars (data not shown).

Histopathological Investigations

Since the nature of muscle fibers may be used to assess disease progression of ALS the clusters including type I muscle fibers in musculus logissimus dorsi were examined regarding the number of fibers in each cluster. This investigation revealed that the frequencies of type I fibers in the two affected boars are significantly decreased in comparison to controls, Fig 14. Statistical evaluation reveals P-values of 3×10^{-6} and 2×10^{-5} for 4905 and 4908, with respect to the control boar, 147, emphasizing highly significant differences. Furthermore a P-value of 0.08 reveals that the two controls are not statistically different, which is also the case for the two affected boars, P = 0.11. The stainings, Fig 14, further highlights the large differences in number of type I fibers, both regarding the size of the clusters and the absolute number, which is also reduced in the two transgenic boars.

Sections from cervical spinal cord of the two the two affected boars and two age matched wild type boars were stained with various peptide antibodies raised against human SOD1. However, only the 100-115 anti-SOD1 peptide antibody proved to be specific with respect to porcine SOD1. Fig. 15 shows a motorneuron from the spinal cord of both an affected boar (4908) and the age matched control boar (147). In Fig. 15A) showing a motor neuron from the affected boar, SOD1 stainings are seen in the motor axon, most likely arising from SOD1 inclusions. In comparison no stainings are seen in the axon of the control. Furthermore, in Fig. 15A large fluorescent compartments are seen in the neuropil which are not present in the control either.

Example 2

A transgenic pig model for Parkinson's disease

Cloning of the porcine SNCA cDNA

The full-length porcine α-synuclein (SNCA) cDNA was isolated from cerebellum by a combination of RT-PCR and RACE. Initially, blast searches using the human SNCA cDNA sequence were carried out with GenBank (http://www.ncbi.nlm.nih.gov/Genbank/index.html) and with the porcine EST data bank at The Danish Institute of Agricultural Sciences (DIAS). Sequence similarity search was performed with gapped alignment using NCBI Blastall with options blastn, minimum value 10-8. The porcine cDNAs thus identified were used to derive oligonucleotide primers for cloning and as queries for further searches in the local genomic DIAS sequence database.

The pig cerebellum tissue used for RT-PCR cloning of porcine SNCA was obtained from an adult pig. After removal, tissue was dissected and pulverized in liquid nitrogen. Total RNA was isolated by the RNeasy method (Qiagen). The integrity of the RNA samples was verified by ethidium bromide staining of the ribosomal RNA on 1% agarose gels.

The porcine SNCA cDNA presented here was isolated using an RT-PCR cloning approach. Synthesis of cDNA was conducted with 5 µg of total RNA isolated from pig cerebellum using SuperScript II RNase H- reverse transcriptase (Invitrogen). The cDNA synthesis was initiated by heating of total RNA, oligo(dT)12-18 primer, dNTP at 65°C for 5 min followed by addition of 200 units reverse transcriptase and then incubation at 42°C for 50 min followed by 70°C for 15 min.

The RT-PCR reaction mix contained: 2.5µl cDNA, 1.5mM MgCl2, 0.2mM dNTP, 0.5µM of each primer SNCA-F: 5'-CCATGGATGTATTCATGAAAGGACTTTCAA-3' (SEQ ID NO:79) and SNCA-R: 5'-CTTCCGGCTCATAGTCCTGATACCC-3' (SEQ ID NO:80), and 1U Phusion DNA polymerase (Finnzymes), in a total volume of 25 µl. PCR amplification was carried out in the total volume using the following program: Denaturation at 94°C for 2 min., 10 cycles of 94°C for 15 s, 55°C for 30 s, 72°C for 40 s, followed by 25 cycles of 94°C for 15 s, 60°C for 30 s, 72°C for 40 s. The PCR program was concluded by an extension at 72°C for 7 min. Twentyfive microlitres of the amplification product was applied to a 1% agarose gel and visualized after electrophoresis by ethidium bromide staining. A fluorescent band of approx. 400 bp was cut out and eluted using the Qiaquick Gel Extraction kit from Qiagen. The eluted PCR product was cloned directly into the pCR TOPO 2.1 vector (Invitrogen) and sequenced in both directions.

To obtain a full-length coding SNCA cDNA, sense and antisense primers derived from the isolated SNCA fragment were used in 5' and 3' RACE (rapid amplification of cDNA ends) experiments. A sense SNCA specific primer was used in combination with a kit anchor primer (Roche Molecular Biochemicals). In brief, for 3'-RACE, an oligodT reverse transcription oligonucleotide primer, 5'-GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTTTV-3' (V = A, C or G) (SEQ ID NO: 81) was used in a reverse transcription reaction. The resultant SNCA cDNA was used as a template for PCR amplification employing the proof-reading DNA polymerase Phusion (Finnzymes), in combination with a kit PCR anchor primer: 5'-GAAAACGCGTATCGATGTTCGAC-3' (SEQ ID NO:82) and a gene-specific primer SNCA-F: 5'-CCATGGATGTATTCATGAAAGGACTTTCAA-3'(SEQ ID NO:83). PCR products were recovered as described above, cloned into the pCR TOPO2.1 vector and sequenced. one PCR amplicon of approx. 800 bp contained a DNA fragment that showed homology to SNCA and which also matched the sequence of the partial SNCA cDNA where the sequences overlapped. For 5'-RACE a reverse transcription oligonucleotide primer, SNCA5-it1: 5'-GGATCCTACATAGAGCACACCCTC-3' (SEQ ID NO:84) was used in a reverse transcription reaction. The synthesized SNCA cDNA was used as a template for PCR amplification employing Phusion DNA polymerase (Finnzymes), in combination with a kit PCR anchor primer: 5'-GAAAACGCGTATCGATGTTCGAC-3' (SEQ ID NO:85) and a gene-specific primer, SNCA5-it2: 5'-TCCCGCTGCTTCTGCCACACCCTG-3' (SEQ ID NO:86). PCR products were recovered as described above, cloned into the pCR TOPO2.1 vector and sequenced. one PCR product contained a DNA fragment that showed homology to SNCA and also matched the sequence of the partial SNCA cDNA where the sequences overlapped.

The interconnectedness between the original cDNA clone and the 5'- and 3'RACE sequences was confirmed by PCR with the primers SNCA5-F: 5'-CAGTCTGTTAGGGGGAGGAGCTTATTTC-3' (SEQ ID NO:87) and SNCA-it3: 5'-CTATAGTTAATATTTATAGGTGCATAGTTCC-3' (SEQ ID NO:88). PCR amplification was carried out in the total volume using the following program: Denaturation at 95°C for 2 min., 10 cycles of touchdown (-0.5oC per cycle) 95°C for 20 s, 60°C for 30 s, 72°C for 45 s, followed by 25 cycles of 95°C for 20 s, 55°C for 30 s, 72°C for 45 s. The PCR program was concluded by an extension at 72°C for 5 min.

DNA sequencing was performed employing the dideoxy chain termination method using BigDye terminator cycle sequencing kit with AmpliTaq DNA polymerase FS (PE

Applied Biosystems). The sequencing analysis was performed on an automated DNA sequencer (ABI PRISM TM Genetic Analyzer Model 3730xl, PE Applied Biosystems). Traces were aligned and visualized using the SEQUENCHER version 4.0.5 for Windows (Gene Codes Corporation).

Characterization of the porcine SNCA cDNA

The SNCA cDNA was amplified by the reverse transcriptase polymerase chain reaction (RT-PCR) using oligonucleotide primers derived from in silico sequences. Partial porcine SNCA EST sequences identified in the DIAS EST library were used to derive primers for RT-PCR amplification of the SNCA cDNA. A 420 bp fragment was obtained which showed a high level of homology to published SNCA sequences. Sense and antisense primers were designed from this sequence and used for 5' and 3'-RACE experiments. With one round of PCR a SNCA cDNA covering the coding and 3'UTR sequence was obtained. Similarly, one round of PCR generated the missing 5'UTR sequence. To confirm that the obtained porcine SNCA fragments were interconnected, a PCR reaction using primers covering the near full-length coding sequence of was performed. This resulted in the 982 bp cDNA sequence shown in Fig.16.

The identity of the porcine SNCA cDNA was established by comparing the deduced polypeptide sequence with other isolated alpha-synuclein proteins. The porcine SNCA cDNA (GenBank Access. No. DQ073395) is 982 bp in length with the translational start site at nucleotide 104 and the TAA stop codon at nucleotide 524. The open reading frame (oRF) of SsSNCA has a G+C content of 50% and it encodes a polypeptide of 140 amino acids with an estimated molecular mass of 14.5 kDa and a pI of 4.6. The encoded porcine □-synuclein protein contains the characteristic motifs of other □-synuclein proteins: five imperfect repeats with a core consensus sequence KTKEGV distributed from the amino terminus to the central part of the protein. As for other □-synucleins eleven central hydrophobic amino acids are missing compared to the homologous ß-synuclein and γ-synuclein.

Amino acid sequence similarity between porcine α-synuclein and other published mammalian α -synuclein proteins was determined by the Clustal method. Multiple alignment of α -synuclein amino acids sequences from pig, human, mouse and rat, cow, chicken and Xenopus (Fig. 17) revealed a very high overall homology. Interestingly, it was found that the amino acid in position 53 which is an alanine in human is a threonine residue in all other species. This particular alanine residue is found substituted to a threonine (Ala53Thr) in familial Parkinsonism.

A very high degree of identity between porcine α -synuclein and most other alpha-synuclein proteins was found. The encoded pig α -synuclein polypeptide exhibits significant sequence identity to human α -synuclein (98%), cow α -synuclein (96%) and mouse and rat α -synuclein (both 94%). The lowest amino acid identity between pig α -synuclein and other α -synuclein proteins was observed with the chicken α -synuclein (84%) and the Xenopus sequence (80%). See fig. 18 for a phylogenetic tree. The Prosite Web site (http://www.expasy.ch/prosite/) was used to analyze the 140 amino acid porcine α -synuclein protein sequence and predicted a molecular weight of 14.5 kDa and identified potential post translational modifications. These include one casein kinase II phosphorylation site, one tyrosine kinase phosphorylation site and five putative myristoylation sites.

Site directed mutagenesis of porcine SNCA

In order to introduce the Ala30Pro mutation into the porcine SCNA, site directed mutagenesis was performed employing the QuickChange® XL Site-Directed Mutagenesis Kit (Stratagene) and accomplished in accordance with manufactures recommendation applying the following primers:

SNCA-A30P-F: 5'-GGGTGTGGCAGAAGCACCGGGAAAGACAAAAGAG -3' (SEQ ID NO: 89)

SNCA-A30P-R: 5'-CTCTTTTGTCTTTCCCGGTGCTTCTGCCACACCC -3' (SEQ ID NO: 90).

The PCR conditions were: Denaturation at 95°C for 1 min., 18 cycles of 95°C for 50 s, 60°C for 50 s and 68°C for 6 min. The PCR program was concluded by an extension at 68°C for 7 min.

To ensure that the mutation of interest was integrated in the porcine SNCA gene, several colonies were picked and grown overnight and plasmids were harvested and sequenced according to standard procedures. A plasmid containing the mutation was chosen as template for the subsequent procedures. Next, the plasmid containing the mutated SNCA cDNA was digested with KpnI and EcoRV releasing the SNCA fragment, which was now cloned into the KpnI and SmaI digested phCMV1 expression vector using standard protocols. XL10-Gold® Ultracompetent Cells (Invitrogen, CA) were transformed with the phCMV1 vector preparation and to ensure that the SNCA insert had integrated correctly into the phCMV1 vector colonies were grown in liquid LB-Amp and plasmids were purified and sequenced according to standard procedures.

Vector constructs containing correctly integrated mutagenized SNCA fragments were selected for following procedures.

Large-scale SNCA DNA preparation

In order to create DNA for incubation of sperm cells large scale PCR reactions were performed. The PCR reactions were carried out in a GeneAmp® PCR System 9700 (Applied Biosystems) in a final volume of 25 µL consisting of 5 µL 5 x Phusion HF buffer, 2 µL dNTP (2.5 mM each) 0.63 µL forward and reverse primer 5 pmol, 0.1 µL Phusion DNA Polymerase (2 U/µL), 1 µL SNCA-phCMV1 template, and 15.6 µL H_2O. The PCR reaction consisted of an initial denaturation at 98°C for 30 sec followed by 30 cycles of denaturation for 10 sec at 98°C, annealing at 74°C for 30 sec and elongation for 95 sec at 72°C followed by a final elongation step at 72°C for 7 min. The following primers were used to amplify the mutagenized SOD1 construct plus the flanking CMV promoter, intron sequence, and SV polyA, generating a fragment of approximately 2100 bp.

phCMVF: 5'-GTCGGAACAGGAGAGCGCACGAGGG-3' (SEQ ID NO: 91)

phCMVR: 5'-GGGTGATGGTTCACGTAGTGGGC-3' (SEQ ID NO: 92)

In order to purify the generated PCR product a "High Pure PCR Product Purification Kit" (Roche) was applied. The suppliers' instructions were followed throughout the purification procedure. The PCR purified fragments were sequenced to check for errors in the sequence. See fig. 19 and 20.

Sperm mediated gene transfer SMGT

Sperm Mediated Gene Transfer, Buffer:

In order to wash the porcine sperm cells and hence remove the sperm liquid, the following optimized buffer is applied:

For 1 liter:

56.1 g	Glucose
3.5 g	EDTA (2 H_2O)
3.5 g	Sodium citrate
1.1 g	Sodium bicarbonate

The components are dissolved in water and the solution is sterilized through a filter. Before the buffer is added to the sperm cells, 6 mg/ml BSA (Bovine Serum Albumine, Fraction V, Sigma) is added.

Selection of Sperm Donor Boars:
The selection of the sperm donor boars are crucial for the outcome of the procedure. A boar station (Hatting KS Viborg), have therefore been contacted and the boars of choice are selected so that the initial sperm motility is ≥90 %. The sperm is collected in sterile 10 mL tubes and transported undiluted at a temperature not below 15°C as this will cause damage to the sperm cells.

Washing procedure:
The following procedure is accomplished as fast as possible (buffer is as indicated above):
5 mL sperm is transferred to a 50 mL Falcon tube
5 mL buffer preheated to 37°C is added
Mix by inverting the tubes
The solution is incubated for 5 min at room temperature (~ 22°C)
40 mL buffer (room temperature) is added
Centrifuge at 800 g, for 10 min at 25°C
Remove the supernatant
Resuspend the pellet in 50 mL buffer (room temperature)
Centrifuge at 800 g, for 10 min at 17°C
Remove the supernatant
Carefully resuspend the pellet in the remaining buffer in the bottom of the Falcon tube.

Examination of the sperm cells:
In order to choose the correct donor cells, the sperm cells from the different boars are examined under a light microscope. The sperm cells originating from the boar having the highest sperm cell motility after the washing procedure are chosen. Next, the sperm cells from the boar of choice are counted.

DNA uptake/incubation:
10^9 sperm cells are diluted into 120 mL 17°C buffer

0.4 µg linearized DNA/ 10^6 sperm cells is added (that is, a total of 400 µg linearized DNA)

Incubate 100 min at 17°C

To avoid sedimentation of the cells, invert the tube every 20 min

Transfer the tube to room temperature, and transport it, still at room temperature to stable facilities. This takes approx. 10 min. The incubated sperm cells are now ready to be applied in artificial insemination.

Animals:

Two recipient sows (Danish Landrace x Yorkshire) at approximately 140 kg were selected due to their natural heating period and used for artificial insemination (1 x 10^9 DNA treated sperm/sow) meeting standard insemination procedures. Insemination was accomplished in the local stable areas at DIAS. Semen was collected from trained Landrace boars that have abstained for 2 days. Semen was treated according to aforementioned procedures. Both sows were examined for pregnancy 24 and 42 days after insemination, showing that only one of the sows was pregnant. Animal care and experimental procedures met local, national and European Union Guidelines.

Test for presence of the transgene:

After 115 days (17.06.2005) 10 normal looking piglets were born, 5 of these were boar piglets and 5 were sow piglets. One of the boar piglets died the following day (17.06.2005). Blood samples were collected from the piglets in 6 mL EDTA blood collection tubes. Furthermore, blood from a wild type animal was collected as well and handled together with the 9 aforementioned animals. At a later stage semen was collected from selected animals and genomic DNA was isolated. DNA was purified according to standard blood purification procedures in special clean laboratories, in order to avoid any possible contamination.

The PCR reaction was performed in a total volume of 10 µL consisting of 1 µL 10 x MgCl2 free reaction buffer, 0.4 µL 50 mM MgCl2, 1 µL of both forward and reverse primer (10 pmol each), 0.5 µL dNTP mix, 0.5 µL DyNazyme EXT DNA polymerase (1U/µL), 0.5 µL DNA template (50 ng), and 5.1 µL H_2O.

Forward and reverse primer used for the above PCR procedure:

PHCMV_682F: 5'-GATTCCCCGTGCCAAGAGTG-3' (SEQ ID NO:93)

SNCA-4R: 5'-TTGCCCAGCTGATCCTTTTTGCCAAAG-3' (SEQ ID NO:94)

The touchdown PCR reaction was accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems) under the following conditions: Initial denaturation at 95°C for 3 min, denaturation at 95°C for 30 sec, touchdown from 62°C to 57°C with a decrement of 0.5°C for 20 sec, followed by 1 min of elongation at 72°C pr cycle. Furthermore, 35 cycles of 30 sec denaturation at 95°C, 20 sec of annealing at 57°C, and 1 min of elongation at 72°C was included together with a final elongation step at 72°C for 7 min.

Blood samples were withdrawn form potentially transgenic piglets and PCR reactions were carried out on purified DNA as described above. Fig. 21 shows that all animals (4363-4371) are positive regarding the transgenic DNA fragment of 800 bp. However, mosaicsm can not be ruled neither the possibility of the various animals having different copy numbers.

Transgene in the germ cells:

In order to transfer the transgene to next generation it is important to ensure that the transgene is present in the germ cells. Therefore, DNA has been extracted from sperm cells from the two boars (4905 and 4908). The purification of DNA was accomplished using a standard purification procedure:

Standard purification procedure:

300 µL of semen was washed in 1 mL 0.9 % NaCl, followed by centrifugation for 5 min at 3000 rpm where after the supernatant was discarded. This step was repeated twice and 20 µL Pronase (20 mg/mL), 20 µL 1 M DTT, and 300 µL buffer S was added to each sample, where after these were left to incubate at room temperature overnight. Subsequently, 180 µL 6 M NaCl was added to each sample and shaken vigorously for approximately 20 seconds. The samples were now centrifuged for 15 min. at 10000 rpm and the supernatant was then carefully transferred to a new Eppendorf tube where the DNA was precipitated adding twice the volume of supernatant and centrifuged at 10000 rpm for 10 min. Subsequently the ethanol was removed and the DNA was air dried and resuspended in 300 µL of nuclease free water.

Buffer S composition: 10 mM Tris HCl (pH 8.0); 100 mM NaCl; 10 mM EDTA (pH 8.0); 0.5 % SDS; H_2O.

Presence of the modified SNCA transgene was examined in DNA purified from sperm cells from boars 4363-4371. As shown in Fig. 22 all boars harbored the transgene in the sperm cells. A PCR of the expected size of 800 bp can be observed in for all animals although at differential amounts.

Phenotypic characterization of boar # 4363

First symptoms were observed in three boars at the age of 17 months. The pigs were examined by Knud Larsen and veterinarian Keld Dahl Winter (Danish Meat). One boar #4363) had the most pronounced symptoms. When standing the boar showed a strongly upward curved (convex) back. Loss of muscle tissue was observed in musculus longissimus dorsi left side while the right side was unaffected. During activity permanent tremor of the tail was observed. More pronounced tremor was seen in the neck especially when the head was raised. Tremor was also visible in the tail and in ear tips. The tremor was intermittent and disappeared partly when the boar was at rest. The tremor in head and neck was worsened when the boar was surprised by visitors and by rising of the head. The boar appeared with a rigid body posture, moved very slowly and did not turn around when people were circling around it. This is not a normal behaviour. The coordination of the limbs was fully normal. However, the movements were very slow. The general state of health was largely unaffected and the boar did not show any signs of pain.

One month later boar # 4363 was examined. Tremor of head, neck and tail had increased significantly and were now present partly as resting tremor. The pronounced tremor symptoms have not been observed in any earlier described syndromes in pigs (pers. comm. Keld Dahl Winter). The boar's movements were very slow and considered inhibitory as no turning towards people approaching at the tail was seen. A normal healthy pig would immediately turn towards an arriving person. Since the latest examination one month earlier the muscular atrophy had increased and spread to both sides of the back. The backline had become more visible and the neural spines were more protruding.

Sixteen days later the boar # 4363 was sacrificed and dissected for further analyses.

Pathological examination of boar # 4363

Boar # 4363 was sacrificed and dissected. Samples from different organs such as heart, liver, kidney, lung, spleen were collected together with samples from testis and selected muscles (musculus longissimus dorsi). Also the brain was taken out and

divides into to halves, both were dissected into discrete regions and either snap-frozen or fixed in formaldehyde. After three weeks fixation different brain samples were embedded in paraffin, sliced with a microtome and subjected to different stainings. Nissl AMG-staining of thin-layer sections from substantia nigra revealed presence of neurons but most of the neurons were shrunken with lacunae and no clear segregation between the nucleus, nucleolus and cytoplasm (Fig. 23). Similarly, as shown in Fig. 24, HE-staining also demonstrated shrunken neurons with numerous lacunae (holes) which is a clear indication of neural degeneration.

A staining procedure for tyrosine hydrolase (TH) was also carried out on the thin layer sections. The results showed as illustrated in Fig. 25, that 1) The number of dopaminergic cells seemed to be reduced and 2) The remaining dopaminergic cells and neuropil seemed to be more rough and unordered.

For comparison a brain sample from a mini-pig was also examined for TH staining. Numerous dopaminergic cells were observed.

A GFAB staining revealed an intense staining in the mesencephalon of boar # 4363, an indication of pronounced inflammation and gliosis (Fig.26). Numerous astrocytes are noted indicative of active inflammation and reactive gliosis.

