Animal Cloning

Database: CAB Abstracts <2000 to 2014 Week 20>
Search Strategy:
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1 (clone or cloning or cloned or clones).mp. [mp=abstract, title, original title, broad terms, heading words] (81788)
2 (ethic* or law* or legal* or legisla* or regulat*).mp. [mp=abstract, title, original title, broad terms, heading words] (319628)
3 (pet or pets or "companion animal" or "pet animal" or "small animal" or dog or dogs or cat or cats).mp. [mp=abstract, title, original title, broad terms, heading words] (119295)
4 1 and 2 and 3
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A selection of results

<1>
Accession Number
20133029356
Author
Gomez, M. C.; Biancardi, M. N.; Jenkins, J. A.; Dumas, C.; Galiguis, J.; Wang, G.; Pope, C. E.
Title
Scriptaid and 5-aza-2'deoxycytidine enhanced expression of pluripotent genes and in vitro developmental competence in interspecies black-footed cat cloned embryos.
Source
Publisher
Wiley-Blackwell
Location of Publisher
Berlin
Country of Publication
Germany
Abstract
Somatic cell nuclear transfer offers the possibility of preserving endangered species including the black-footed cat, which is threatened with extinction. The effectiveness and efficiency of somatic cell nuclear transfer (SCNT) depends on a variety of factors, but inappropriate epigenetic reprogramming of the transplanted nucleus is the primary cause of the developmental failure of cloned embryos. Abnormal epigenetic events such as DNA methylation and histone modifications during SCNT perturb the expression of imprinted and pluripotent-related genes that, consequently, may result in foetal and neonatal abnormalities. We have demonstrated that pregnancies can be established after transfer of black-footed cat cloned embryos into domestic cat recipients, but none of the implanted embryos developed to term and the foetal failure has been associated to aberrant reprogramming in cloned embryos. There is growing evidence that modifying the epigenetic pattern of the chromatin template of both donor cells and reconstructed embryos with a combination of inhibitors of histone deacetylases and DNA methyltransferases results in enhanced gene reactivation and improved in vitro and in vivo developmental competence. Epigenetic modifications of the chromatin template of black-footed cat donor cells and reconstructed embryos with epigenetic-modifying compounds enhanced in vitro development, and regulated the expression of pluripotent genes, but these epigenetic modifications did not improve in vivo developmental competence.
Publication Type
The cyclin-dependent kinase 5 regulatory subunit-associated protein 1-like 1 (CDKAL1) gene encodes methylthiotransferase, and the gene contains risk variants for type 2 diabetes in humans. In this study, we performed complementary DNA cloning for Cdkal1 in the cat and dog and characterized the tissue expression profiles of its messenger RNA. Cat and dog Cdkal1 complementary DNA encoded 576 and 578 amino acids, showing very high sequence homology to mammalian CDKAL1 (>88.4%). Real-time polymerase chain reaction analyses revealed that Cdkal1 messenger RNA is highly expressed in smooth muscle and that tissue distribution of Cdkal1 is similar in cats and dogs. Genotyping analysis of single-nucleotide polymorphism for cat Cdkal1 revealed that obese cats had different tendencies from normal cats. These findings suggest that the cat and dog Cdkal1 gene is highly conserved among mammals and that cat Cdkal1 may be a candidate marker for genetic diagnosis of obesity.
Accession Number
20113218067
Author
Kim MinJung; Oh HyunJu; Park JungEun; Kim, G. A.; Hong SoGun; Jang Goo; Kwon MoSun; Koo BonChul; Kim TeoAn; Kang SungKeun; Ra JeongChan; Ko CheMyong; Lee ByeongChun
Title
Generation of transgenic dogs that conditionally express green fluorescent protein.
Source
Publisher
Wiley-Blackwell
Location of Publisher
Hoboken
Country of Publication
USA
Abstract
We report the creation of a transgenic dog that conditionally expresses eGFP (enhanced green fluorescent protein) under the regulation of doxycycline. Briefly, fetal fibroblasts infected with a Tet-on eGFP vector were used for somatic cell nuclear transfer. Subsequently reconstructed oocytes were transferred to recipients. Three clones having transgenes were born and one dog was alive. The dog showed all features of inducible expression of eGFP upon doxycycline administration, and successful breeding resulted in eGFP-positive puppies, confirming stable insertion of the transgene into the genome. This inducible dog model will be useful for a variety of medical research studies.
Publication Type
Journal article.

