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DISSERTATION

**FELINE NIEMANN-PICK DISEASE TYPE C – THERAPEUTIC STUDIES AND
GENETIC CHARACTERIZATION**

Submitted by

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Department of Pathology

In partial fulfillment of the requirements

For the Degree of Doctor of Philosophy

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Fort Collins, Colorado

Fall 2000

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WE HEREBY RECOMMEND THAT THE DISSERTATION PREPARED UNDER OUR SUPERVISION BY KYRA LYNN SOMERS ENTITLED FELINE NIEMANN-PICK DISEASE TYPE C – THERAPEUTIC STUDIES AND GENETIC CHARACTERIZATION BE ACCEPTED AS FULFILLING IN PART REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY.

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ABSTRACT OF DISSERTATION

FELINE NIEMANN-PICK DISEASE TYPE C – THERAPEUTIC STUDIES AND GENETIC CHARACTERIZATION

Niemann-Pick Disease Type C (NPC) is an autosomal recessive neurovisceral storage disorder in which defective intracellular transport of cholesterol results in lysosomal lipid accumulation. Clinical manifestations are heterogeneous, but usually include neonatal jaundice, onset and progression of neurological signs, hepatosplenomegaly, neurovisceral storage and premature death. The lysosomal storage in NPC involves a complex lipidosis characterized by accumulation of unesterified cholesterol, phospholipids and sphingomyelin. A feline model of NPC has been characterized and is clinically, biochemically, and morphologically equivalent to the major form of human NPC, NPC1. Chapters one and two of this dissertation describe therapeutic trials conducted in the feline model of NPC, while chapters three and four focus on the genetic characterization of the feline model of NPC.

Chapter one discusses the results of a diet study conducted in the feline model of NPC. The study goal of the cholesterol restricted diet was to lower the amount of low density lipoprotein (LDL) available to cells, hypothetically reducing subsequent lysosomal accumulation of unesterified cholesterol and other lipids. Results indicated liver lipid concentrations of unesterified cholesterol, cholesterol ester, and phospholipids in NPC affected treated kittens were similar to those seen in NPC affected untreated kittens. Ganglioside concentrations in the NPC affected treated kittens and NPC affected untreated kittens were also similar. Histologic findings in liver sections from NPC affected treated kittens showed a diffuse uniform microvacuolar pattern within hepatocytes and Kupffer cells, compared to a heterogeneous macro/micro vacuolar pattern and prominent nodular fibrosis in NPC affected untreated kittens. Similar differences in vacuolar patterns were seen in splenic macrophages. Neurological progression of disease was not altered and dietary cholesterol restriction did not significantly decrease storage in NPC affected treated kittens.

Chapter two describes the findings of a drug study, in which a potent ganglioside synthesis inhibitor, N-butyldeoxynojirimycin (NB-DNJ) was evaluated as a potential therapy for NPC. The predominant storage material outside of the central nervous system (CNS) includes unesterified cholesterol, phospholipids

and sphingomyelin. This is in contrast to the storage seen within the central nervous system, which is predominantly glycosphingolipids and in particular, gangliosides GM2 and GM3. A drug study was conducted to determine if NB-DNJ would prevent and/or slow disease manifestation in this feline model of NPC. Preliminary results from this study were encouraging with evidence of decreased ganglioside storage within the CNS and delayed clinical disease progression.

Chapter three summarizes complementation studies that were performed to determine if the gene responsible for the major form of human NPC and the feline model of NPC are orthologous. Cell fusions between human NPC and feline NPC fibroblasts were conducted to assess whether the multinucleated heterokaryons that were formed showed a reversal of the NPC phenotype. Cultured fibroblasts from NPC affected humans and NPC affected cats were hybridized and then analyzed for complementation by challenging the cells with LDL and subsequently staining with the fluorescent antibiotic filipin to visualize any abnormal accumulation of unesterified cholesterol. All of the multinucleated cells formed from the fusion of feline NPC fibroblasts and human NPC1 fibroblasts retained the NPC staining phenotype. This indicated an absence of

complementation and suggested that the underlying defect in the major form of human NPC, NPC1, and this feline model of NPC involve orthologous genes.

Chapter four describes the molecular genetic characterization of the feline model of NPC. Using human based PCR primers, initial fragments of the feline NPC1 cDNA were amplified and sequenced. Utilizing these sequences, feline specific PCR primers were generated and designed to amplify six bands which overlap and span the entire expected feline *NPC1* open reading frame. Ninety-eight percent of the feline NPC1 cDNA has been sequenced and a single base substitution (G2870C) has been identified in all NPC affected cats evaluated. Additionally, known carriers are heterozygous at the same allele. This mutation results in an amino acid change from cysteine to serine. The mutation site was utilized to design a PCR based assay for the identification feline NPC heterozygotes. Analysis to determine if cytogenetic abnormalities exist in NPC affected cats was performed. R-banded metaphase chromosome spreads of normal and known heterozygotes were generated. Karyotyping revealed that mutations resolvable at the cytogenetic level were not evident, supporting a small mutation. Utilizing FISH techniques, NPC1 PAC clones were used to determine the specific chromosomal location of NPC gene. Genetic characterization of feline NPC confirmed that the gene responsible for NPC in this feline model is

the orthologous gene that is mutated in the major form of human NPC, further substantiating the value of this colony as an animal model for NPC1.

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DISSERTATION INTRODUCTION

Niemann-Pick Disease Type C (NPC) is an inborn error of metabolism characterized by lysosomal accumulation of lipids. Like many other lysosomal storage disorders, neurological abnormalities are present due to storage within the brain (1). Most lysosomal storage disorders result from a hydrolase deficiency, but that is not the case with NPC. Many several storage diseases have been identified in domestic animals (2). Development and characterization of animal models of lysosomal storage diseases has proven very useful in both the elucidation of pathophysiology and evaluation of therapeutic modalities.

NPC was first described in 1958 by Crocker and Farber. Increased tissue sphingomyelin was identified in a patient and the "new disease", NPC, was grouped with the other documented sphingomyelinase deficiencies, Niemann-Pick Diseases Type A and B (3). Niemann-Pick Disease Type C is now known to not be due to a sphingomyelinase deficiency, but the historical classification scheme persists (4, 5).

Niemann-Pick Disease Type C is an autosomal recessive inherited disease characterized by defective intracellular transport of exogenous, low density lipoprotein (LDL) derived cholesterol (6, 7). Uptake of LDL cholesterol is normal, but the NPC defect results in delayed cholesterol esterification and the subsequent accumulation of unesterified cholesterol that can be visualized by staining with the fluorescent antibiotic filipin (8, 9). The predominant storage material outside of the central nervous system (CNS) includes unesterified cholesterol, phospholipids and sphingomyelin. This is in contrast to the storage seen within the CNS, which is predominantly glycosphingolipids (GSL) and in particular, gangliosides GM2 and GM3. Ganglioside accumulation has been associated with ectopic dendritogenesis in several storage diseases(10). Cytological findings include vacuolated hepatocytes and vacuolated macrophages in the both the spleen and bone marrow (11, 12).

Disease Manifestations of NPC

The clinical manifestations of human NPC include neonatal jaundice, hepatosplenomegaly, and a progressive neurodegenerative course marked by ataxia, dystonia, and dementia (13, 14). Niemann-Pick Disease Type C is panethnic and clinically heterogeneous, with varied ages of onset that are divided into acute (infantile), sub-acute (juvenile) and chronic (adult) categories (15). Prominent findings within the CNS include increased ganglioside accumulation, which is associated with the formation

of ectopic dendrites, (16) and axonal spheroid formation with subsequent neuroaxonal dystrophy and cell death. GABAergic cells, including Purkinje cells in the cerebellum, are particularly affected (17). Recently, filipin staining of NPC neurons has shown storage of unesterified cholesterol within neurons, contrary to earlier reports that cholesterol did not accumulate within the CNS of NPC patients (18, 19). Other abnormalities within the nervous system include a demyelinating and sensory polyneuropathy (20) in addition to the formation of neurofibrillary tangles (NFT's) consisting of paired helical filaments composed of tau proteins; these are similar to NFT's in Alzheimer's disease (21, 22).

Animal Models of NPC

Several models for NPC exist, including two murine models, the BALB/c LSD mouse and C57BL/KsJ (spm) mouse, in addition to the feline model that is the subject of this dissertation (9, 23). Both murine models have been shown to be genetic orthologs of the major form of human NPC, NPC1 (24, 25).

The feline model of NPC has been characterized and is phenotypically, morphologically, and biochemically identical to human NPC1 (17, 26-29). NPC affected cats typically present with clinical neurological signs between 8 and 12 weeks of age with rapid progression to severe dysmetria and ataxia, and death by 7 to 10 months of age.

Biochemical abnormalities include increased serum cholesterol and bilirubin concentrations, and increased serum alkaline phosphatase, aspartate aminotransferase and alanine aminotransferase activities. Storage within the viscera is evident and includes vacuolization of hepatocytes, Kupffer cells, and macrophages. Within the CNS, axonal spheroids and ectopic dendrites are evident and by electron microscopy, membranous cytoplasmic inclusions are seen within neurons (27, 28).

Complementation studies using cultured fibroblasts from NPC affected cats and NPC1 affected humans suggested that the gene responsible for the NPC phenotype in this colony of cats is orthologous to the gene responsible for the major form of human NPC, NPC1 (30). Studies performed as part of this dissertation have since confirmed that the feline NPC gene is also an ortholog of the human NPC1 gene (Somers et al, unpublished data). Additionally, findings in feline NPC heterozygotes revealed morphological and biochemical abnormalities within the CNS, manifestations that have not yet been reported in carriers of genetic neuronal storage diseases (31).

Therapy for NPC

Currently, there is no effective treatment for NPC despite numerous attempts including bone marrow transplantation, cholesterol lowering diets and drugs, and the administration of ganglioside synthesis inhibitors (18, 32-36). Bone marrow transplants

have been performed in NPC cats and humans. Results for both species were similar and although there was a slight delay in clinical disease progression, the overall pattern of the disease course and subsequent premature death were not altered (32) (Brown et al, unpublished data).

Clinical trials in human beings using cholesterol lowering drugs and cholesterol restricted diets have had mixed results. In one study, dietary cholesterol restriction and treatment with cholesterol lowering agents, such as DMSO and lovastatin, were effective in decreasing plasma and hepatic cholesterol concentration; however, neurological function was not evaluated in one study, while no clinical benefit was noted in the other (33, 34). On the other hand, a single case study suggested that diet modification and cholesterol lowering agents might delay neurological deterioration on a short-term basis (35).

Most recently, treatment efforts have been targeted towards decreasing the abnormal ganglioside accumulation within the CNS. The predominant storage material outside of the CNS includes unesterified cholesterol, phospholipids and sphingomyelin, in contrast to the storage seen within the CNS, which is predominantly glycosphingolipids (GSL) and in particular, gangliosides (GM2 and GM3) (37-39). Ganglioside accumulation has

been associated with ectopic dendritogenesis in NPC, as well as in several other storage diseases, and may be a contributing factor to the neurological deterioration (40).

Molecular Bases of NPC

In Tay-Sachs and Sandhoff diseases, the predominant storage in the CNS is GM2 ganglioside (41-43). In two separate studies, N-butyldeoxynojirimycin (NB-DNJ) was used to treat Tay-Sachs or Sandhoff mice. Both studies showed NB-DNJ was successful in preventing the accumulation of GM2 within the brain (36, 44). Additionally, the Sandhoff mice showed delayed symptom onset, reduced storage in peripheral tissues and increased life expectancy. Clinical studies are currently underway to treat type 1 Gaucher disease, a related disorder that involves GSL accumulation in peripheral tissues, but not the CNS (45).

These findings suggested that NB-DNJ might have a beneficial effect on GSL accumulation in the treatment of NPC and associated neurological dysfunction. NB-DNJ is an imino sugar and potent inhibitor of glycosphingolipid synthesis. NB-DNJ inhibits the N-linked oligosaccharide processing enzymes α -glucosidases I and II, and the ceramide specific glucosyltransferase that catalyses the first step in glycosphingolipid biosynthesis. The drug is water-soluble, is not metabolized and is excreted intact by the kidney (46-48). Treatment of HL-60 cells with NB-DNJ results in morphological changes

of secretory granules and the Golgi apparatus, both of which are non-cytotoxic and fully reversible upon withdrawal of the NB-DNJ (49). The drug is well tolerated by adult mice. However, when young mice were treated with NB-DNJ, extensive depletion of GSL within the liver and lymphoid organs was noted without any overt lesions, and the treated mice did grow more slowly (50). The administration of a less toxic inhibitor such as N-butyldeoxygalactonojirimycin may avoid some of the negative side effects associated with NB-DNJ (51).

Other studies using double knockout mice revealed that the absence of ganglioside accumulation had no impact on the clinical NPC disease course and that visceral storage remained unchanged (18). NPC model mice were bred with mice carrying a mutated GalNAcT gene, which is responsible for the synthesis of GM2. No reduction in visceral storage was noted in the double mutants. However, they had significant reduction in the characteristic NPC brain lesions, including neuronal storage and decreased staining of neurons with filipin, but no improvement in the clinical NPC phenotype. Demyelination and neurodegeneration as determined by apoptotic cells and loss of Purkinje cells persisted as a prominent feature in the double mutants (18). These findings raise questions about the true role of ganglioside accumulation and the formation of ectopic dendrites as they relate to NPC and the characteristic neurological deterioration.

Only recently has the molecular basis of NPC begun to come to light. In 1993, Carstea et al first documented the linkage of NPC to human chromosome 18 (52).

Complementation studies indicated that there were at least two genes that could be implicated in causing NPC (6, 53). The most common complementation group (major form) is now designated as NPC1 and accounts for greater than 95% of all NPC cases.

The major form of human NPC (NPC1) has been mapped to chromosome 18q11; the human NPC gene (NPC1) has been identified and sequenced (24, 52). Studies also indicated that the gene responsible for the NPC phenotype in two murine models was linked to mouse chromosome 18, and homology studies showed that mouse chromosome 18 was syntenic with areas of human chromosomes 18 and 5(25). Over thirty different mutations of the NPC1 gene have been identified in humans (24, 54, 55). It has also been shown that Niemann-Pick disease type D (NPD), which arose from a founder effect in Nova Scotia, is an allelic variant of NPC (56).

The NPC1 gene codes for a 1278 amino acid protein. The putative NPC1 protein is predicted to have thirteen transmembrane regions and three large hydrophilic loops (57).

The NPC1 protein has been shown to reside in late endosomes and to transiently interact with lysosomes and the trans-Golgi network (58). The exact function of the NPC1 protein remains unknown. However, it has been shown to be a transport protein that is critical for the movement of endocytosed material (58, 59). Several possible

functions of the NPC1 protein have been proposed and include 1) direct transporting that would facilitate the movement of cholesterol out of the lysosomes, 2) docking/fusion role that would mediate the interaction of cholesterol-laden vesicles and endosomes, or 3) functioning as a molecular pump (57). The mechanism by which the mutation in the NPC1 gene and resultant C957S amino acid substitution contributes to the pathogenesis of NPC remain unknown. The 957 cysteine residue is conserved across multiple species and is likely critical to the structure and subsequent function of the NPC1 protein (60).

The pathogenesis of the brain dysfunction in NPC is still not understood. It is clear that outside the central nervous system (CNS), the NPC1 lesion results from a processing defect of LDL-derived cholesterol, but it is widely accepted that exogenous cholesterol is not presented to the CNS because of the blood-brain barrier. This means that the NPC1 protein must have other functions, at least within the CNS, which have yet to be identified. Overall, the NPC1 protein is not closely related to any other known proteins, but the membrane orientation of the NPC1 sterol sensing domain (SSD) is identical to those of HMG CoA reductase and SCAP, known mediators of cholesterol homeostasis (61).

Characterization of the feline NPC1 cDNA sequence confirmed that the gene responsible for the NPC phenotype in the feline model is indeed the ortholog of the

human NPC1 gene. Strong nucleotide and amino acid sequence homology exists between the cat and human, which is actually greater than that between the human and mouse (Somers et al, unpublished data). This is not surprising given that comparative genomic studies have shown that the cat is phylogenetically more closely related to humans than the mouse, and that the overall feline-human syntenic chromosomal conservation is greater than the mouse-human (62). Based on these findings, the NPC feline colony will serve an extremely valuable model for further evaluation of the NPC1 protein and development of future treatment modalities.

Although the exact function of the NPC1 protein remains unknown, the field is rapidly advancing and it is probable that the elucidation of the function of the NPC1 protein will be determined in the very near future. These discoveries will play a pivotal role in understanding disease pathogenesis in NPC, in both the peripheral tissues and the CNS, and are vital to the development of rational treatment modalities.

The specific aims of the research presented in this dissertation were:

- 1) To evaluate dietary cholesterol restriction and ganglioside synthesis inhibitors as potential treatment modalities in the feline model of Niemann-Pick Disease Type C.

- 2) To characterize the gene responsible for the NPC phenotype in the feline model and to identify the mutation(s) in this cat colony.

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CHAPTER ONE

DIETARY CHOLESTEROL RESTRICTION IN A FELINE MODEL OF NIEMANN-PICK DISEASE TYPE C

INTRODUCTION

The primary defect in Niemann-Pick Disease Type C (NPC) leads to abnormal processing of cholesterol, specifically exogenous cholesterol that enters cells via LDL receptor mediated pathways (1). This results in the accumulation of several lipids, including unesterified cholesterol. A diet study was conducted in this feline model of NPC to evaluate the effect of dietary cholesterol restriction on disease progression. The cholesterol restricted diet was targeted at reducing the amount of low density lipoprotein available to cells, hypothetically to prevent the subsequent accumulation of unesterified cholesterol in the lysosomes.

Clinical trials using low cholesterol diets in human beings have had mixed results. In one study, dietary cholesterol restriction and treatment with cholesterol lowering agents, such

as DMSO and lovastatin, were effective in decreasing plasma and hepatic cholesterol concentration (2,3). However, neurological function was not evaluated in one study, while no clinical benefit was noted in the other. On the other hand, a single case study suggested that diet modification and cholesterol lowering agents may delay neurological deterioration on a short-term basis (4). The aim of this study was to evaluate the impact of dietary cholesterol restriction on disease progression in feline NPC. The hypothesis was that restriction of dietary cholesterol would prevent cellular lipid accumulation and halt or delay clinical disease progression.

MATERIALS AND METHODS

Animals

Two NPC affected treated cats and two NPC affected non-treated cats were evaluated. Historical data from NPC affected non-treated cats were also used. Cats were fed controlled diets beginning at eight weeks of age and were maintained for 150 and 180 days respectively. The cats were individually housed and fed twice daily; the weight of food consumed was recorded. Cats were cared for according to the principles outlined in the National Institutes of Health Guide for the Care and Use of Laboratory Animals, under the guidelines of the Institutional Animal Care and Use Committee (ACUC), and housed in a facility certified by the American Association for Accreditation of Laboratory Animal Care (AAALAC) at Colorado State University. At the end of study, animals were

euthanized with an overdose of intravenous barbituate (40mg/lb pentobarbital), complete necropsies were performed and tissues for analyses were collected.