Very interestingly, a specific antibody staining for α-synuclein, using Ab raised against human α -synuclein, revealed patches of large □-synuclein aggregates throughout the mesencephalon (Fig. 27). α -synuclein s located in the cell bodies and extracellular sorroundings

In conclusion, all pathological examinations of boar # 4363 are clearly indicative for PD. However, no classical Lewy bodies are observed. Lewy bodies are a cardinal symptom of PD and presence of Lb is needed to recapitulate the development and progression of PD. The explanation for the missing LBs could easily be that boar # 4363 was sacrificed too early in the progression of disease. As the boar was at the age of 18 months and showing a large row of the clinical symptoms of PD but without complete resting tremor it was what could be expected at this particular stage.

Fig. 23 shows a Nissl staining of substantia nigra isolated from boar # 4363. The figures clearly demonstrate that there are fewer cells present than expected from a normal healthy individual. Furthermore, neurons in substantia nigra look abnormal and also presence of cytoplasmatic vacuoles and shrinking of cells is indicative of an abnormal condition. Lewy bodies are not visible in this staining.

Example 3

A transgenic pig Model animal of Alzheimer's Disease

PSEN1 and PSEN2 Isolation and sequencing

Pig brain, lymphocyte, and liver RNA was isolated with the TRI-reagent (Sigma). For RT-PCR of PSEN1 the following primers were used (PSEN1forward, 5'-TGGAGGAGAACACATGAAAGAAAG-3' (SEQ ID NO: 95); PSEN1-forward-EcoR1 5'-GGGGAATTCTGGAGGAGAACACATGAAAGAAAG-3' (SEQ ID NO:96); PSEN1reverseEcoR1, 5'-GGGGAATTCCCTGACTTTGTTAGATGTGGACAC-3' (SEQ ID NO:97). The RT-PCR reaction was incubated at 50°C for 60 min with the reverse primer followed by PCR with the PSEN1forward-EcoR1 and PSEN1reverse-EcoR1 primers at conditions (94°C for 3 min, 35 cycles of; 94°C, 45 sec; 62°C, 30 sec; 68°C, 2 min, followed by a final elongation step at 68°C for 7 min). Amplified DNA fragments were purified from agarose gels and either directly sequenced or EcoR1 cloned into pCDNA3 followed by DNA purification and sequencing. For RT-PCR of PSEN2 the following primers were used (PSEN2-forward, 5'-GCCATGCTCACTTTCATGGC-3'; PSEN2-reverse (SEQ ID NO: 98), 5'-CACGACTGCGTCCAGTGACC-3' (SEQ ID NO: 99). The reverse transcription reaction was accomplished using the Invitrogen reverse transcription system (Invitrogen) and 5 µg of total-RNA according to the manufacturer's instructions. Subsequently, the PCR reaction was carried out at the following conditions: (94°C for 3 min, 35 cycles of; 94°C, 45 sec; 60°C, 30 sec; 68°C, 2 min, followed by a final elongation step at 68°C for 7 min). Amplified DNA fragments were purified from agarose gels and either directly sequenced or cloned into pCR® 2.1-TOPO® Vector (Invitrogen) followed by DNA purification and sequencing. The porcine pSEN1 and pSEN2 cDNA sequences were submitted to GenBank (Accession numbers DQ853416, and DQ853415, respectively)

BAC-hybridisation

Radioactive probes were generated employing the nick translation kit from Invitrogen which incorporated [α-32P]dCTP into the PCR generated PSEN1-exon8 fragment. High-density colony BAC filters (a generous gift from Dr. P. D. Jong) of the porcine genome were screened with the PSEN1-exon8 probe. The filters were pre-hybridized, hybridized, washed and autoradiographed according to standard methods. Positive

spots were localised and BAC DNA of positive clones was isolated using the alkaline lysis method described by Zhang et al. (1996). BAC clone 388G9 contained the PSEN1 genomic sequence and was used for intronic sequence generation.

Generation of intron sequence information

The BAC clone 388G9 was sequenced with primers located in exons 5, 7, 8 and 9 and pointing towards the intronic sequences. Table 8 shows the applied primers. All exon and flanking intronic sequences were deposited as a gapped submission to GenBank (Accession number DQ86246).

Table 8 Sequences of primers and real time PCR probes

Primer and probes	Sequence	SEQ ID NO:	Application
PS1 Exon 5 forward primer1	5'-GGAGGTGGTAATGTGGTTGG-3'	100	BAC sequencing
PS1 Exon 5 reverse primer1	5'-CCAACCATAAGAAGAACTGGG-3'	101	BAC sequencing
PS1 Exon 7 forward primer1	5'-CCTATAACGTTGCCATGGATTAC-3'	102	BAC sequencing
PS1 exon 7 reverse primer1	5'-CACAGCCAAGATGAGCCAC-3'	103	BAC sequencing
PS1 Exon 8 forward primer1	5'-GCTGGTTGAAACAGCTCAGGAG-3'	104	BAC sequencing
PS1 Exon 8 reverse primer1	5'-CCAGCAAACGAAGTGGGCCATTTG-3'	105	BAC sequencing
PS1 Exon 9 forward primer1	5'-CAACAATGGTGTGGTTGGTG-3'	106	BAC sequencing
PS1 Exon 9 reverse primer1	5'-GGATACCTTCCTTTGGGCTTC-3'	107	BAC sequencing
PS1 Exon 5 forward primer2	5'-GACACTTACCTGGGGCTTTGTG-3'	108	SNP screening
PS1 Exon 5 reverse primer2	5'-CCAAGTAAGGTGAGACAGGAAAACC-3'	109	SNP screening
PS1 Exon 7 forward primer2	5'-GCTACGAGTATGAAGGTGGGATATG-3'	110	SNP screening
PS1 exon 7 reverse primer2	5'-CCAGGAGTCAAGATAACTGG-3'	111	SNP screening
PS1 Exon 8 forward primer2	5'-CCACCATCTGTTTACCTGCTA-3'	112	SNP screening
PS1 Exon 8 reverse primer2	5'-GGCCATCATTACATGTGTTTG-3'	113	SNP screening
PS1 Exon 9 forward primer2	5'-GGTGACATTAAGAAGTTTGGTGACTTG-3'	114	SNP screening
PS1 Exon 9 reverse primer2	5'-GGGTGTTACCACAGCTTGGAG-3'	115	SNP screening
PS1 forward primer	5'-GTGATTTCAGTATACGATTTAGTGGCTG-3'	116	Real Time PCR
PS1 reverse primer	5'-CACCAACCACACCATTGTTGAC-3'	117	Real Time PCR
PS1 MGB probe	5'-VIC-TTGTGTCCAAATGGC-3'	118	Real Time PCR
PS2 forward primer	5'-GGAGGAAAGGGGCGTGAAG-3'	119	Real Time PCR
PS2 reverse primer	5'-CACAAACCGATGAGGATGGC-3'	120	Real Time PCR
PS2 MGB probe	5'-VIC-CTGGAACACCACGCTGG-3'	121	Real Time PCR
GAPDH forward primer	5'-GACTCATGACCACGGTCCATG-3'	122	Real Time PCR
GAPDH reverse primer	5'-GTCAGATCCACAACCGACACG-3'	123	Real Time PCR
GAPDH MGB probe	5'-VIC-CATCACTGCCACCCAGA-3'	124	Real Time PCR

SNP screening

Exons 5, 7, 8 and 9 and flanking intron sequences were amplified by PCR (primers listed in table 8 under SNP-screening application). Exon 5 and flanking intron sequences were amplified at conditions 50 ng DNA; 94 oC for 3 min and 35 cycles; 94°C, 30 sec; 60°C, 20 sec; 72°C, 1 min. Exon 7 and flanking intron sequences were amplified at conditions 50 ng DNA; 94°C for 3 min and 35 cycles; 94°C, 20 sec; 58°C, 20 sec; 72°C, 1 min. Exon 8 and flanking intron sequences were amplified at conditions 50 ng DNA; 94°C for 3 min and 35 cycles; 94°C, 45 sec; 64°C, 30 sec; 72°C, 1 min. Exon 9 and the flanking intron sequences were amplified at conditions 50 ng DNA; 94°C for 3 min and 35 cycles; 94°C, 20 sec; 58°C, 20 sec; 72°C, 1 min. All PCR products were incubated with exozap at 37 °C for 1 hour and sequenced with the forward amplification primer. The sequences were analyzed using PolyBace and checked manually in Consed.

Hybrid cell mapping

A porcine-rodent somatic cell hybrid panel was used for physical mapping (Yerle et al., 1996) of both PSEN1 and PSEN2. For PSEN1 the exon 9 forward and reverse primers 2 were used for amplification of the probe fragment. For PSEN2 the PCR primers (PSEN2exon12F; 5'-GTTTGTGTCTGACCCTCCTGCTGC-3' (SEQ ID NO: 125) and PSEN2exon12R; 5'–CAGATGTAGAGCTGGTGGGGAGG-3'(SEQ ID NO: 126)) were used for amplification of the probe fragment. PCR's were performed in a total volume of 10 µL containing 10 ng DNA, 1 x PCR buffer, 2.5 mM of each dNTP, 5 pmol of each primer, and 0.5 U of Taq polymerase (Bioline) under the following conditions: 94°C for 3 min; 35 cycles of 94°C for 20 s, 65°C for 20 s and 72°C for 20 s, and a final elongation step for 5 min at 72°C.

Immunohistochemistry

Fetal pig brains were immersion fixed in formalin and paraffin-embedded tissue blocks were produced from various brain regions. 10 micrometer coronal sections were then obtained on coated glass slides. The sections were deparaffinized and pretreated with proteinase K for 6 min. The slides were blocked with BSA (1 mg/ml) for 10 min. Immunohistochemical demonstration of PSEN1 and PSEN2 was performed using the EnVision+ System-HRP-DAB (DAKO). The anti-PSEN1 antibody was a rabbit polyclonal antiserum 520 (a generous gift from Dr. Poul Fraser, Toronto, Canada) used

in 1:100 dilution with incubation time 2 hours. The anti-PSEN2 antibody was the mouse monoclonal antibody, APS 26, used in 1:33 dilution with incubation time 2 hours (abcam). Nuclei were counterstained in haematoxylen solution. The slides were finally coverslipped with Faramount Aqueous Mounting Medium (DAKO).

Real-time quantitative PCR assay

Total RNA was isolated from cerebellum, frontal cortex, hippocampus, brainstem, and basal ganglia from 60, 80, 100, and 115 days old porcine fetuses using the TRI Reagent™ (Sigma) in compliance with the manufacturer's instructions. Three separate tissues were applied for each type of tissue and time in gestation, yielding a total of 60 samples. The reverse transcription reaction was accomplished using an Invitrogen reverse transcription system (Invitrogen) and 5 µg of RNA according to the manufacturer's instructions. Quantitative real time PCR was performed using the TaqMan® assay and PCR amplification in an ABI-PE prism 7900 sequence detection system (PE Applied Biosystems). Primers and MGB probes were designed using the Primer Express Software 2.0 (PE Applied Biosystems), so that both forward and reverse primer spanned an exon-exon junction. The MGB probe was synthesized with VIC as a reporter dye. After an initial screening with different control genes GAPDH was chosen as the endogenous control and the MGB-probe was synthesized with VIC as a reporter dye. The primers and probes are detailed in table 8. Separate mixtures for PSEN1, PSEN2, and GAPDH were prepared and consisted of 5 µL 2X TaqMan® Universal PCR Master Mix, 0.3 µL of each primer (10 µM), 0.25 µL probe (5 µM), 2 µL of a 5-fold diluted cDNA template, and H_2O to a final volume of 10 µL. Real-time PCR was done under the following conditions: 2 min at 50°C, 10 min at 95°C, 40 cycles of 95°C for 15 sec and 60°C for 1 min. For both PSEN1, PSEN2, and GAPDH PCRs were performed in triplicate. The cycle threshold (Ct) values corresponding to the PCR cycle number at which fluorescence emission in real time reaches a threshold above baseline emission were determined in SDS 2.2 (PE Applied Biosystems). To compare expression patterns in the various brain tissues at different developmental stages mRNA template concentrations for GAPDH, PSEN1, and PSEN2 were calculated using the standard curve method. Standard curves were constructed using 8 fold dilution of day 115 frontal cortex cDNA (4, 2, 1, 0.5, 0.25, 0.125, and 0.0625 µL). The mRNA quantity of each amplicon was calculated for each standard and experimental sample.

Statistical analysis

The equality of PSEN1 and PSEN2 expression levels between different time of gestation within the 5 sampled tissues were tested for statistical significance using the standalone software REST© [52]. The statistical model applied was the Pair Wise Fixed Reallocation Randomisation Test. The assumption regarding normal distribution of the data was avoided, and differences in expression between groups were assessed using the means for statistical significance by randomization. The level of probability was set at $P < 0.05$ as statistically significant and 50000 randomization steps were implemented in each comparison.

Results

PSEN1 and PSEN2 cDNA and protein sequence

To determine the cDNA sequence of porcine PSEN1 we designed a set of primers based on the conserved 5' and 3' untranslated regions between the rodent, bovine, and human PSEN1. Using RT-PCR, the cDNA representing the entire pig PSEN1 open reading frame was amplified, cloned and sequenced. The porcine cDNA was throughout the sequence homologous to human PSEN1 (90 %) but only homologous to human PSEN2 in short dispersed regions. The porcine PSEN1 protein has a length of 467 amino acids, which compares well with the 467 amino acids of the human and mouse counterparts (fig. 28). Multiple amino acid sequence alignment of PSEN1 revealed a 92 % sequence identity between pig and human (fig. 28). Furthermore, 34 changes were observed between the two sequences, 11 of these being conservative. Comparison of pig and mouse revealed a sequence identity of 89% and 16 of 50 amino acid changes were conservative. The cow PSEN1 has a length of 478 amino acids and a sequence identity of 94% to porcine, 12 of 28 changes being conservative, and hence, cow PSEN1 is the PSEN1 variant that shows the highest degree of identity to the porcine counterpart. Mutations in human PSEN1 can be cause Alzheimer's disease and it is noteworthy that none of the amino acid changes between pig and human are located in positions known to cause Alzheimer's disease. (fig. 28) (www.molgen.ua.ac.be/ADMutations). By contrast, at position 318 where human PSEN1 contains a non-pathogenic polymorphism, E318G, a Q residue is present at the equivalent position in pig, cow, and mouse PSEN1 [53]. Two other non-pathogenic polymorphisms R35Q and F175S present in human PSEN1 are in the porcine PSEN1 R and F, respectively (fig. 28) [54,55].

The human PSEN2 cDNA sequence was used to blast NCBI porcine databases as well as an in house porcine database allowing the design of primers corresponding to the

5'-end of the coding region and the 3'-non-coding region of the putative porcine PSEN2. The primers amplified a porcine cDNA fragment of approximately 1.4 kb and sequence analysis revealed high sequence homology with human PSEN2 (92 %) but only homologous to human PSEN1 cDNA in small dispersed regions, demonstrating that the porcine orthologous of PSEN2 was identified. Analysis of the porcine PSEN2 open reading frame showed that the porcine PSEN2 protein consisted of 448 amino acid residues, as do the human and mouse orthologous (fig. 29). Multiple amino acid sequence alignment of PSEN2 revealed 97.8 % sequence identity between pig and human, and 1 of the observed 10 changes was conservative (fig. 29). Comparison of pig and mouse showed a sequence identity of 95%, 8 of the 20 changes being conservative. The cow PSEN2 has a length of 449 amino acids and a sequence identity of 98.2 %, where 4 of the 8 changes are of conservative. Thus, as observed for PSEN1, also the bovine PSEN2 protein shows the highest degree of identity to the porcine counterpart. Moreover, it should be noted that none of the observed changes between the sequences of the different species are located in PSEN2 positions identified to be mutated in Alzheimer's disease patients (fig. 29) (www.molgen.ua.ac.be/ADMutations). At position 334 a non-pathogenic polymorphism, P334R, has been identified in human PSEN2 [54,56], and the proline residue was conserved in the porcine cDNA.

The amino acid sequence for porcine PSEN1 shows 64% identity to porcine PSEN2 and particularly amino acids in the transmembrane domains and the C-terminus are conserved (data not shown). Also the two aspartic acid residues located in transmembrane domain 6 (D257 in PSEN1 and D263 in PSEN2) and transmembrane domain 7 (D385 in PSEN1 and D363 in PSEN2), and the "PAL" sequence, (P433, A434, L435 in PSEN1 and P414, A415, L416 in PSEN2) are conserved in both porcine PSEN1 and PSEN2, consistent with the essential role of these residues for the protease catalytic function of the presenilins [54,57,58].

Mapping of porcine PSEN1 and PSEN2

A porcine-rodent somatic cell hybrid panel was used for the chromosomal mapping of porcine PSEN1 and PSEN2 genes (data not shown) [59]. Statistical evaluation applying the "Interpreting PCR data" program (http://www.toulouse.inra.fr/lgc/pig/pcr/pcr.htm) showed a chromosomal localization for the PSEN1 gene to chromosome 7q12-q26 with a probability of 0.4494 and a correlation of 1, and for the PSEN2 gene to chromosome 10p11-p16 with a probability

of 0.9959 and a correlation of 0.7255. The specified regions of porcine chromosomes 7 and 10 have synteny with human chromosomes 14 and 1, respectively. This is in agreement with mapping of the human PSEN1 gene to 14q24.3 and the human PSEN2 gene to 1q31-q42.

Single nucleotide polymorphism screening of porcine PSEN1

To examine for genetic variation in porcine PSEN1, we resequenced exons 5, 7, 8, and 9 in a large animal material consisting of 900 Landrace/Yorkshire crossbreed sows and a pig breed panel consisting of 55 Landrace, Duroc, Yorkshire and Hampshire breeds. These exons were chosen for sequence analysis because they constitute "hotspots" for mutations in familiar Alzheimer's disease. However, no SNP's were identified in the 4 exonic regions (data not shown). Next, we extended the polymorphism analysis to include intronic sequences, which identified a C/T SNP at position 58 in intron 8 (position 1163 in the sequence deposited in DQ86246) as well as two C/T polymorphisms at positions 52 and 92 and a G/A polymorphism at position 117 in intron 10 (positions 1535, 1575, and 1600 in the DQ86246). The genotyping data are summarized in table 9 and 10. All breeds except Hampshire were polymorphic in intron 8 and at positions 52 and 92 in intron 10, whereas only the Yorkshire breed was polymorphic at position 117 in intron 10. Genotype frequencies were in accordance with Hardy-Weinberg equilibrium, indicating that no selective disadvantage is associated with the SNPs.

PSEN expression in the developing porcine brain

PSEN1 and PSEN2 have been shown to be widely expressed during embryonic development and especially the expression profile in the CNS is well characterized [60-62]. Here, we measured the mRNA expression levels of PSEN1 and PSEN2 in hippocampus, cerebellum, frontal cortex, basal ganglia, and brain stem from dissected porcine foetus brains at days 60, 80, 100 and 115 of gestation using three biological samples for each of the time points. Day E115 corresponds to the normal day of birth. The PCR analyses were performed in triplicates. The requirement for a proper internal control gene was met by normalization to the GAPDH expression level to compensate for inter-PCR variation with respect to RNA integrity and sample loading. Although housekeeping gene expression has been reported to vary considerably within different tissues or treatments, we did not find any significant differential expression of GAPDH within the 5 different porcine brain tissues at the various developmental stages. The

standard curve for the control GAPDH (R^2 = 0.98), PSEN1 (R^2 = 0.98), and PSEN2 (R^2 = 0.98) were generated by plotting Ct values versus log µL of cDNA. The slope of the regression line was used to calculate the amount of cDNA and thus mRNA in each sample. All GAPDH cDNA's generated almost identical Ct values within each type of tissue (data not shown) and accordingly the mRNA expression levels of PSEN1 and PSEN2 were normalized to the GAPDH expression level. Ethidium bromide-staining after real time PCR confirmed specific amplification of the relevant PCR products (data not shown).

PSEN1 and PSEN2 were expressed in all 5 tissues at the 4 time points evaluated. However, it should be noted, that for both PSEN1 and PSEN2 the mean standard deviation is considerable, reflecting a high heterogeneity among animals. In basal ganglia the PSEN1 expression levels did not vary significantly between the different times of gestation (fig. 30). In frontal cortex, cerebellum, and hippocampus the PSEN1 expression level was significantly lower at day 115 of gestation compared to day 60 (P = 0.001, P = 0.036, and P = 0.003, respectively), yielding a reduction of 5, 2, and 3 times for the said tissues (fig. 30). Furthermore, the reduction in PSEN1 expression in frontal cortex is also significant at day 80 compared to day 60 (P = 0.003). Similarly, PSEN1 expression is gradually reduced in hippocampus during the time period of gestation (fig. 30). Moreover, the same tendency is seen in cerebellum, however the reduction in expression levels is only significant between day 100 and 115 (P = 0.015) and day 60 and 115 (P = 0.036).

For PSEN2 no differential expression was observed in frontal cortex. In hippocampus the only significant variation was seen as an increase in expression level between day 60 and 80 of gestation (P = 0.015) (fig. 30). Also in the brain stem, PSEN2 is upregulated between day 60 and 80 of gestation (P = 0.032) (fig. 30). In cerebellum and basal ganglia the expression levels of PSEN2 are up-regulated between day 80 and 100 (P = 0.003, and P = 0.03) (fig. 30). When comparing the overall expression levels of PSEN1 and PSEN2, an approximately three fold lower PSEN2 expression level is observed. In conclusion, the real time PCR analysis showed significant, albeit small, alterations in the expression levels of PSEN1 and PSEN2 mRNA in different brain compartments during embryonic brain development, which likely reflect biological importance.

To examine the localization of the PSEN1 and PSEN2 proteins *in situ* we utilized immunohistochemical stainings at embryonic day 100 brain slides with antibodies for PSEN1 and PSEN2. PSEN1 staining was more intense and diffusible outside cell

bodies than observed for the PSEN2 staining (fig. 31). We note that all PSEN2 stained regions also were positive for PSEN1 staining (fig. 31). No clear alterations in localization or intensity of PSEN1 and PSEN2 staining were detected in analysis of other embryonic time points or brain regions (data not shown). Intracellular immunostaining was confined to the cytoplasm with a distinct sparing of the nuclei. The immunostaining was observed in all parts of the CNS, especially in neurons but also to some extend in astrocytes (fig. 31 and data not shown). In cortex both pyramidal and nonpyramidal cells were stained (fig. 31). Also all hippocampus CA subfields and the granule cells were PSEN positive (fig. 31). The immunohistochemical analysis supports that the PSEN proteins are located in the majority, if not all, of the neurons. Moreover, all PSEN2 stained cell types were also positive for PSEN1 staining in accordance with the observed redundancies in PSEN1 and PSEN2 functions [63,64].

