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In order to elucidate the cellular and molecular processes which are involved in Norrie disease (ND), we have used gene targeting technology to generate ND mutant mice. The murine homologue of the ND gene was cloned and shown to encode a polypeptide that shares 94% of the amino acid sequence with its human counterpart. RNA in situ hybridization revealed expression in retina, brain and the olfactory bulb and epithelium of 2 week old mice. Hemizygous mice carrying a replacement mutation in exon 2 of the ND gene developed retrolental structures in the vitreous body and showed an overall disorganization of the retinal ganglion cell layer. The outer plexiform layer disappears occasionally, resulting in a juxtaposed inner and outer nuclear layer. At the same regions, the outer segments of the photoreceptor cell layer are no longer present. These ocular findings are consistent with observations in ND patients and the generated mouse line provides a faithful model for study of early pathogenic events in this severe X-linked recessive neurological disorder.
of 1.9 kbp. The open reading frame (ORF) of 399 bp is completely contained within exons 2 and 3 and gene expression is restricted to brain and retina as revealed by Northern blot analysis.

The predicted gene product contains 133 amino acid residues, is probably secreted and particularly rich in cysteines. Database searches revealed homologies of the ND protein with the cysteine-rich domain of mucins and with proteins involved in cell interaction and differentiation processes (20). Moreover, computer-aided analysis suggests that the third structure of the human gene product revealed striking similarities with the transforming growth factor β (TGFβ) (21). These observations point to a role of the ND gene product in developmental and differentiation processes. However, little is known about the histological, cellular and molecular mechanisms which are involved in the pathogenesis of this disease. To shed more light on the sequence of events involved in the manifestation of ND, we have established an animal model for this disorder by targeted mutagenesis of the Norrie disease (mND) gene of the mouse.

**RESULTS**

The mouse Norrie disease (mND) gene and its expression pattern

A human complementory DNA clone, pTF35 (12), which spans the entire ORF and parts of the 5′ and 3′ noncoding regions, was used as probe to screen a mouse brain cDNA library. Isolated cDNAs detected a 1.8 kbp transcript in mouse brain by Northern blot hybridization (Fig. 1). X-chromosomal localization was established by dosage Southern blot hybridization (data not shown) and confirmed later on by hybridization of gene targeted XY embryonic stem cell lines with the deleted 283 bp exon 2 (Fig. 1b, 1c). There is a high degree of nucleotide sequence conservation between the human and mouse ND gene. Sequence comparison yielded identity values of 91.7% for the ORF and 82.3% for the entire cDNA. The exon–intron structure of the mND gene was established by cloning the cDNA hybridizing genomic EcoRI fragments from mouse strain 129/SvJ DNA and subsequent sequencing of intron–exon junctions with cDNA-derived primers. The gene consists of three exons hybridizing to EcoRI fragments of 2.5, 6.5 and 4.0 kbp, respectively, and encodes a polypeptide of 131 amino acids. The human and mouse protein sequences are 94% identical, with only minor substitutions (Fig. 2).

In order to investigate tissue specific expression of the mND gene, RNA in situ hybridization was carried out. Expression was low and evenly distributed in almost all tissues of mouse embryos from 12.5 to 18.5 days post conception (d.p.c.), including the eye, ear and brain. Enhanced expression was visible in the developing olfactory bulb at 14.5 d.p.c. (data not shown). Here, high expression is restricted to differentiating neurons of the marginal layer. Two weeks after birth, the expression within the olfactory bulb becomes restricted to the mitral cell layer and the sensory layer of the olfactory epithelia (Fig. 3g–k). High expression levels
Figure 3. RNA in situ hybridization of a mND gene riboprobe to a transversal cryosection of a mouse head 2 weeks after birth. Bright field (a, c, e, g and i) and corresponding dark field (b, d, f, h and k) images are shown. High expression is visible in the olfactory epithelium and the retina and lower expression levels were detected in the cerebellum (b). The high magnifications of the different tissues show expression within the Purkinje cell layer of the cerebellum (c and d), the retinal ganglion and inner nuclear layers (e and f), the mitral cells of the bulbus olfactorius (g and h) and in the olfactory epithelium (i and k). ce: cerebellum, cor: cortex, epl: external plexiform layer, gcl: ganglion cell layer, gl: granular layer, glo: glomerular layer, hi: hippocampus, inl: inner nuclear layer, ipl: internal plexiform layer, le: lens, lp: lamina propria, ml: mitral cell layer, mo: molecular layer, nc: nasal cavity, ns: nasal septum, ole: olfactory epithelium, pl: Purkinje cell layer. Bars a and b: 1 mm; c-k: 100 μm.
Figure 4. Gene targeting of the murine ND gene. (a) Targeting strategy. A portion of exon 2 (black box) was replaced by a neomycin resistance cassette (neo, shaded box). The targeting vector contained the thymidine kinase gene of the herpes simplex virus (hsvtk) as additional selection marker. Correctly targeted clones will show a 4.8 \text{kbp} \text{BamHI} and a 16.8 \text{kbp} \text{BgII} fragment with the 3' and 5' probes, respectively. Both of these probes are located external to the targeted 6.5 \text{kbp} \text{EcoRI} fragment. Restriction sites: B, \text{BamHI}; B*, \text{BamHI} introduced by \text{in vitro} mutagenesis; Bg, \text{BglII}; E, \text{EcoRI}; K, \text{KpnI}; X, \text{Xhol}. (b) Autoradiogram of a Southern blot containing \text{BamHI} digested DNA of seven targeted embryonic stem cell lines (TCL) and controls 129/SvJ; liver DNA from mouse strain 129/SvJ; E14; DNA of non-targeted embryonic stem cells, SNLH9; DNA isolated from feeder cells) after hybridization with the 3' probe (top) and the substituted 283 bp fragment from exon 2 (bottom).