Cholesterol Restricted Diet

A cholesterol restricted diet, formulated in conjunction with veterinary nutritionists and a commercial pet food company (Ralston Purina™), contained less than 2.6 mg of cholesterol per 100 grams of diet on a dry matter basis (Table 1). The diet was soybean based and included menhaden fish oil as the only source of cholesterol. (Cats are true carnivores and require an exogenous arachidonic acid source (menhaden fish oil), precluding a cholesterol free diet). The cholesterol restricted diet was mixed and stored as a powder at 4°C then mixed with water just prior to feeding. The control diet included two commercial pet foods (dry Meow Mix™ and canned Science Diet™ Feline Growth) containing 41.7 mg and 484.4 mg of cholesterol per 100 grams of diet on a dry matter basis respectively. Cholesterol content of all diets was determined by gas separation chromatography at Woodson-Tenent Laboratories (Des Moines, IA, USA).

Clinical Neurological Assessment

Neurological examinations of NPC affected treated and untreated cats were conducted every two weeks beginning at eight weeks of age. Standard evaluation of postural, reflex

and cranial nerve function was performed by a board certified veterinary neurologist who was unaware of the treatment status of individual cats.

Serum Biochemical Analyses

Cats were bled for serum biochemical analyses by jugular venipuncture following a 12 hour fast. Serum chemistry analyses were performed on an automated analyzer (Hitachi 704 or 911; Boehringer-Mannheim Corporation, Indianapolis, IN, USA). Analytes included serum bilirubin, cholesterol and albumin concentrations, and serum alkaline phosphatase (ALP) and alanine aminotransferase (ALT) activities. Serum for biochemical analyses was collected every four weeks beginning at two weeks of age.

Liver Lipid Analyses

Analyses of unesterified cholesterol, cholesterol ester and phospholipids in liver tissue were performed at the end of the study. Lipid extraction of fresh frozen liver was performed by the method of Folch (5). Briefly, a known weight of liver was extracted with chloroform-methanol (2:1 v/v) and filtered; 1/5 volume of water was added to the filtrate. Phases were separated by centrifugation and the lower phase was used for quantification of individual lipids. Total and individual lipids were quantified using standard methods (6) and expressed as nmol lipid/g wet weight tissue.

Brain Ganglioside Analyses

Cerebral cortex was collected at necropsy and frozen at -70°C . Gangliosides were extracted and purified by modified Suzuki method (7) and separated by high performance thin layer chromatography (HPTLC). Plates were scanned by densitometry (Quick-Scan Flur-Vis densitometer, Helena Laboratories, Beaumont, Texas, USA); G_{M1} , G_{M2} , and G_{M3} gangliosides were quantified.

Morphological Analyses

Light microscopic examination of liver, spleen and brain was performed at the end of the study. Tissues were collected at necropsy, fixed in 10% neutral buffered formalin, processed routinely, sectioned at $6\mu\text{m}$, and stained with hematoxylin and eosin (H&E). Cerebellar tissue sections stained with H&E were quantitatively assessed by enumeration of Purkinje cells (CNIH Image software, version 1.61, W. Rasband, National Institutes of Health, Bethesda, MD) and counting of axonal spheroid numbers per 40X objective field averaged over eight fields.

Statistical Analysis

The number of NPC affected treated cats was inadequate for statistical comparison. Data for the two NPC affected treated cats are actual values while data for NPC affected untreated cats are means with standard deviation or ranges.

RESULTS

Clinical Neurological Assessment

Age of onset and rate of progression of neurological disease in the two NPC affected cats fed the cholesterol restricted diet were not different from NPC affected untreated cats. In general, NPC affected cats display intention head tremors between 8 and 12 weeks of age with a mean onset at 10.25 weeks of age. The NPC affected treated cats in the study showed neurological signs at 8 and 9 weeks of age and progressed neurologically at the same rate as NPC affected untreated cats. The intention tremors became more pronounced over time. Dysmetria during ambulation and hypermetric limb movements with truncal swaying were noted. By 19 to 23 weeks of age, NPC affected cats maintained a crouched position and would fall to either side when moving. Slow initiation and hypermetria of postural reactions were noted, and intention tremors had progressed to whole body involvement. Between the ages of 20 and 33 weeks, cats were unable to right themselves from lateral recumbency. Overtime, the tremors became less apparent, cats developed disuse muscle atrophy and menace response was lost. Both treated and untreated cats were euthanized between 7 and 9 months of age.

Serum Biochemical Analyses

Previously identified biochemical abnormalities in the feline model of NPC include increased serum ALP, ALT, and AST activities, increased serum bilirubin and cholesterol

concentrations and decreased serum albumin concentration (8,9). Serum abnormalities are not present in feline NPC heterozygotes (10).

Serum ALP activity and cholesterol concentration were lower in one NPC affected treated cat, as compared to NPC affected untreated cats from 12 weeks of age until the last sampling, and were comparable to values seen in the normal cats. Serum albumin concentrations were higher in both NPC affected treated cats compared to NPC affected untreated cats and similar to those seen in normal cats. Both NPC affected treated kittens had normal serum bilirubin concentrations. Serum biochemical data are summarized in Table 2.

Tissue Lipid Analyses

Liver lipid concentrations in NPC affected treated cats were similar to those in NPC affected untreated cats (Table 3). Ganglioside concentrations of G_{M1} , G_{M2} , and G_{M3} in the cerebral cortical grey matter of the NPC affected treated cats remained unchanged when compared to ganglioside concentrations in NPC affected untreated cats (Table 4).

Morphological Analyses

Hepatocyte cytoplasm was vacuolated in both the NPC affected treated and NPC affected untreated cats. In the NPC affected treated cats, cytoplasmic vacuolar changes

were diffuse and uniform throughout each hepatic lobule; all hepatocytes were swollen and rounded. The vacuoles were small, round, clear, and of almost uniform diameter. Occasional cells had larger vacuoles. By contrast, in the NPC affected untreated cats, cytoplasmic vacuoles were markedly variable in size and were usually larger than those seen in the NPC affected treated cats (Figure 1.1, 1.2). In the NPC affected untreated cats, narrow bands of fibrous tissue were present in the limiting plates of the lobules and extended through the lobules in a random fashion, disrupting the orderly arrangement of the hepatic cords. Fibrosis was not evident in NPC affected treated cats. Individual hepatocytes were occasionally surrounded by thin bands of collagen. Hepatocytes near the collagenous bands were smaller than more distant hepatocytes or those in the NPC affected treated cats (Figure 1.3, 1.4).

Splenic macrophages had similar differences in vacuolization (Figure 1.5, 1.6).

Macrophages in the NPC affected treated cats contained many small uniform clear cytoplasmic vacuoles, while in the NPC affected untreated cats, vacuoles were more variable in size, with larger cytoplasmic vacuoles predominating.

Purkinje cell numbers decrease with age in all NPC affected cats (11). Cerebellar

Purkinje cell concentration in both NPC affected treated and untreated cats was similar, but reduced compared to that of normal cats. The number of Purkinje cells seen in NPC

affected untreated cats was 1.1 (SD \pm 0.54) per 100 μm^2 , compared to the two NPC affected treated cats, which were 1.3 and 0.7 per 100 μm^2 respectively. Normal control cats had a mean of 2.0 (SD \pm 0.48) Purkinje cells per 100 μm^2 . Large round hypereosinophilic axonal spheroids were prominent in the cerebellar granular and Purkinje cell layers in both NPC affected treated cats and NPC affected untreated cats (Figure 1.7, 1.8). A mean of 1.4 (SD \pm 0.27) axonal spheroids per 40X objective field was seen in the NPC affected untreated cats, compared to 1.6 and 1.4 in the two NPC affected treated cats. No axonal spheroids were seen in normal control cats.

DISCUSSION

Dietary cholesterol restriction did not significantly impact disease progression in the two NPC affected treated cats in this study. Hepatic parameters, particularly serum albumin and cholesterol concentrations and serum ALT and ALP activity, appear to have improved in one kitten. The apparent improvement in these parameters, as well as the change in vacuolar patterns in the liver and spleen sections of the NPC affected treated cats, may be related to alterations in liver lipid metabolism following dietary cholesterol restriction. However, other dietary variables such as phytosterols and vitamin E content may have contributed to the results. Phytosterols are present in high concentrations in

soybeans and are known to reduce cholesterol absorption (12). Vitamin E has been shown to be beneficial in lowering serum lipid concentrations. Despite the potential presence and beneficial impact of other cholesterol attenuating substances in the diet, no significant change in disease progression was seen.

It appears that reduced dietary cholesterol has little impact on brain lesions and ganglioside storage was not decreased in NPC affected treated cats. Perhaps this is related to the fact that while visceral tissues store unesterified cholesterol and phospholipids in addition to glycolipids, NPC affected brains store predominantly gangliosides (G_{M2} and G_{M3}). Ganglioside synthesis inhibitors such as N-butyldeoxynojirimycin have shown promise as a potential therapy for NPC (13). Other studies involving double mutant mice (NPC model mice crossed with mice unable to synthesize G_{M2} and complex gangliosides) showed that the absence of ganglioside storage in the central nervous system (CNS) had no impact on the clinical NPC course of the disease (14). These finding suggested that ganglioside storage may be a secondary event and the primary mechanism for neurological dysfunction in NPC likely remains to be identified.

This study would have been improved by increasing the number of affected treated cats, including normal treated controls and starting the diet at an earlier age, but there was a

very limited supply of NPC affected kittens and the diet would have been difficult to administer prior to weaning of kittens (eight weeks of age). Earlier weaning is not well tolerated by NPC affected kittens, which tend to not do well in general. Although the number of animals evaluated may be too small to draw definitive conclusions, dietary cholesterol restriction did not impact disease progression in these two NPC affected treated cats. These findings are important and consistent with studies in people, suggesting the key to treating NPC lies elsewhere and that other treatment modalities need to be explored. This animal model may be valuable for future studies of intracellular cholesterol metabolisms and the development and evaluation of novel treatment modalities for NPC.

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Table 1

Composition of Cholesterol Restricted Diet

Dietary Component	Proportion of Diet (%)
Soy Bean Meal	50.00
Wheat Germ Meal	16.00
Canola Oil	25.00
Menhaden Fish Oil	0.15
Molasses	4.20
Purina™ Mineral Mix	0.20
Purina™ Vitamin Mix	0.70
Taurine	0.10
Calcium Oxide	0.80
Potassium Phosphate	2.54
Zinc	0.03
Sodium Chloride	0.20
Methionine	0.08

Table 2**Serum Biochemical Analytes**

Serum Analyte	AUTC (n=12)		S22	S96	Normal (n=32)	
	Mean	Range			Mean	Range
Alkaline Phosphatase (IU/L)	500	310-670	370	230	230	120-340
Alanine Aminotransferase (IU/L)	310	230-400	500	215	70	40-95
Cholesterol (mg/dl)	210	160-310	180	145	105	60-175
Bilirubin (mg/dl)	0.3	0.2-0.4	0.1	0.2	0.1	0-0.2
Albumin (gm/dl)	2.7	2.6-2.8	3.3	3.4	3.1	2.3-3.9

AUTC – NPC affected untreated control

S22, S96 – NPC affected treated (actual values)

Normal – untreated controls

Table 3**Liver Lipid Concentrations (nmol/g wet tissue weight)**

Lipid	AUTC (n=6)		S22	S96	Normal (n=14)	
	Mean	Range			Mean	Range
Unesterified Cholesterol	45,800	31,000-72,550	66,600	47,525	3900	1200-6800
Cholesterol Ester	760	150-2350	3,680	690	2000	500-6300
Total Phospholipids	46,100	35,840-60,800	56,660	61,390	25,400	11,870-28,780
Sphingomyelin	5790	3200-11380	12,330	10,790	1150	100-2200
Phosphatidycholine	10,600	4300-15,700	11,230	9900	4670	2280-6240

AUTC – NPC affected untreated control

S22, S96 – NPC affected treated (actual values)

Normal – untreated controls

Table 4

Cerebral Cortex Ganglioside Concentrations ($\mu\text{g}/\text{mg}$ of tissue)

Ganglioside	AUTC (n=6)		S96	Normal (n=11)	
	Mean	Range		Mean	Range
GM1	0.068	0.037-0.125	0.048	0.118	0.34-0.137
GM2	0.034	0.011-0.083	0.036	0.010	0.008-0.026
GM3	0.038	0.002-0.124	0.029	0.002	0.0-0.009

AUTC – NPC affected untreated control

S96 – NPC affected treated (actual values)

Normal – untreated controls

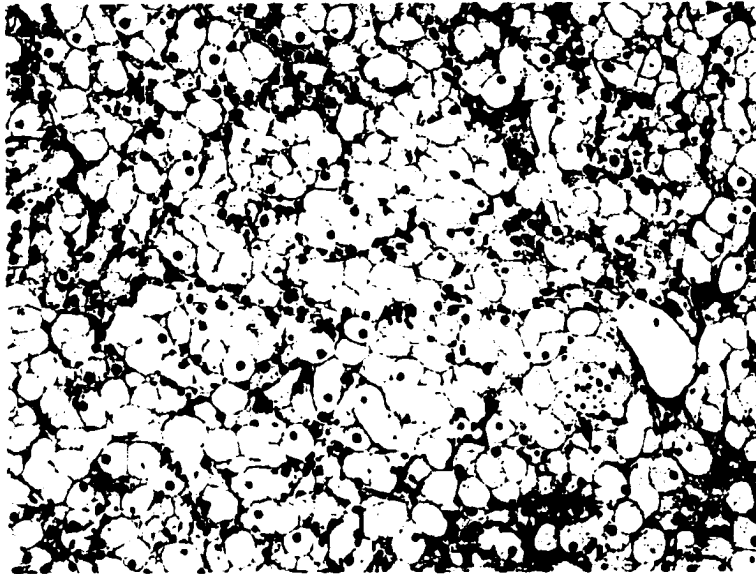


FIGURE 1.1
Liver (H&E 100X)
NPC affected treated cat with discrete
microvacuolar pattern in cytoplasm of hepatocytes.

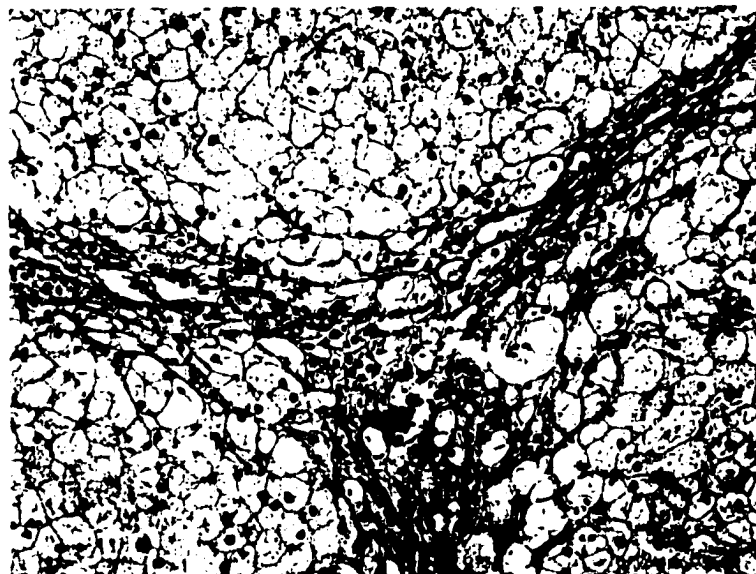


FIGURE 1.2
Liver (H&E 100X)
NPC affected untreated cat with a mixed
micro-macro vacuolar pattern in cytoplasm of
hepatocytes and prominent fibrosis.

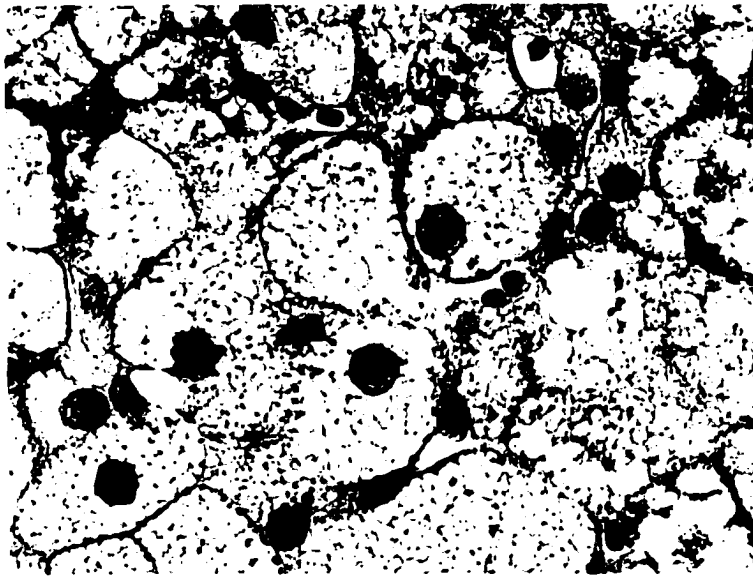


FIGURE 1.3
Liver (H&E 500X)
NPC affected treated cat with discrete
microvacuolar pattern in cytoplasm of hepatocytes.

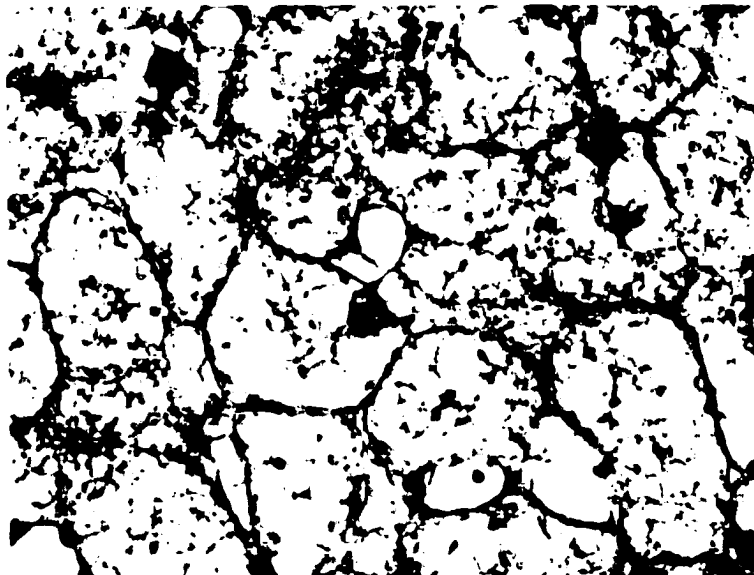


FIGURE 1.4
Liver (H&E 500X)
NPC affected untreated cat with a mixed micro-
macro vacuolar pattern in cytoplasm of hepatocytes.

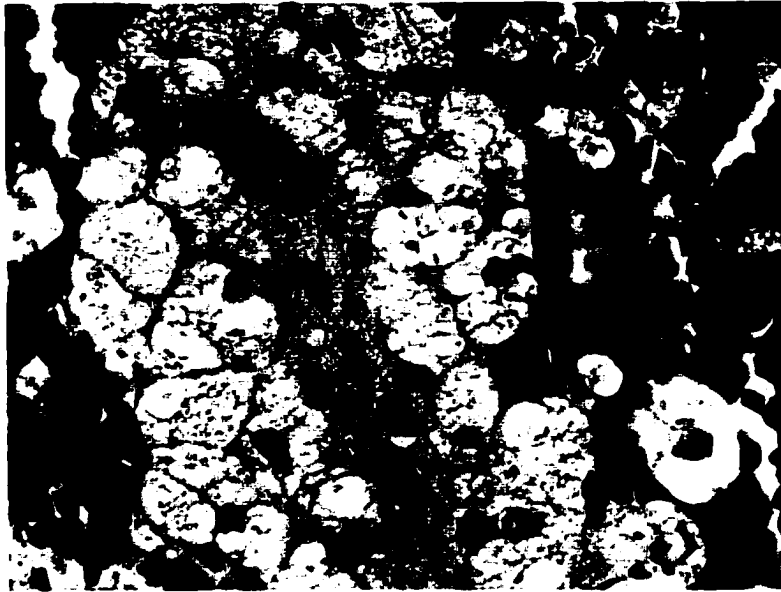


FIGURE 1.5
Spleen (H&E 100X)
NPC affected treated cat with a micro- vacuolar pattern
within macrophages.