Table 9. Genotype-frequencies of a C/T SNP in position 1163 (DQ86246) in PSEN1 intron 8 in a pig breed-panel.

Breed	No. of animals	Genotype frequencies SNP position 1163		
		C/C	T/T	C/T
Landrace	14	0	0.71	0.29
Duroc	15	0	0.60	0.40
Hampshire	17	1	0	0
Yorkshire	14	0	0.62	0.38

Table 10. Genotype-frequencies for three SNPs in PSEN1 intron 10 (DQ86246) in a pig breed-panel.

Breed	No. of animals	Genotype frequencies SNP position 1535/1575			SNP position 1600		
		C/C	T/T	C/T	G/G	A/A	G/A
Landrace	14	0.71	0	0.29	1	0	0
Duroc	14	0.57	0.07	0.36	1	0	0
Hampshire	11	0	1	0	1	0	0
Yorkshire	16	0.63	0	0.37	0.69	0	0.31

Example 4

Model animal of diseases related to Trinucleotide Repeat Sequences

Human TNR disease causing regions are in most cases also identifiable in the primate and rodent genomes [65-67]. However, in rodents the TNR regions in general are composed of significantly fewer TNR units and are less polymorphic. As TNR sequences are rapidly evolving and may functionally influence the affected genes, changes in such regions have the potential to participate in functional diversification [65, 68]. To analyse how the disease causing TNR regions identified in humans have evolved in the porcine genome, we analysed porcine TNRs. We here describe that in terms of TNR tract lengths the porcine TNRs in general represent an intermediate between rodent and humans and that several of the TNRs are polymorphic in the pig. In addition, the length of TNRs was in several of the porcine loci comparable to the lengths normally identified in primates.

Genomic samples

Genomic DNA was prepared from unrelated (no common parents and grandparents) Duroc, Landrace, Hampshire, Yorkshire, and Goettingen minipig males according to standard procedures. The DNA was isolated from EDTA stabilized blood using a salting out procedure [69].

PCR and sequencing of genomic DNA

To sequence porcine genomic TNR regions flanking sequences conserved between mouse and humans were identified and corresponding PCR primers designed. 50 ng of Duroc pig genomic DNA was used in PCR with conditions 95°C 30", 58°C 30", 72°C 1', 35 cycles. Standard taq polymerase PCR conditions were used except for the inclusion of 1 M Betaine and 5% DMSO. After agarose gel electrophoresis analysis DNA of expected size was purified and sequenced. If the intensity of bands or the sequencing result was evaluated inadequate for further analysis new PCR primers were designed either based on the evolutionary approach or nested according to determined sequences. By this scheme the following optimized primer sets were used to amplify genomic TNR regions (all PCR reactions run for 35 cycles with 50 ng genomic DNA as input): SCA1: SCA1+, CAGCGCTCCCAGCTGGAGG (SEQ ID NO: 127); SCA1-,

GGAYGTACTGGTTCTGCTGG(SEQ ID NO:128); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSO. SCA2: SCA2NyTRI-, GCCACCGTAGAGGAGGAGGAAG(SEQ ID NO:129); SCA2TRI(+), CTCACCATGTCGCTGAAGC(SEQ ID NO:130); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSO. SCA3: SCA3-I7+, CCATGGGAATAGTTTTTCTCATG (SEQ ID NO:131); SCA3exon10(-), GGTTGGCTTTTCACATGGATGTG (SEQ ID NO:132); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSO. SCA6: SCA6nyTRI+, CGGCCACACGTGTCCTATTC (SEQ ID NO:133); SCA6NYTRI-, GGCCGCTGGGGGCCGCTCG (SEQ ID NO:134); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSo. SCA7: SCA7Tri(+), GGAGCGGAAAGAATGTCGGAG (SEQ ID NO:135); SCA7Tri(-), CCCACAGATTCCACGACTGTC (SEQ ID NO:136); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSO. SCA17: pTBP-, GAAGAGCTGTGGAGTCTGG (SEQ ID NO:137); pTBP+, CTATCCATTTTGGAGGAGCAG (SEQ ID NO:138); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSo. DRPLA: Drpla-Ny+, GGAGGCCAGTCCACTGCTCAC (SEQ ID NO:139); Drpla-Ny-, GGGAGACATGGCATAAGGGTG (SEQ ID NO:79); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSO. SMBA: ARTri+, X; ARTri-, X, 94°C 45", 58°C 30", 72°C 2'. HD:, pHUNNYRE+, CCGCCATGGCGACCCTGGAAA (SEQ ID NO:140); pHUNNYRE-, GGTGGCGGCTGAGGAGGCTG (SEQ ID NO:141); 95°C 30", 65°C 30", 72°C 1' with betaine and DMSO. FMR1: FMR1(Ny+1), CGTTTCGGTTTCACTTCCGGTG (SEQ ID NO:142); FMR1Zoo-, CCGCACTTCCACCACCAGCTC (SEQ ID NO:143); 95°C 30", 60°C 30", 72°C 1' with betaine and DMSO. FMR2: FMR2-Ny-, TGCGGCGGCAGCAGCCGCTAC (SEQ ID NO:1444); FMR2(Ny+2), CCCCTGTGAGTGTGTAAGTGTG (SEQ ID NO:145); 95°C 30", 58°C 30", 72°C 1' with betaine and DMSo. SCA12: SCA12TRI(+), GGGAGGAGCCTCGCCTTTAATG (SEQ ID NO:146); SCA12Tri(-), CGCGACAAAATGGTGCCTTTC (SEQ ID NO:147), 95°C 30", 58°C, 30", 72°C1' with betaine and DMSO. DMPK: gDMPKpoly+, GCCCTGCTGCCTTCTCTAGGTC (SEQ ID NO:148); gDMPKpoly-, CCCCAGCTCTAGCCCTGTGATC (SEQ ID NO:149), 94°C 30", 64°C 30", 72°C 2'. DNA fragments were purified from agarose gels using GFX columns (Amersham Biosciences) and sequenced according to standard procedures. DNA fragments were amplified from Duroc, Landrace, Hampshire, Yorkshire, and Goettingen minipig male genomic DNA.

Sequence information for TNRs in Homo sapiens (human), Pan troglodytes (chimpanzee), Canis familiaris (dog), Rattus norvegicus (rat), Mus musculus (mouse),

and Monodelphis domestica (opossum) was extracted from genome browsers at NCBI (www.ncbi.nlm.nih.gov/Genomes).

Microsatellite analysis on sows and offspring originating from boars with extended TNRs

Genotyping of different Huntingtin allele lengths was performed by microsatellite analysis in a porcine material consisting of 14 Duroc boars, 611 Landrace and Landrace x Yorkshire crossbred sows and 349 offspring originating from 4 of the Duroc boars and the aforementioned sows. The following primers were used; Fw: FAM-CCGCCATGGCGACCCTGGAAA (SEQ ID NO:150), Rw: GGTGGCGGCTGAGGAGGCTG (SEQ ID NO:151). The amplicon was amplified in a total volume of 10 µL in a mixture consisting of: 50 ng of genomic DNA, 5 pmol of each primer, 2.5 mM dNTPs, 1 µL of 10 x reaction buffer, 0.5 µL DMSO, 2.5 µL 4 M Betaine, and 5 U Taq DNA polymerase (Applied Biosystems, USA). PCR amplification was as follows : initial denaturation for 4 min at 95°C, and 35 cycles at 95°C for 30 sec, 64°C for 30 sec, 72°C for 1 min. An extension step of 72°C for 5 min was added after the final cycle. PCR products were denatured with formamide and electrophoresis was carried out on a 3730 DNA Analyzer (Applied Biosystems, USA) using the recommended protocol. Size analyses of DNA fragments were accomplished with the GeneMapper® Software Ver 3.0 (Applied Biosystems, USA). The internal size standard GeneScan-LIZ 500 (Applied Biosystems, USA) was employed for allele sizing.

Accession numbers

The determined porcine TNR regions and flanking sequences were submitted to genebank and have been assigned the following accession numbers: SCA1 (DQ915251, DQ915252), SCA2 (DQ915254), SCA3 (DQ915255, DQ915256), SCA6 (DQ915259, DQ915260, DQ915261), SCA7 (DQ915262), SCA17 (DQ915258), DRPLA (DQ915263, DQ915264), SMBA (DQ915257), HD (DQ915274, DQ915275, DQ915276, DQ915277, DQ915278, DQ915279, DQ915280, DQ915281, DQ915282), FMR1 (DQ915269, DQ915270, DQ915271, DQ915272, DQ915273), FMR2 (DQ915268), SCA12 (DQ915265, DQ915266, DQ915267), DMPK (DQ915253).

Results

To sequence porcine genomic regions homologous to human disease causing TNRs we first identified flanking sequences showing highly conserved regions between

mouse and humans. Employing this PCR approach 12 porcine genomic loci corresponding to human disease causing TNRs were amplified. The identified TNRs were located in coding regions and 5´-UTRs. The DMPK 3'-UTR TNR was amplified using primers based on EST sequences available in Genbank. To search for TNR polymorphisms in different porcine breeds we included Duroc, Landrace, Hampshire, Yorkshire and Goettingen minipig. For each of the pig breeds a number of animals were analysed assuring the detection of common alleles (allele frequency > 10%).

Porcine genomic sequences homologous to human non-coding TNR expansion regions. We first addressed porcine genomic sequences homologous to human non-coding TNRs.

DMPK: In the 3´-UTR of the human myotonic dystrophy protein kinase gene, DMPK, a CTG TNR is located [19-23]. The normal size of this TNR varies between 5 and 37. Expansions from above 50 to several thousand CTG repeats result in myotonic dystrophy. A CTG TNR consisting of 4 CTG repeats in all the pig breeds studied (Duroc, Landrace, Yorkshire, Hampshire, and minipigs) (fig. 32) was identified at the same localization in the porcine DMPK. No length variation in the DMPK TNR was identified (fig. 32). The repeat number found is below the minimum number of CTG repeats (5 CTGs) observed in humans. In the mouse the TNR sequence of DMPK is composed of 2 CAG repeats flanked by single CTG repeats (fig. 32). In dog and rat a single CTG is present flanked by other types of TNRs (fig. 32).

SCA12: The SCA12 CAG TNR within the 5´-UTR of the human PPP2R2B gene normally varies in size from 7 to 28 repeats and in the expanded form from above 65 to 78 TNRs [27]. Three alleles consisting of 8, 9, and 10 CAG repeats were identified in the porcine breeds (fig. 32). The most abundant allele in Duroc contained 8 CAG repeats, whereas the most abundant allele in Hampshire contained 10 CAG repeats (fig. 32). An allele containing 9 CAG repeats was the only allele observed in Landrace, Yorkshire and Minipigs (fig. 32). The presence of long uninterrupted CAG TNRs in the porcine SCA12 locus is distinct from the mouse and rat SCA12 locus which is composed of CAG TNRs interrupted with CAC and GAG triplets (fig. 32). Notably, the lengths of the porcine SCA12 alleles are comparable and even higher than SCA12 allele lengths identified in some humans (fig. 32).

FMR1/FRAXA: In the promoter region of the human FMR1 gene, 6 to 52 CGG repeats are normally present [24, 25]. Expansions in the range of 55 to 200 repeats result in the pre- mutation while the full mutation ranges from 200 to several thousand repeats

resulting in fragile X syndrome. The sequence of the FMR1 TNR region in Duroc showed the presence of two alleles: a 14 CGG repeat allele with a frequency of 90% and a 13 CGG repeat allele with a frequency of 10% (fig. 32). Sequence analysis of the FMR1 TNR in the other porcine breeds showed a high degree of FMR1 TNR length polymorphisms. A 15 CGG repeat allele was identified in Duroc, Hampshire and Yorkshire (fig. 32). This allele was the most common in Yorkshire, whereas a 9 CAG repeat allele was also identified in Hampshire and a 12 CAG repeat allele in Duroc and Minipigs. No allele polymorphism was observed in Landrace. All the porcine FMR1 alleles were longer than the homologous mouse TNR sequence which is composed of 6 CGG repeats and 2 CGG repeats separated by a CGA (fig. 32). The dog FMR1 TNR has a size similar to the pig TNR (fig. 32). In the most common type of human FMR1 TNR allel two groups of CGG repeats are separated by an AGG triplet (fig. 32). Also the chimpanzee FMR1 TNR is highly polymorphic and includes AGG triplet interruptions [70]. Interestingly, the porcine FMR1 TNR length exceeds the minimal length present in the human FMR1 CGG TNR prone to expand.

FMR2/FRAXE: The number of CCG repeats in the TNR of the 5´end of the human FMR2 gene varies from 6 to 35 [26]. Expansions containing from 61 to 200 repeats result in the pre-mutation and expansions above 200 repeats result in the full mutation and the fragile X syndrome. The homologous region in the porcine FMR2 gene was found to contain 7 CCG repeats in all breeds analysed (fig. 32). The porcine TNR length exceeds the length of the homologous mouse TNR which is composed of 4 CCG repeats (fig. 32). Furthermore, the length of the porcine CCG TNR is longer than the minimal CCG allele length identified in humans (fig. 32).

Porcine genomic sequences homologous to human poly-glutamine coding TNR expansion regions.

Next we addressed the sequence of poly-glutamine coding TNR sequences of nine porcine loci. SCA1: In the human SCA1 locus CAG TNR expansions in the ATX1 protein causes spinocerebellar ataxia [71, 73]. The human SCA1 TNR region is characterized by the presence of 12 CAG repeats followed by two CAT repeats flanking a CAG triplet [28]. The CAG TNR prone to expand is normally composed of between 6 and 39 repeats and the expanded version consists of 41 to 81 repeats. The porcine SCA1 TNR is composed of two CAG repeats separated by eight proline encoding triplets (fig. 33). However, in Minipigs a variant was detected; the most common allele having a CAG TNR duplication (fig. 33). The dog SCA1 region includes

6 CAG repeats (fig. 33). The mouse and rat homologous region is composed of two CAG repeats and three proline coding triplets (fig. 33). Thus, in terms of CAG repeat numbers the porcine and rodent SCA1 TNRs are similar but distinct from the homologous human TNR (fig. 33). However, due to the presence of numerous proline codons (CCX) the porcine SCA1 TNR have increased complexity compared to the TNR in rodents.

SCA2: The SCA2 TNR expansion, affecting the ATX2 protein, results in spinocerebellar ataxia [73]. This TNR normally consists of 15 to 30 CAG repeats and the expanded form ranges from 35 to 59 triplets [29]. The porcine locus is composed of 7 CAG repeats separated by two CAA triplets (fig. 33). Accordingly, the region encodes a stretch of nine poly-glutamines. No polymorphism whatsoever was observed in the porcine SCA2 TNR region. The dog SCA2 TNR had proline interruptions in the poly-glutamine stretch (fig. 33). The homologous rodent SCA2 TNR is composed of CAG repeats separated by a proline encoding triplet (fig. 33).

SCA3: In the human SCA3 locus a CAG TNR expansion in the ataxin-3 gene above 54 repeats results in ataxia whereas the normal number of CAG repeats varies between 12 and 36 [30-32]. In pigs a five CAG TNR allele was identified in Duroc, Hampshire, and Landrace whereas five and six CAG TNR alleles were identified in Yorkshire and Minipigs (fig. 33). In terms of the number of encoded poly-glutamines the porcine SCA3 TNR region is homologous to the mouse SCA3 TNR region (fig. 33) and well below the critical number in the human counterpart. The dog SCA3 TNR encodes 12 glutamines but includes several CAA interrupting triplets (fig. 33).

SCA6: The SCA6 TNR expansion in the CACNA1A voltage dependent calcium channel results in ataxia [33]. The normal number of TNRs is between 4 and 18 and expansions from 21 to 27 TNRs are disease causative. In pigs a SCA6 allele was identified composed of 5 and 4 CAG repeats separated by a CAA triplet thereby encoding a poly-glutamine stretch of 10 (fig. 33). In Minipigs longer SCA6 alleles composed of 7 or 9 CAG repeats followed by the CAA triplet and 4 CAG repeats (fig. 33) were identified. These alleles encode stretches of 12 and 14 poly-glutamines, respectively. The poly-glutamine stretches encoded by the porcine SCA6 TNR region were comparable in length to the normal range encoded by the human SCA6 sequence, and the 14 poly-glutamine stretch identified in Minipigs matches the upper range of the more common human alleles (fig. 33). In dog a 10 CAG SCA6 TNR was present (fig. 33). We note the absence of a SCA6 TNR in rodents and a high degree of divergence in the CACNA1A

sequence between rodents and pig, dog, and primates at the particular genomic position.

SCA7: The TNR of the human SCA7 locus in the N-terminal end of the ataxin-7 protein is normally composed of 7 to 35 CAG repeats [54]. Disease causing expansions range from 37 to 200 repeats. The TNR of the porcine SCA7 locus contains 5 CAG repeats and no polymorphisms were observed in the breeds (fig. 33). Similarly, the TNR of the mouse SCA7 locus contains 5 CAG repeats (fig. 33). Interestingly, a SCA7 allele with 5 CAG repeats has also been identified in humans. Note that the SCA7 CAG repeats are flanked by a poly-alanine stretch and a glutamine and proline rich stretch highly variable between the examined mammalian genomes (data not shown).

DRPLA: CAG expansions within the human atrophin-1 gene results in dentatorubral-pallidoluysian atrophy (DRPLA) [36]. The normal range of repetitive CAG repeats is from 3 to 25, and in patients with DRPLA allele sizes have expanded to 49 to 88 CAG repeats. The most common natural occurring human allele encodes a stretch of 17 poly-glutamines. In the porcine atrophin-1 TNR, six CAG repeats flanked by multiple CAG and CAA triplets resulting in an allele encoding 14 poly-glutamines (fig. 33) was identified. Moreover, in Minipigs an allele with seven CAGs resulting in a 15 poly-glutamine encoding allele was observed (fig. 33). This means that the length of the porcine atrophin-1 poly-glutamine stretches is above the minimal length observed in humans. The TNR of the mouse atrophin-1 gene encodes six glutamines with an interrupting proline and from the rat gene is encoded 11 glutamines highly interrupted by proline residues (fig. 33). The dog atrophin-1 TNR encodes a stretch of 12 poly-glutamines (fig. 33). In mammalians the atrophin-1 TNR is flanked by histidine rich stretches polymorphic between the examined mammalian genomes (data not shown).

SCA17: A CAG expansion in the TATA box binding protein (TBP) gene is causative of the SCA17 phenotype resulting in ataxia [35]. The human TNR region is composed of two groups of CAG repeats separated by multiple CAA and CAG triplets. Expansions normally progress from the larger of the two CAG groups. The normal stretch of encoded poly-glutamines varies between 29 and 42 whereas poly-glutamine stretches from 47 to 55 have been identified in SCA17 patients. The porcine SCA17 TNR region encodes 26 poly-glutamines and thus is the largest poly-glutamine encoding TNR identified in pigs (fig. 33). The pig SCA17 sequence is composed of four groups of CAG TNRs intervened by CAA triplets (fig. 33). The longest CAG group consists of 10 CAGs. No allele polymorphism was identified in porcine SCA17. In comparison, mouse SCA17 TNR encodes 13 poly-glutamines and a maximum of three CAG triplets in one

stretch (fig. 33). The dog SCA17 TNR encodes 22 glutamines but includes several alanine interruptions (fig. 33).

SBMA: CAG repeat expansions in exon 1 of the androgen receptor (AR) gene on the X-chromosome results in spinal and bulbar muscular atrophy (Kennedy's disease) [37]. The normal length of the human CAG TNR is between 11 and 33 CAG copies and in diseased individuals the expansion ranges from 38 to 62. In the pig an AR allele encoding 7 poly-glutamines interrupted by a single CTG leucine triplet was identified (fig. 33). No TNR variation was observed between the different porcine breeds. In mouse and rat the AR TNR sequence encodes 3 glutamines interrupted by a single AGG arginine triplet or CGG arginine triplet, respectively (fig. 33). The dog AR TNR is composed of a 10 CAG repeats (fig. 33). Note, in mammalians the TNR is flanked by a proline and glutamine rich stretch highly polymorphic between the examined mammalian genomes (data not shown).

HD: The CAG TNR in the Huntingtin gene is located in the 5'-end of the coding region. Normally, the gene contains from 6 to 35 CAG repeats and in Huntington's disease patients more than 35 CAG repeats are present [74]. A large degree of variation was observed in the pig Huntingtin TNR region (fig. 33). This difference was due both to a variable number of CAG repeats but also due to the absence or presence of a CAA triplet which separates the continuous CAG theme into two groups (fig. 33). Alleles with sizes encoding 13 to 24 poly-glutamines from were identified. Highly interesting, in Duroc, an allele composed of a stretch of 21 uninterrupted CAGs, a CAA triplet, and two CAGs resulting in the encoding of a total of 24 poly-glutamines (fig. 33) was identified. This allele represents the largest number of uninterrupted CAGs identified in the analysis of porcine TNRs. The long allele was specifically identified in Duroc and has an allele frequency of 20%. The Minipig Huntingtin gene and polymorphisms therein were described previously [75]. The numbers of poly-glutamines encoded by porcine Huntingtin TNRs are indeed comparable to the human repeat and are for the 24 poly-glutamine allele even above the number of poly-glutamines most frequently found in human Huntingtin alleles. In contrast the mouse Huntingtin TNR region encodes seven poly-glutamines intervened by a CAA triplet and the dog TNR region 10 poly-glutamines (fig. 33). The Huntingtin TNR is flanked by a proline and glutamine rich stretch polymorphic between the examined mammalian genomes (data not shown).