Accession Number
20113186588
Author
Hong IlHwa; Jeong YeonWoo; Shin TaeYoung; Hyun SangHwan; Park JinKyu; Ki MiRan; Han SeonYoung; Park Sell; Lee JiHyun; Lee EunMi; Kim AhYoung; You SangYoung; Hwang WooSuk; Jeong KyuShik
Title
Morphological abnormalities, impaired fetal development and decrease in myostatin expression following somatic cell nuclear transfer in dogs.
Source
Publisher
Wiley-Blackwell
Location of Publisher
Hoboken
Country of Publication
USA
Abstract
Several mammals, including dogs, have been successfully cloned using somatic cell nuclear transfer (SCNT), but the efficiency of generating normal, live offspring is relatively low. Although the high failure rate has been attributed to incomplete reprogramming of the somatic nuclei during the cloning process, the exact cause is not fully known. To elucidate the cause of death in cloned offspring, 12 deceased offspring cloned by SCNT were necropsied. The clones were either stillborn just prior to delivery or died with dyspnea shortly after birth. On gross examination, defects in the anterior abdominal wall and increased heart and liver sizes were found. Notably, a significant increase in muscle mass and macroglossia lesions were observed in deceased SCNT-cloned dogs. Interestingly, the expression of myostatin, a negative regulator of muscle growth during embryogenesis, was down-regulated at the mRNA level in tongues and skeletal muscles of
SCNT-cloned dogs compared with a normal dog. Results of the present study suggest that decreased expression of myostatin in SCNT-cloned dogs may be involved in morphological abnormalities such as increased muscle mass and macroglossia, which may contribute to impaired fetal development and poor survival rates.

Publication Type
Journal article.

<6>
Accession Number
20103294899
Author
Zhang JiaXin; Sang Ming; Zhao Wei; Ai HongXin; Shui Yan; Li JianFeng; Song Ren; Zhang ShuangQuan
Title
Molecular characterization of the canine cytokine TWEAK (CD255) and its receptor, Fn14 (CD266).
Source
Veterinary Immunology and Immunopathology; 2010. 137(1/2):172-175. 7 ref.
Publisher
Elsevier Ltd
Location of Publisher
Oxford
Country of Publication
UK
Abstract
TWEAK is a member of the tumor necrosis factor superfamily. The interaction of TWEAK with its receptor Fn14 regulates multiple cellular responses, including stimulation of proliferation, migration, apoptosis, angiogenesis, and induction of proinflammatory cytokines. This paper reports for the first time the molecular cloning of dog TWEAK and Fn14. The open reading frame (ORF) of dog TWEAK is 750 bp, its genomic DNA consists of seven exons and six introns and is approximately 10 kb in size by computer-assisted analysis. Sequence similarity at the amino acid level between dog TWEAK and human or mouse was 95 and 92%, respectively. The ORF of dog Fn14 contains 390 bp. Sequence similarity at the amino acid level between dog Fn14 and human, or mouse, or frog was 95, 93 and 64%, respectively. Real-time quantitative PCR analysis revealed that both TWEAK and Fn14 are constitutively expressed in various tissues in dog. Furthermore, we verified dTWEAK interacted with dFn14 by yeast two-hybrid assay. Our results suggest that the TWEAK-Fn14 pathway is evolutionarily highly conserved. It will be helpful for investigation on the biological role of the TWEAK/Fn14 system in this important animal model. Furthermore, it provides insight into the molecular evolution of the emerging TWEAK and Fn14 families.
Publication Type
Journal article.