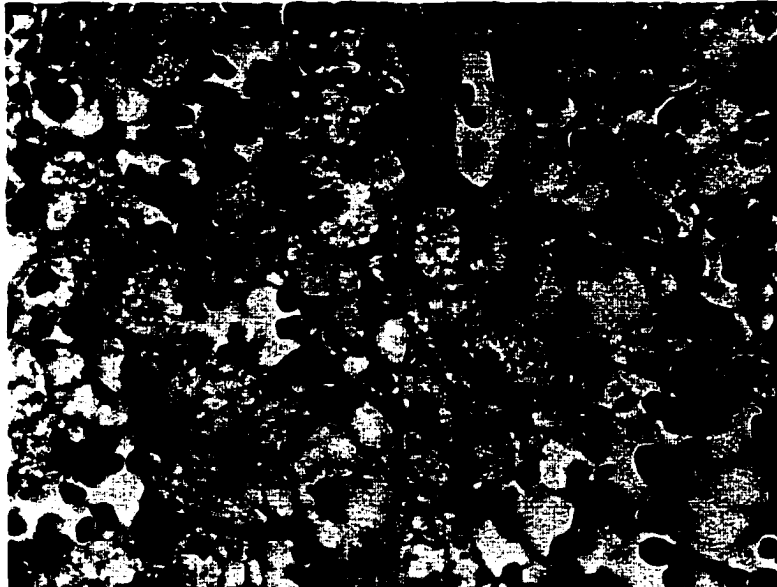


FIGURE 1.6
Spleen (H&E 100X)
NPC affected untreated cat with a mixed micro-macro
vacuolar pattern within macrophages.



FIGURE 1.7
Cerebellum (H&E 100X)
NPC affected untreated cat with axonal spheroids
and Purkinje cell loss.



FIGURE 1.8
Cerebellum (H&E 100X)
NPC affected untreated cat with axonal
spheroids and Purkinje cell loss.

CHAPTER TWO

EFFECT OF N-BUTYLDEOXYNOJIRIMYCIN IN A FELINE MODEL OF NIEMANN-PICK DISEASE TYPE C

INTRODUCTION

Niemann-Pick Disease Type C (NPC) is an inherited storage disorder characterized by a cholesterol metabolism defect that results in lysosomal accumulation of several types of lipid. The predominant storage material outside the central nervous system (CNS) includes unesterified cholesterol, phospholipids and sphingomyelin (1, 2), in contrast to the storage seen within the CNS, which is predominantly glycosphingolipids (GSL) and in particular, gangliosides (GM2 and GM3) (3, 4). Ganglioside accumulation has been associated with ectopic dendritogenesis in NPC, as well as in several other storage diseases, and may be a contributing factor to the neurological deterioration (3).

The primary goal of this pilot study was to evaluate the impact of the ganglioside synthesis inhibitor, N-butyldeoxynojirimycin (NB-DNJ), on clinical disease progression

and brain ganglioside accumulation in NPC affected cats. N-butyldeoxynojirimycin is an imino sugar that inhibits the ceramide-specific glucosyltransferase that catalyzes the first step of GSL biosynthesis (5, 6). The rationale for this study was that NB-DNJ has been used to successfully prevent the accumulation of GM2 within the brain of Tay-Sachs and Sandhoff mice, in which GM2 is stored (7). Additionally, the Sandhoff mice showed delayed symptom onset, reduced storage in peripheral tissues and increased life expectancy. These findings suggested that NB-DNJ might have a beneficial effect on GSL accumulation in the treatment of NPC and associated neurological dysfunction. NB-DNJ is a potent inhibitor of glycosphingolipid synthesis.

NB-DNJ inhibits the N-linked oligosaccharide processing enzymes α -glucosidases I and II, and the ceramide specific glucosyltransferase which catalyses the first step in glycosphingolipid biosynthesis. The drug is water-soluble, is not metabolized and is excreted intact by the kidney. The hypothesis for this study was that administration of NB-DNJ to NPC affected cats would prevent and/or slow clinical disease progression and decrease brain ganglioside accumulation in the feline model of NPC.

This NB-DNJ drug study was a collaborative effort with Drs. Stephen Walkley and Mark Zervas (Albert Einstein College of Medicine, Bronx, NY) who conducted a concurrent

drug study in NPC mice to evaluate the effect of NB-DNJ on clinical disease progression and ganglioside storage.

MATERIALS AND METHODS

Animals

Cats were divided into four groups that consisted of NPC affected treated cats (n=3), NPC affected untreated cats (n=12, includes historical data), normal treated cats (n=4), and normal untreated cats (established reference ranges). Cats were housed and cared for according to the principles outlined in the National Institutes of Health Guide for the Care and Use of Laboratory Animals, under the guidelines of the Institutional Animal Care and Use Committee (ACUC), and housed in an American Association for Accreditation of Laboratory Animal Care (AAALAC) certified facility at Colorado State University.

NB-DNJ was donated by Oxford GlycoSciences (Abingdon, United Kingdom). The drug was administered as a powder mixed with cat food, or if cats would not eat the food, it was mixed with a small amount of water and administered orally using a syringe. An initial dose of 1200-mg/kg body weight divided bid was given, based on the dosage used in mice. This dose was hepatotoxic; increased liver enzyme activities were markedly increased within 24 hours of administration. The dose was immediately decreased to

150 mg/kg body weight divided bid and later to 50 - 100 mg/kg body weight divided bid, depending on appetite, and presence of weight loss, vomiting, or diarrhea. Table 2.1 summarizes the individual cat status, age at start of study and number of days on treatment for each NB-DNJ dosage.

Clinical Neurological Assessment

Neurological examinations of NPC affected cats were conducted on a bi-weekly basis beginning at 6 weeks of age and continuing until the end of the study. Evaluation of postural, reflex and cranial nerve function was performed by a board certified veterinary neurologist unaware of the treatment status of individual cats. Additionally, all cats were monitored on a daily basis for changes in clinical behavior and eating habits. Normal controls were not neurologically examined.

Hematology and Serum Biochemical Analyses

Complete blood counts and serum biochemical profiles were performed weekly (or more frequently if indicated) and began one week prior to the first administration of the drug. Blood was collected by jugular venipuncture following a 12 hour fast and prior to the morning administration of the drug. Serum analyses were performed on all NPC affected treated and NPC untreated cats and treated normal controls. Serum chemistry analyses were performed on an automated analyzer (Hitachi 704 or 911; Boehringer-

Mannheim Corporation, Indianapolis, IN, USA). Analytes included serum cholesterol, bile acids and bilirubin concentrations, and serum alkaline phosphatase (ALP), alanine aminotransferase (ALT), and aspartate aminotransferase (AST) activities. Serum for measurement of NB-DNJ concentration was collected and frozen at multiple time points throughout the study. All serum samples were batch analyzed by Oxford GlycoSciences (Abingdon, United Kingdom).

Brain Ganglioside Analyses

Animals were pre-medicated with a combination of butorphanol, acepromazine and glycopyrolate (BAG protocol) and deeply anesthetized with isoflurane. Sections of cerebral cortex were collected and frozen at -70°C ; the CNS was immediately perfused with 4% paraformaldehyde and 0.1% glutaraldehyde in 0.1 M phosphate buffer followed by immersion fixation in the same fixative for 4 hours.

High Performance Thin Layer Chromatography (HPTLC)

Samples for HPTLC were collected from the left hemisphere from the midline to the lateral extent of cortex in the coronal plane at midline along the anterior posterior axis. Frozen brain tissue was homogenized, then total lipids were extracted by the method of Folch (8). A volume of total lipid extract equivalent to 10 mg dry weight was partitioned. The upper phase was purified by SEP PAK C18 chromatography and dried under N_2 ,

re-suspended, and the extract spotted on silica gel 60-coated glass-backed, HPTLC plates. After drying, plates were developed in chloroform:methanol:0.22% CaCl₂ (55:45:10). To image gangliosides, the plate was sprayed with a fine mist of resorcinol and incubated at 100C for 35 minutes until a purple color reaction occurred. Lipids were identified by comparison with authentic ganglioside standards.

Immunohistochemistry (IHC)

Samples for IHC were collected from the right hemisphere from the midline to the lateral extent of cortex in the coronal plane at midline along the anterior posterior axis. Fixed brain tissue sections were processed for immunocytochemistry. Antibody to GM2 ganglioside was employed to observe ganglioside concentration in treated versus untreated cats in a qualitative manner. The cerebral cortex, and the Purkinje cells, and granule cells within the cerebellum were evaluated. Sections for immunocytochemistry were reacted free floating in wells containing the appropriate reagents. Sections were pre-treated with 0.5% hydrogen peroxide in methanol to inactivate endogenous peroxidases, washed in phosphate buffered saline (PBS) , then pre-incubated for one hour in either 10% normal goat or horse serum to block nonspecific antibody binding. Sections were incubated overnight with antibody against GM2 ganglioside (1:1000 dilution, P. Livingston, Memorial Sloan Kettering Medical Center). After an 18 hour incubation at 4C, tissue sections were washed in 0.01 M PBS, incubated for one hour at

room temperature with a biotinylated antibody against the host species of the primary antibody, washed again, and incubated for 1 hour with the avidin-horseradish peroxidase reagent kit (Vectastain ABC kit, Vector, Laboratories). Peroxidase label was demonstrated using a 0.05% 3,3' diaminobenzidine/0.01% hydrogen peroxide mixture diluted in 0.05 M TRIS-HCL pH 7.4. Sections were mounted on gel-coated slides, dehydrated in graded ethanol, and cover slipped in permount.

Morphological Analyses

Tissues for light microscopy were collected at necropsy, fixed in 10% neutral buffered formalin, processed routinely, sectioned at 6 μ m, and stained with hematoxylin and eosin (H&E). Liver, spleen, adrenal gland, lymph node, kidney, lung, myocardium, thyroid, intestine, and ovaries were examined.

RESULTS

Clinical Neurological Examinations

Progression of clinical neurological disease in the two older NPC affected treated cats was delayed compared to that of NPC affected untreated cats. Onset of clinical signs appeared to be delayed in the youngest NPC affected treated cat compared to NPC affected untreated controls. Cats placed on the drug treatment after the onset of clinical signs had less severe intention tremors compared to age-matched NPC untreated cats.

Additionally, the cat that began treatment at 21 weeks became ataxic at a much later time point compared to NPC affected untreated cats. The NPC affected treated cat that began treatment at 13 weeks of age died at 21 weeks of age (from pneumonia) and had no evidence of ataxia.

The cat that began the drug treatment at 7 weeks of age, prior to the onset of clinical signs, was clinically normal at 11 weeks, the age of death. This is in contrast to NPC affected untreated cats that typically show signs of subtle head intention tremors by 10 weeks of age (n=12), although onset as late as 12 weeks (2 out of 12 kittens or 17%) has been noted. This cat had severe hypoglycemia that was likely the cause of death and possibly attributable to the drug treatment. The age of onset for clinical neurological signs for each cat / group is summarized in Table 2.2. Values given for NPC affected untreated cats (AUTC) are group means (n=12) and include historical data.

Hematology, Serum Biochemical Analyses and Serum Drug Concentrations

Abnormalities seen in the complete blood counts included lymphocytosis, likely attributable to an excitement response that is common in young cats. At different time points, transient neutrophilia with low to normal lymphocyte concentration was present; this combination is most consistent with an endogenous steroid induced stress response.

Mild hypoproteinemia characterized by hypoglobulinemia was seen in all groups and likely reflects the limited antigenic exposure of cats in a closed research colony; this has been a consistent observation in this particular colony of cats. Hypercholesterolemia of comparable magnitudes was seen in both NPC affected treated and NPC affected untreated cats. Transient hypoglycemia was noted in one NPC affected treated cat and one normal treated cat. Increased serum AST and ALT activities were seen in all groups except the non-treated normal controls, and was exacerbated by increased dosages of NB-DNJ (Figures 2.1, 2.2 and 2.4). Mild increases in serum ALP activity and serum phosphorus were seen in all groups of cats and is most consistent with normal increases seen in young growing animals. Additionally, increases in serum ALP activity in normal treated cats which were greater than increases associated with bone growth were seen as a NB-DNJ dose related response. Serum ALP activity was decreased in NPC affected treated cats relative to NPC affected untreated cats. NPC affected non-treated cats had serum ALP activities that were greater than the age related increases seen in normal young cats (Figures 2.3 and 2.4). Bile acids were mildly increased in all groups except the normal non-treated control cats, and occasional concurrent hyperbilirubinemia was noted. The increases seen in the NPC affected treated and untreated cats were comparable to increases seen historically in all NPC affected cats. The increased bile acids in the normal treated cats appeared to be associated with high drug dosages.

Serum drug concentrations were determined for multiple time points and various drug dosages. At drug dosages of 50-75 mg/kg/day, cats had a mean serum drug concentration of 1916 ng/ml (range 150-5548 ng/ml); at dosages of 100-150 mg/kg/day, cats had a mean serum concentration of 19,255 ng/ml (range 11,316-30,000 ng/ml). Increases in administered drug dosages correlated with increases in serum concentrations of NB-DNJ up to 100 mg/kg/day at which point the serum drug concentration reached a plateau (Figure 2.5).

Brain Ganglioside Analyses

HPTLC

Analysis of cerebral cortex demonstrated qualitatively decreased concentrations of GM3 and GM2 gangliosides in the cerebral cortex of one NPC affected treated cat evaluated to date. Analysis of cerebral cortex of normal treated and normal untreated cats showed that they have undetectable levels of GM3 and GM2 gangliosides compared to NPC affected cats (Figure 2.6).

Immunohistochemistry

Immunocytochemical staining of the cerebral cortex and cerebellum with anti-GM2 antibody showed a qualitative reduction in storage material in the NPC affected treated cat. In the cerebral cortex reduced storage was most apparent in the pyramidal

neurons, while in the cerebellum the reduction was most notable in the granule cell layer (Figures 2.7 and 2.8). In the NPC affected untreated cat, punctate vesicular GM2 labeling was extensive and intensely labeled numerous pyramidal cells of the cerebral cortex. Also, Purkinje cells of the cerebellar cortex and the entire granule cell layer displayed marked GM2 labeling.

Morphological Analyses

Liver

Inflammatory cells were present in the portal and periportal regions of the livers of one NPC affected treated cat and the adult treated normal control cat. The typical NPC related vacuolization of hepatocytes and Kupffer cells was similar in both the NPC affected treated and NPC affected untreated cats.

Adrenal

One treated normal cat and one treated affected cat had moderate to severe adrenal cortical degeneration. Foci of swollen degenerate cells and areas of calcification were present in the zona fasciculata of the adrenal cortex.

Other Tissues

Mild intestinal cryptitis was present in one NPC affected treated cat. No other morphological abnormalities, besides the typical NPC vacuolization, were noted in sections of kidney, lung, lymph node, spleen, myocardium, pancreas or thyroid

evaluated from cats in each of the treatment groups. No differences in NPC related lesions were noted in tissues from NPC affected treated cats compared to tissues from NPC affected untreated cats.

DISCUSSION

Progression of clinical neurological disease in the two older NPC affected treated cats was slower than progression of disease in the NPC affected untreated cats. Onset of clinical signs was possibly delayed in the youngest NPC affected treated cat that was clinically normal at 11 weeks of age, compared to NPC affected untreated cats that typically show clinical signs by 10 weeks of age. Both HPTLC and immunocytochemical staining suggested that ganglioside accumulation in NPC affected treated cats was qualitatively less, compared to the NPC affected untreated cats. These results are similar to those seen in NPC affected mice treated with NB-DNJ (Zervas, Somers et al, submitted to Science 10/2000). However the study duration was limited and the number of treated cats was small.

The qualitative reduction of GM2 and GM3 ganglioside storage within the CNS is significant in light of concurrent clinical neurological improvement, and may implicate ganglioside accumulation as a possible contributing factor to neurological dysfunction in NPC. The apparent reduction in gangliosides based on HPTLC was subjective and may

be a result of sample loading. Quantitative analysis of gangliosides is crucial for definitive interpretation of data and analyses are pending.

The dosage used in mice (1200mg/kg/day) was hepatotoxic in cats based on increased liver enzyme activities (AST, ALT and ALP) and abnormalities in hepatic function indicators (serum bile acid and bilirubin concentrations). These serum abnormalities correlated with increased dosages of NB-DNJ. The cat treated prior to the onset of clinical signs died at an early point in this study and the death was likely due to hypoglycemia. Hypoglycemia may have been related to the drug or possibly a result of anorexia that was also noted in the cat. Decreased liver function can result in hypoglycemia, but no evidence of end stage liver disease was present in the cat.

Previous studies using NB-DNJ in mice have documented weight loss and lymphoid depletion. Although weight loss was seen in the treated cats, no lymphoid depletion was identified. However, adrenal cortical necrosis was seen in two treated cats (one normal and one NPC affected). Differences in drug administration to mice compared to cats may account for some of the different types of toxicity observed in the two species. The NB-DNJ was incorporated into dry mouse chow, thus mice consumed the drug over a long period of time whereas cats received bolus doses of the drugs twice daily. Moreover, mice require two times the NB-DNJ dose used in humans to achieve the same serum concentration (7). Additionally, cats may be uniquely sensitive to NB-DNJ

due to species related differences in liver metabolism. Pharmacokinetic studies would be useful for determining ideal ND-DNJ dosages to be used in cats. The administration of a less toxic inhibitors such as N-butyldeoxygalactonojirimycin may avoid some of the negative side affects associated with NB-DNJ (9).

Interestingly, studies using double knockout mice revealed that the absence of ganglioside accumulation had no impact on NPC related neurological signs and that visceral storage remained unchanged. NPC model mice were bred with mice carrying a mutated GalNAcT gene, which is responsible for the synthesis of GM2. No reduction in visceral storage was noted in the double mutants. However, they had significant reduction in neuronal storage and decreased staining of neurons with filipin, but no improvement in the clinical NPC phenotype (10). Demyelination and neurodegeneration as determined by apoptotic cells and loss of Purkinje cells persisted as a prominent feature in the double mutants. These findings raise questions about the true role ganglioside accumulation and the formation of ectopic dendrites as they relate to NPC and the characteristic neurological deterioration.

In addition to ectopic dendritogenesis, a prominent feature in the brain of NPC cats is the formation of axonal spheroids. These are found predominantly on GABAergic cells including the Purkinje cells (11). Axonal spheroid formation is a prelude to neuroaxonal dystrophy and subsequent cell death. The progressive loss of Purkinje cells is strongly

associated with worsening of the clinical NPC phenotype (11). Axonal spheroids are thought to result from a block in retrograde transport (12). Perhaps the NPC1 protein is critical to the retrograde transport of endocytosed material from the distal axons, and possibly formation of axonal spheroids, followed by neuroaxonal dystrophy and eventual cell death is responsible for the NPC phenotype. The NPC1 protein has been demonstrated to be crucial for retrograde transport within the endocytic system and when defective, results in non-specific storage of numerous materials(13-15) .

The preliminary results of this limited pilot study are encouraging and additional studies should be performed. Ganglioside synthesis inhibitors show more promise than any treatment modality evaluated to date; human clinical trials using NB-DNH to treat NPC were initiated in the Fall of 2000. This feline model of NPC is a valuable resource for the continued evaluation of ganglioside synthesis inhibitors and well as other therapeutic modalities.