The porcine Huntingtin TNR length is meiotic stable

Since a long uninterrupted CAG TNR sequence was present in the Huntingtin gene of Duroc pigs, we next examined if this sequence was stably inherited or prone to retractions or expansions. For this purpose we used a porcine material consisting of Duroc boars crossed with Landrace and Landrace/Yorkshire crossbread sows. The genotyping of different Huntingtin allele lengths was performed by microsatellite analysis. From the boar cohort, four heterozygous boars were identified having both a 161 bp fragment and a 140 bp fragment corresponding to 24 and 17 glutamines, respectively. The genotyping result of the 4 heterozygous boars was verified by DNA sequencing. The genotyping data from the cohort of the 611 sows used in the breeding scheme resulted in the identification of the alleles also present in the pure Landrace and Yorkshire breeds. Furthermore, two new Huntingtin alleles encoding 14 and 15 glutamines not present in the pure breeds were identified in the sow cohort (table 11). Also the 24 poly-glutamine encoding allele was present in the sow population, however only at a low frequency (0.3 %, table 11). Interestingly, no alleles were identified with a size less than 13 poly-glutamines or a poly-glutamine number of 19, 20, 21, 22, or 23 (table 1 and data not shown). However, since the population of sows was not completely unrelated, the allele frequency calculations are only indicative. The group of genotyped offspring consisted of 349 pigs. All these 349 animals had a genotype in accordance with the inheritance of a maternal and paternal Huntingtin allele without any TNR retractions or expansions (table 12). Thus, we could not identify any evidence for transmission instability of Huntingtin TNRs.

Table 11. Meiotic stability of porcine *Huntingtin* (CAG)24 and (CAG)17 alleles.

Female haplotypes

Male haplotypes		Q=13 L=128 F=0.18	Q=14 L=131 F=0.02	Q=15 L=134 F=0.05	Q=16 L=137 F=0.025	Q=17 L=140 F=0.51	Q=18 L=143 F=0.21	Q=24 L=161 F=0.003
	Q=17 L=140	Q=13,17 L=128,140 N=24	Q=14,17 L=131,140 N=0	Q=15,17 L=134,140 N=11	Q=16,17 L=137,140 N=2	Q=17,17 L=140,140 N=88	Q=18,17 L=143,140 N=49	Q=24,17 L=161,140 N=0

Q=24 L=161	Q=13,24 L=128,161 N=18	Q=14,24 L=131/,161 N=0	Q=15,24 L=134,161 N=10	Q=16,24 L=137,161 N=1	Q=17,24 L=140,161 N=115	Q=18,24 L=143,161 N=31	Q=24,24 L=161,161 N=0

The paternal genotype was 140/161. The sow haplotypes are indicated together with the frequency (F) within the breeding cohort. For all offspring a genotype could be assigned in accordance with transmission of both paternal and maternal alleles not subjected to expansions or retractions. A total of 349 offspring were genotyped. The genotypes are visualized according to the length (L) of the analysed fragments. Q indicates the number of glutamines encoded from the TNR alleles. N indicates the number of offspring with the indicated genotype.

Example 5

Animal model of chondrodysplasia

Only a very limited amount of knowledge is available regarding the presence of collagen X in permanent cartilages, such as trachea, in comparison to growth plate cartilages. We isolated the full length cDNA encoding collagen X from porcine trachea illustrating that collagen X is not solely present in hypotrophic chondrocytes of calcifying matrix typically present in long bones. However, in humans collagen X have, previously been shown in trachea especially in elderly individuals where ossification occur in the tracheal cartilage as a result of the progressing age. Furthermore, in developing rat tracheal cartilage, collagen X was confined to the peripheral uncalcified region of the cartilage [76] indicating that collagen X might play a role beside providing the molecular structural environment in relation to endochondral ossification, however this is not confirmed in humans [77].

Materials and Methods

RNA Isolation

The pig trachea tissue used for RT-PCR cloning of COLA was obtained from an adult pig. Tissue was dissected and pulverized in liquid nitrogen after removal. Total RNA was isolated by RNeasy method (Qiagen). The integrity of RNA samples was verified by ethidium bromide staining of the ribosomal RNA on 1.5 % agarose gels.

DNA Constructs

Generation of a porcine COL10A1 clone was accomplished in the following way: RNA derived from adult porcine trachea was employed in a cDNA synthesis using conditions where 5 µg of total RNA was mixed with 1 µL of oligo (dT)12-18 (500 µg/mL), and DEPC treated H_2O to a final volume of 12 µL. The mixture was incubated at 70°C for 10 min, after which 4 µL of 5 x first-strand buffer, 2 µL of 0.1 mM DTT, 1 µL of 10 mM dNTP mix and 1 µL (200 U/µL) of Superscript II (Invitrogen) was added and the sample was further incubated at 42°C for 1 hour followed by an inactivation step at 70°C for 15 min. oligonucleotides used for RT-PCR cloning were derived from the genomic COL10A1 sequence (Accession number: AF222861) and also contained linkers (Bgl II in the sense primer and Eco RI in the antisense primer) for subsequent cloning. The RT-PCR reaction mix contained 2.5 µL cDNA, 1.5 mM MgCl2, 0.2 mM dNTP, 10 pmol of each primer (COL-F: 5'-AACAGATCTATGCTGCCACAAACAGCCCTTTTGCT -3' (SEQ ID NO:152) and COL-R: 5'-GCAGAATTCTCACATTGGAGCCACTAGGAATCCT-3'(SEQ ID NO:153), and 1.0 U Phusion Fidelity DNA polymerase (Finnzymes), in a total volume of 25 µL using the following conditions: denaturation at 98°C for 2 min., followed by 30 cycles of 98°C for 10 s., 60°C for 30 s., and 72°C for 1 min. The PCR program was concluded by a final extension step at 72°C for 5 min. The PCR was accomplished in a GeneAmp® PCR System 9700 (Applied Biosystems). The amplification product was applied to a 1% ethidium bromide stained agarose gel and a fluorescent band of approximately 2000 bp was isolated using standard procedures and cloned into the pCR®2.1-TOPO vector (Invitrogen, CA) and sequenced in both forward and reverse direction applying standard procedures to ensure that they harboured the CoL10A1 amplicon. The COL10A1 plasmid DNA was digested with Eco RI and ligated into a phCMV1 (Gene Therapy Systems Inc.) expression vector pre-digested with Eco RI. The successful cloning of COL10A1 into the phCMV1 vector was confirmed by sequencing.

In order to create DNA for incubation of sperm cells, large scale PCR reactions were performed. The PCR reactions were carried out in a GeneAmp® PCR System 9700 (Applied Biosystems) in a final volume of 25 µL consisting of 5 µL 5 x Phusion HF buffer, 2 µL dNTP (2.5 mM each) 0.63 µL forward and reverse primer 5 pmol, 0.1 µL Phusion DNA Polymerase (2 U/µL), 1 µL COL10A1-CMV1 template, and 15.6 µL H_2O. The PCR reaction consisted of an initial dnaturation at 98°C for 30 sec followed by 30 cycles of denaturation for 10 sec at 98°C, annealing at 74°C for 30 sec and elongation for 95 sec at 72°C followed by a final elongation step at 72°C for 7 min. The following

primers were used to amplify the COL10A1 construct plus the flanking CMV promoter, intron/enhancer sequence, and SVpolyA, generating a fragment of approximately 3600 bp.

phCMVF: 5'-GTCGGAACAGGAGAGCGCACGAGGG-3' (SEQ ID NO:154)

phCMVR: 5'-GGGTGATGGTTCACGTAGTGGGC-3' (SEQ ID NO:155)

In order to purify the generated PCR product a "High Pure PCR Product Purification Kit" (Roche) was applied. The suppliers' instructions were followed throughout the purification procedure. The PCR purified fragments were sequenced to check for errors in the sequence.

Preparation of Sperm and DNA Uptake

First and second semen ejaculate, were collected from 8 different boars yielding 16 semen fractions in total. All fractions of spermatozoa had an initial motility of 90 prior to the washing procedure. Seminal fluid was quickly removed by washing the sperm in Fertilization Buffer (FB) consisting of 56.1 g Glucose, 3.5 g EDTA ($2H_2O$), 3.5 g Sodium Citrate ($2H_2O$), and 1.1 g sodium bicarbonate dissolved in 1 liter of sterilized water. Furthermore 6 mg/ml BSA (Fraction V, Sigma) was added. Briefly, 5 mL of FB/BSA prewarmed to 37°C was added to 5 mL of undiluted semen and left for 5 minutes at room temperature. Next, FB/BSA at room temperature was added to 50 ml and centrifuged for 10 minutes at room temperature at 500g. The supernatant was removed and semen was resuspended in 50 mL FB/BSA at room temperature and further centrifuged at 500g at 17°C, after which, the supernatant was removed again and the spermatozoa was resuspended in 15 mL of FB/BSA. Next, in order to select the optimal donor cells, the spermatozoa from the different boars were quickly examined under a light microscope. The sperm cells originating from the boar having the highest sperm cell motility after the washing procedure were chosen as vehicles for the subsequent transgenic procedures. Furthermore, the atozoa were counted.

1×10^9 sperm cells from the chosen donor boar were incubated for 100 minutes at 17°C with the linear CoL10A1 DNA fragment in a concentration of 0.4 µg DNA/10^6 spermatozoa in a suspension of 120 mL FB/BSA. The container was inverted every 20 minutes to prevent sedimentation of spermatozoa. Finally, the mixture was incubated 10 minutes at room temperature and employed in artificial insemination of a sow in natural heat.

Animals

Semen was collected from trained Danish Landrace boars that had abstained for 2 days. one recipient sow (Danish Landrace x Yorkshire) at approximately 140 kg were selected due to its natural heating period and used for artificial insemination (1 x 10^9 DNA treated spermatozoa/sow) meeting standard insemination procedures. Insemination was accomplished in the local stable areas at DIAS. The sow was examined for pregnancy 24 and 42 days after insemination, showing that was successfully pregnant. After ended gestation period 6 boar and 6 sow piglets were naturally born and blood samples were withdrawn from the piglets three days after birth in EDTA and serum tubes. Due to economical reasons, 9 animals were sacrificed and hence 2 boars and 1 sow piglet were kept for later investigation. The sow was sacrificed at the age of 7 month since severe phenotypic alterations were present. Animal care and experimental procedures met local, national and European Union Guidelines.

DNA and RNA Studies

DNA was prepared from EDTA stabilized blood samples from the 12 piglets. RNA was prepared from snap frozen tissues from the sacrificed sow (heart, kidney, liver, lung, skin, ovary, musculus longissimus dorsi, musculus semimembranosus, and musculus triceps brachii). To avoid any contamination, all DNA and RNA samples were extracted in special clean laboratory facilities under highly stringent experimental conditions using standard protocols.

PCR and RT-PCR

To ensure the presence of the transgene, 50 ng of genomic DNA from each animal, isolated from blood samples were amplified using the following primers: phCMV_430F: 5'-GTCTCCACCCCATTGACGTC -3' (SEQ ID NO:156) and phCMV_646R: 5'-GGATCGGTCCCGGTGTCTTC-3' (SEQ ID NO:157) yielding a fragment of 217 bp using the following sample mix 1 µL 10 x $MgCl_2$ free reaction buffer, 0.4 µL 50 mM $MgCl_2$, 10 pmol of each primer, 5 mM dNTP-mix, and 0.5 U Dynazyme Ext DNA polymerase. The reaction was performed in a total volume of 10 µL and accomplished as a touchdown PCR in a GeneAmp® PCR system 9700 (Applied Biosystems) under the following conditions: Initial denaturation at 95°C for 3 min, denaturation at 95°C for 30 sec, touchdown from 62 °C to 57 oC with a decrement of 0.5 °C for 20 sec, followed by 1 min of elongation at 72°C pr cycle. Furthermore, 35 cycles of 30 sec denaturation

at 95°C, 20 sec of annealing at 57 °C, and 1 min of elongation at 72°C was included together with a final elongation step at 72°C for 7 min.

Southern Blot Analysis

Transgene integration was determined by Southern blot analysis of DNA from musculus longissimus dorsi from the affected sow. 10 µg of genomic DNA from the affected sow and from a wild type pig was digested with Bgl II and double digested with Bgl II and Bam HI, respectively, and separated on a 0.9% agarose gel, blotted to a nylon membrane and probed with [32P]-labelled collagen X NC1 fragment derived from PCR amplification using the following primers NC1_F: 5´-GCTCTAGAGGTCCCACCCACCCGAAGG-3' (SEQ ID NO:158) and NC1_R: 5'-TCTCTAGATCACATTGGAGCCACTACGAA-3' (SEQ ID NO:159).

Histopathology

From the right foreleg tissues from the growth plates (physis) and metaphyses of femur, ulna and radius were sampled together with the articular areas including the articular-epiphyseal cartilage complex of the shoulder-, elbow-, and carpal joints. From the two hind legs similar tissue samples were collected from the hip and knee joints, i.e. from the femoral and tibial bones. Also the osteo-chondral junction of three ribs was sampled for histology. All tissues were fixed in 10% neutral buffered formalin followed by decalcification in a solution containing 3.3% formaldehyde and 17% formic acid for 2 weeks. The tissues were processed through graded concentrations of alcohol and xylene, and embedded in paraffin wax blocks. Tissue sections of 4-5 µ were stained by haematoxylin and eosin (HE), and in selected cases by Van Gieson for collagen and safranin o for cartilage matrix [78,79].

Results

Sperm Mediated Gene Transfer and Genetically Modified Pigs

In order to establish transgenic pigs which could shed light on the functional role of collagen X a COL10A1 cDNA wild type construct was generated. Interestingly, the porcine COL10A1 cDNA was isolated from trachea using primers generated from the previously known COL10A1 sequence [80]. The cDNA fragment was initially cloned into the pCR®2.1-TOPO vector and subsequently successfully removed to the phCMV1 expression vector facilitating constitutive expression qua the CMV promoter. In order to impede possible truncation of important elements following SMGT, the

COL10A1 DNA fragment employed in the transgenic procedure, include additional nucleotides 5' and 3' prime to the CMV promoter and the polyA fragment which, constitutes a fragment of approximately 3600 bp in total, fig 34.

Initially, eight Danish Landrace boars were used as sperm donors and the sperm fraction showing the highest motility after the initial washing procedure, introduced to remove seminal fluid, was chosen in the subsequent DNA incubation procedure. After ended gestation period 12 normal looking piglets were naturally born and PCR analysis, of DNA isolated from blood, amplifying a 217 bp DNA fragment, located in the 5' –prime phCMV fragment of the construct, showed that all 12 piglets harboured the transgene, see fig 35. However, due to economical reasons only 3 piglets were kept for phenotypical investigations.

Phenotypic Description

At the age of approximately 5½ month one of the three transgenic animals, a sow, developed clinical manifestations of lameness. The sow was oppressed in its movements rising from primarily difficulties with the forelegs, had a toddling gait, a curved back, which however could be a compensation for the abnormalities arising from the fore legs. The signs became slightly worse and at the age of approximately seven month the sow would only walk when forced to, and it would immediately bent down on the elbows and walk on these. However, for ethical reasons the sow was sacrificed at this point.

Southern Blot Analysis

Southern blot analysis, shown in fig. 36, performed on tissue from musculus longissimus dorsi from the diseased sow and a normal wild type pig reveals additional bands in the affected pig, when digested with Bgl II and Bam HI in comparison to the control using the entire collagen NC1 domain as a radiolabelled probe. This therefore, led us to conclude that the transgene has become integrated into the genome of the affected pig. Unfortunately, Bgl II did only digest the genomic DNA to a limited degree, and hence no difference is seen regarding additional bands in the unidigestion using this enzyme alone (lane 1 and 2).

Expression Analysis

Expression of the COL10A1 construct was accomplished by RT-PCR using primers located in COL10A1 exon 2 and COL10A1 exon 3 on total RNA isolated musculus triceps brachii, ovary, kidney, skin, liver, lung, musculus longissmus dorsi, musculus semimembranosus, heart, and liver, spleen, kidney, lung, and heart from a wild type control. The RT- PCR analysis revealed expression of collage X in kidney, lung, and heat in the affected sow, although only very limited amounts of transcript are present in kidney, fig 37. However, since the PCR is only qualitative, the judgement of expression levels within the samples should be taken with precaution, although the same amount of total RNA has been used in the cDNA synthesis. Furthermore, no expression of CoL10A1 is present in the wild type control tissues.

Histopathology

The articular-epiphyseal area of the humeral trochlea constituting the proximal portion of the elbow joint, revealed severe alterations, see fig 38. The cartilage was retained with contents of hypertrophied chondrocytes. Within areas of retained cartilage formation of clefts were regularly seen, and in the depth irregular cavitations filled with fibrinous material were present along with eosinophilic streaks. Moreover, the distal growth plates of both ulna and radius were irregular with localized areas of retained cartilage. Lesions were not present within sections from the ribs, the articular-epiphyseal areas or the growth plates of the hind legs.

Thus in conclusion, the integration and expression of the COL10A1 transgene gave rise to a dyschondroplasia phenotype affecting especially the two fore limbs of a sow. The alterations present in the transgeneic sow, resembles osteochondrosis which is known to affect younger animals, and is characterised by similar lesions of the articular-epiphyseal cartilage complex [41] as observed in the forelegs of the present sow.

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Claims

1. A non-human animal model for a hereditary autosomal dominant disease, wherein the non-human animal model expresses at least one phenotype associated with said hereditary autosomal dominant disease obtained by a genetic determinant.

2. A non-human animal model for a hereditary autosomal dominant disease, wherein the non-human animal model expresses at least one phenotype associated with said hereditary autosomal dominant disease obtained by sperm-mediated gene transfer.

3. The model according to claim 1 or 2, wherein the autosomal dominant disease is a protein conformation disease.

4. The model according to claim 1 or 2, wherein the autosomal dominant hereditary disease is Amyotrophic Lateral Sclerosis (ALS).

5. The model according to claim 1 or 2, wherein the autosomal dominant hereditary disease is Alzheimer's Disease.

6. The model according to claim 1 or 2, wherein the autosomal dominant hereditary disease is Parkinson's Disease.

7. The model according to claim 1 or 2, wherein the autosomal dominant hereditary disease is diseases related to Trinucleotide Repeats.

8. The model according to claim 7, wherein the autosomal dominant hereditary disease is Huntington's Chorea.

9. The model according to claim 1 or 2, wherein the autosomal dominant hereditary disease is dyschondroplasia.

10. A pig model for a hereditary autosomal dominant disease, wherein the pig model expresses at least one phenotype associated with said hereditary autosomal disease obtained by a genetic determinant.

11. A pig model for a hereditary autosomal dominant disease, wherein said disease is a protein conformation disease obtained by a genetic determinant.

12. A pig model for a hereditary neurodegenerative autosomal domainant disease obtained by a genetic determinant.

13. A pig model for amyotrophic lateral sclerosis obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with Amyotrophic Lateral Sclerosis.

14. A pig model for Alzheimer's Disease obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with Alzheimer's Disease.

15. A pig model for Parkinson's Disease obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with Parkinson's Disease.

16. A pig model for diseases related to Trinucleotide Repeats obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with a disease related to Trinucleotide Repeats.

17. A pig model for Huntington's chorea obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with Huntington's chorea.

18. A pig model for dyschondroplasia obtained by a genetic determinant, wherein the pig model expresses at least one phenotype associated with chondrodysplasia.

19. The non-human animal model according to claim 1, wherein the non-human animal is a pig.

20. The model according to any of claims 10 to 18, wherein the pig is not a mini-pig.

21. The model according to claim 20, wherein the pig belongs to the species of S. domesticus.

22. The model according to claim 20, wherein the pig is selected from the group consisting of Landrace, Yorkshire, Hampshire, Duroc, Chinese Meishan, Berkshire and Piêtrain, including any combination thereof.

23. The model according to claim 19, wherein the pig is an inbred pig.

24. The model according to any of claims 10-18, wherein the pig is a mini-pig.

25. The model according to claim 24, wherein the mini-pig is selected from the group consisting of Goettingen, Yucatan, Bama Xiang Zhu, Wuzhishan and Xi Shuang Banna, including any combination thereof.

26. The model according to any of claims 1 to 25 obtainable by a sperm mediated gene transfer method (SMGT) comprising the steps of

i) providing semen from a male, non-human animal

ii) providing a genetic determinant capable of establishing said at least one phenotype associated with said hereditary disease when the genetic determinant is expressed in said non-human animal model,

iii) contacting said semen and said genetic material,

iv) fertilising an oocyte from a female, non-human animal with the semen and the genetic determinant, and

v) incubating said fertilised oocyte under conditions allowing said fertilised oocyte to develop into said non-human animal model.

27. A method for producing the model according to any of claims 1 to 25, said method comprising the steps of

i) providing semen from a male, non-human animal

ii) providing at least one genetic determinant capable of establishing said at least one phenotype associated with said hereditary disease when the at least one genetic determinant is expressed in said non-human animal model

iii) contacting said semen and said at least one genetic determinant,

iv) fertilising an oocyte from a female, non-human animal with the semen and the genetic material, and

v) incubating said fertilised oocyte under conditions allowing said fertilised oocyte to develop into said non- human animal model.

28. The method of claim 27, wherein said model expresses at least one phenotype associated with a hereditary disease.

29. The method of claim 28, wherein the hereditary disease is autosomal dominant.

30. The method of claim 28, wherein the hereditary autosomal disease is as defined in any of claims 1-18.

31. The method of claim 24, wherein the non-human animal is a pig.

32. The method of claim 31, wherein the pig is not a mini-pig.

33. The method of claim 32, wherein the pig belongs to the species of S. domesticus.

34. The method of claim 32, wherein the pig is selected from the group consisting of Landrace, Yorkshire, Hampshire, Duroc, Chinese Meishan, Berkshire and Piêtrain, including any combination thereof.

35. The method of claim 31, wherein the pig is an inbred pig.

36. The method of claim 31, wherein the pig is a mini-pig.

37. The method of claim 36, wherein the mini-pig is selected from the group consisting of Goettingen, Yucatan, Bama Xiang Zhu, Wuzhishan and Xi Shuang Banna, including any combination thereof.