<7>
Accession Number
20103167839
Author
Rissetto, K. C.; Rindt, H.; Selting, K. A.; Villamil, J. A.; Henry, C. J.; Reinero, C. R.
Title
Cloning and expression of canine CD25 for validation of an anti-human CD25 antibody to compare T regulatory lymphocytes in healthy dogs and dogs with osteosarcoma.
Source
Veterinary Immunology and Immunopathology; 2010. 135(1/2):137-145. 47 ref.
Publisher
Elsevier Ltd
Location of Publisher
Oxford
Country of Publication
UK

Abstract

T regulatory cells (Tregs) are a unique subset of T helper cells that serve to modify/inhibit effector cells of the immune system and thus are essential to prevent autoimmunity. Overzealous Treg activity may contribute to impaired immune responses to cancer. Tregs can be phenotypically identified by proteins expressed on the cell surface (CD4 and CD25) and inside the cell (forkhead box3 (FoxP3)), although in dogs, no anti-canine CD25 antibody exists. We hypothesized that a mouse anti-human CD25 antibody definitively recognizes the canine protein and can be used to identify Tregs in dogs. We describe cloning and transfection of the canine CD25 gene into human HeLa cells with subsequent expression of the canine protein on the cell surface detected using an anti-human CD25 antibody in a flow cytometric assay. Validation of this antibody was used to identify CD4+CD25+FoxP3+Tregs in 39 healthy dogs and 16 dogs with osteosarcoma (OSA). Results were expressed in five different ways and showed significantly fewer %CD4+CD25+T lymphocytes expressing FoxP3 in blood of older dogs (>=7 years) compared with the other two age groups (<2 and 2-6 years) (p<0.001) and fewer %CD4+CD25+FoxP3+Tregs in the tumor draining lymph nodes of OSA patients compared to the unrelated lymph node (p=0.049). However, there was no significant difference in % Tregs in the peripheral blood or lymph nodes between the control dogs and those with OSA. While the CD25 antibody can be successfully used in a flow cytometric assay to identify Tregs, this study does not support clinical utility of phenotypic recognition of Tregs in dogs with OSA.

Publication Type
Journal article.

Accession Number
20093016746

Author

Title
The antiretroviral potency of APOBEC1 deaminase from small animal species.

Source

Publisher
Oxford University Press

Location of Publisher
Oxford

Country of Publication
UK

Abstract
Although the role of the APOBEC3-dependent retroelement restriction system as an intrinsic immune defense against human immunodeficiency virus type1 (HIV-1) infection is becoming clear, only the rat ortholog of mammalian APOBEC1s (A1) thus far has been shown to possess antiviral activity. Here, we cloned A1 cDNAs from small animal species, and showed that similar to rat A1, both wild-type and Delta vif HIV-1 infection was inhibited by mouse and hamster A1 (4- to 10-fold), whereas human A1 had negligible effects. Moreover, rabbit A1 significantly reduced the infectivity of both HIV-1 virions (>300-fold), as well as that of SIVmac, SIVagm, FIV and murine leukemia virus. Immunoblot analysis showed that A1s were efficiently incorporated into the HIV-1 virion, and their packaging is mediated through an interaction with the nucleocapsid Gag domain. Interestingly, there was a clear accumulation of particular C-T changes in the genomic RNAs of HIV-1 produced in their presence, with few G-A changes in the proviral DNA. Together, these data reveal that A1 may function as a defense mechanism, regulating retroelements in a wide range of mammalian species.

Publication Type
Journal article.

Accession Number
Regulatory T cells (Treg) are increased and directly infected by feline immunodeficiency virus (FIV) and likely play a role in other feline autoimmune, neoplastic, and infectious diseases. Phenotypically, Treg are best characterized by surface expression of CD4 and CD25 and intranuclear expression of the forkhead transcription factor Foxp3. Our objective was to clone and sequence feline FOXP3 for the purpose of developing assays to enhance studies of feline Treg. We determined the feline FOXP3 is 1293 nucleotides in length and codes for a protein that shares high homology to other species. A splice variant devoid of exon 2 was also identified. A real-time PCR assay was developed and used to show Foxp3 mRNA expression occurs primarily in CD4+CD25+ T cells. Two cross-reacting antibodies were identified by immunocytochemical staining of HEK293 cells transfected with feline FOXP3. The antibody labeling confirmed the nuclear localization of the protein. A flow cytometric assay was also validated and used to correlate the phenotypic and functional characteristics of feline Treg induced by treatment of lymph node lymphocytes with flagellin or LPS in combination with mitogen or IL2. Together, these studies provide useful tools to further investigate Foxp3 and Tregs in cats.
stomach revealed that the motilin receptor was localized in neuronal cell bodies and fibers. This is the first study detailing the cloning, expression, and functional characterization of the dog motilin receptor. Determination of the full sequence and functional properties of the dog motilin receptor will provide useful information enabling us to interpret previous and future studies of motilin agonists in dogs.