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Table 2.1**Age at Study Start and Number of Day on Each Drug Dosage**

Cat ID	NPC Status	Age in weeks at study start	Days on 1200 mg/kg/day	Days on 150 mg/kg/day	Days on 100 mg/kg/day	Days on 50 mg/kg/day	Total days on Drug
161	Normal	136	0	0	11	8	19
218	Normal	21	1	20	23	11	54
235	Normal	13	0	0	0	144	144
232	Normal	7	0	0	9	14	23
222	Affected	21	1	20	23	11	54
231	Affected	13	0	0	0	156	156
233	Affected	7	0	0	9	14	23

Table 2.2

Age in weeks for onset of neurological signs

Cat ID	Treatment Status	Age at Study Start	Intention Tremors	Ataxia	Falling	Age at Death
222	treated	21	11	29	none	33
231	treated	13	6	none	none	20
233	treated	7	none	none	none	11
AUTC	untreated	N/A	10	14.5	24.5	33

AUTC – affected untreated controls (n=12)

Mean Serum AST Activity Compared to NB-DNJ Dose

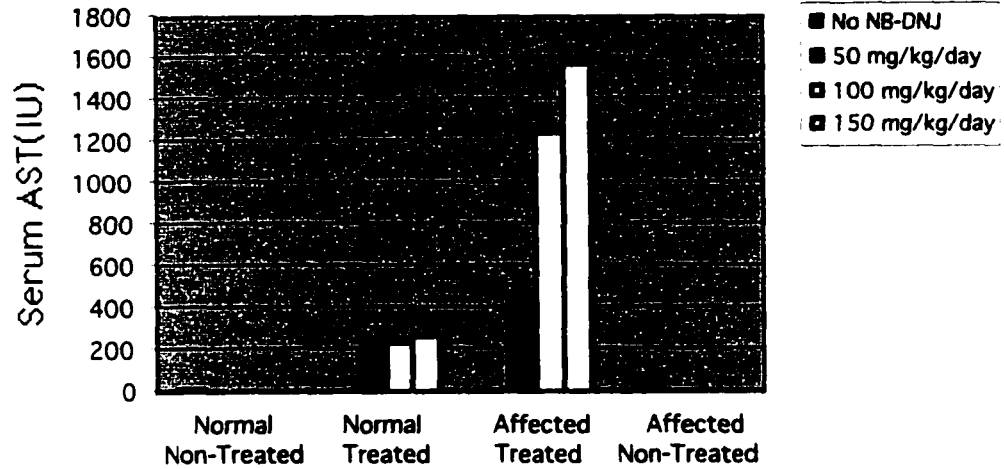


FIGURE 2.1

Serum AST increased as the dosage of NB-DNJ increased; the magnitude of this increase was greater in NPC affected treated cats compared to that of normal treated cats.

Mean Serum ALT Activity Compared to NB-DNJ Dose

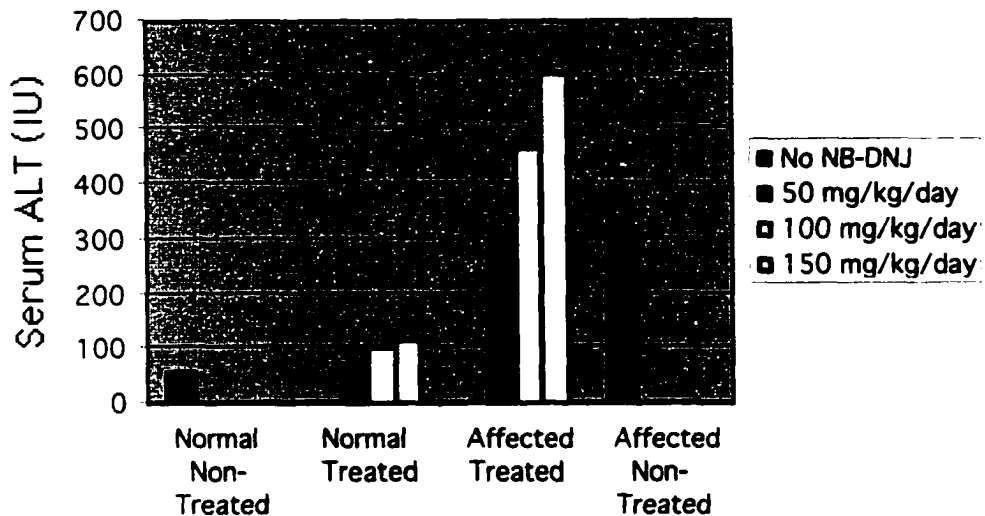


FIGURE 2.2

Serum ALT activity increased as the dosage of NB-DNJ increased; the magnitude of increase was greater in NPC affected treated cats compared to normal treated cats. ALT activity in NPC affected non-treated cats was also increased.

Mean Serum ALP Activity Compared to NB-DNJ Dose

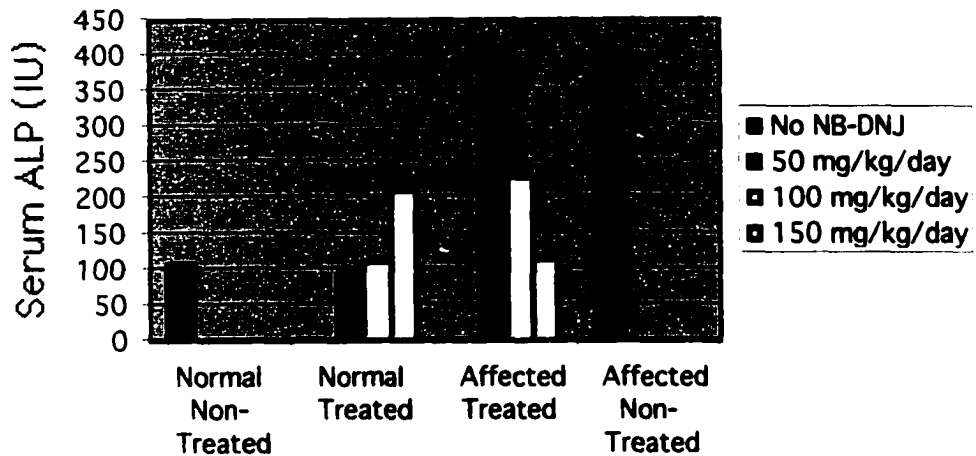


FIGURE 2.3

Serum ALP activity increased in normal treated cats as the dosage of NB-DNJ increased while serum ALP activity decreased in NPC affected treated cats as the NB-DNJ dose increased. ALP activity in NPC affected non-treated cats was also increased.

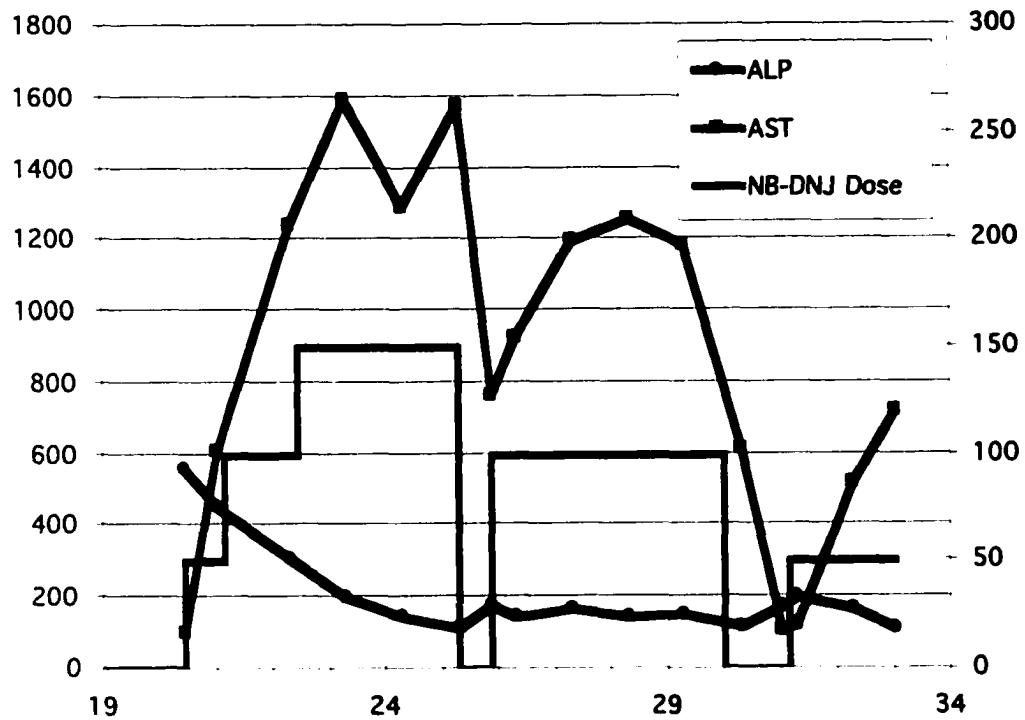


Figure 2. 4

NB-DNJ Dose Versus Serum ALP and AST Activity

Data from one NPC affected treated cat.

Serum ALP and AST (IU, y-axis)
 Serum NB-DNJ on the right (ng/ml)

As the serum NB-DNJ concentration increased, serum ALP activity decreased and serum AST activity increased.

Mean Serum NB-DNJ Concentration Compared to NB-DNJ Dose

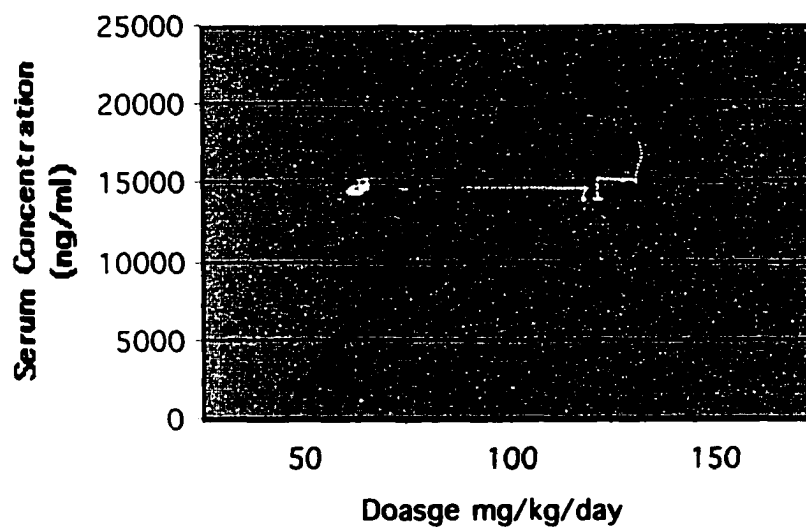


FIGURE 2.5

Serum concentration of NB-DNJ increased as the drug dosage was increased up to approximately 100/mg/kg at which point serum concentrations reached a plateau of ~20,000 ng.ml.



Figure 2.6

HPTLC Plate - Ganglioside Content of Cerebral Cortex

- Lane 1 - Normal treated cat
- Lane 2 - NPC affected non-treated cat
- Lane 3 - NPC affected treated
- Lane - 4 Normal non-treated cat

Lane 3 shows decreased GM3 and GM2 content compared to lane 4.

Lanes 5-9 correspond to murine samples from a concurrent study

- Lane 5 - Normal non-treated mouse
- Lane 6 - NPC affected non-treated mouse
- Lanes 7 and 8 - NPC affected treated mice
- Lane 8 - Normal treated mouse

Lanes 7 and 8 show decreased GM3 and GM2 content compared to lane 6.

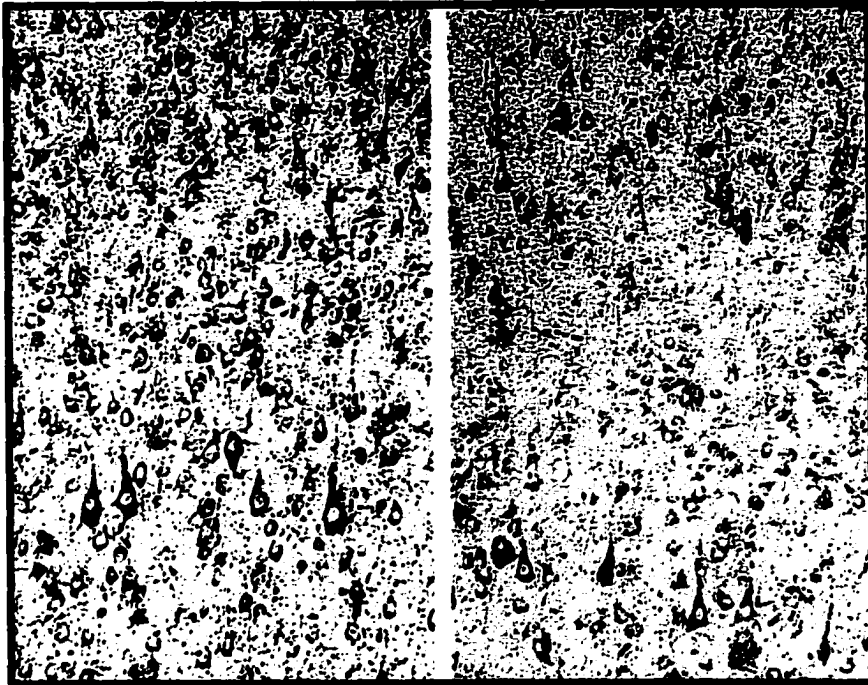


Figure 2.7

Immunocytochemistry of Anti-GM2 Reactivity in Cerebral Cortex

Left - NPC affected non-treated cat

Right - NPC affected treated cat

GM2 immunoreactivity is less apparent in the NPC affected treated cat on the right.

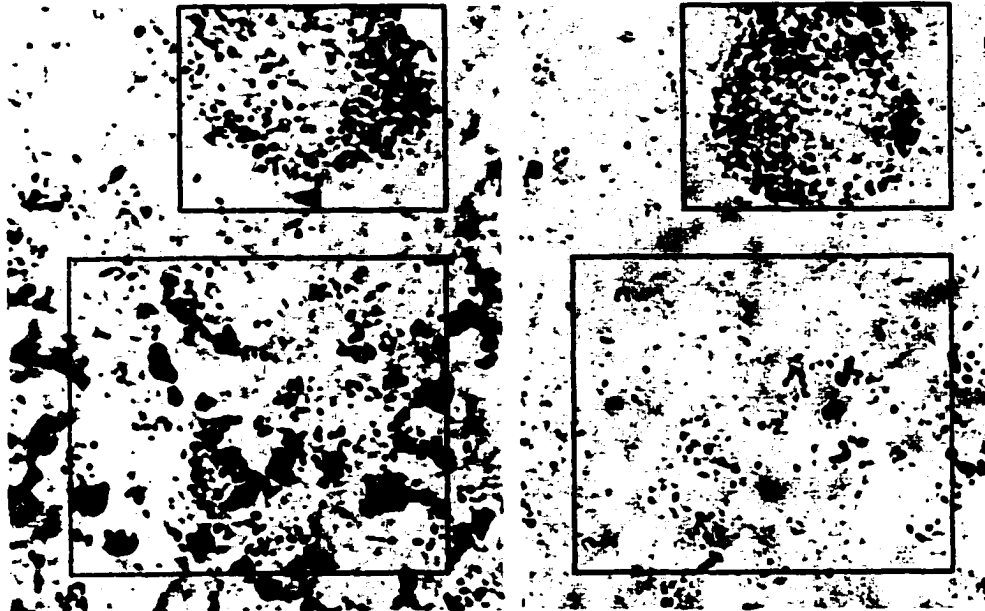


Figure 2.8

GM2 Immunoreactivity in the Cerebellum

Left side represents an NPC affected non-treated cat, which displays more anti-GM2 reactivity than is seen in the NPC affected NB-DNJ treated cat on the right.

The decreased immunoreactivity is more apparent in the granule cell layer (red box) than in the Purkinje cells (black box)

CHAPTER THREE

COMPLEMENTATION STUDIES IN HUMAN AND FELINE NIEMANN-PICK DISEASE

TYPE C

INTRODUCTION

Complementation studies involve restoration of normal cellular function after the hybridization of two different cell lines. Normal cellular function can be restored when a competent cell line provides the missing genetic information that is responsible for the production of the absent or defective gene product. When two cell lines are crossed and no restoration of normal cellular function occurs, the mutation in each cell line involves the homologous gene. Complementation studies can be used to identify diseases in which mutation of two separate genes result in a common phenotype that is otherwise indistinguishable. This has been demonstrated in human Niemann-Pick Disease Type C (NPC) (1,2,3). Additionally, complementation studies have been used to confirm that animal models that appear to represent a human disease have the same genetic basis (4,5). Complementation studies were used to identify a murine model of

NPC that belongs to the same complementation group as the major form of childhood NPC (6).

The feline model of NPC has been shown to be clinically, biochemically, and morphologically identical to the major form of human NPC, NPC1 (7,8,9,10). Niemann-Pick Disease Type C is characterized by the abnormal accumulation of unesterified cholesterol in lysosomes that can be visualized by staining cultured fibroblasts with the fluorescent antibiotic filipin, which specifically binds unesterified cholesterol.

In this study, complementation experiments using cultured fibroblasts from NPC affected cats and NPC-1 affected humans were conducted to determine if this feline model involves the gene orthologous to the human gene, *NPC1*. Cell fusions between human NPC and feline NPC fibroblasts were conducted to assess whether the multinucleated heterokaryons that were formed showed a reversal of the NPC phenotype.

Specific Aims - Complementation studies were performed to determine if the gene responsible for the major form of human Niemann-Pick type C disease (NPC) and the feline model of NPC are orthologous.

Hypothesis – Cell fusions between feline NPC fibroblasts and human NPC fibroblasts will result in the formation of multinucleated heterokaryons without the restoration of

normal cellular function, and this lack of complementation can be visualized by the retention of normal NPC phenotype as seen with filipin staining.

MATERIALS AND METHODS

Fibroblast strains and cell fusion

The following cell lines were evaluated: human NPC1 affected fibroblasts (two unrelated patients), feline NPC affected fibroblasts (three cats from the NPC colony), and feline normal fibroblasts (two cats from outside the NPC colony). Crosses performed are summarized in Table 1. Fibroblasts were cultured using standard protocols, and cell fusions were performed according to the methods of Brul et al (11). Fibroblasts were cultured in 25cm² flasks in regular media (Minimal Essential Media (MEM) supplemented with 10% fetal calf serum (FCS), 2% L-glutamine (Irvine Scientific) and gentamycin). Cell strains from confluent flasks were mixed and co-cultured in a ratio of 1:1 for three days. Cell fusions were performed on day 4 according to the following protocol. Media was removed from flasks of co-cultured fibroblasts and cells were rinsed with MEM; 0.6 ml of 41% (vol/vol) polyethylene glycol 1000 (PEG 1000, Sigma) in MEM with 8.75% (vol/vol) dimethyl sulfoxide (DMSO) was then added. After 2 minutes of rocking, 0.6ml of 25% PEG in MEM was added followed by another 2 minutes of rocking. The PEG suspension was diluted two more times at 2-minute intervals with the addition of 4 mls of

MEM at each time point. The final suspension was aspirated and the cells were rinsed with MEM. The hybrids were then cultured for 3 days in regular media.

Assessment of Complementation

Following fusion, fibroblasts were cultured for three days in MEM supplemented with 10% FCS, 2% L-glutamine and gentamycin under 5% CO₂/95% air. On day four, the media was changed to 5% lipoprotein deficient media (LPDS, Bionetics). Cells were cultured for another 48 hours and then transferred to Lab Tek Chamber slides (NUNC) for an additional 48 hours. Cells were challenged with low density lipoprotein (LDL, Bionetics) at a concentration of 50ug/ml for 24 hours, then fixed with 3% paraformaldehyde and stained with the fluorescent antibiotic filipin. Slides were viewed by fluorescent microscopy, and multinucleated cells were evaluated for complementation.