38. The method of claim 27, wherein the contacting said semen and said genetic material occurs in a buffer composition comprising i) glucose and ii) a citrate salt and/or a bicarbonate salt, preferably the sodium salt thereof, optionally in combination with iii) a compound capable of chelating divalent metal ions, such a e.g EDTA, and further optionally in combination with iv) Bovine Serum Albumine (BSA), including any combination of i) and ii) with iii) or iv).

39. A method for evaluating the response of a therapeutical treatment of a hereditary disease, said method comprising the steps of

a. providing the non-human animal model according to any of claims 1 to 25,

b. treating said non-human animal with at least one pharmaceutical composition exerting an effect on said at least one phenotype, and

c. evaluating the effect observed.

40. The method of claim 39 comprising the further step of advising on medical treatment based on the afore-mentioned observed effects.

41. A non-human sperm cell comprising at least one genetic determinant exerting at least one dominant phenotype for at least one hereditary disease when expressed in a non-human animal host organism.

42. The non-human sperm cell according to claim 41, wherein the hereditary disease is an autosomal dominant disease.

43. The non-human sperm cell according to claim 41, wherein the hereditary autosomal disease is as defined in any of claims 1-18

44. The non-human sperm cell according to any of claims 41 to 43, wherein the genetic determinant is of mammalian origin, including human origin or porcine origin.

45. The non-human sperm cell according to any of claims 41 to 43, wherein said model is genetically modified

46. A method for producing the non-human sperm cell according to any of claims 41 to 44, said method comprising the steps of

a. providing a non-human sperm cell,
b. providing at least one genetic determinant exerting a dominant phenotype for a hereditary disease when expressed in a non-human animal host organism,
c. contacting said non-human sperm cell and said at least one genetic determinant, wherein said contacting results in the uptake of the genetic determinant into the non-human sperm cell.

47. The method of claim 46, wherein the non-human sperm cell is a pig sperm cell.

48. The method of claim 46, wherein the hereditary disease is an autosomal dominant disease as defined in any of claims 1 to 18.

49. A composition comprising a non-human sperm cell in combination with at least ond genetic determinant exerting at least one dominant phenotype for at least one hereditary disease when expressed in a non-human animal host organism.

50. The composition according to claim 49, wherein the hereditary disease is an autosomal dominant disease as defined in any of claims 1 to 18.

51. The composition according to any of claims 49 to 50, wherein the genetic determinant is of human origin or porcine origin.

52. A method for fertilising an oocyte by sperm-mediated gene transfer, said method comprising the steps of providing the non-human sperm cell according to any of

claims 41 to 44 and introducing said non-human sperm cell into the oocyte to be fertilised.

53. A method for fertilising an oocyte by sperm-mediated gene transfer, said method comprising the steps of providing the composition according to any of claims 50 to 51 and introducing said composition into the oocyte to be fertilised.

54. An embryo obtained by fertilising an oocyte with the non-human sperm cell according to any of claims 41 to 44.

55. An embryo obtained by fertilising an oocyte with the composition according to any of claims 49 to 50.

56. A method for the cultivation and development of the embryo according to any of claims 54 or 55, said method comprising the step of cultivating said embryo under conditions allowing the embryo to develop into a non-human animal offspring expressing said genetic determinant and exerting a dominant phenotype for a hereditary disease.

57. A method for screening the efficacy of a pharmaceutical composition, said method comprising the steps of

a. providing the non-human animal model according to any of claims 1 to 25,
b. expressing in said animal model said at least one genetic determinant and exerting said dominant phenotype for said hereditary disease,
c. administering to said non-human animal the pharmaceutical composition the efficacy of which is to be evaluated, and
d. evaluating the effect, if any, of the pharmaceutical composition on the phenotype exerted by the genetic determinant when expressed in the non-human model.

```
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421   GGAAGTCGTT TGGCCTGTGG TGTAATTGGG ATCACCCAGT AA
```

Fig. 1

```
1    ATGGCGACGA AGGCCGTGTG TGTGCTGAAG GGCGACGGCC CGGTGCAGGG CACCATCTAC
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421  GGAAGTCGTT TGGCCTGTGG TGTAATTGGG ATCACCCAGT AA
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Fig. 2

```
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R.norvegicus    MAMKAVCVLKGDGPVQGVIHFEQKASGEPVVVSGQITGLTEGEHGFHVHQYGDNTQGCTT 60
H.sapiens       MATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKGLTEGLHGFHVHEFGDNTAGCTS 60
s.scrofa        MATKAVCVLKGDGPVQGTIYFELK-GEKTVLVTGTIKGLAEGDHGFHVHQFGDNTQGCTS 59
                ** ************** * ** * .  .* : * *.**:** ******::**** ***:

M.musculus      AGPHFNPHSKKHGGPADEERHVGDLGNVTAGKDGVANVSIEDRVISLSGEHSIIGRTMVV 120
R.norvegicus    AGPHFNPHSKKHGGPADEERHVGDLGNVAAGKDGVANVSIEDRVISLSGEHSIIGRTMVV 120
H.sapiens       AGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTLVV 120
S.scrofa        AGPHFNPESKKHGGPKDQERHVGDLGNVTAGKDGVATVYIEDSVIALSGDHSIIGRTMVV 119
                ******* *:***** *:**********:*.***** * *** **:***:*.*****:**

M.musculus      HEKQDDLGKGGNEESTKTGNAGSRLACGVIGIAQ 154
R.norvegicus    HEKQDDLGKGGNEESTKTGNAGSRLACGVIGIAQ 154
H.sapiens       HEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ 154
S.scrofa        HEKPDDLGRGGNEESTKTGNAGSRLACGVIGITQ 153
                  *** ****:**********************.*
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Fig. 3

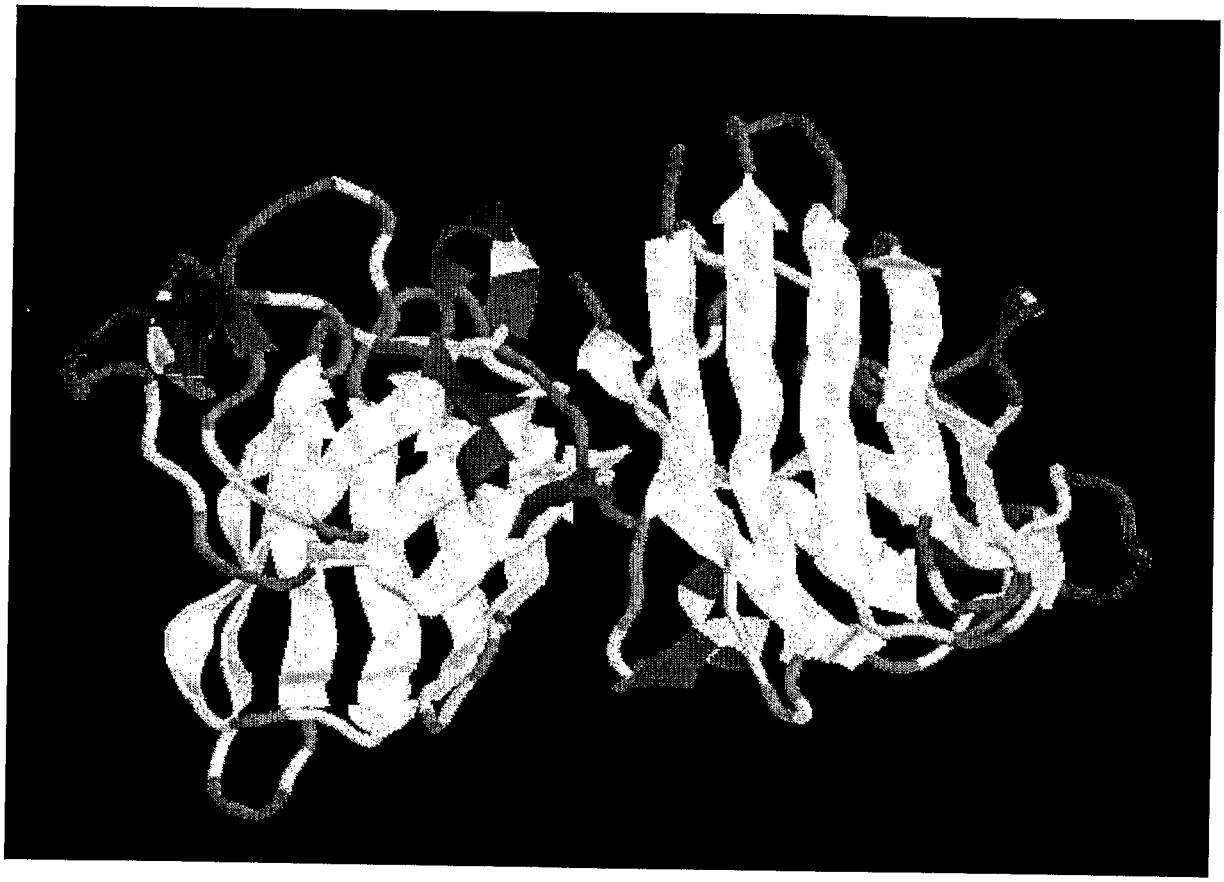

Fig. 4

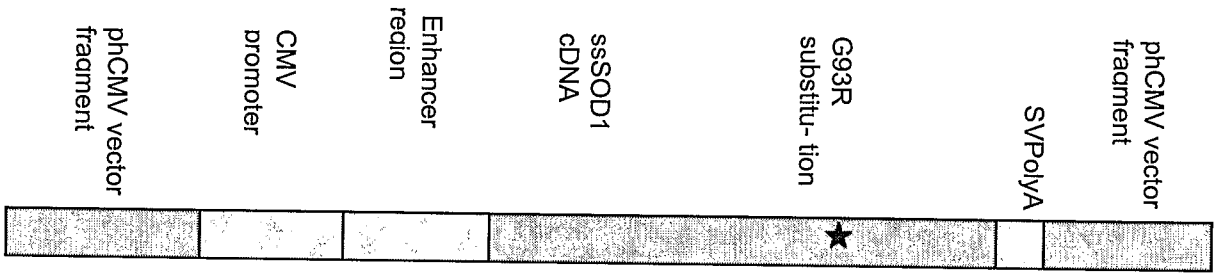
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Fig. 5

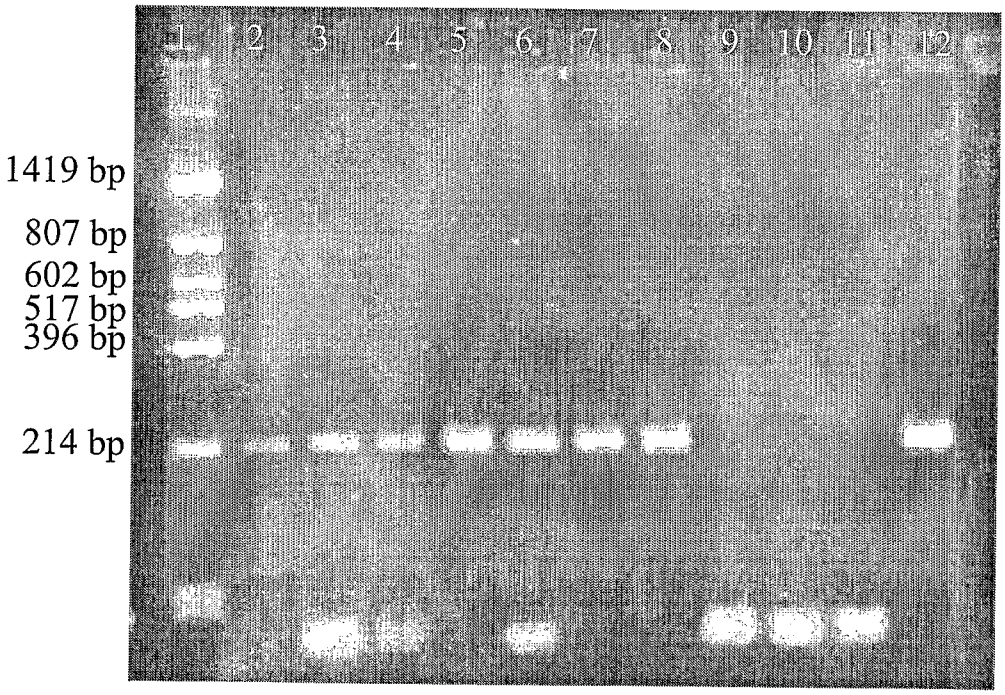

Fig. 6

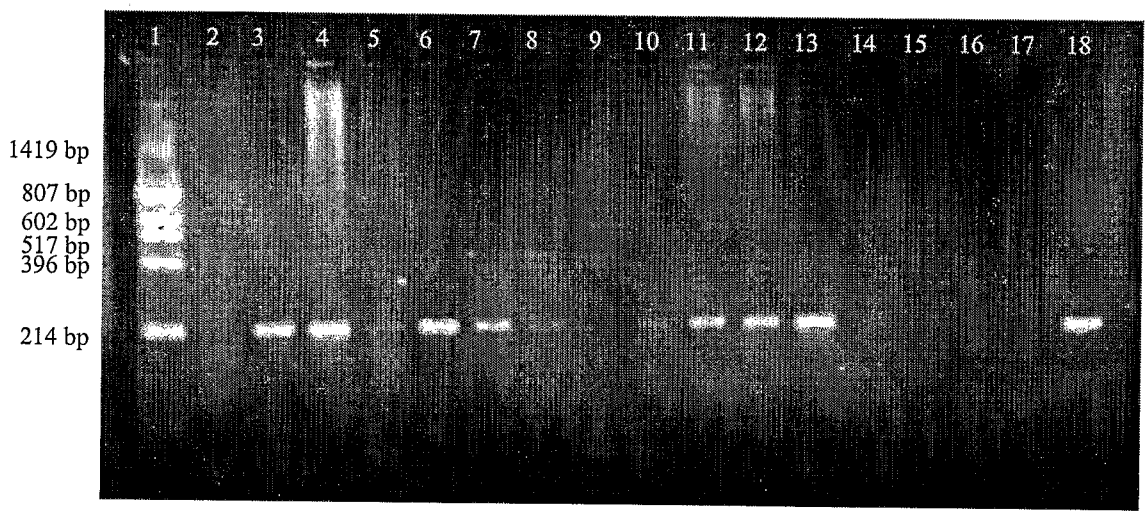
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Fig. 7

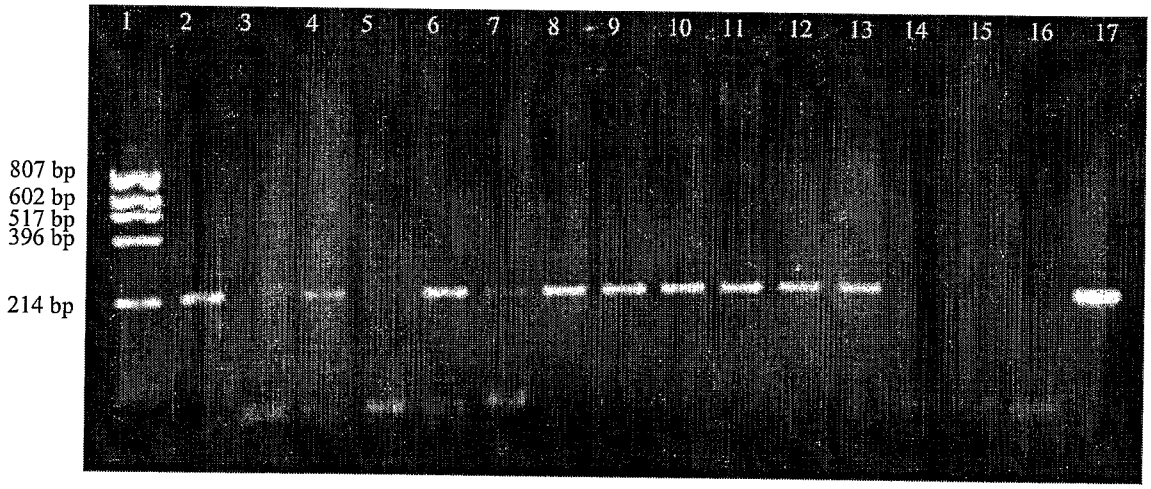
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Fig. 8

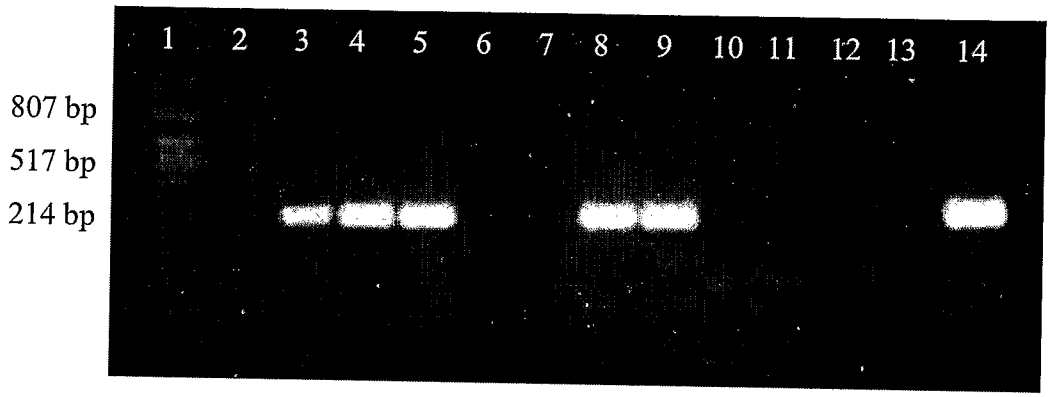


Fig. 9

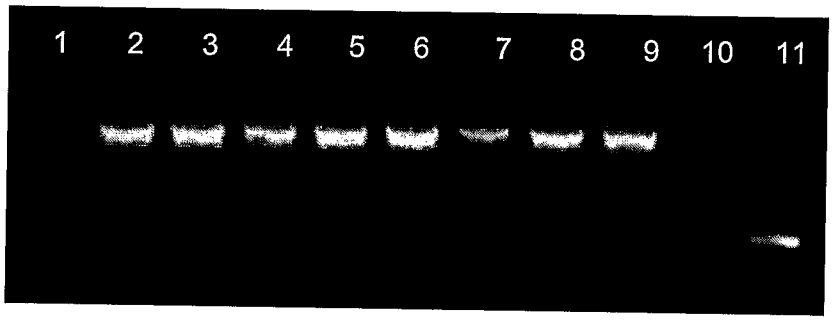


Fig. 10

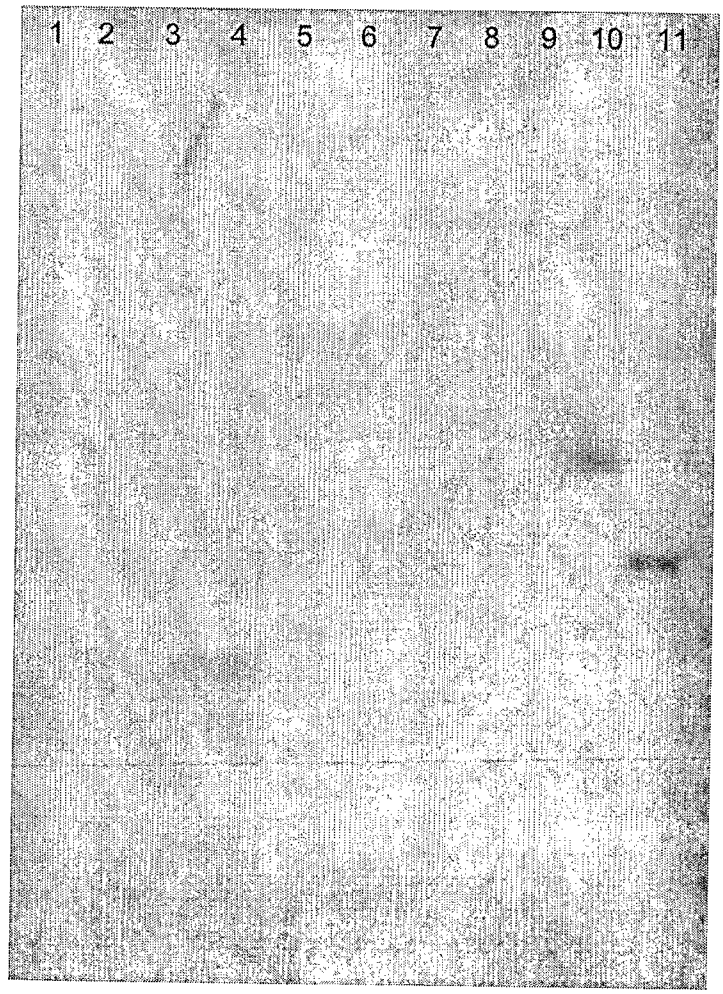
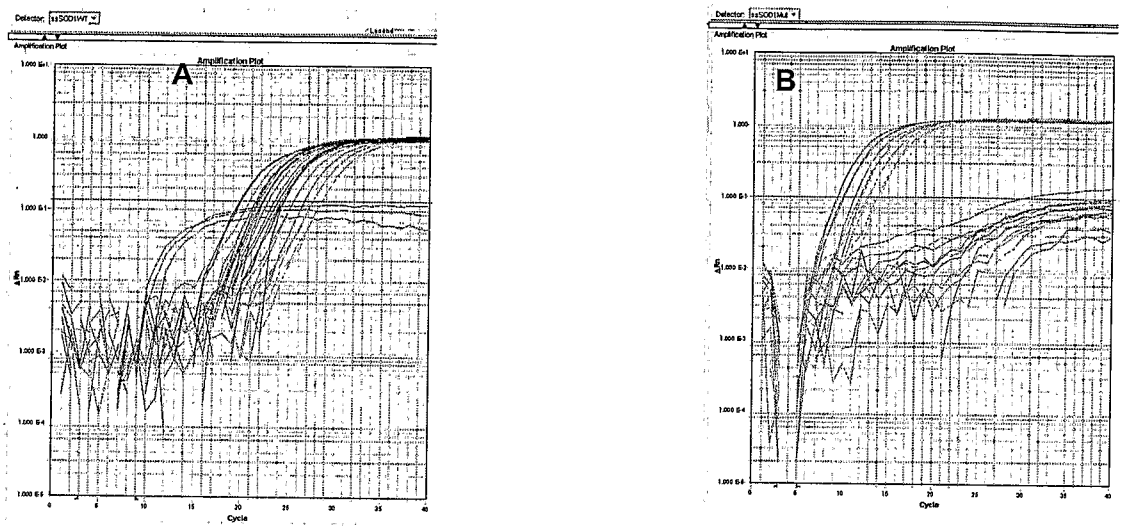