Publication Type
Journal Article.

Accession Number
20073098813

Author
Haworth, K. E.; Healy, C.; McGonnell, I. M.; Binns, M.; Sharpe, P. T.

Title
Characterisation of the genomic canine Fgf8 locus and screen for genetic variants in 4 dogs with different face types.

Source

Publisher
Informa Healthcare

Location of Publisher
Abingdon

Country of Publication
UK

Abstract
We are investigating the genetic basis of morphological differences in skull shape between domestic dogs of different breeds using a candidate gene approach to identify genes involved in the genetic regulation. One such candidate is Fgf8. Fgf8 is a signalling molecule important in the embryonic development and patterning of the craniofacial region. Mice conditional null for the expression of Fgf8 after E9.5 have a short foreface and a wide skull (Trumpp et al. 1999). Using a combination of bioinformatics and PCR cloning, we have characterised the genomic loci of the canine Fgf8 gene. Like the mouse homologue, it is composed of six exons and we also predict that like the mouse, there are eight alternative isoforms that are generated by alternative splicing events. We have identified a short 200 bp sequence upstream of the Fgf8 gene that is highly conserved between species and have predicted putative transcription factor binding sites using the Transfac database. Genetic analysis of 4 dogs with different skull types identified genetic variation. None of the variants however, were predicted to have any functional significance.

Publication Type
Journal article.

Accession Number
20063239869

Author
Mizuno, T.; Baba, K.; Goto, Y.; Masuda, K.; Ohno, K.; Tsujimoto, H.

Title
Genomic cloning of feline Fas ligand gene and characterization of the transcription regulatory region.

Source
Veterinary Immunology and Immunopathology; 2006. 114(3/4):305-312. 21 ref.

Publisher
Elsevier

Location of Publisher
Amsterdam

Country of Publication
Netherlands

Abstract
The feline Fas ligand gene was molecularly cloned from a feline genomic library and its genomic organization was determined. The feline Fas ligand gene contained four exons and spanned approximately 10 kb in the genome, and thus had the same structure as the human Fas ligand gene. The promoter region of the feline Fas ligand gene was further characterized by deletion mapping. The region between nucleotides -459 and -172 relative to the ATG codon was essential for the promoter activity when transfected into human and feline lymphoid cells. The characterization of the feline Fas ligand gene in the present study will be useful for further investigations of the regulatory mechanism of feline Fas ligand expression.

Publication Type
Journal article.
The interaction between two genes, Agouti and Melanocortin-1 receptor (Mc1r), produces diverse pigment patterns in mammals by regulating the type, amount, and distribution pattern of the two pigment types found in mammalian hair: eumelanin (brown/black) and pheomelanin (yellow/red). In domestic dogs (Canis familiaris), there is a tremendous variation in coat colour patterns between and within breeds; however, previous studies suggest that the molecular genetics of pigment-type switching in dogs may differ from that of other mammals. Here we report the identification and characterization of the Agouti gene from domestic dogs, predicted to encode a 131-amino-acid secreted protein 98% identical to the fox homologue, and which maps to chromosome CFA24 in a region of conserved linkage. Comparative analysis of the Doberman Pinscher Agouti cDNA, the fox cDNA, and 180 kb of Doberman Pinscher genomic DNA suggests that, as with laboratory mice, different pigment-type-switching patterns in the canine family are controlled by alternative usage of different promoters and untranslated first exons. A small survey of Labrador Retrievers, Greyhounds, Australian Shepherds, and German Shepherd Dogs did not uncover any polymorphisms, but we identified a single nucleotide variant in black German Shepherd Dogs predicted to cause an Arg-to-Cys substitution at codon 96, which is likely to account for recessive inheritance of a uniform black coat.