Verification of Interspecies Fusions

To verify that interspecific fusions had occurred, fibroblasts from human and feline cell lines were differentially labeled with fluorescent cell tracking dyes prior to fusion. Cell tracking dyes used for this study were 5-(and 6)-((4-chloromethyl) benzoyl) amino tetramethyl rhodamine (CMTMR; Molecular Probes), which appears red, and 5-

chloromethylfluorescein diacetate (CMFDA; Molecular Probes), which appears green.

The dyes, as supplied by the manufacturer, were brought up in DMSO to a stock concentration of 5mM. Stock solutions were stored at 4°C in 100µl aliquots. For staining, the dyes were further diluted to 10µM by adding 4µl of 5mM stock dye to 2mls 1X PBS (phosphate buffered saline). Human cells were stained in 10µM CMTMR (red) and feline cells were stained in 10µM CMFDA (green) for 30 minutes at 37°C. Dyed cells were co-cultured and fused by the preceding protocol, then viewed by dual fluorescence microscopy to evaluate multinucleated cells for interspecific fusion. Multinucleated heterokaryons resulting from interspecific fusion would be expected to appear yellow.

RESULTS

Complementation Analysis

All of the visualized multinucleated cells derived from each of the crosses between human NPC affected fibroblasts and feline NPC affected fibroblasts retained the NPC staining phenotype characterized by a prominent perinuclear fluorescence with filipin, indicative of a lack of complementation (Figure 1). Multinucleated cells formed between different feline NPC affected cells all retained the NPC phenotype. Crosses performed between normal feline fibroblasts and NPC affected human or NPC affected feline fibroblasts each resulted in multinucleated heterokaryons that exhibited loss of the NPC

staining phenotype as visualized by the absence of perinuclear fluorescence with filipin, indicating restoration of normal cellular function. (Figure 2).

Interspecific Fusions

Fusions between CMTMR stained human cells (red) and CMFDA stained feline cells (green) resulted in the formation of multinucleated cells with dual fluorescence, which appears yellow (Figure 3).

DISCUSSION

Complementation studies are based upon restoration of normal cellular functions as a result of hybridization of a defective cell with a competent cell. Our goal was to determine if the gene responsible for the NPC phenotype in the feline model of NPC is orthologous to the gene that is mutated in the major group of human NPC, NPC-1. The absence of complementation in all visualized multinucleated cells formed between the fusion of human NPC affected fibroblasts and feline NPC affected fibroblasts suggests that this feline model of NPC and major form of human NPC, NPC-1 arise from mutations of orthologous genes. Attempts to simultaneously filipin stain and track fibroblasts with the fluorescent dyes were not successful, as the tracking dyes did not survive the filipin staining protocol. However, in the verification of interspecific fusion, the

multinucleated heterokaryons that were identified as human/feline hybrids represented greater than 75% of all the multinucleated cells present. Considering this, the retention of the NPC phenotype in every multinucleated cell seen after the fusion of NPC1 affected human and NPC affected feline fibroblasts is significant. Thus, normal cellular function was not restored after hybridization of NPC human and NPC feline fibroblasts, indicating a lack of complementation. Based on these findings, this feline colony appears to have a mutation of the gene orthologous to that responsible for the major form of human NPC1 and will serve as a valuable model for future studies, including evaluating efficacy of gene therapy.

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Table 1

Crosses performed for complementation analyses

<u>Human</u>		<u>Feline</u>		<u>Feline</u>		<u>Feline</u>
NPC-H1	X	NPC-F1		NPC-F1	X	NPC-F2
		NPC-F2				NPC-F3
		NPC-F3				NOR-F
		NOR-F		NPC-F2	X	NOR-F3
NPC-H2	X	NPC-F1				NOR-F
		NPC-F2		NPC-F3	X	NOR-F
		NPC-F3				
		NOR-F				

NPC-H1, NPC-H2 represent NPC affected human fibroblast strains

NPC-F1, NPC-F2, NPC-F3 represent NPC affected feline fibroblast strains

NOR-F represents normal feline fibroblast strain



Figure 3.1

The two mononuclear fibroblasts exhibit the perinuclear fluorescence that is typical of the NPC phenotype. The multinucleated cell was formed following the fusion of NPC affected human and NPC affected feline fibroblasts. The persistent presence of marked perinuclear fluorescence is indicative of a lack of complementation. (filipin, 400X)



Figure 3.2

Multinucleated fibroblast formed after fusion of NPC affected human fibroblasts and normal feline fibroblasts. Note the absence of the perinuclear fluorescence in the multinucleated cell, indicative of complementation and restoration of normal cellular phenotype. Human mononuclear cells retained the NPC staining phenotype. (filipin., 400X)

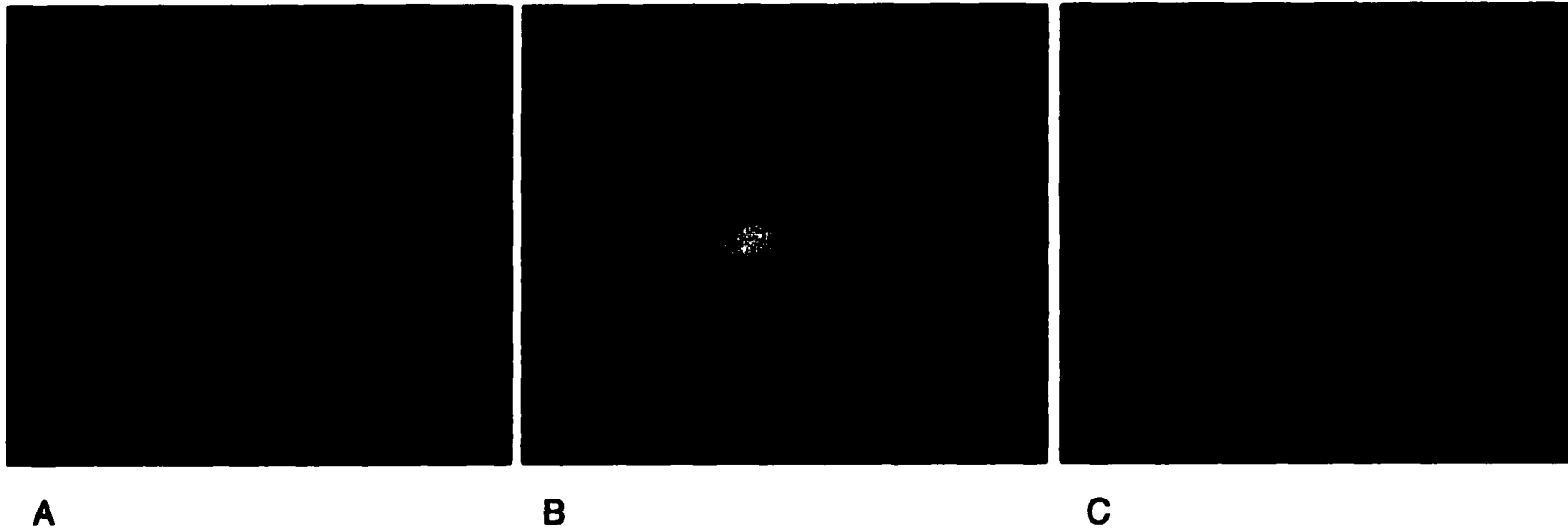


Figure 3.3

(A) Feline NPC affected fibroblasts stained with CMFDA. (C) Human NPC affected fibroblasts stained with CMTMR. (B) Multinucleated heterokaryon as indicated by the dual (yellow) fluorescence as a result of fusion between human and feline cells. (1000X)

CHAPTER FOUR

GENETIC CHARACTERIZATION OF FELINE NIEMANN-PICK DISEASE TYPE C

INTRODUCTION

Niemann-Pick Disease Type C (NPC) was first described over thirty years ago, but only in recent years have the details of the molecular basis of this disease begun to be discovered. In 1993, Carstea et al (1) first documented the linkage of NPC to human chromosome 18. In 1996, complementation studies indicated that at least two genes could be implicated in causing the NPC phenotype (2). The most common complementation group (major form) is now designated as NPC1 and accounts for greater than 95% of all human NPC cases. The human NPC1 gene has been mapped to chromosome 18q11, and has been identified and sequenced (3). Numerous different mutations have been documented in NPC patients and many of the mutations are clustered in the terminal third of the gene(4). The gene responsible for the NPC phenotype in two murine models is linked to the mouse chromosome 18, which is syntenic with areas of human chromosomes 18 and 5 (5).

A feline model of NPC has been characterized and is phenotypically, morphologically, and biochemically identical to human NPC1 (6, 7). Complementation studies using cultured fibroblasts from NPC affected cats and NPC1 affected humans suggest that the gene responsible for the NPC phenotype in this colony of cats is orthologous to the gene responsible for the major form of human NPC, NPC1 (8). Characterization of the feline NPC cDNA was performed to confirm that the gene was an ortholog of human *NPC1* and to identify the mutation responsible for the NPC phenotype in this feline model. The hypotheses for this work were that feline Niemann-Pick Disease Type C involves the gene that is orthologous to the NPC1 gene in humans, and a mutation in this gene results in the NPC phenotype in this cat colony.

MATERIALS AND METHODS

Feline NPC cDNA sequence and mutation analysis

RNA was extracted from frozen liver (20mg) or cultured fibroblasts (confluent T25 flask) using the RNeasy mini kit (QIAGEN, Santa Clara, CA). Extracted RNA (12.5µl) was used for cDNA synthesis (Advantage RT-for-PCR kit, CLONTECH, Palo Alto, CA) (CLONTECH kit #K1402-1, Palo Alto, CA). First strand cDNA (5µl) was used for subsequent PCR reactions (CLONTECH kit #K1905-1, Palo Alto, CA). Human NPC1-specific PCR primers were kindly provided by Drs. Eugene Carstea and Jill Morris. Initially, 36 different human NPC primer pair combinations were used with feline

fibroblast-derived cDNA template. Standard PCR protocols were used. Of these primer pairs, eight amplified bands that were of the expected size based on the known human sequence. From these initial eight primer pair combinations that amplified bands, three primer pair combinations were chosen that incorporated sections of the 5', middle, and 3' regions of the cDNA sequence. These three primer pairs amplified single, discrete bands of the expected molecular weight. The three amplified fragments were cloned into the pCR II-TOPO vector using the TOPO TA Cloning kit (Invitrogen, Carlsbad, CA). Ligated products were transformed into competent Topo-10 cells, and 100 μ l of the cell culture was plated on LB-plates with 50 μ g/ml of ampicillin. Colonies with inserts (white colonies) were selected. Colonies were cultured overnight in LB medium containing 50 μ g/ml of ampicillin. Plasmid DNA was isolated (Qiagen Miniprep kit #27104, Santa Clara, CA). Plasmids were digested with EcoR1, run out on a 1.5% agarose gel in 1XTAE for 30 min, and then evaluated for the expected inserts. Clones were sequenced using Sanger di-deoxy chain termination methodology on an ABI 377 Automated DNA Sequencer. ABI sequence data files were analyzed using ABI Sequence Navigator software (version 1.0.1). Based on the sequence data, feline specific primers were generated (Table 4.1), and the majority of the open reading frame of the feline NPC cDNA was subsequently cloned and sequenced (Figure 4.1). Multiple runs in both directions for each cat were used to generate a consensus sequence. Redundant

sequence data were generated from three NPC affected cats, four NPC obligate heterozygote cats and three normal control cats.

Identification of Heterozygotes

Whole blood was collected in EDTA, and 500µl was used for DNA extraction (Qiagen kit #51104, Santa Clara, CA) then used for subsequent PCR and restriction digests. Feline specific PCR primers were used to amplify an approximately 103 base-pair fragment that incorporates the mutation site. The primary PCR products were then digested with the restriction enzyme Mwo1 and subsequently analyzed by gel electrophoresis. The NPC mutation results in an unrecognizable restriction site for restriction enzyme Mwo1. Thus, no cutting occurs when the NPC mutation is present.

The Mwo1 Restriction Site:

GCNNNNN NNG**C**

CGNN NNNNNC**G**

The bold "G" is the mutation site in feline NPC, the underlined 'G' is the base that is changed from a "T" in the feline sequence to a "G" with an engineered primer used for the PCR reaction. The "space" denotes the restriction site for Mwo1. Primers used for amplification were:

(sense) 5'-CTC-TAGG-TAC-CCG-AAT-AGG-CTT-TGC-3'

(antisense) 5'-CGA-TCG-GTG-CTG-TTG-TAG-CCT-CTA-3'

A thymidine nucleotide at 2879 location (9 nucleotides downstream of mutation site) changed to guanine (underlined "C" above) to provide a MwoI site with normal sequence.

DNA extracted from whole blood was used in PCR reactions to amplify the ~105bp fragment that spans the mutation site. Primers used for the carrier assay are identified above. PCR conditions were as follows: initial denaturing for 3 min. at 95°C, then 30 cycles of (95°C for 1 minute / 56°C for 45 seconds / 72°C for 1 minute). The reaction contained 3% DMSO. PCR product (10µl) was used for the MwoI digestion. The restriction digest included 0.5µl of the restriction enzyme, 2.5µl of the provided buffer and 12µl of distilled water, for a total of 25µl. The restriction digest was run for 2 hours at 55°C. The entire 25µl sample plus 5µl of marking dye was loaded onto a 3% Metaphor gel with ethidium bromide and run in 1X TBE buffer at 90v for 1.5-3 hours. Final bands were visualized with an ultraviolet light source.

The PCR based assay for the identification of heterozygotes was used to screen all cats currently in the NPC colony. Additionally, RNA was extracted from frozen fibroblasts of deceased animals using the RNeasy mini kit (QIAGEN, Santa Clara, CA) then cDNA was synthesized (Clontech kit #K1905-1, Palo Alto, CA) and evaluated with the assay.

COLLABORATIVE STUDIES

Karyotyping

Karyotyping of NPC obligate heterozygotes and NPC affected cats was performed in collaboration with Dr. Elizabeth McNeil, Colorado State University. Metaphase slides for karyotyping were made from pokeweed stimulated peripheral blood lymphocytes.

Chromosomes were stained with DAPI and Chromomycin A3 and R-banding was enhanced with a computer imaging system (9). Chromosome number was determined from 20 metaphase spreads. Full karyotypes were performed for 5 metaphase spreads. R-banded metaphase chromosome spreads of normal and known heterozygotes were generated. Comparisons of maternal to paternal chromosome pairs as well as to existing normal-cat metaphase chromosomes were made.

Cytogenetic localization of Feline NPC

Fluorescence in situ hybridization (FISH) analysis using feline PAC clones was conducted in collaboration with the laboratory of Dr. Stephen O'Brien (National Cancer Institute, Frederick, MD). Feline PAC clones were labeled with biotin-11 (Sigma) by nick translation (10) and the final probe size of less than 500bp was verified on a 1.2% gel with appropriate markers. Metaphase spreads of domestic cat (FCA#215) were prepared by standard cytogenetic techniques (11) and FISH analysis was performed (12). Briefly, the metaphase spreads were denatured in 70% formamide 2XSSC in an

80C oven for 90 seconds and dehydrated in cold 70%, 90% and 100% ethanol. 400ng of labeled probe, 10ug of salmon sperm carrier DNA, and 3ug of cat COT-1 DNA were resuspended in 50% formamide-10% dextran sulfate-2XSSC and denatured for 10 minutes at 75C. The denatured probe cocktail was layered on the denatured metaphase chromosomes and placed in a humidifying box at 37C. Following 48 hours of incubation, and post-hybridization washes, the hybridized biotin labeled probes were detected with fluorescein isothiocyanate (FITC) conjugated to avidin DCS (5mg/ml, Vector Labs).

Fluorescence signals were captured as gray scale images using Zeiss Axioskop epi-fluorescence microscope with a cooled charged couple device camera (Photometrics CE 250), and Apple Macintosh power PC, and the Oncor Image system. Gray scale images were computer enhanced, pseudocolored, and merged using Oncor image software. Images of Dapi stained chromosomes were merged with FITC detected signals allowing for direct visualization, chromosome identification and chromosome assignment.

NPC Immunoreactivity Evaluation

Studies using rabbit anti-mouse NPC1 antibody and anti-human NPC1 antibody were performed in collaboration with W. Sherman Garver, (University of Arizona College of Medicine, Tucson, Arizona. Immunoblot analyses using immune and preimmune serum on normal feline liver homogenates were conducted.

Immunoblot analysis

Frozen liver from a normal cat was homogenized on ice in 0.32 molar sucrose.

Homogenates were electrophoresed through SDS/5% polyacrylamide gels, transferred to nitrocellulose membranes, and Western blotted for NPC1 using rabbit anti-human and anti-mouse NPC1 polyclonal antibodies. Immunoreactive bands were visualized using a labeled goat anti-rabbit secondary IgG and enhanced chemiluminescence detection.

RESULTS

cDNA and mutation analysis

To date, 97% of the estimated 3834 base pair cDNA sequence has been determined.

The feline nucleotide sequence has greater than 86% homology with the human sequence while the predicted feline amino acid sequence has greater than 90% identity with the human amino acid sequence (Figure 4.2). A single base substitution of guanine for cytosine (G2870C) was identified in all NPC affected cats evaluated (n=5). Carriers were heterozygous for the same allele (Figures 4.3 - 4.5). This point mutation results in an amino acid substitution of a conserved cysteine for serine (C957S) (Figure 4.6).

Heterozygote Identification

The Mwo1 restriction site is present in normal cats and both copies of the NPC gene is cleaved, resulting in a single visual band at approximately 80bp. NPC affected cats are

homozygous for the mutation at the restriction site, resulting in no cleavage of either copy, thus a single band is visualized at approximately 103bp. Feline NPC heterozygotes can be identified by the presence of two bands, one that has been cut (wild type~80bp) and one that remains uncut (mutant~103bp) (Figure 4.7). All previously known obligate heterozygotes and NPC affected cats were correctly identified (NPC affected N=3, NPC obligate heterozygote N=4, Normal N=4). An additional 33 cats from the NPC colony were screened; two additional female and five additional male carriers were identified.

COLLABORATIVE STUDIES

Karyotyping

Mutations resolvable at the cytogenetic level were not detected in NPC obligate heterozygotes or NPC affected cats (Figure 4.8). The normal karyotypes supported a small mutation.

Chromosomal Localization

Hybridization data using feline NPC PAC localized the NPC-1 gene to chromosome D3q1 (Figure 4.9).

The feline NPC1 protein and antibody investigations

Immunoblot analysis of liver homogenates from normal cats revealed that no cross-reaction with the feline NPC protein was evident with either the rabbit anti-human NPC1 or rabbit anti-murine NPC1 antibodies.

DISCUSSION

Characterization of the feline NPC1 cDNA sequence confirmed that the gene responsible for the NPC phenotype in the feline model is indeed the ortholog of the human NPC1 gene. Strong nucleotide and amino acid sequence homology exists between the cat and human, which is actually greater than that between the human and mouse. This is not surprising given that comparative genomic studies have shown that the cat is phylogenetically more closely related to humans than the mouse, and that the overall feline-human syntenic chromosomal conservation is greater than the mouse-human (13). This degree of homology is underscored by the high efficiency of the human based primers used in the initial PCR amplification of the feline cDNA sequence. The feline NPC gene localized to chromosome D3; D3 has been shown to be homologous to human chromosome 18, the chromosome to which the human NPC1 gene has been localized (1, 13).