Fig. 11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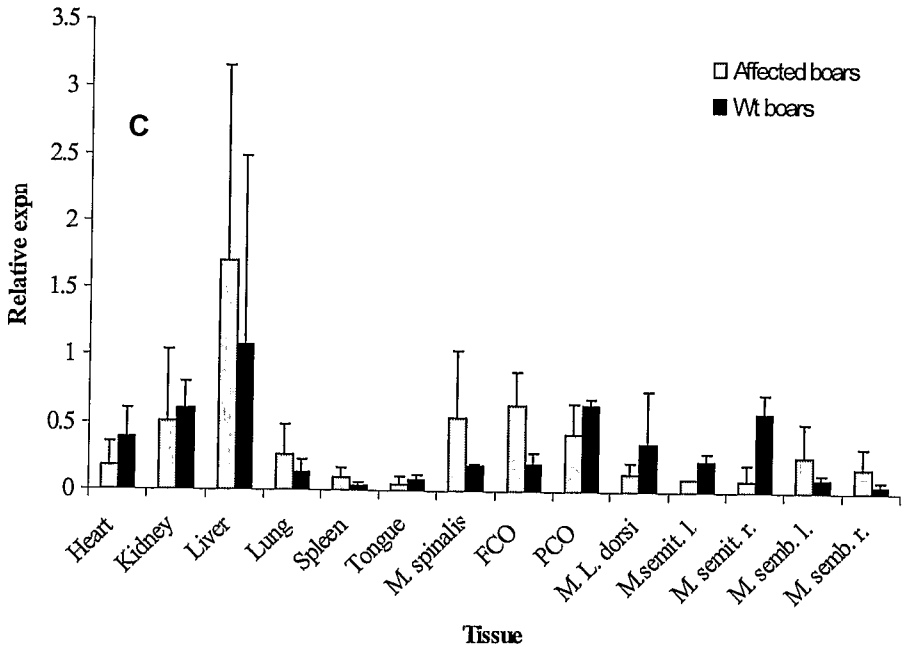
B
Amplification Plot
Cycle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Lung
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Tongue
M. spinalis
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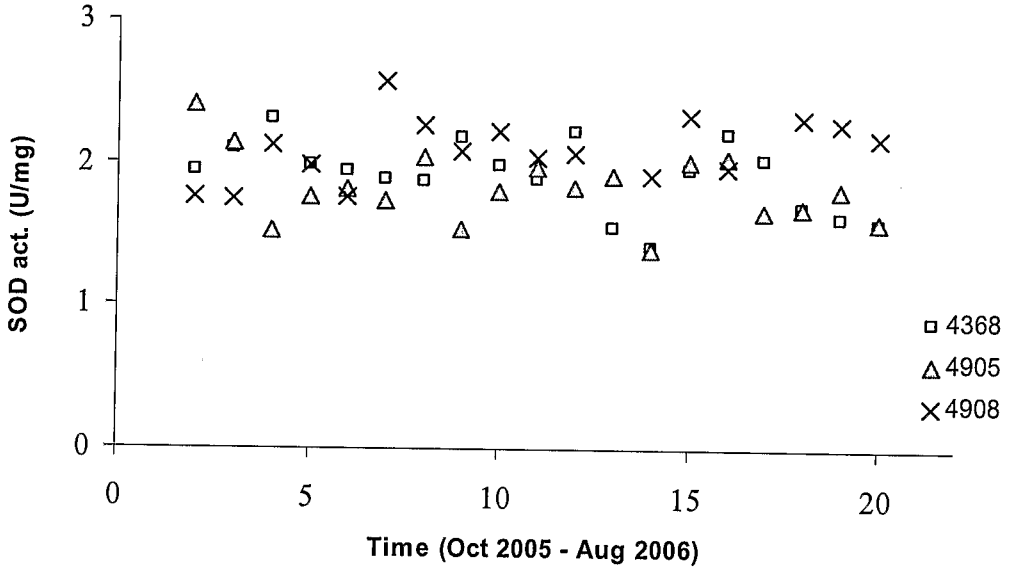
M. semb. l.
M. semb. r.
Tissue

Fig. 12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Time (Oct 2005 - Aug 2006)
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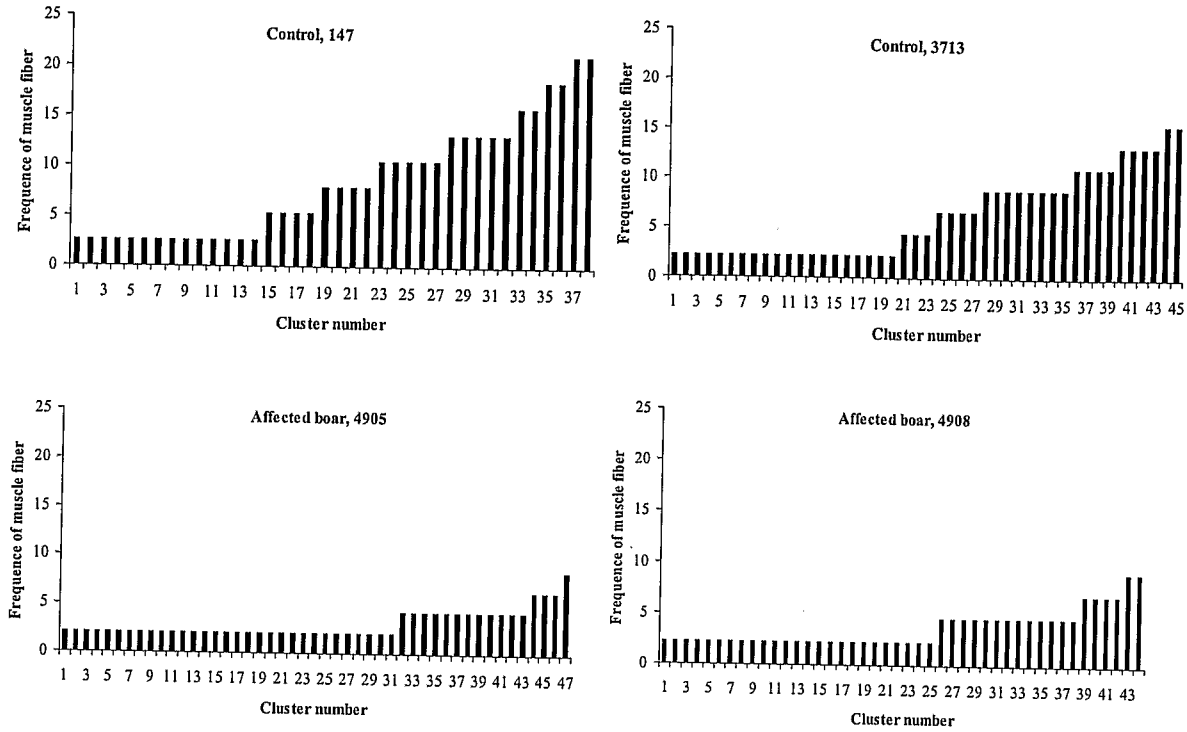
4908

Fig. 13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Frequence of muscle fiber
Cluster number

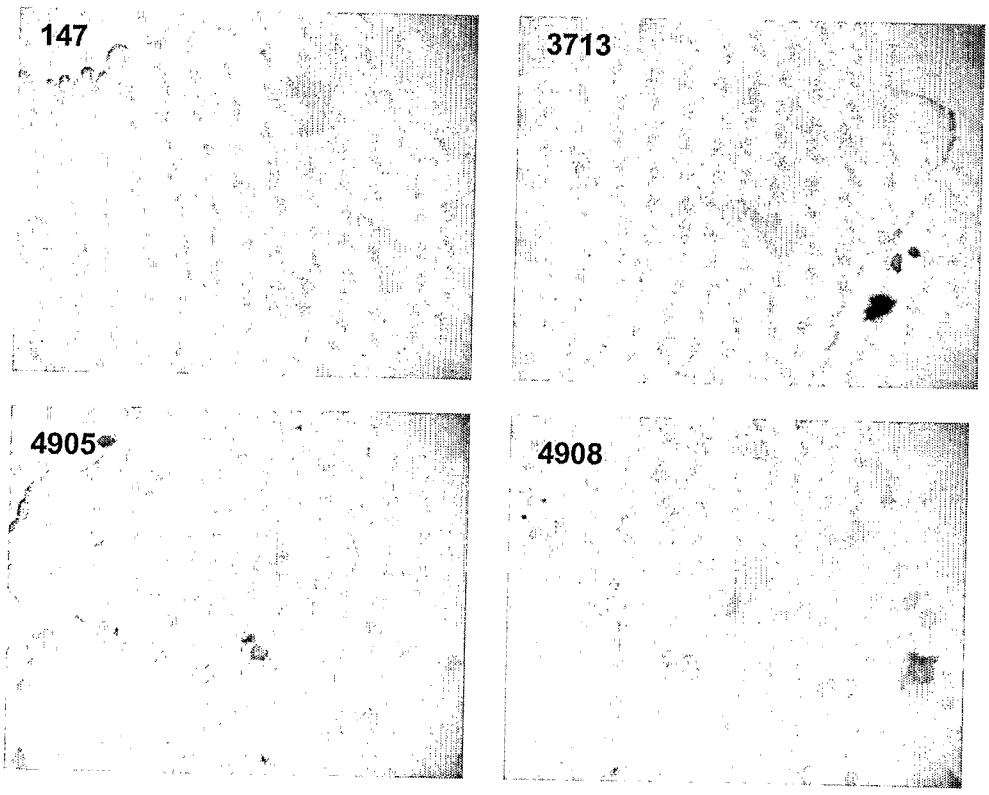

147
3713
4905
4908

Fig. 14

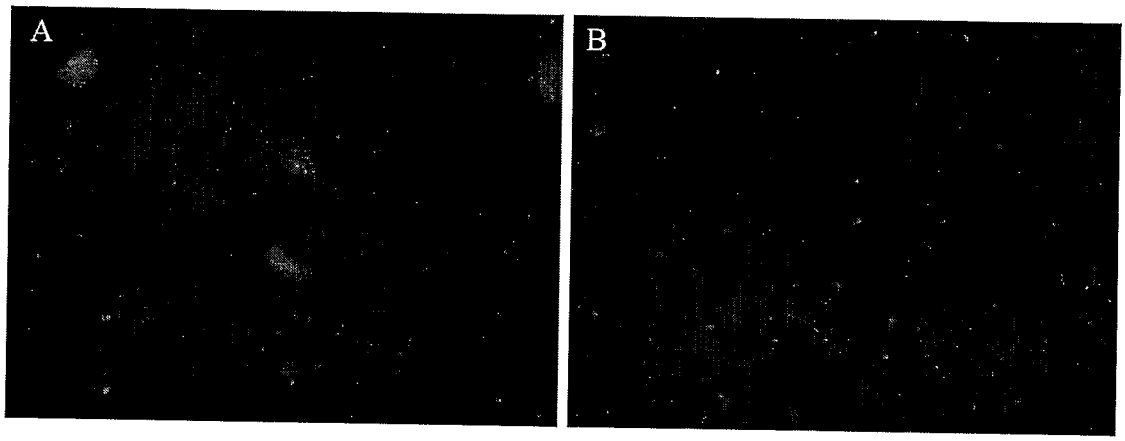


Fig. 15

```
   1  cagtctgtta gggggaggag cttatttctc cattccggtg tgatccagga acagctgttt
  61  tccctccagc tctgaaagtg tggggtaaag gaattcatta gccatggatg tattcatgaa
 121  aggactttca aaagccaagg agggagtcgt ggctgctgct gaaaaaacca aacagggtgt
 181  ggcagaagca gcgggaaaga caaaagaggg tgtgctctat gtaggatcca aaaccaagga
 241  aggagtggtt catggtgtga caacagtggc tgagaagacc aaagagcaag tgacaaatgt
 301  tggagaggca gtggtgacag gggtgacagc ggtagcacag aagacagtgg aaggagcagg
 361  gagcattgca gctgccactg gctttggcaa aaaggatcag ctgggcaaga atgaagaagg
 421  agccccccag gagggaattc tggaagatat gcctgtggat cctgacaatg aagcttatga
 481  aatgccttcc gaggaagggt atcaggacta tgaaccggaa gcctaagggg tatctttgct
 541  cccagtttcc tgagatctgc tgacagacgt gccatcctgt ccaagtgccc cgttcccacc
 601  tgcccagtcg tgaccttctc tcaacgcttt cacagtgtct tttgaagtct tccatgagca
 661  gtgactggag tatctgtacc cgccccacct cggttccggt gcttccctct cactgaatat
 721  atggtagcag ggtcttgtgt gctgtggctg ttgtggcttc gaacctaaaa tgtttaatga
 781  aaaacaccta agtgactacc acttatttct aaatctattt tttgttgctg ttgagaaatt
 841  gtgagtgatt tactctccta agatttaaaa gtgtcttttc aggattccgt cgaagaataa
 901  tgatgtatgg cgaaatttgt taatatatac aatacttaaa catgtgagca tggaactatg
 961  cacctataaa tattaactat ag
```

Fig. 16

```
                                                ↓
SsSNCA      MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTK   60
HsSNCA      MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTK   60
BtSNCA      MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGRTKEGVLYVGSKTKEGVVHGVTTVAEKTK   60
MmSNCA      MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAETTK   60
RnSNCA      MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTK   60
XlSNCA      MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTK   60
GgSNCA      MDVFMKGLNKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSRTKEGVVHGVTTVAEKTK   60
            ******** ********************** ********** ********* **** **

SsSNCA      EQVTNVGEAVVTGVTAVAQKTVEGAGSIAAATGFGKKDQLGK-NEEGAPQEGILE---DM  116
HsSNCA      EQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGK-NEEGAPQEGILE---DM  116
BtSNCA      EQVTNVGEAVVTGVTAVAQKTVEGAGSIAAATGFGKKDHMGK-GEEGASQEGILE---DM  116
MmSNCA      EQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGK-GEEGYPQEGILE---DM  116
RnSNCA      EQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGK-GEEGYPQEGILE---DM  116
XlSNCA      EQVSNVGGAVVTGVTAVAHKTVEGAGNFAAATGLVKKDQ-K--NESGFGPEGTMENSENM  117
GgSNCA      EQVSNVGGAVVTGVTAVAQKTVEGAGNIAAATGLVKKDQLAKQNEEGFLQEGMVNNT-DI  119
            *** *** ********** *******  *****  ***      * *   **

SsSNCA      PVDPDNEAYEMPSEEGYQDYEPEA 140
HsSNCA      PVDPDNEAYEMPSEEGYQDYEPEA 140
BtSNCA      PVDPDNEAYEMPSEEGYQDYEPEA 140
MmSNCA      PVDPGSEAYEMPSEEGYQDYEPEA 140
RnSNCA      PVDPSSEAYEMPSEEGYQDYEPEA 140
XlSNCA      PVNPNNETYEMPPEEEYQDYDPEA 141
GgSNCA      PVDPENEAYEMPPEEEYQDYEPEA 143
            ** *  * **** ** **** ***

                                                ↓
```

Fig. 17

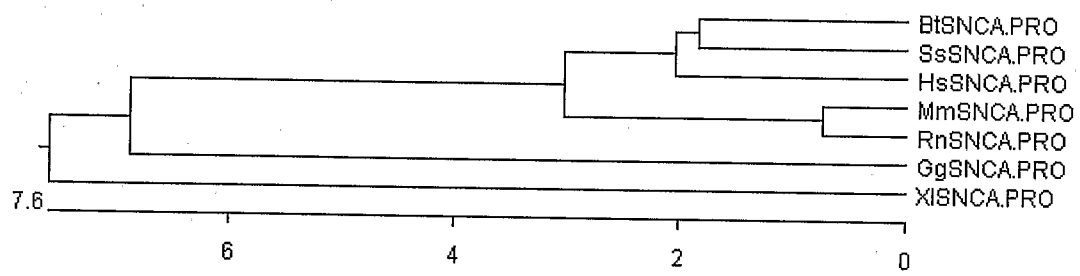

BtSNCA.PRO
SsSNCA.PRO
HsSNCA.PRO
MmSNCA.PRO
RnSNCA.PRO
GgSNCA.PRO
XlSNCA.PRO
7.6
6
4
2
0

Fig. 18

```
   1  cagtctgtta gggggaggag cttatttctc cattccggtg tgatccagga acagctgttt
  61  tccctccagc tctgaaagtg tggggtaaag gaattcatta gccatggatg tattcatgaa
 121  aggactttca aaagccaagg agggagtcgt ggctgctgct gaaaaaacca aacagggtgt
 181  ggcagaagca ccgggaaaga caaaagaggg tgtgctctat gtaggatcca aaaccaagga
 241  aggagtggtt catggtgtga caacagtggc tgagaagacc aaagagcaag tgacaaatgt
 301  tggagaggca gtggtgacag gggtgacagc ggtagcacag aagacagtgg aaggagcagg
 361  gagcattgca gctgccactg gctttggcaa aaaggatcag ctgggcaaga atgaagaagg
 421  agcccccag gagggaattc tggaagatat gcctgtggat cctgacaatg aagcttatga
 481  aatgccttcc gaggaagggt atcaggacta tgaaccggaa gcctaagggg tatctttgct
 541  cccagtttcc tgagatctgc tgacagacgt gccatcctgt ccaagtgccc cgttcccacc
 601  tgcccagtcg tgaccttctc tcaacgcttt cacagtgtct tttgaagtct tccatgagca
 661  gtgactggag tatctgtacc cgccccacct cggttccggt gcttccctct cactgaatat
 721  atggtagcag ggtcttgtgt gctgtggctg ttgtggcttc gaacctaaaa tgtttaatga
 781  aaaacaccta agtgactacc acttatttct aaatctattt tttgttgctg ttgagaaatt
 841  gtgagtgatt tactctccta agatttaaaa gtgtcttttc aggattccgt cgaagaataa
 901  tgatgtatgg cgaaatttgt taatatatac aatacttaaa catgtgagca tggaactatg
 961  cacctataaa tattaactat ag
```

Fig. 19

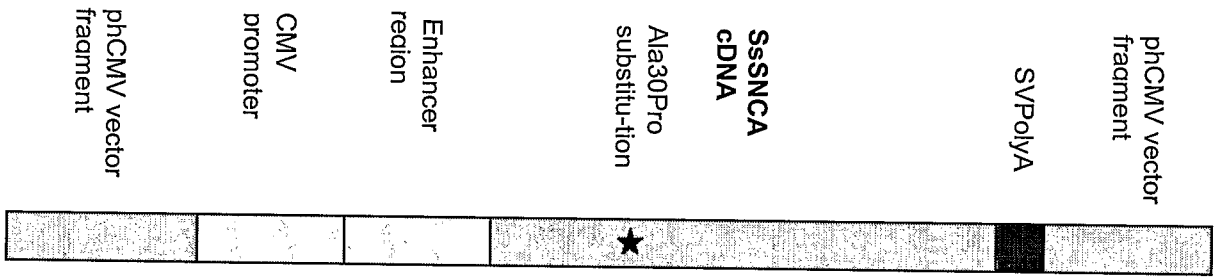

phCMV vector fragment
SVPolyA
SsSNCA cDNA
Ala30Pro substitu-tion
Enhancer region
CMV promoter
phCMV vector fragment