Thiopurine S-methyltransferase (TPMT) plays an important role in the metabolism of thiopurine drugs. In humans, a common genetic polymorphism for TPMT is a major factor responsible for individual variation in the toxicity and therapeutic efficacy of these drugs. Dogs (Canis familiaris) are also treated with thiopurine drugs and, similar to humans, they display large individual variations in thiopurine toxicity and efficacy. We set out to determine whether dogs might also display genetically determined variation in TPMT activity. As a first step, we observed that canine red blood cell (RBC) TPMT activity in samples from 145 dogs varied over a nine-fold range. That variation was not associated with either the age or sex of the animal. Subsequently, we cloned the canine TPMT cDNA and gene. The canine cDNA encoded a protein that was 81.2% identical to the enzyme encoded by the most common TPMT allele in humans. A genotype-phenotype correlation analysis was performed by resequencing the canine TPMT gene using DNA samples from 39 animals selected for high, low or intermediate levels of RBC TPMT activity. We observed nine polymorphisms in these 39 DNA samples, including three insertion/deletion events and six single nucleotide polymorphisms (SNPs), one of which was a nonsynonymous cSNP (Arg>Sup>97</sup>Gln). However, when the variant allozyme at codon 97 was expressed in COS-1 cells, it did not display significant differences in either basal levels of TPMT activity or in substrate kinetics compared with the wild-type allozyme. Six of the nine canine TPMT polymorphisms were associated with 67% of the variation in level of RBC TPMT activity in these 39
blood samples. When those six SNPs were assayed using DNA from all 145 animals studied, 40% of the phenotypic variance in the entire population sample could be explained by these polymorphisms. Therefore, inheritance is a major factor involved in the regulation of variation in RBC TPMT in the dog, just as it is in humans. These observations represent a step towards the application of pharmacogenetic and pharmacogenomic principles to companion animal drug therapy.

Publication Type
Journal article.

<16>
Accession Number
20023138838

Author
Wiedmeyer, C. E.; Solter, P. F.; Hoffmann, W. E.

Title
Kinetics of mRNA expression of alkaline phosphatase isoenzymes in hepatic tissues from glucocorticoid-treated dogs.

Source
American Journal of Veterinary Research; 2002. 63(8):1089-1095. 41 ref.

Publisher
American Veterinary Medical Association

Location of Publisher
Schaumburg

Country of Publication
USA

Abstract
Objective: To clone segments of the canine liver alkaline phosphatase (LALP) and corticosteroid-induced alkaline phosphatase (CIALP) genes and use those clones to determine the tissue source of CIALP, the kinetics of LALP and CIALP mRNA expression for glucocorticoid-treated dogs, and the correlation between LALP and CIALP transcript concentrations and isoenzyme activities. Sample Population: Tissues obtained from 7 dogs treated with prednisone (1 mg/kg, SC, q 24 h) for up to 32 days and 1 untreated (control) dog. Procedure: Gene segments of LALP and CIALP were obtained by reverse transcription-polymerase chain reaction (RT-PCR) assay. The tissue source of CIALP and IALP mRNA was determined by northern blot analysis of tissues from 1 of the glucocorticoid-treated dogs. Hepatic tissues and serum samples were obtained from the 6 remaining glucocorticoid-treated dogs on days 0, 2, 5, 10, and 32 of prednisone treatment, and relative expression of LALP and CIALP mRNA was correlated with LALP and CIALP activity. Results: A 2246-base pair (bp) segment of canine LALP and a 1338-bp segment of CIALP were cloned. Northern blot analysis revealed CIALP mRNA expression in hepatic tissues only after glucocorticoid treatment. Kinetics of LALP and CIALP mRNA expression in the liver of glucocorticoid-treated dogs paralleled liver and serum activities of LALP and CIALP. Conclusions and Clinical Relevance: The liver is the most likely source for CIALP in dogs. Analysis of kinetics of serum and hepatic LALP and CIALP mRNA suggests that after glucocorticoid treatment, both are regulated by modification of mRNA transcript concentrations, possibly through differing mechanisms.

Publication Type
Journal article.