The position of the single missense mutation (G2870C) identified in this colony is consistent with reports of several mutations in people involving the terminal third of the

NPC1 gene(14). Over thirty different mutations of the NPC1 gene have been identified in humans(3, 15, 16). Given the fact that this is an inbred colony of cats from a single queen and son mating, arising from a single ancestor, genetic heterogeneity was not expected. This is similar to the founder effect identified in the allelic variant of NPC, Niemann-Pick disease type D (NPD), identified in Nova Scotia (17).

The NPC1 gene codes for a 1278 amino acid protein. The putative NPC1 protein is predicted to have thirteen transmembrane regions and three large hydrophilic loops (18) (Figure 4.10). The NPC1 protein has been shown to reside in late endosomes and to transiently interact with lysosomes and the trans-Golgi network (19). The exact function of the NPC1 protein remains unknown. However, it has been shown to be a transport protein that is critical for the movement of endocytosed material (19, 20). Several thoughts on the possible functions of the NPC1 protein have been proposed and include

- 1) direct transporting that facilitates the movement of cholesterol out of the lysosomes,**
- 2) a docking/fusion role that mediates the interaction of cholesterol-laden vesicles and endosomes, or 3) acting as a molecular pump (18). The mechanism(s) by which the mutation in the NPC1 gene and resultant C957S amino acid substitution leads to disease pathogenesis in NPC remains unknown. The 957 cysteine residue is conserved across multiple species and is likely critical to the structure and subsequent function of the NPC1 protein (21).**

The pathogenesis of the brain dysfunction in NPC is still not understood. It is clear that outside the central nervous system (CNS), the NPC1 lesion results from a processing defect of LDL-derived cholesterol, but it is widely accepted that exogenous cholesterol is not presented to the CNS because of the blood-brain barrier. Thus, the NPC1 protein must have other functions, at least within the CNS, which have yet to be identified. Overall, the NPC1 protein is not closely related to any other known proteins, but the membrane orientation of the NPC1 sterol sensing domain (SSD) is identical to those of HMG CoA reductase and SCAP, known mediators of cholesterol homeostasis (22).

The development of a PCR assay to identify feline NPC heterozygotes has greatly facilitated colony management and should result in an increased number of affected kittens produced. The ability to rapidly and accurately genotype offspring is a significant improvement over previous methods, composed of breeding trials and filipin staining of cultured fibroblasts to determine heterozygosity. The maintenance of this colony and the availability of affected animals will be valuable for further characterization of the NPC molecular defect and evaluation of potential treatment modalities.

Sequence analysis of the 5' end of the feline NPC1 cDNA has not been completed.

Efforts are currently underway to isolate the remaining 5' end of the feline cDNA sequence (approximately 100bp). Thus far, 3734 bases of the anticipated 3834 base

pair cDNA have been identified. Early attempts have relied on primers based on the known human and mouse NPC1 cDNA sequence, but the 5' region tends to have less homology across species and the area is often G:C rich, making amplification of this area more difficult. Future efforts to isolate the 5' end of the cDNA will utilize 5' SMART RACE (CLONTECH, Palo Alto, CA) and/or the feline PAC clones generated in Stephen O'Brien's laboratory.

Studies conducted with rabbit anti-human NPC1 and anti-mouse NPC1 antibodies resulted in no reaction with the feline NPC1 protein. This was not surprising given that the antibodies were generated against 19 amino acid residues in the human and mouse, each of which showed only partial sequence homology to the predicted feline amino acid sequence (15 of 19 in the human and 14 of 19 in the mouse). A suitable region of the predicted amino acid sequence of the feline NPC protein against which to generate antibodies was identified. The residues are in the same region as those used for the development of the anti-mouse NPC1 and anti-human NPC1 antibodies, which have both proven reactive (20, 23). A feline NPC specific polyclonal antibody has been ordered from Research Genetics (Huntsville, Alabama) and will be available by the end of 2000.

Although the exact function of the NPC1 protein remains unknown, the field is rapidly advancing and it is probable that the elucidation of the function(s) of the NPC1 protein will be determined in the very near future. These discoveries will play a pivotal role in understanding disease pathogenesis in NPC, in both the peripheral tissues and the CNS, and are vital to the development of rational treatment modalities.

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Table 4.1**Overlapping Primer Pairs Used for Sequencing of the Feline NPC Gene**

#	Primer Pairs	Forward	Reverse	Band	Size
1	f103sn / f957asn	CATCTGGAGATAAGAGGTAC	TGCCATGTAGGTGATCCAC	A	854
2	3F / f1197asn	CTGCCTCTACAGTTTCTGTCCA	GGGAGAAGAAGATGATGGG	B	809
3	RTEsn / RTGasn	GCTTGGACGCCATGTAT	AGCACGGAATGGCTGTT	C	693
4	f1366sn / f2435asn	ACACACTTACCAGCCGTACC	TGAAGAAGGGAGTCGATGAG	D	1070
5	f2447sn / 18R	TACCAGCGAGATGAACGTC	GCGTTAAATATCTGCTGCACCT	E	653
6	f2787sn / f3531asn	TGTGTACTTTGTCCTGGAGG	TGACCAAGATCATAGCGATG	F	744
7	f3370sn / f3997asn	TGTCTTCTACGAACAGTACCTG	ACGACCCACAGACACAGTTC	G	627
8	F1755sn / f2329asn	CTTGTGTTAGGAGGCTATGATG	CATACTTAGGAGCCACTTCTCC	H	574

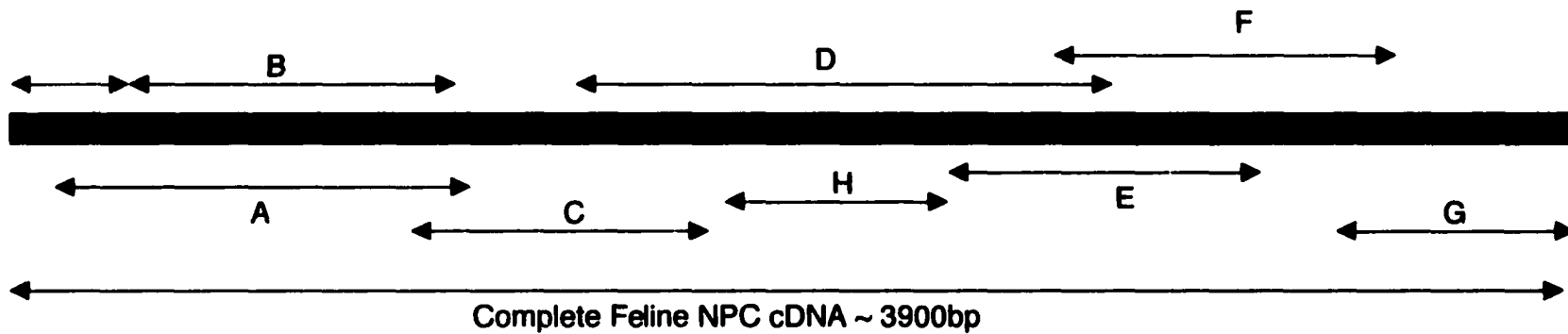


Figure 4.1

The Feline NPC cDNA

The complete feline NPC cDNA is expected to be approximately 3900bp.

Fragments for the overlapping segments are designated by letters A-H.

Details about bands A-H (size and primers used) are listed in Table 4.1

The red arrow denotes the first 103 missing bases of the expected open reading frame that remain to be identified.

Figure 4.2

Sequence data for the NPC1 gene

Nucleotide sequence from: normal cat (Feline-Normal Bands 1-6) and normal human (human).

Amino acid sequence from: normal cat (feline aa sequence) and normal human (human aa)

The start codon in the human sequence is designated by a blue box.

The site of the feline NPC mutation is in the orange box (nt 2870).

The region used to generate the feline specific anti-feline NPC1 antibody is represented by the green box (aa1257-1275).

	-120	-110	-100	-90	
Feline - Normal Bands 1-6 human feline aa sequence human aa	TTT GCTCCTGCTC CTCCGCTCCT CCTGCGCGGG GTGCTGA ==>				
	F A P A P P L L L R G V L ==>				
	-80	-70	-60	-50	
Feline - Normal Bands 1-6 human feline aa sequence human aa	AAC AGCCCCGGGA AGTAGAGCCG CCTCCGGGGA GCCCAAC ==>				
	K Q P G E V E P P P G S P T ==>				
	-40	-30	-20	-10	
Feline - Normal Bands 1-6 human feline aa sequence human aa	CAG CCGAACGCCG CCGGCGTCAG CAGCCTTGCG CGGCCAC ==>				
	S R T P P A S A A L R G H ==>				
	0	10	20	30	
Feline - Normal Bands 1-6 human feline aa sequence human aa	AGC ATG CCGCTC GCGGCCTGGC CCTTGGCCTC CTCTCTGC ==>				
	S M T A R G L A L G L L L ==>				
	4	50	60	70	
Feline - Normal Bands 1-6 human feline aa sequence human aa	TGC TACTG TG TCCAGCGCAG GTGTTTTAC AGTCTG ==>				
	L L L C P A Q V F S Q S C ==>				
	80	90	100	110	
Feline - Normal Bands 1-6 human feline aa sequence human aa	TGT TTGGTATGGA GAGTGTGGAA TTGCATATGG GGACAAG ==>				
	V W Y G E C G I A Y G D K ==>				
	120	130	140	150	
Feline - Normal Bands 1-6 human feline aa sequence human aa	AGG TACAACCTGCA AATATTCAGG GCCACCAAAA CCCTTGC ==>				
	AGG TACAATTGCG AATATTCAGG CCCACCAAAA CCATTGC ==>				
	R Y N C K Y S G P P K P L ==>				
	R Y N C E Y S G P P K P L ==>				
	160	170	180	190	
Feline - Normal Bands 1-6 human feline aa sequence human aa	CGA AGGATGGTA TGACTTAGTG CAGGAGCTCT GTCCAGG ==>				
	CAA AGGATGGATA TGACTTAGTG CAGGAACCTCT GTCCAGG ==>				
	P K D G Y D L V Q E L C P G ==>				
	P K D G Y D L V Q E L C P G ==>				
	200	210	220	230	
Feline - Normal Bands 1-6 human feline aa sequence human aa	ATT CTCCTTGGAC AATGTCAGTC TTGTGTGCGA TGTGCAG ==>				
	ATT CTCCTTGGC AATGTCAGTC TCTGTGTGTA TGTTCGG ==>				
	F F L D N V S L C C D V Q ==>				
	F F F G N V S L C C D V R ==>				

	240	250	260	270
Feline - Normal Bands 1-6	CAG	CTCCGGACAC	TGAAAGACAA	CCTGCAGCTG
human	CAG	CTTCAGACAC	TAAAAGACAA	CCTGCAGCTG
feline aa sequence	Q	L R T	L K D N	L Q L P L
human aa	Q	L Q T	L K D N	L Q L P L
	280	290	300	310
Feline - Normal Bands 1-6	AGT	TTCTGTCCAG	ATGTCCATCC	TGTTTCTATA
human	AGT	TTCTGTCCAG	ATGTCCATCC	TGTTTTTATA
feline aa sequence	Q	F L S R	C P S	C F Y N L V
human aa	Q	F L S R	C P S	C F Y N L L
	320	330	340	350
Feline - Normal Bands 1-6	GAA	CCTGTTTTGC	GAGCTGACGT	GTAGCCCTCG
human	GAA	CCTGTTTTGT	GAGCTGACAT	GTAGCCCTCG
feline aa sequence	N	L F C	E L T	C S P R Q S
human aa	N	L F C	E L T	C S P R Q S
	360	370	380	390
Feline - Normal Bands 1-6	CAG	TTTCTGAATG	TTACAGCAAC	TGAAGATTAT
human	CAG	TTTTTGAATG	TTACAGCTAC	TGAAGATTAT
feline aa sequence	Q	F L N V T A T	E D Y V D	
human aa	Q	F L N V T A T	E D Y V D	
	400	410	420	430
Feline - Normal Bands 1-6	CTG	TTACAAACCA	GACTAAAACA	AATGTAAAAG
human	CTG	TTACAAACCA	GACGAAAACA	AATGTAAAAG
feline aa sequence	P	V T N Q	T K T	N V K E L Q
human aa	P	V T N Q	T K T	N V K E L Q
	440	450	460	470
Feline - Normal Bands 1-6	GTA	CTACATTGGA	GAGAGTTTTG	CCAATGCCAT
human	ATA	CTACGTCGGA	CAGAGTTTTG	CCAATGCAAT
feline aa sequence	Y	Y I G	E S F	A N A M Y N
human aa	Y	Y V G	Q S F	A N A M Y N
	480	490	500	510
Feline - Normal Bands 1-6	GCC	TGCCGGGACG	TGGAGGCCCC	CTCCAGTAAT
human	GCC	TGCCGGGATG	TGGAGGCCCC	CTCAAGTAAT
feline aa sequence	A	C R D	V E A P	S S N D K
human aa	A	C R D	V E A P	S S N D K
	520	530	540	550
Feline - Normal Bands 1-6	CCC	TGGGACTGCT	GTGTGGGAAG	GACGCCGAAG
human	CCC	TGGGACTCCT	GTGTGGGAAG	GACGCTGACG
feline aa sequence	A	L G L L	C G K	D A E A C N
human aa	A	L G L L	C G K	D A D A C N
	560	570	580	590
Feline - Normal Bands 1-6	TGC	CACTAACTGG	ATTGAGTACA	TGTTCAAGTAA
human	TGC	CACCAACTGG	ATTGAATACA	TGTTCAATAA
feline aa sequence	A	T N W	I E Y	M F S K D N
human aa	A	T N W	I E Y	M F N K D N

	600	610	620	630
Feline - Normal Bands 1-6 human feline aa sequence human aa	GGC CAGGCACCTT GGA CAGGCACCTT G Q A P F T I T P I F S D G Q A P F T I T P V F S D	TCACCATCAC TTACCATCAC	ACCCATTTT TCCTGTGTTT	TCAGATC TCAGATT
	640	650	660	670
Feline - Normal Bands 1-6 human feline aa sequence human aa	TTC CAACCCATGG L P T H G M E P M N N A T K F P V H G M E P M N N A T K	GATGGAGCCC GATGGAGCCC	ATGAACAATG ATGAACAATG	CCACCAA CCACCAA
	680	690	700	710
Feline - Normal Bands 1-6 human feline aa sequence human aa	GGG CTGTGACGAG G C D E S V D E V T G P C G C D E S V D E V T A P C	TCTGTGGAGC TCTGTGGATG	AGGTCACCGG AGGTCACAGC	GCCGTGC ACCATGT
	720	730	740	750
Feline - Normal Bands 1-6 human feline aa sequence human aa	AGC TGCCAGGACT S C Q D C S I V C G P K P S C Q D C S I V C G P K P	GCTCAATGT GCTCTATGT	TTGTGGCCCA CTGTGGCCCC	AAGCCCC AAGCCCC
	760	770	780	790
Feline - Normal Bands 1-6 human feline aa sequence human aa	AGC CCCACCGCC Q P P P P P V P W R I L G L Q P P P P P A P W T I L G L	TCCTGTGCC TCCTGTCTCC	TGGAGAATCT TGGACGATCC	TGGCCT TTGGCTT
	800	810	820	830
Feline - Normal Bands 1-6 human feline aa sequence human aa	GGA CGCCATGTAT D A M Y V I M W I T Y M A D A M Y V I M W I T Y M A	GTCATCATGT GTCATCATGT	GGATCACCTA GGATCACCTA	CATGGCA CATGGCG
	840	850	860	870
Feline - Normal Bands 1-6 human feline aa sequence human aa	TTT TTGCTTGRT F L L V F F G A F F A L W F L L V F F G A F F A V W	TTTTTGGAGC TTTTTGGAGC	ATTTTTTGCT ATTTTTTGCA	TTGTGGT GTGTGGT
	880	890	900	910
Feline - Normal Bands 1-6 human feline aa sequence human aa	GCT ACAGAAAACG C Y R K R Y F V S E Y T P I C Y R K R Y F V S E Y T P I	CTATTTTGT GTATTTTGT	TCCGAGTACA TCCGAGTACA	CCCCCAT CTCCCAT
	920	930	940	950
Feline - Normal Bands 1-6 human feline aa sequence human aa	TGA TAGCAACATA D S N I A F S V N A N D R D S N I A F S V N A S D K	GCTTTCTCTG GCTTTTCTG	TAAATGCCAA TAAATGCAAG	TGACAGA TGACAAA

Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> ⁹⁹⁰ GGG GAGGCGTCCT ⁹⁹⁰ GCTGCGACGC ⁹⁹⁰ GCTTGGTGCG ⁹⁹⁰ GCATTTC GGA GAGGCGTCCT GCTGTGACCC TGTCAGCGCA GCATTTC G E A S C C D A L G A A F G E A S C C D P V S A A F </p> <p>1000 1010 1020 1030</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> AGG GCTGTCTGAG GCGGCTCTTC TCACAGTGGG GCTCTTT AGG GCTGCTTGAG GCGGCTGTTC ACACGCTGGG GGTCTTT E G C L R R L F S Q W G S F E G C L R R L F T R W G S F </p> <p>1040 1050 1060 1070</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> CTG CGTCCGAAAC CCGGCCCCA TCATCTTCTT CTCCTTG CTG CGTCCGAAAC CCTGGCTGTG TCATTTTCTT CTCGCTG C V R N P G P I I F F S L C V R N P G C V I F F S L </p> <p>1080 1090 1100 1110</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> GCC TTCATTGCCG CCTGTCTTTC AGGCCTGGTG TTTGTGC GTC TTCATTACTG CGTGTTCGTC AGGCCTGGTG TTTGTCC A F I A A C S S G L V F V V F I T A C S S G L V F V </p> <p>1120 1130 1140 1150</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> GGG TCACGACCAA TCCAGTTGAC CTGTGGTCAG CTCCCAG GGG TCACAACCAA TCCAGTTGAC CTCTGGTCAG CCCCAG R V T T N P V D L W S A P S R V T T N P V D L W S A P S </p> <p>1160 1170 1180 1190</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> CAG CCAGGCGCGC CTCGAGAAAG AGTACTTTGA CACGCAC CAG CCAGGCTCGC CTGGAAAAAG AGTACTTTGA CCAGCAC S Q A R L E K E Y F D T H S Q A R L E K E Y F D Q H </p> <p>1200 1210 1220 1230</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> TTT GGGCCTTTCT TCCGCACGGA GCAGCTCATC ATCCAGG TTT GGGCCTTTCT TCCGCACGGA GCAGCTCATC ATCCGGG F G P F F R T E Q L I I Q F G P F F R T E Q L I I R </p> <p>1240 1250 1260 1270</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> CCC CCCACACCAG TGCACACACT TACCAGCCAT ACCCCTC CCC CTCCTCACTGA CAAACACATT TACCAGCCAT ACCCTTC A P H T S A H T Y Q P Y P S A P L T D K H I Y Q P Y P S </p> <p>1280 1290 1300 1310</p>
Feline - Normal Bands 1-6 human feline aa sequence human aa	<p> AGG ATCCGATGTG CCCTTCGGAC CTCCGCTTGA CCTCGCG GGG AGCTGATGTA CCCTTTGGAC CTCCGCTTGA CATAAG G S D V P F G P P L D L A G A D V P F G P P L D I Q </p>