Fig. 20

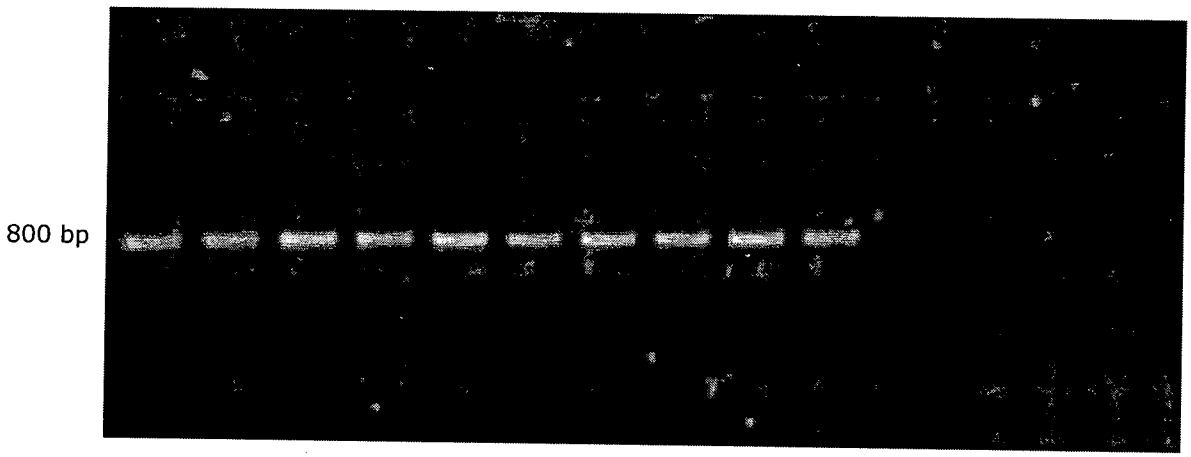


Fig. 21

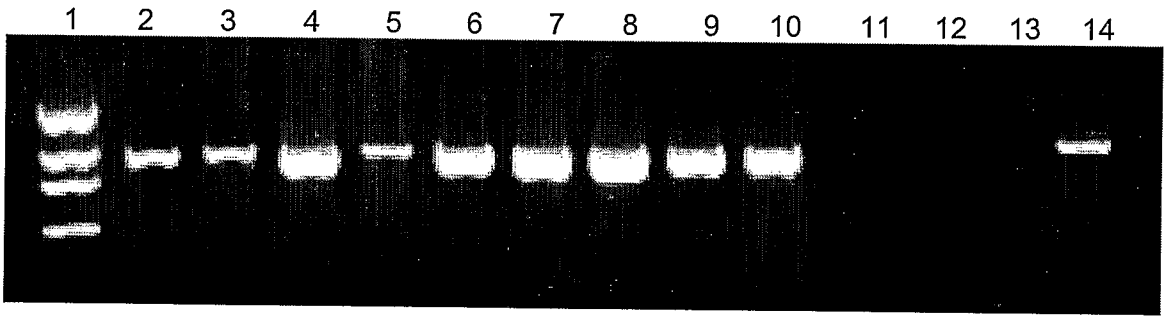


Fig. 22

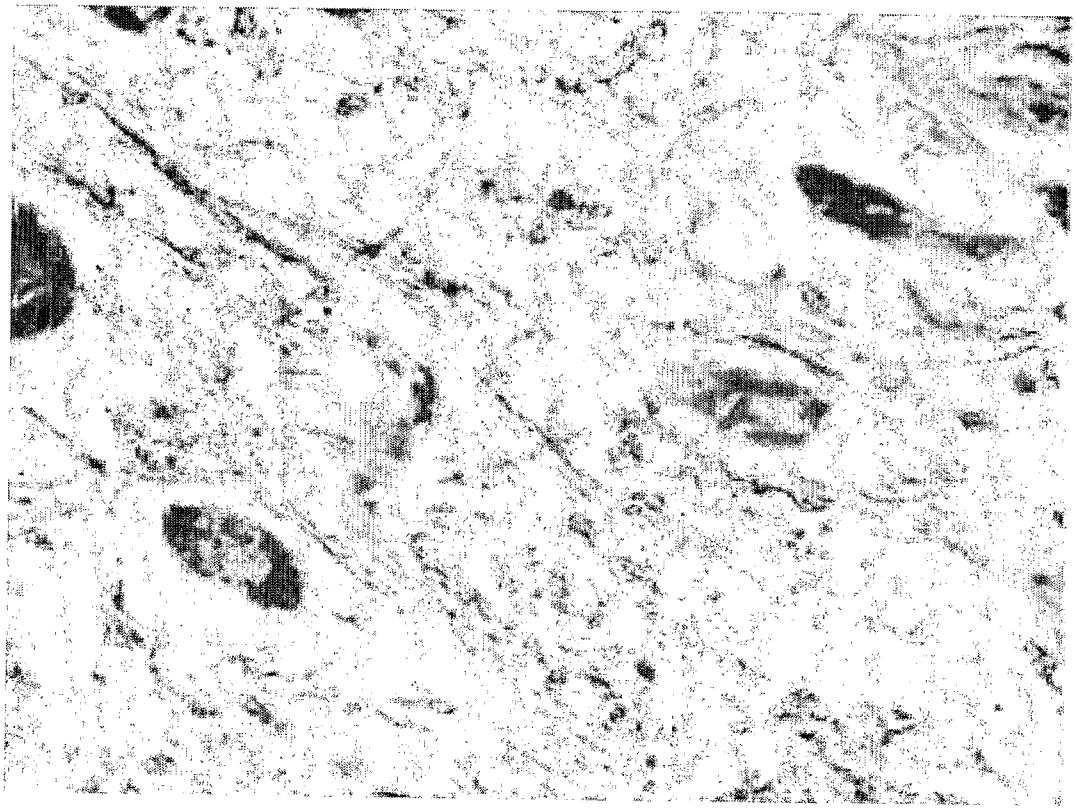


Fig. 23

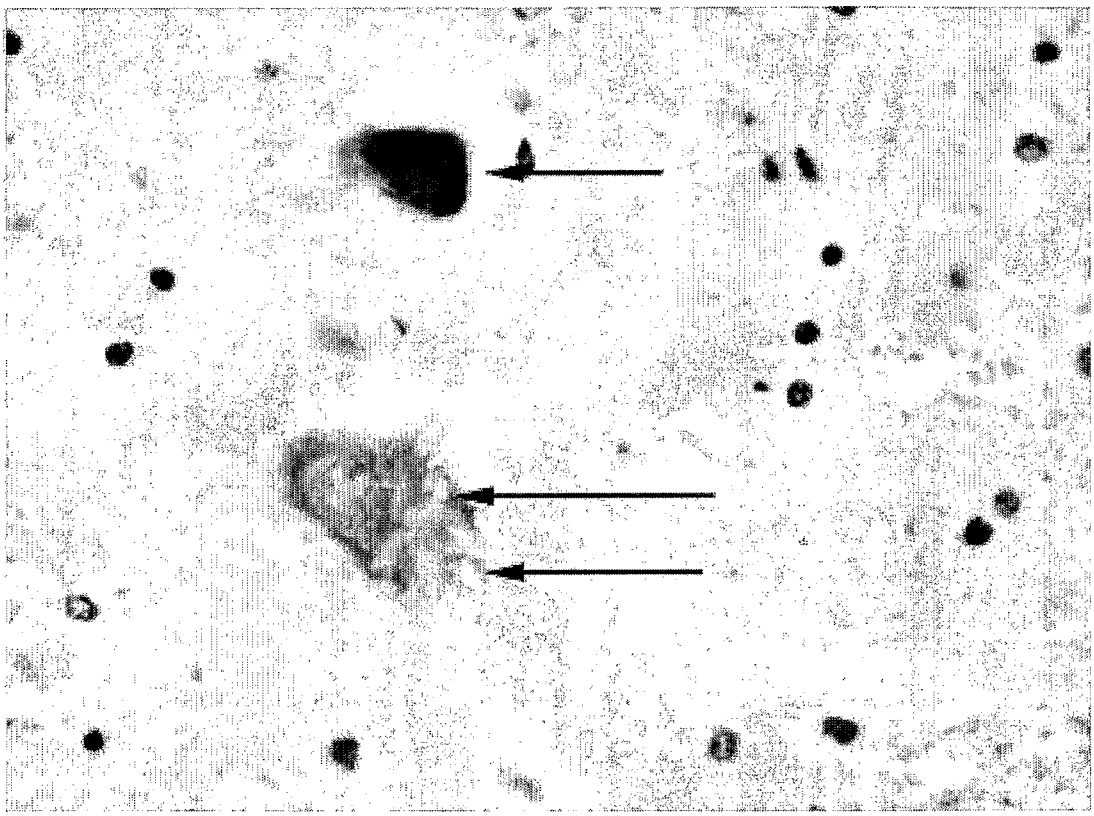
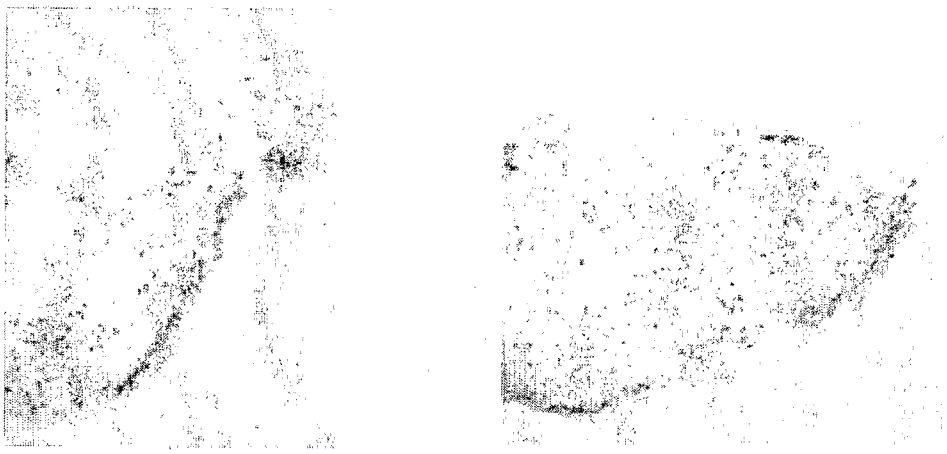


Fig. 24

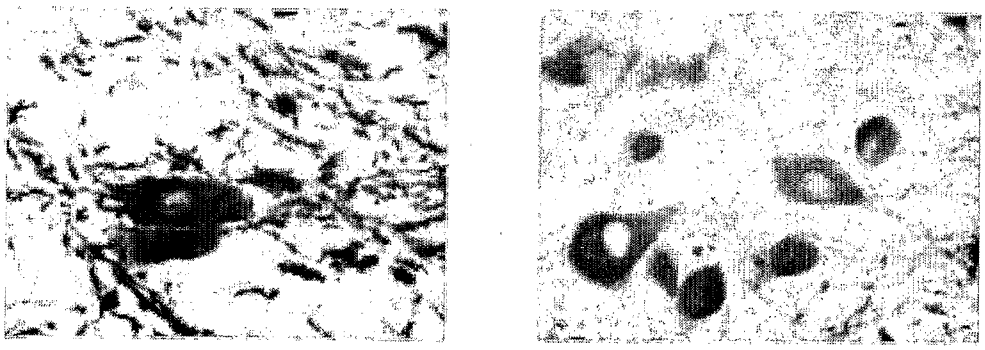
A B

Comparison to normal minipig brain

CK1 Minipig



The number of dopaminergic cells seems to be reduced

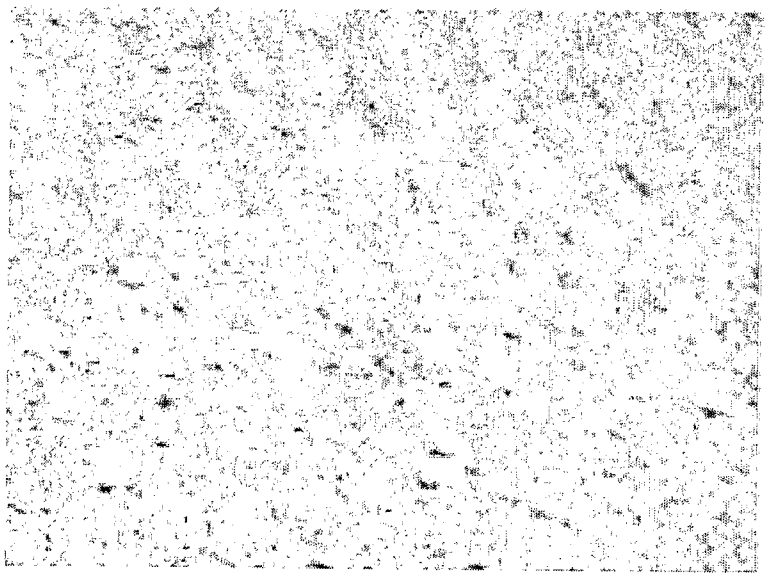


The remaining dopaminergic cells and neuropil seems to be more rough and unordered

Fig. 25

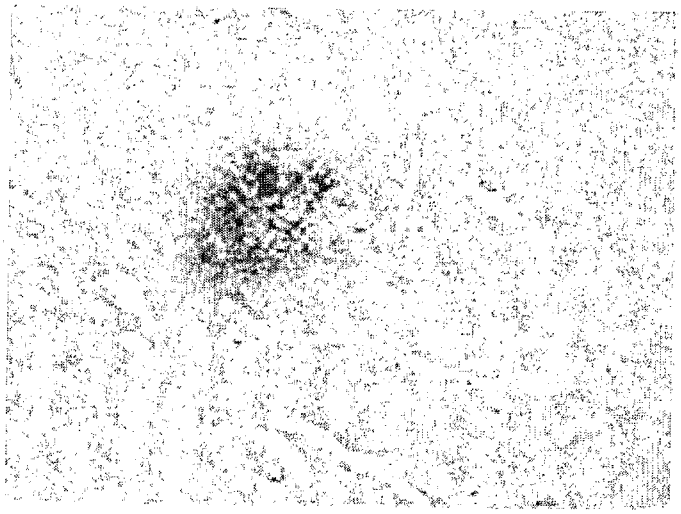
CK1, GFAB-staining

Patches of intense GFAB-staining is noted the mesencephalon.

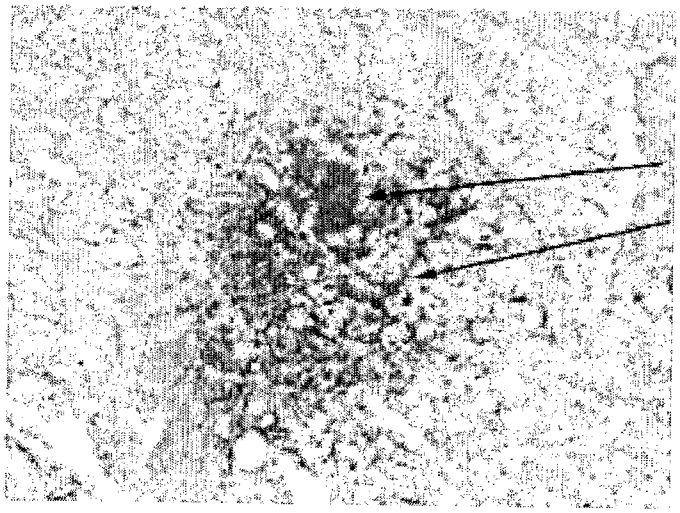


Numerous astrocyttes is noted indicative of active inflammation and reactive gliosis.

Fig. 26



Patches of large alfasynuclein aggregates are visible throughout the mesencephalon



Alfasynuclein is located in the cell bodies and extracellular surroundings

Fig. 27

```
                                                                Q
S.scrofa    PSEN1 MTELPAPLSYFQNAQMSEDNHVSNNVSSQNDSRERHEHSIERRRRGNSESLSNGGAQGNS 60
B.taurus    PSEN1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDSRERHEHGNERRRRGNTESVSNGRAPSSS 60
H.sapiens   PSEN1 MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEH-NDRRSLGHPEPLSNGRPQGNS 59
M.musculus  PSEN1 MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQ-HDRQRLDNPEPISNGRPQSNS 59
                ***:***************.* *. : ****.:**:::  :*:  .:.*.:*** . ..*
                                    +  +  +   +  + + +        +          + +++
S.scrofa    PSEN1 RQVVEQEEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 120
B.taurus    PSEN1 QQVVEQEEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 120
H.sapiens   PSEN1 RQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 119
M.musculus  PSEN1 RQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFT 119
                :*****:**************************************************
                +  +              +   +   +  ++     ++         + ++  +++ ++S ++
S.scrofa    PSEN1 EDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSF 180
B.taurus    PSEN1 EDTETVAQRALHSILNAVIMISVIVIMTILLVVLYKYRCYKVIHAWLIVSSLLLLFFFSF 180
H.sapiens   PSEN1 EDTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSF 179
M.musculus  PSEN1 EDTETVGQRALHSILNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSF 179
                ******.**********.*******:**********************:***********
                   ++                      +  +   ++  + +  +    +  + + + + +
S.scrofa    PSEN1 IYLGEVFKTYNVAMDYITVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIK 240
B.taurus    PSEN1 IYLGEVFKTYNVAMDYISVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIK 240
H.sapiens   PSEN1 IYLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIK 239
M.musculus  PSEN1 IYLGEVFKTYNVAVDYVTVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIK 239
                **************:**::**************:****************************
                      +   +      +   +++++  + + ++++   + + + +++
S.scrofa    PSEN1 YLPEWTAWLILAVISVYDLVAVLCPNGPLRLLVETAQERNETLFPALIYSSTMVWLVNMA 300
B.taurus    PSEN1 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 300
H.sapiens   PSEN1 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 299
M.musculus  PSEN1 YLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMA 299
                ***************************:****:******************************
                                       G
S.scrofa    PSEN1 EGDPEAQRKVSKNSNYNAQSTG-----------ESQDSVTESDDGGFSEEWEAQRDSRLG 349
B.taurus    PSEN1 EGDPEAQRKVSKNSNYNAQRPANSPVTTTGTESESQDPVTESDDGGFSEEWEAQRDSRLG 360
H.sapiens   PSEN1 EGDPEAQRRVSKNSKYNAESTER----------ESQDTVAENDDGGFSEEWEAQRDSHLG 349
M.musculus  PSEN1 EGDPEAQRRVPKNPKYNTQRAER----------ETQDSGSGNDDGGFSEEWEAQRDSHLG 349
                ********:*.**.:**:: .              *:**. : .***************:**
                    +   +      +            ++  +  + +   +++ +          +   +
S.scrofa    PSEN1 PHHSTAESRSAVQDLSRSIPATEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 409
B.taurus    PSEN1 PHHSTAESRSAVQDLSSSILASEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 420
H.sapiens   PSEN1 PHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 409
M.musculus  PSEN1 PHRSTPESRAAVQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA 409
                **:**.***:***:** ** : ************************************
                +       +     + +    +  +++  +
S.scrofa    PSEN1 CFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
B.taurus    PSEN1 CFVAILIGLCLTLLLLAIFKKALPALPVSITFGLIFYFATDYLVQPFMDQLAFHQFYI 478
H.sapiens   PSEN1 CFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
M.musculus  PSEN1 CFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
                ***************************:******:************************
```

Fig. 28

29/39

```
S.scrofa    PSEN2 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGLEDGESAAQWRSQDSEEDHEE-D 59
B.taurus    PSEN2 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQDGRQGLEDGESAAQWRSQESEEDHEEED 60
H.sapiens   PSEN2 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEE-D 59
M.musculus  PSEN2 MLAFMASDSEEEVCDERTSLMSAESPTSRSCQEGRPGPEDGESTAQWRTQESEEDCEE-D 59
                   **:************************.****:** * ****.:****:*:.*** ** *
                     +
S.scrofa    PSEN2 PDRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQL 119
B.taurus    PSEN2 PDRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQL 120
H.sapiens   PSEN2 PDRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQL 119
M.musculus  PSEN2 PDRYACSGAPGRPSGLEEELTLKYGAKRVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQL 119
                   ****.***.****.*************:**********************************
                     +       +           +       +
S.scrofa    PSEN2 IYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLITSSLML 179
B.taurus    PSEN2 IYTPFSEDTPSVGQRLLNSVLNTLIMISVIVTMTIFLVVLYKYRCYKFIHGWLIMSSLML 180
H.sapiens   PSEN2 IYTTFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLML 179
M.musculus  PSEN2 IYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLML 179
                   ***.*:************************.********************** *****
                                                                    +           +
S.scrofa    PSEN2 LFLFTYIYLGEVLKTYNVAMDYPTLFLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALM 239
B.taurus    PSEN2 LFLFTYIYLGEVLKTYNVAMDYPTLFLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALM 240
H.sapiens   PSEN2 LFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALM 239
M.musculus  PSEN2 LFLFTYIYLGEVLKTYNVAMDYPTLFLAVWNFGAVGMVCIHWKGPLALQQAYLIVISALM 239
                   *************************:*:******************.*******:*****

S.scrofa    PSEN2 ALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV 299
B.taurus    PSEN2 ALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV 300
H.sapiens   PSEN2 ALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV 299
M.musculus  PSEN2 ALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV 299
                   ************************************************************

                                                      R
S.scrofa    PSEN2 WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLPGYPGEELEEEEERG 359
B.taurus    PSEN2 WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLPGYPGEELEEEEERG 360
H.sapiens   PSEN2 WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPDVFEPPLPGYPGEELEEEEERG 360
M.musculus  PSEN2 WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEAFEAPLPGYPGEELEEEEERG 359
                   ************************************:.**.**.**************

S.scrofa    PSEN2 VKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPIS 419
B.taurus    PSEN2 VKLGLGDFIFYSVLVGKAAAMGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPIS 420
H.sapiens   PSEN2 VKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPIS 419
M.musculus  PSEN2 VKLGLGDFIFYSVLVGKAAATGNGDWNTTLACFIAILIGLCLTLLLLAVFKKALPALPIS 419
                   ******************** *.**********:**************************
                                      +         +
S.scrofa    PSEN2 ITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
B.taurus    PSEN2 ITFGLIFYFSTDNLVRPFMDTLASHQLYI 449
H.sapiens   PSEN2 ITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
M.musculus  PSEN2 ITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
                   ******************************
```

Fig. 29

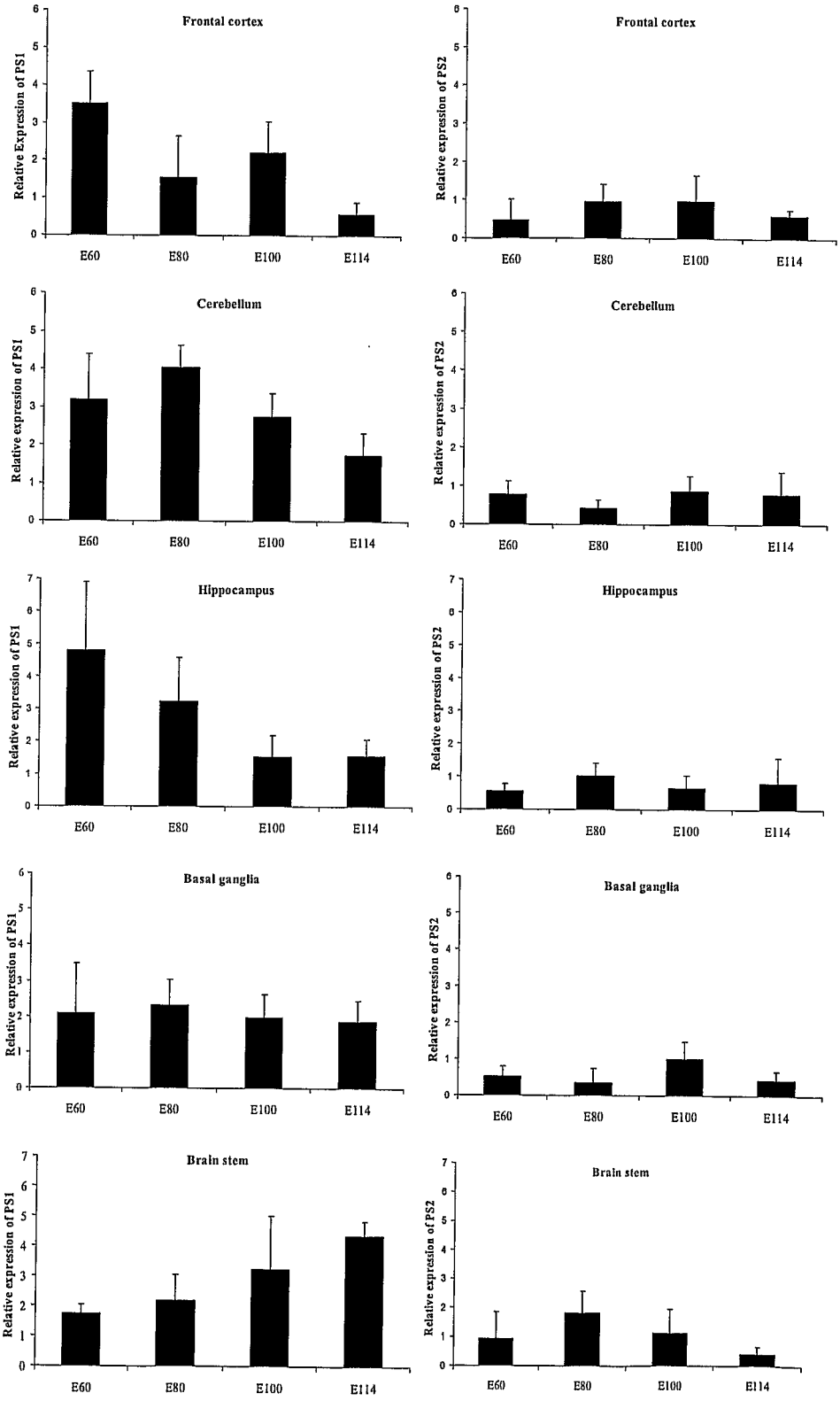

Frontal cortex
Relative Expression of PS1
Frontal cortex
Relative expression of PS2
Cerebellum
Relative expression of PS1
Cerebellum
Relative expression of PS2
Hippocampus
Relative expression of PS1
Hippocampus
Relative expression of PS2
Basal ganglia
Relative expression of PS1
Basal ganglia
Relative expression of PS2
Brain stem
Relative expression of PS1
Brain stem
Relative expression of PS2
E60
E80
E100
E114