	1320	1330	1340	1350
Feline - Normal Bands 1-6	ATC TTGCACCAGG	TTCTTGACTT	ACAAACTGCC	ATCGAAA
human	ATA CTGCACCAGG	TTCTTGACTT	ACAAATAGCC	ATCGAAA
feline aa sequence	I L H Q	V L D L	Q T A	I E
human aa	I L H Q	V L D L	Q I A	I E
	1360	1370	1380	1390
Feline - Normal Bands 1-6	ATA TCACTGCATC	TTATAACAAT	GAGACCGTGA	CACTTCA
human	ACA TTACTGCCTC	TTATGACAAT	GAGACTGTGA	CACTTCA
feline aa sequence	N I T A S	Y N N	E T V	T L Q
human aa	N I T A S	Y D N	E T V	T L Q
	1400	1410	1420	1430
Feline - Normal Bands 1-6	AGA CATCTGCGTG	GCCCCCTGT	CACCCTATAA	CAAGAAC
human	AGA CATCTGCTTG	GCCCCCTTTT	CACCGTATAA	CACGAAC
feline aa sequence	D I C V	A P L	S P Y N	K N
human aa	D I C L	A P L	S P Y N	T N
	1440	1450	1460	1470
Feline - Normal Bands 1-6	TGC ACCATTCTGA	GCGTGTTAAA	TACTTCCAG	AACAGCC
human	TGC ACCATTTTGA	GTGTGTTAAA	TACTTCCAG	AACAGCC
feline aa sequence	C T I L	S V L N	Y F Q	N S
human aa	C T I L	S V L N	Y F Q	N S
	1480	1490	1500	1510
Feline - Normal Bands 1-6	ATT CCATGCTGGA	CCATGAAATA	GGAGATGACT	TCTTTGT
human	ATT CCGTGCTGGA	CCACAAGAAA	GGGACGACT	TCTTTGT
feline aa sequence	H S M L D	H E I	G D D	F P V
human aa	H S V L D	H K K	G D D	F F V
	1520	1530	1540	1550
Feline - Normal Bands 1-6	GTA TGCAGATTAC	CACACGCACT	TGCTATACTG	TGTACGG
human	GTA TGCCGATTAC	CACACGCACT	TTCTGTACTG	CGTACGG
feline aa sequence	Y A D Y	H T H	L L Y C	V R
human aa	Y A D Y	H T H	F L Y C	V R
	1560	1570	1580	1590
Feline - Normal Bands 1-6	GCT CCTGCCCTCTC	TGAACGATAC	CAGTTTGCTC	CATGATC
human	GCT CCTGCCCTCTC	TGAATGATAC	AAGTTTGCTC	CATGACC
feline aa sequence	A P A S	L N D T	S L L	H D
human aa	A P A S	L N D T	S L L	H D
	1600	1610	1620	1630
Feline - Normal Bands 1-6	CTT GCCTGGGTAC	ATTCGGTGGG	CCAGTGTTC	CGTGGCT
human	CTT GTCTGGGTAC	GTTGGGTGGA	CCAGTGTTC	CGTGGCT
feline aa sequence	P C L G T	F G G	P V F	P W L
human aa	P C L G T	F G G	P V F	P W L
	1640	1650	1660	1670
Feline - Normal Bands 1-6	TGT GTTAGGAGGC	TATGATGATC	AAAATTACAA	TAATGCC
human	TGT GTTGGGAGGC	TATGATGATC	AAAACTACAA	TAACGCC
feline aa sequence	V L G G	Y D D	Q N Y N	N A
human aa	V L G G	Y D D	Q N Y N	N A

	1680	1690	1700	1710
Feline - Normal Bands 1-6	ACA	GCCCTTG	TGGA TTACCTTTCC	TGTCATAAAT TACTATA
human	ACT	GCCCTTG	TGGA TTACCTTTCC	TGTCATAAAT TACTATA
feline aa sequence	T	A L V	I T F P	V N N Y Y
human aa	T	A L V	I T F P	V N N Y Y
	1720	1730	1740	1750
Feline - Normal Bands 1-6	ATG	ATACAGAGAG	GCTCCAGAAG	GCCCACGTCT GGGAAAA
human	ATG	ATACAGAGAA	GCTCCAGAGG	GCCCAGGCCT GGGAAAA
feline aa sequence	N	D T E R	L Q K	A H V W E K
human aa	N	D T E K	L Q R	A Q A W E K
	1760	1770	1780	1790
Feline - Normal Bands 1-6	AGA	GTTTATTAAT	TTTGTGAAAA	ACTACAAGAA TCCAAT
human	AGA	GTTTATTAAT	TTTGTGAAAA	ACTACAAGAA TCCAAT
feline aa sequence	E	F I N	F V K	N Y K N P N
human aa	E	F I N	F V K	N Y K N P N
	1800	1810	1820	1830
Feline - Normal Bands 1-6	CTG	ACCATTTCTT	TCACTACTGA	GCGAAGTATT GAAGATG
human	CTG	ACCATTTCCCT	TCACTGCTGA	ACGAAGTATT GAAGATG
feline aa sequence	L	T I S	F T T E	R S I E D
human aa	L	T I S	F T A E	R S I E D
	1840	1850	1860	1870
Feline - Normal Bands 1-6	AAC	TAAATCGTGA	AAGTAACGGT	GATATTTTCA CTGTTAT
human	AAC	TAAATCGTGA	AAGTGACAGT	GATGTCTTCA CCGTGT
feline aa sequence	E	L N R E	S N G	D I F T V I
human aa	E	L N R E	S D S	D V F T V V
	1880	1890	1900	1910
Feline - Normal Bands 1-6	AAT	CAGCTATGCC	ATCATGTTTC	TGTACATTTTCA CATAGCC
human	AAT	TAGCTATGCC	ATCATGTTTC	TATATATTTTCT CCTAGCC
feline aa sequence	I	S Y A	I M F	L Y I S I A
human aa	I	S Y A	I M F	L Y I S I A
	1920	1930	1940	1950
Feline - Normal Bands 1-6	TTG	GGGCACATCA	AAAGCTGTAG	CAGGCTTCTA GTGGACT
human	TTG	GGGCACATCA	AAAGCTGTAG	CAGGCTTCTG GTGGATT
feline aa sequence	L	G H I	K S C S	R L L V D
human aa	L	G H I	K S C R	R L L V D
	1960	1970	1980	1990
Feline - Normal Bands 1-6	CTA	AAATCTCCCT	CGGCATCGCG	GGGATCCTCA TTGTGTT
human	CGA	AGGTCTCACT	AGGCATCGCG	GGCATCTTGA TCGTGCT
feline aa sequence	S	K I S L	G I A	G I L I V L
human aa	S	K V S L	G I A	G I L I V L
	2000	2010	2020	2030
Feline - Normal Bands 1-6	GAG	CTCAGTGGCG	TGCTCGTTGG	GCATCTTTAG CTACGTT
human	GAG	CTCGGTGGCT	TGCTCCTTGG	GTGTCTTCAG CTACATT
feline aa sequence	S	S V A	C S L	G I F S Y V
human aa	S	S V A	C S L	G V F S Y I

	2040	2050	2060	2070
Feline - Normal Bands 1-6 human feline aa sequence human aa	GGG ATCCCCCTCA GGG TTGCCCTTGA G I P L T L I V I E V I P G L P L T L I V I E V I P	CCCTCATTGT CCCTCATTGT	GATCGAAGTC GATCGAAGTC	ATCCCAT ATCCCGT
	2080	2090	2100	2110
Feline - Normal Bands 1-6 human feline aa sequence human aa	TCC TGGTGCTGGC TCC TGGTGCTGGC F L V L A V G V D N I F I L F L V L A V G V D N I F I L	TGTTGGGGTG TGTTGGAGTG	GACAACATCT GACAACATCT	TCATTCT TCATTCT
	2120	2130	2140	2150
Feline - Normal Bands 1-6 human feline aa sequence human aa	GGT CCAGACCTAC GGT GCAGGCCTAC V Q T Y Q R D E R L H G E V Q A Y Q R D E R L Q G E	CAGCGAGATG CAGAGAGATG	AACGTCTTCA AACGTCTTCA	TGGAGAA AGGGGAA
	2160	2170	2180	2190
Feline - Normal Bands 1-6 human feline aa sequence human aa	ACT CTGGATCAGC ACC CTGGATCAGC T L D Q Q L G R V L G E V T L D Q Q L G R V L G E V	AGCTGGGCAG AGCTGGGCAG	GGTCTTAGGA GGTCTTAGGA	GAAGTGG GAAGTGG
	2200	2210	2220	2230
Feline - Normal Bands 1-6 human feline aa sequence human aa	CTC CTAGTATGTT CTC CCAGTATGTT A P S M F L S S F S E A V A A P S M F L S S F S E T V A	CCTGTCATCC CCTGTCATCC	TTTTCAGAGG TTTTCTGAGA	CTGTAGC CTGTAGC
	2240	2250	2260	2270
Feline - Normal Bands 1-6 human feline aa sequence human aa	ATT TTTCTTAGGA ATT TTTCTTAGGA F F L G A L S K M P A V H F F L G A L S V M P A V H	GCGTGTCAA GCATTGTCCG	AGATGCCGGC TGATGCCAGC	TGTTTAC CGTGCAC
	2280	2290	2300	2310
Feline - Normal Bands 1-6 human feline aa sequence human aa	ACC TTCTCTCTGT ACC TTCTCTCTCT T F S L F A G M A V L I D T F S L F A G L A V F I D	TTGCCGGGAT TTGCCGGGATT	GGCAGTCTTC GGCAGTCTTC	ATCGACT ATTGACT
	2320	2330	2340	2350
Feline - Normal Bands 1-6 human feline aa sequence human aa	TCC TTCTTCAGAT TTC TTCTGCAGAT F L L Q I T C F V S L L G L F L L Q I T C F V S L L G L	TACCTGTTTC TACCTGTTTC	GTGAGTCTCT GTGAGTCTCT	TGGGGTT TGGGGTT
	2360	2370	2380	2390
Feline - Normal Bands 1-6 human feline aa sequence human aa	AGA CATTAAAGCGT AGA CATTAAACGT D I K R Q E K N R L D V L D I K R Q E K N R L D I F	CAAGAGAAAA CAAGAGAAAA	ACCGTCTGGA ATCGGCTAGA	TGTTCTT CATCTTT

	2400	2410	2420	2430	
Feline - Normal Bands 1-6	TGC	TGTGTCAGAG	GCTCTGAAGA	TGGAACCAAGT	GTCCAGG
human	TGC	TGTGTCAGAG	GTGCTGAAGA	TGGAACAAGC	GTCCAGG
feline aa sequence	C	C V R	G S E D	G T S	V Q
human aa	C	C V R	G A E D	G T S	V Q
	2440	2450	2460	2470	
Feline - Normal Bands 1-6	CTT	CAGAGAGCTG	CTTGTTCGG	CTCTTCAAGC	ACTCCTA
human	CCT	CAGAGAGCTG	TTTGTTCGC	TTCTTCAAAA	ACTCCTA
feline aa sequence	A	S E S C	L F R	L F K	H S Y
human aa	A	S E S C	L F R	F F K	N S Y
	2480	2490	2500	2510	
Feline - Normal Bands 1-6	TTC	TCCACTTCTG	CTTAAGGACT	GGATGAGACC	AATTGTG
human	TTC	TCCACTTCTG	CTAAAGGACT	GGATGAGACC	AATTGTG
feline aa sequence	S	P L L	L K D	W M R	P I V
human aa	S	P L L	L K D	W M R	P I V
	2520	2530	2540	2550	
Feline - Normal Bands 1-6	ATA	GCAATATTTG	TGGGTGTCCT	GTCATTCAGT	GTTGCGA
human	ATA	GCAATATTTG	TGGGTGTTCT	GTCATTCAGC	ATCCGAG
feline aa sequence	I	A I F	V G V L	S F S	V A
human aa	I	A I F	V G V L	S F S	I A
	2560	2570	2580	2590	
Feline - Normal Bands 1-6	TCC	TGAACAAAGT	GGAATCGGA	TTGGATCAGT	CTCTTTC
human	TCC	TGAACAAAGT	AGATATTGGA	TTGGATCAGT	CTCTTTC
feline aa sequence	V	L N K V	E I G	L D Q	S L S
human aa	V	L N K V	D I G	L D Q	S L S
	2600	2610	2620	2630	
Feline - Normal Bands 1-6	AAT	GCCAGATGAC	TCCTACGTGA	TGGATTATTT	CAAGTCC
human	GAT	GCCAGATGAC	TCCTACATGG	TGGATTATTT	CAAATCC
feline aa sequence	M	P D D	S Y V	M D Y	F K S
human aa	M	P D D	S Y M	V D Y	F K S
	2640	2650	2660	2670	
Feline - Normal Bands 1-6	CTC	AAA TACC	TGCATGCAGG	TCCACCTGTG	TACTTTG
human	ATC	AGTCAGTACC	TGCATGCGGG	TCCGCTGTG	TACTTTG
feline aa sequence	L	K Y	L H A G	P P V	Y F
human aa	I	S Q Y	L H A G	P P V	Y F
	2680	2690	2700	2710	
Feline - Normal Bands 1-6	TCC	TGGAGGAAGG	GCATGACTAC	ACCTCTCTGA	AAGGGCA
human	TCC	TGGAGGAAGG	GCACGACTAC	ACTTCTTCCA	AGGGGCA
feline aa sequence	V	L E E G	H D Y	T S L	K G Q
human aa	V	L E E G	H D Y	T S S	K G Q
	2720	2730	2740	2750	
Feline - Normal Bands 1-6	GAA	CATGGTGTGC	GGAGGCATGG	GCTGCAATAA	CGACTCC
human	GAA	CATGGTGTGC	GGCGGCATGG	GCTGCAACAA	TGATTCC
feline aa sequence	N	M V C	G G M	G C N N	D S
human aa	N	M V C	G G M	G C N N	D S

	2760	2770	2780	2790
Feline - Normal Bands 1-6 human feline aa sequence human aa	CTG GTGCAGCAGA	TATTCAACGC	GGCCAGCTA	GACAGCT
	CTG GTGCAGCAGA	TATTTAACGC	GGCGCAGCTG	GACAACT
	L V Q Q	I F N A	A Q L D S	
	L V Q Q	I F N A	A Q L D N	
	2800	2810	2820	2830
Feline - Normal Bands 1-6 human feline aa sequence human aa	ATA CCCGAATAGG	CTTTGCTCCC	TCTTCCTGGA	TCGACGA
	ATA CCCGAATAGG	CTTCGCCCCC	TCGTCCTGGA	TCGACGA
	Y T R I G	F A P S S W	I D D	
	Y T R I G	F A P S S W	I D D	
	2840	2850	2860	2870
Feline - Normal Bands 1-6 human feline aa sequence human aa	TTA CTTTGATTGG	GTCAAGCCTC	AGTCTTCTG	CTGTAGA
	TTA TTTGACTGG	GTGAAGCCAC	AGTCGTCTG	CTGTAGA
	Y F D W	V K P Q S S	C C R	
	Y F D W	V K P Q S S	C C R	
	2880	2890	2900	2910
Feline - Normal Bands 1-6 human feline aa sequence human aa	GTC TACAACAGCA	CCGATCGGTT	CTGCAATGCT	TCAGTGG
	GTG GACAATATCA	CTGACCAGTT	CTGCAATGCT	TCAGTGG
	V Y N S	T D R F	C N A S V	
	V D N I	T D Q F	C N A S V	
	2920	2930	2940	2950
Feline - Normal Bands 1-6 human feline aa sequence human aa	TTG ACCCTGCCTG	CATCCGCTGC	AGGCCCTCA	CCCAGGA
	TTG ACCCTGCCTG	CGTTCGCTGC	AGGCCTCTGA	CTCCGGA
	V D P A C	I R C R P L	T Q E	
	V D P A C	V R C R P L	T P E	
	2960	2970	2980	2990
Feline - Normal Bands 1-6 human feline aa sequence human aa	GGG CAAACAGAGG	CCTCAAGGTG	GAGACTTCAT	GAGATTC
	AGG CAAACAGAGG	CCTCAGGGGG	GAGACTTCAT	GAGATTC
	G K Q R	P Q G G D F M	R F	
	G K Q R	P Q G G D F M	R F	
	3000	3010	3020	3030
Feline - Normal Bands 1-6 human feline aa sequence human aa	CTG CCCATGTTCC	TTTCTGATAA	CCCGAACCCC	AAGTGCG
	CTG CCCATGTTCC	TTTCTGATAA	CCCTAACCCC	AAGTGTC
	L P M F	L S D N	P N P K C	
	L P M F	L S D N	P N P K C	
	3040	3050	3060	3070
Feline - Normal Bands 1-6 human feline aa sequence human aa	GCA AAGGGGGACA	TGCTGCTTAC	AGTTCGGCAG	TTAACAT
	GCA AAGGGGGACA	TGCTGCCTAT	AGTTCGGCAG	TTAACAT
	G K G G H	A A Y S S A	V N I	
	G K G G H	A A Y S S A	V N I	
	3080	3090	3100	3110
Feline - Normal Bands 1-6 human feline aa sequence human aa	CCT CGGCAATGAC	ACGGGT G	TCGGAGCCAC	TTACTTC
	CCT CCTTGGCCAT	GGCACCAGGG	TCGGAGCCAC	GTACTTC
	L G N D	T G V G A T	Y F	
	L L G H	G T R V G A T	Y F	

	3120	3130	3140	3150
Feline - Normal Bands 1-6	ATG ACCTACCACA	CCGTGCTTCA	GACGTCTGCT	GACTTTA
human	ATG ACCTACCACA	CCGTGCTGCA	GACCTCTGCT	GACTTTA
feline aa sequence	M T Y H	T V L Q	T S A D	F
human aa	M T Y H	T V L Q	T S A D	F
	3160	3170	3180	3190
Feline - Normal Bands 1-6	CTG ACGCCATGAG	AAAAGCCAAC	CTCATCGCCA	GTAACAT
human	TTG ACGCTCTGAA	GAAAGCCCGA	CTTATAGCCA	GTAATGT
feline aa sequence	T D A M R	K A N L	I A S N	I
human aa	I D A L K	K A R L	I A S N	V
	3200	3210	3220	3230
Feline - Normal Bands 1-6	CAC CAAAACCATG	GGCCTTGAAG	GAAGTAATTA	CCGTGTG
human	CAC CGAAACCATG	GGCATTAAACG	GCAGTGCCTA	CCGAGTA
feline aa sequence	T K T M	G L E G	S N Y R	V
human aa	T E T M	G I N G	S A Y R	V
	3240	3250	3260	3270
Feline - Normal Bands 1-6	TTC CCATACAGTG	TGTTCTATGT	CTTCTACGAA	CAGTACC
human	TTT CCTTACAGTG	TGTTTTATGT	CTTCTACGAA	CAGTACC
feline aa sequence	F P Y S	V F Y V	F Y E Q	Y
human aa	F P Y S	V F Y V	F Y E Q	Y
	3280	3290	3300	3310
Feline - Normal Bands 1-6	TGA CCATTATTGA	TGACACGATC	TTTAACCTCA	GCGTGTG
human	TGA CCATCATTGA	CGACACTATC	TTCAACCTCG	GTGTGTC
feline aa sequence	L T I I D	D T I F	N L S V	S
human aa	L T I I D	D T I F	N L G V	S
	3320	3330	3340	3350
Feline - Normal Bands 1-6	CCT GGGAGCCATC	TTCTTAGTGA	CCGTGATTCT	CCTGGGC
human	CCT GGGCGCGATA	TTTCTGGTGA	CCATGGTCTT	CCTGGGC
feline aa sequence	L G A I	F L V T	V I L L	G
human aa	L G A I	F L V T	M V L L	G
	3360	3370	3380	3390
Feline - Normal Bands 1-6	TGT GATCTGTGGT	CTGCAGTGAT	CATGTGTATC	ACCATCG
human	TGT GAGCTCTGGT	CTGCAGTCAT	CATGTGTGCC	ACCATCG
feline aa sequence	C D L W	S A V I	M C I T	I
human aa	C E L W	S A V I	M C A T	I
	3400	3410	3420	3430
Feline - Normal Bands 1-6	CTA TGATCTTGGT	CAACATGTTT	GGCGTCATGT	GGCTGTG
human	CCA TGGTCTTGGT	CAACATGTTT	GGAGTTATGT	GGCTCTG
feline aa sequence	A M I L	V N M F	G V M W	L W
human aa	A M V L	V N M F	G V M W	L W
	3440	3450	3460	3470
Feline - Normal Bands 1-6	GGG CATCAGTCTG	AATGCAGTTT	CCTTGGTCAA	CCTGGTT
human	GGG CATCAGTCTG	AACGCTGTAT	CCTTGGTCAA	CCTGGTG
feline aa sequence	G I S L	N A V S	L V N L	V
human aa	G I S L	N A V S	L V N L	V

	3480	3490	3500	3510	
Feline - Normal Bands 1-6	ATG	AGCTGTGGCA	TTTCCGTGGA	GTTCTGCAGC	CACATAA
human	ATG	AGCTGTGGCA	TCTCCGTGGA	GTCTGCAGC	CACATAA
feline aa sequence	M	S C G	I S V E	F C S	H I
human aa	M	S C G	I S V E	F C S	H I
	3520	3530	3540	3550	
Feline - Normal Bands 1-6	CGA	GAGCATTAC	AGTGAGCATG	AAGGGCAGCC	GTGCACA
human	CCA	GAGCGTTAC	GGTGAGCATG	AAAGGCAGCC	CGGTGGA
feline aa sequence	T	R A F T	V S M	K G S	R A Q
human aa	T	R A F T	V S M	K G S	R V E
	3560	3570	3580	3590	
Feline - Normal Bands 1-6	ACG	GGCAGAAGAG	GCGCTCGCTC	ACATGGGCAG	TTCTGTG
human	GCG	CGCGGAAGAG	GCACTGCCCC	ACATGGGCAG	CTCCGTG
feline aa sequence	R	A E E	A L A	H M G S	S V
human aa	R	A E E	A L A	H M G S	S V
	3600	3610	3620	3630	
Feline - Normal Bands 1-6	TTC	AGTGAATCA	CACTAACAAA	ATTGGAGGG	ATTGTGG
human	TTC	AGTGAATCA	CACTTACAAA	ATTGGAGGG	ATTGTGG
feline aa sequence	F	S G I	T L T K	F G G	I V
human aa	F	S G I	T L T K	F G G	I V
	3640	3650	3660	3670	
Feline - Normal Bands 1-6	TAT	TGGCCTTTC	CAAATCTCAG	ATTTCCAGA	TATTTTA
human	TGT	TGGCTTTTC	CAAATCTCAA	ATTTCCAGA	TATTTTA
feline aa sequence	V	L A F A	K S Q	I F Q	I F Y
human aa	V	L A F A	K S Q	I F Q	I F Y
	3680	3690	3700	3710	
Feline - Normal Bands 1-6	CTT	CAGGATGTAT	TGGCTATGG	TCTTACTGGG	AGCCACC
human	CTT	CAGGATGTAT	TGGCCATGG	TCTTACTGGG	AGCCACT
feline aa sequence	F	R M Y	L A M	V L L G	A T
human aa	F	R M Y	L A M	V L L G	A T
	3720	3730	3740	3750	
Feline - Normal Bands 1-6	CAC	GGCTTGATCT	TCCTCCCGGT	CTTACTCAGC	TACATAG
human	CAC	GGATTAATAT	TCTCCTCGT	CTTACTCAGT	TACATAG
feline aa sequence	H	G L I	F L P V	L L S Y	I
human aa	H	G L I	F L P V	L L S Y	I
	3760	3770	3780	3790	
Feline - Normal Bands 1-6	GCC	CATCAATAAA	TAAAGCCAAA	AGCTTGCCCA	CTCAAGA
human	GGC	CATCAGTAAA	TAAAGCCAAA	AGTTGTGCCA	CTGAAGA
feline aa sequence	G	P S I	N K A K	S L A	T Q E
human aa	G	P S V	N K A K	S C A	T E E
	3800	3810	3820	3830	3840
Feline - Normal Bands 1-6	GCA	ATACAAAGGT	ACAGAGCGAG	AACAACCTCT	AAATTTC TAG
human	GCG	ATACAAAGGA	ACAGAGCGG	AACGGCTTCT	AAATTTC TAG
feline aa sequence	Q	Y K G	T E R	E Q	L L N F *
human aa	R	Y K G	T E R	E R	L L N F *

Figure 4.3

Electropherogram from normal feline sequence that is homozygous for guanine (G) at the mutation site.

4.4

Electropherogram from an NPC affect cat that is homozygous for cytosine (C) at the mutation site.

4.5

Electropherogram from an obligate NPC heterozygote that has both guanine (G) and cytosine (C) and is heterozygous at the mutation site.

T C T T C T T **G** C T G T A G A G

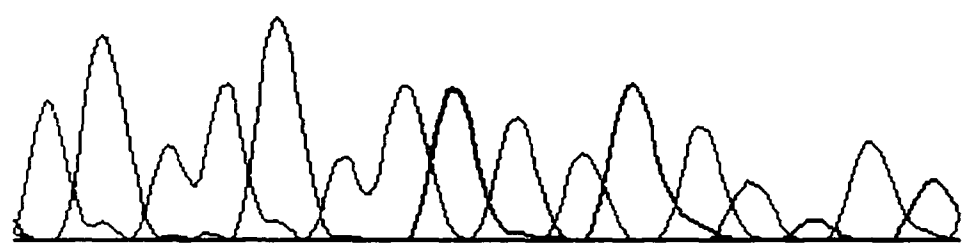


Figure 4.3 2870

T C T T C T T C C T G T A G A G

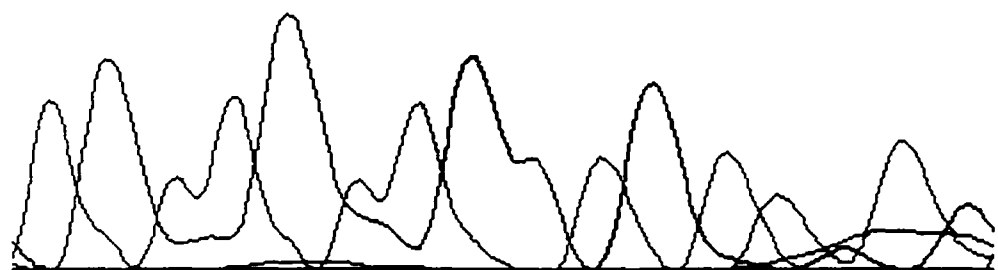


Figure 4.4 2870

T C T T C T T **N** C T G T A G A G

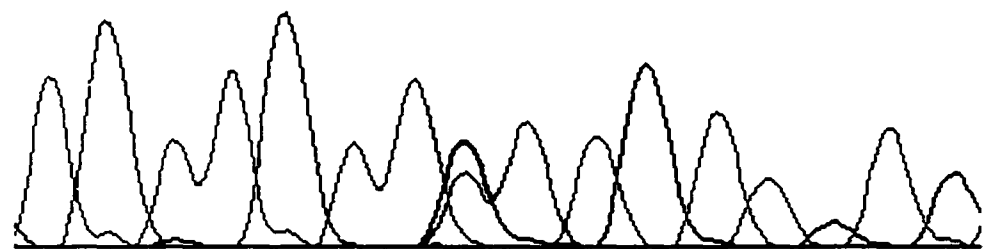


Figure 4.5 2870

Feline NPC Affected	AAGCCTCAGT	CTTCTTC	CCG	TAGAGTCTAC	AACAGCACCG
	K P Q	S S	S	C R V Y	N S T
Feline NPC Heterozygote	AAGCCTCAGT	CTTCTTC	CCG	TAGAGTCTAC	AACAGCACCG
	K P Q	S S	?	C R V Y	N S T
Feline Normal	AAGCCTCAGT	CTTCTTC	CCG	TAGAGTCTAC	AACAGCACCG
	K P Q	S S	C	C R V Y	N S T

Figure 4.6

Base and amino acid sequences from NPC affected, NPC heterozygote, and normal cats.

The area in the red box represents the site of the NPC mutation and illustrates the resulting amino acid from the C957S substitution.

NPC affected cats with serine and normal cats with cysteine.

The "N" and the "?" for the NPC heterozygotes reflects the heterozygous alleles of carriers.

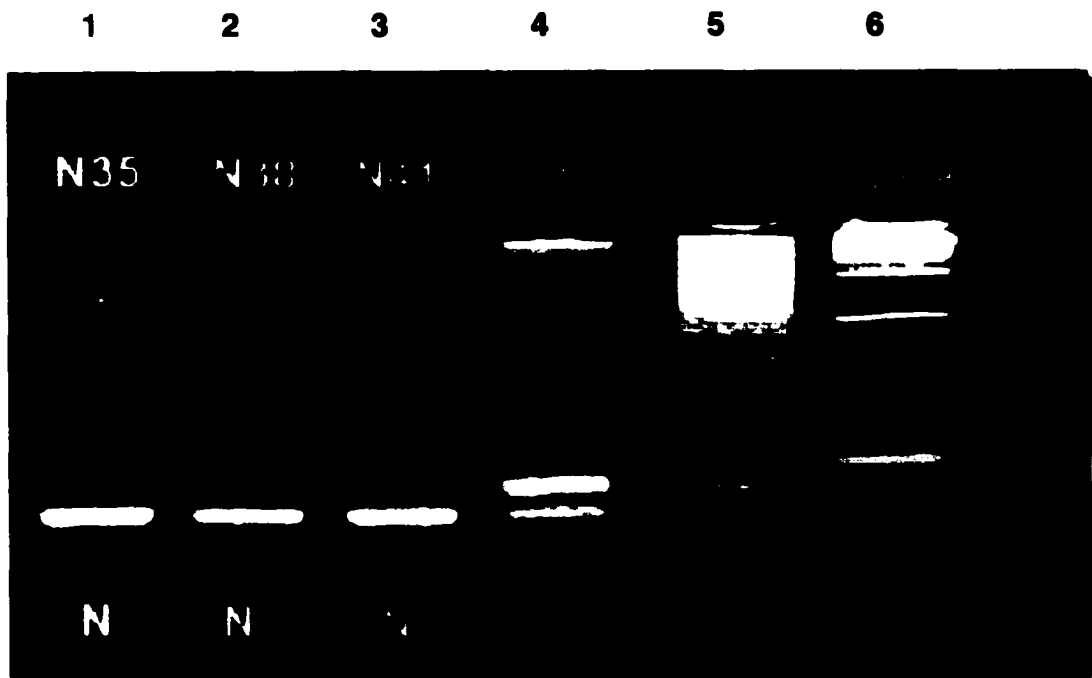


Figure 4.7

Gel from PCR based carrier assay

Lanes 1-3 represent normal genotypes with a single band at ~80bp.

Lane 4 represents a carrier with two bands, the cut wild type at ~80bp and the uncut mutant at ~100bp.

Lane 5 represents a homozygous affected cat with both bands uncut.

Lane 6 is the marker.

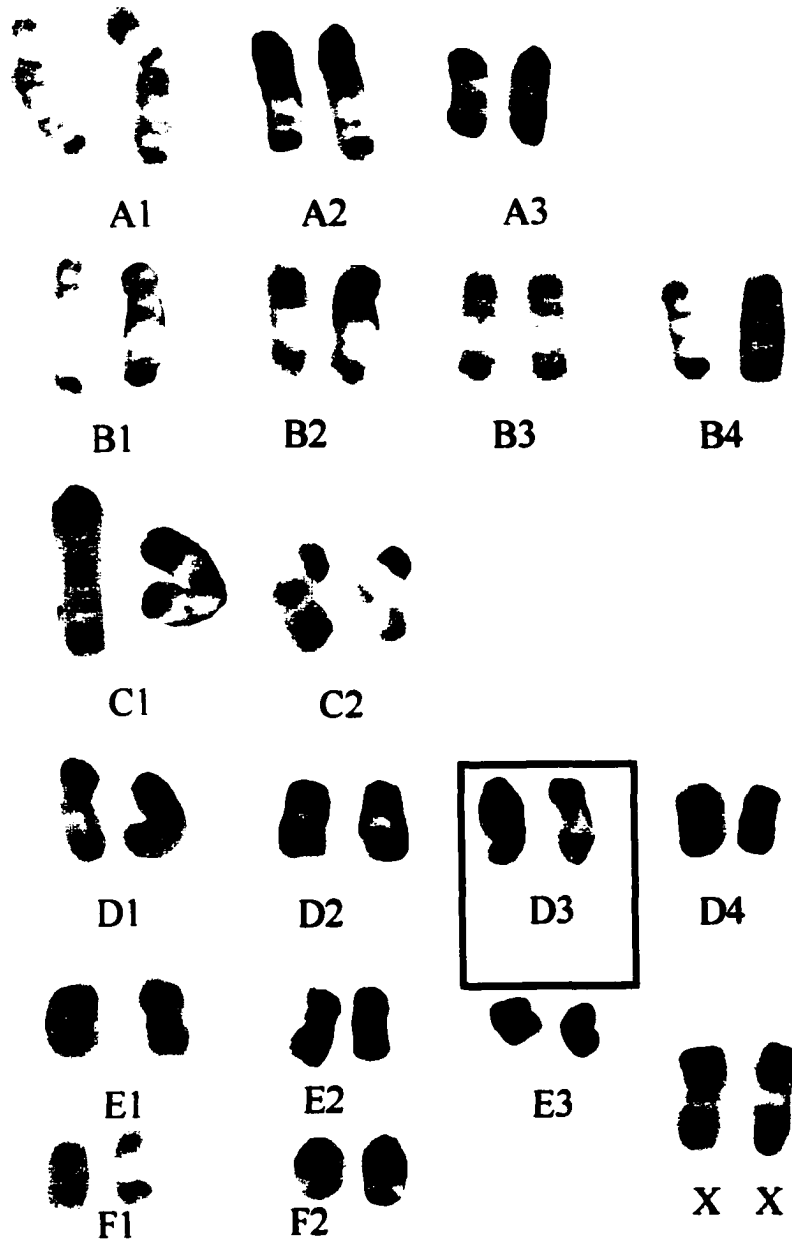


Figure 4.8

Karyotype of NPC obligate heterozygote.

D3, in the red box, is homologous to human chromosome 18.

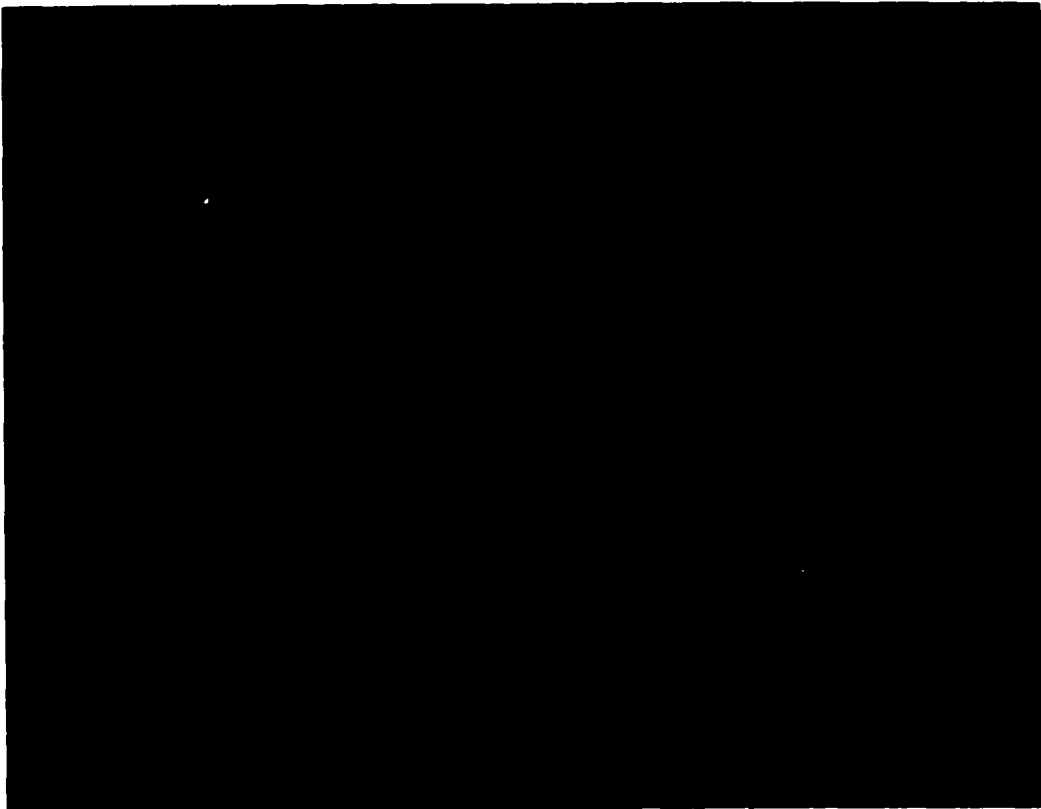


Figure 4.9

FISH analysis of the feline *NPC1* chromosomal localization.

Chromosomes outlined by yellow boxes represent D3, where the feline *NPC1* gene localizes and a homolog of human chromosome 18, the localization site of the human *NPC1*

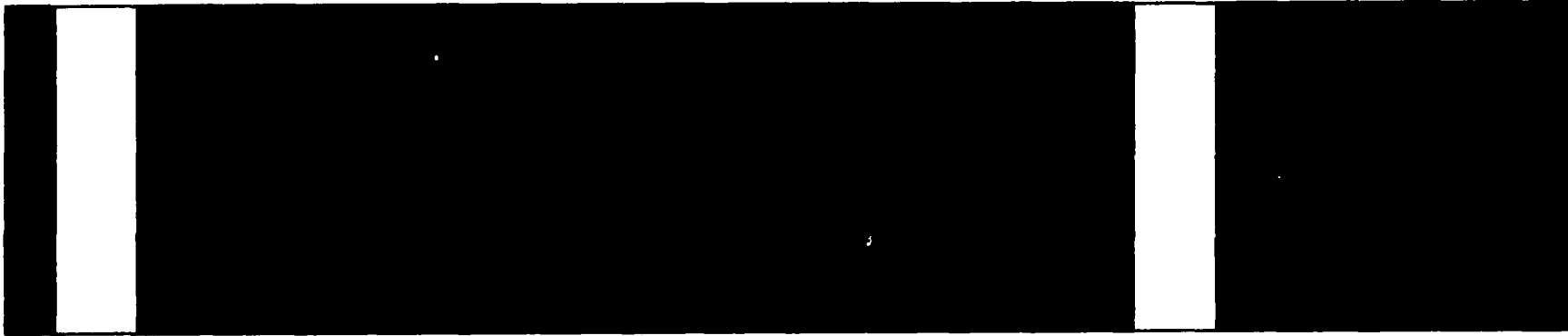






Figure 4.10

The Predicted Human NPC1 Protein

-  **13 Transmembrane domains**
-  **NPC1 critical regions**
-  **NH₂-terminus has an endoplasmic reticulum targeting sequence**
-  **COOH-terminus a lysosomal targeting sequence**