Fig. 30

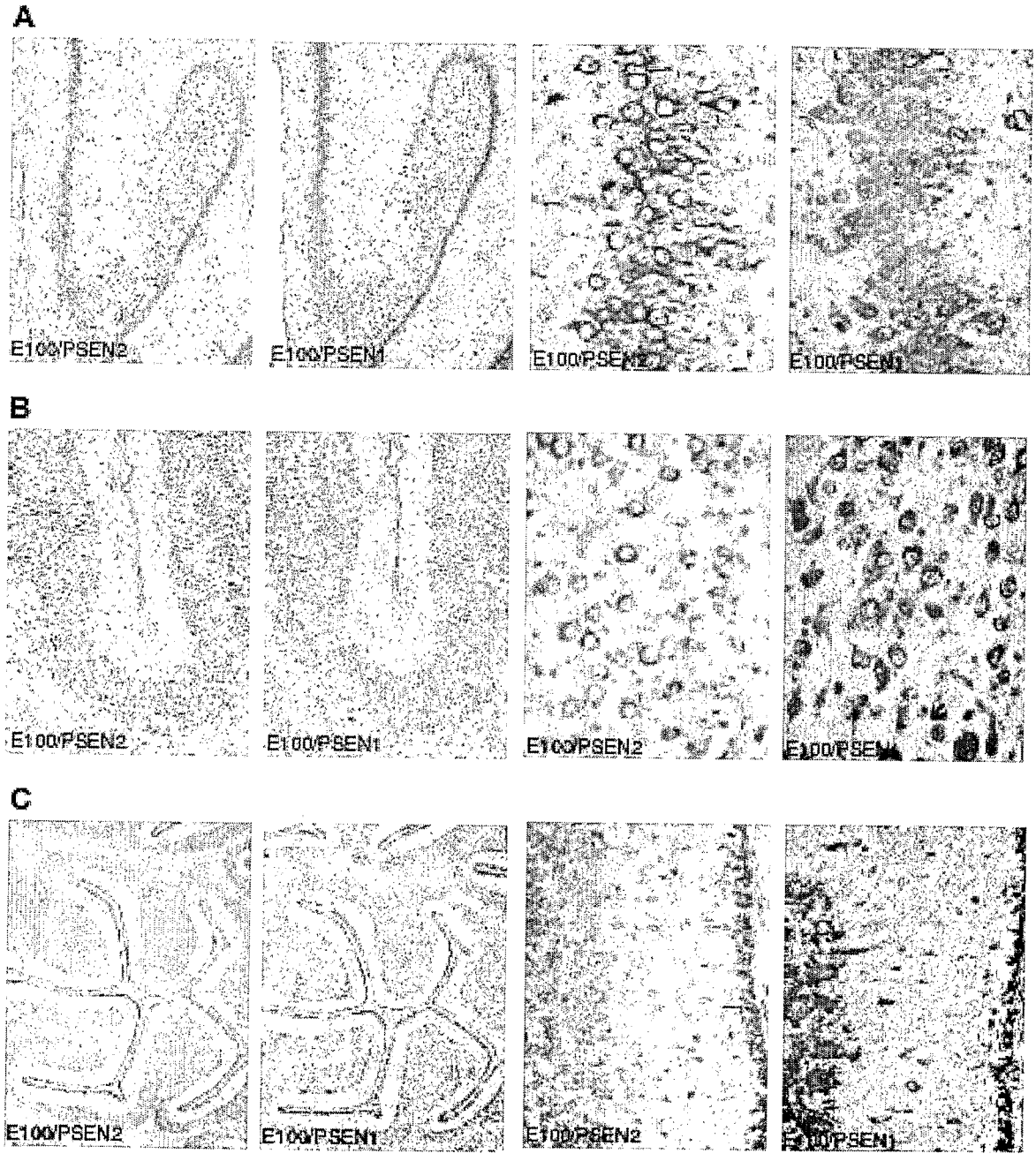

A
E100/PSEN2
E100/PSEN1
E100/PSEN2
E100/PSEN1
B
E100/PSEN2
E100/PSEN1
E100/PSEN2
E100/PSEN1
C
E100/PSEN2
E100/PSEN1
E100/PSEN2
E100/PSEN1

Fig. 31

DMPK:

Pig	(CTG)4	
Human	(CTG)n	normal n=5-37 / En>50
Chimp	(CTG)8 GTG	
Dog	CCG CAG CCG CTG CCG	
Rat	(CTA)2 CTG CAG CCC	
Mouse	CTG (CAG)2 CTG	

SCA12:

Pig(Duroc)	CTG (CAG)n (CTG)2	n=8(0.7), 9(0.3)
Pig(Hamp)	CTG (CAG)n (CTG)2	n=8(0.2), 10(0.8)
Pig(Land)	CTG (CAG)n (CTG)2	n=9
Pig(York)	CTG (CAG)n (CTG)2	n=9
Pig(Mini)	CTG (CAG)n (CTG)2	n=9
Human	CTG (CAG)n CTG	normal n=7-28 (10) / En>65
Chimp	CTG (CAG)11 CTG	
Dog	N.P.	
Rat	CTG (CAG)4 CAC (CAG)3 CTG	
Mouse	CTG (CAG)2 GAG (CAG)2 CAC (CAG)3 CTG	

FMR1/FRAXA:

Pig(Duroc)	(CGG)n	n=12 (<0.1), 13(0.2), 14 (0.9), 15 (<0.1)
Pig(Hamp)	(CGG)n	n= 9(0.2), 13(0.1), 14(0.6), 15(0.1)
Pig(Land)	(CGG)n	n=14
Pig(York)	(CGG)n	n=13(0.1), 14(0.4), 15(0.5)
Pig(Mini)	(CGG)n	n=12(0.3), 13(0.3), 14(0.4)
Human	(CGG)14 AGG (CGG)n	normal n=6-52 / En>200
Chimp	(CGG)9 AGG CGG AGG (CGG)16 AGG CGG	
Dog	(CGG)12	
Rat	(CGG)4 CGA CGG	
Mouse	(CGG)6 CGA (CGG)2	

FMR2/FRAXE:

Pig	(CCG)7 CTG CCG	
Human	CCG GAC (CCG)n CTG CCG	normal n=6-35 / En>200
Chimp	N.P.	
Dog	N.P.	
Rat	(CCG)2 CCA (CCG)2 CTG CCG	
Mouse	(CCG)4 (CTG)2 CCG	

Fig. 32

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SCA1:

Pig(Duroc)	(CAG)n (CCG)4 CCA CCG CCA CCG CAG	n=1	Q=2, P=8
Pig(Hamp)	(CAG)n (CCG)4 CCA CCG CCA CCG CAG	n=1	Q=2, P=8
Pig(Land)	(CAG)n (CCG)4 CCA CCG CCA CCG CAG	n=1	Q=2, P=8
Pig(York)	(CAG)n (CCG)4 CCA CCG CCA CCG CAG	n=1	Q=2, P=8
Pig(Mini)	(CAG)n (CCG)4 CCA CCG CCA CCG CAG	n=1(0.2), 2(0.8)	Q=3, P=8
Human	(CAG)n CAT CAG CAT (CAG)m	normal n+m=6-39 (15) / E(n+m)>40	Q=28, H=2
Chimp	(CAG)10 CAT CAG CAT (CAG)10		Q=21, H=2
Dog	(CAG)6		Q=6
Opossum	CAG CCG CAG		Q=2, P=1
Rat	CCC CCT CCG (CAG)2		Q=2, P=3
Mouse	CCC CCT CCG (CAG)2		Q=2, P=3

SCA2:

Pig	(CAG)2 (CAA)2 (CAG)5		Q=9
Human	(CAG)n CAA (CAG)4 CAA (CAG)m (CCG)2	normal n+m=13-33 (15) / E(n+m)>34	Q=21, P=2
Chimp	(CAG)9 (CAA)6 (CAG)3 CAA (CAG)7 (CCG)2		Q=26, P=2
Dog	CAG CAA (CAG)5 (CCG)2 (CAG)2 CCG CAG (CCG)2		Q=10, P=5
Opossum	N.P.		
Rat	CAG CCG CAG CCG		Q=2, P=2
Mouse	CAG CCG CAG CCG		Q=2, P=2

SCA3:

Pig(Duroc)	(CAG)n CAA	n=6	Q=7
Pig(Hamp)	(CAG)n CAA	n=6	Q=7
Pig(Land)	(CAG)n CAA	n=6	Q=7
Pig(York)	(CAG)n CAA	n=5(0.2), 6(0.8)	Q=6,7
Pig(Mini)	(CAG)n CAA	n=5(0.5), 6(0.5)	Q=6,7
Human	(CAG)2 CAA AAG CAG CAA (CAG)n	normal n=12-36 (15) / En>54	Q=14
Chimp	(CAG)5 CAA AAG CAG CAA (CAG)11		Q=19
Dog	(CAG)2 (CAA)2 (CAG)6 CAA CAG		Q=12
Opossum	N.P.		
Rat	CAA CAG CAT CAG CAA CAG GAA		Q=6
Mouse	CAA (CAG)5 GAG		Q=6

SCA6:

Pig(Duroc)	(CAG)n CAA (CAG)4	n=5	Q=10
Pig(Hamp)	(CAG)n CAA (CAG)4	n=5	Q=10
Pig(Land)	(CAG)n CAA (CAG)4	n=5	Q=10
Pig(York)	(CAG)n CAA (CAG)4	n=5	Q=10
Pig(Mini)	(CAG)n CAA (CAG)4	n=7(0.5), 9(0.5)	Q=12,14
Human	(CAG)n	normal n=4-18 (13) / En>20	Q=13
Chimp	(CAG)11		Q=11
Dog	(CAG)10		Q=10
Opossum	CAG (CCG)2 CAG CCG CCA CAG		Q=3, P=4
Rat	N.P.		
Mouse	N.P.		

SCA7:

Pig	(CAG)5		Q=5
Human	(CAG)n	normal n=7-35 (10) / En>37	Q=10
Chimp	(CAG)8		Q=8
Dog	(CAG)8		Q=8
Opposum	(CAG)2 CAC CAG CAC CAG (CAC)2 (CAG)4		Q=8, H=4
Rat	(CAG)4		Q=4
Mouse	(CAG)5		Q=5

Fig. 33

DRPLA:

Pig(Duroc)	CAG		CAA	(CAG)n	CAA	CAG	CAA	CAG	(CAA)2	n=6	Q=14
Pig(Hamp)	CAG		CAA	(CAG)n	CAA	CAG	CAA	CAG	(CAA)2	n=6	Q=14
Pig(Land)	CAG		CAA	(CAG)n	CAA	CAG	CAA	CAG	(CAA)2	n=6	Q=14
Pig(York)	CAG		CAA	(CAG)n	CAA	CAG	CAA	CAG	(CAA)2	n=6	Q=14
Pig(Mini)	CAG		CAA	(CAG)n	CAA	CAG	CAA	CAG	(CAA)2	n=6(0.7), 7(0.3)	Q=14,15
Human	CAG		CAA	CAG		CAA	(CAG)n			normal n=3-25 (13) / En>49	Q=17
Chimp	CAG		CAA	CAG		CAA	(CAG)12				Q=16
Dog				(CAG)8	CAA	CAG	CAA	CAG			Q=12
Opossum	(CAG)6		CAA	CAG							Q=8
Rat	(CAG)5	(CCA		CAG)4	CCG				(CAA)2		Q=11, P=5
Mouse	(CAG)3		CCA	CAG					(CAA)2		Q=6, P=1

SCA17:

Pig	(CAG)3				(CAG)4	CAA	(CAG)6	CAA	(CAG)10	CAA				Q=26
Human	(CAG)3	(CAA)3			(CAG)8	CAA	CAG	CAA	(CAG)n	CAA	CAG		n=9-22 (18) En>26	Q=38
Chimp	(CAG)3	(CAA)3			(CAG)25	CAA	CAG							Q=30
Dog	CAA (CAG)3	(CAG)6	GCC		(CAG)4	GCC	(CAG)5	CAA	(CAG)2	GCC				Q=22
Opossum	(CAG)8	CAA	(CAG)2	CAA										Q=12
Rat	(CAG)8	CAA	(CAG)3	CAA	(CAG)2									Q=14
Mouse	(CAG)3	CAA	CAG	CAA	(CAG)3	(CAA)2	(CAG)2							Q=13

SBMA:

Pig	(CAG)4	CTG	(CAG)3											Q=7
Human	(CAG)n	CAA											normal n=11-37 (22) / En>37	Q=23
Chimp	(CAG)21	CAA												Q=22
Dog	(CAG)10													Q=10
Opossum	(CAG)	CAC	(CAG)7											Q=8
Rat	(CAG)2	CGG	CAG											Q=3
Mouse	(CAG)2	AGG	CAG											Q=3

Huntingtin:

Pig(Duroc)	(CAG)n					CAA	(CAG)2						n=14(0.6), 21(0.2)	Q=17, 24
	(CAG)5	CAA	(CAG)8	CAA	(CAG)2								(0.2)	Q=17
Pig(Hamp)	(CAG)n					CAA	(CAG)2						N=14(0.7), 15(0.3)	Q=17, 18
Pig(Land)	(CAG)14					CAA	(CAG)2						(0.8)	Q=17
	(CAG)5	CAA	(CAG)9	CAA	(CAG)2								(0.2)	Q=18
Pig(York)	(CAG)14					CAA	(CAG)2						(0.5)	Q=17
	(CAG)5	CAA	(CAG)n	CAA	(CAG)2								n=4(0.2), 7(0.1), 8(0.2)	Q=13,16,17
Pig(Mini)	(CAG)14					CAA	(CAG)2						(0.2)	Q=17
	(CAG)5	CAA	(CAG)n	CAA	(CAG)2								n=8(0.2), 9(0.6)	Q=17,18
Human	(CAG)n	CAA	CAG										normal n=6-35 (18) / En>35	Q=20
Chimp	(CAG)13	CAA	CAG											Q=15
Dog	(CAG)4	CAA	(CAG)5											Q=10
Opossum	(CAG)6													Q=6
Rat	(CAG)2	CAA	(CAG)5											Q=8
Mouse	(CAG)2	CAA	(CAG)4											Q=7

Fig. 33 continued/

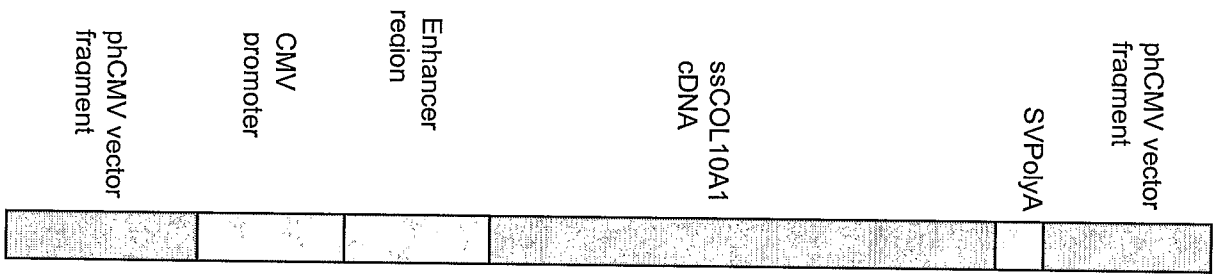
phCMV vector fragment
CMV promoter
Enhancer region
ssCOL10A1 cDNA
SVPolyA
phCMV vector fragment

Fig. 34

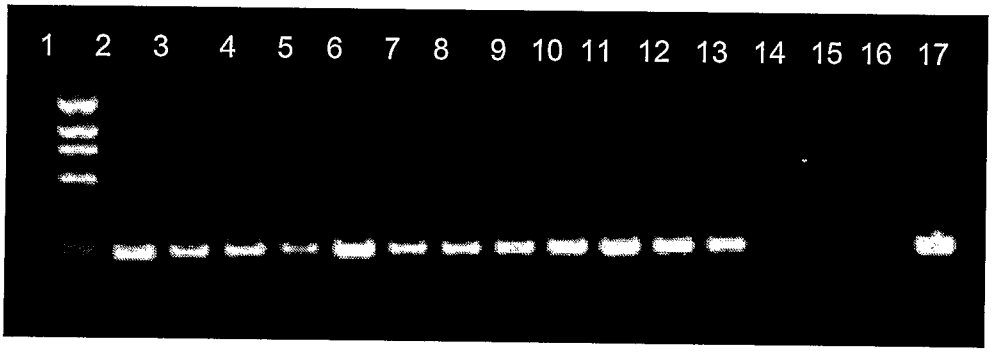

Fig. 35

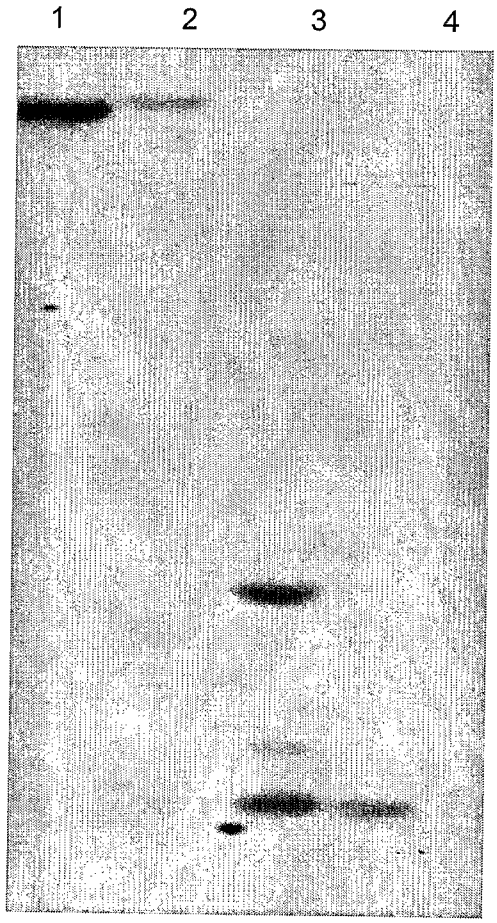

Fig. 36

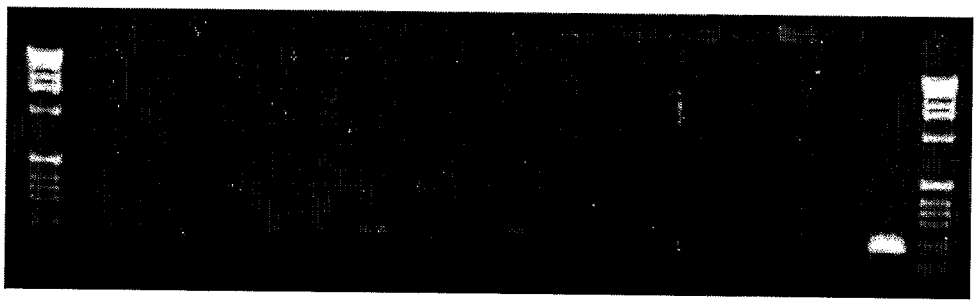

Fig. 37

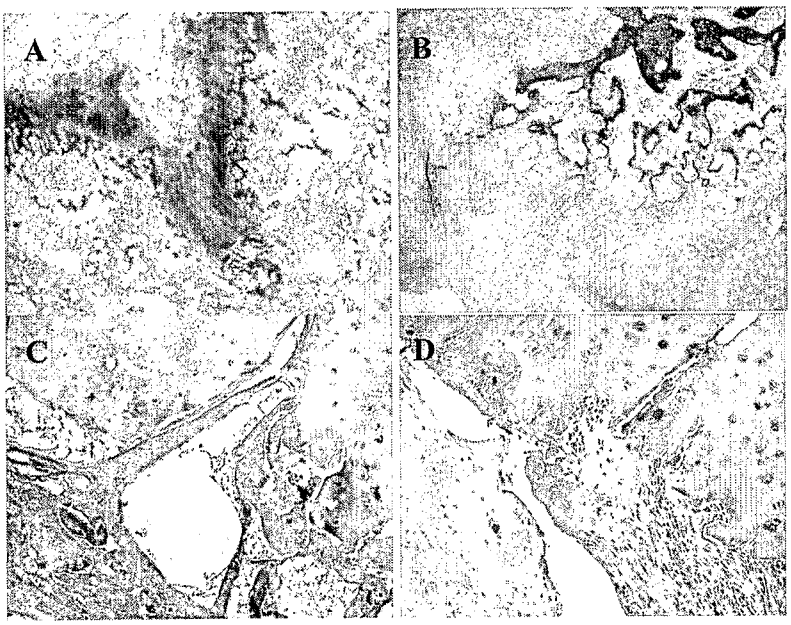

Fig. 38