were also observed in the inner nuclear layer as well as the ganglion cell layer of the retina (Fig. 3c,f) and in Purkinje cells of the cerebellum of 2 week old mice (Fig. 3c,d). We were not able to detect any specific expression in the ear in animals at the age of 4 weeks. Moreover, there was no significant expression in gonads, kidney, liver, lung, spleen, gut, and tongue of adult animals (4–6 months).

Gene targeting of murine embryonic stem (ES) cells

To replace the wild-type ND gene by an inactive gene copy in mouse embryonic stem cells, we designed a construct carrying a deletion of the protein coding portion of exon 2, which removes the 56 N-terminal amino acids of the ND gene product as shown in Figure 4a. Prior to gene targeting in ES cells from mouse strain 129, a genomic 6.5 \text{kbp} \text{EcoRI} fragment carrying exon 2 of that strain was preparatively cloned, because it had been shown previously that isogenic gene targeting constructs yield the highest efficiencies (22). Subsequently, this \text{EcoRI} fragment was recloned in a \text{BamHI} deficient pBluescript SK– vector and a second \text{BamHI} site was introduced behind the boundary between exon 2 and intron 2 by \text{in vitro} mutagenesis. This and the \text{BamHI} site 5' to the ATG start codon, were used to replace 283 bp of exon 2 by a neomycin resistance cassette, in the opposite transcriptional orientation. Additionally, the HSVtk gene was introduced in front of the 5’ end of the homologous \text{EcoRI} fragment, again in opposite orientation to the mND gene (Fig. 4a), to allow for negative selection against random integration events with FIAU.

After electroporation of this construct and selection with G418, 192 resistant clones were obtained, seven of which gave the expected diagnostic 4.8 \text{kbp} \text{BamHI} fragment after hybridization with a 3' probe (Fig. 4a,b). With a 5' probe, six of these clones
Figure 5. PCR-genotyping of mouse tail DNA. (a) Genotyping strategy. Amplification of the endogenous wild-type locus with two intron primers results in a fragment of 486 bp, while from the targeted locus two fragments of 271 and 214 bp are being amplified by using combinations of intron primers and neo-cassette primers. (b) Ethidium bromide stained agarose gel of PCR fragments derived from hemizygous mutant mice (-), as well as heterozygous (+-) and homozygous (++) females.

showed also the diagnostic 16.8 kbp BglII fragment indicative for a faithful homologous recombination upstream of exon 2. The loss of the coding segment of exon 2 was confirmed by using the replaced fragment as probe (Fig. 4b). All properly targeted cell lines were karyotyped prior to injection. Five cell lines containing the normal number of 40 acrocentric chromosomes were injected into C57Bl/6 blastocysts and embryos were transferred to pseudopregnant carrier mothers. One of the cell lines gave rise to chimeric male offspring that transmitted the mutation through the germ line. F1 heterozygous females were mated with wild-type (wt) males and the offspring (F2) was genotyped by PCR with primer combinations allowing the identification of the wild type as well as the mutant allele in a single assay (Fig. 5a,b).

Analysis of ND mice

In the F1 offspring of heterozygous females, the four expected genotypes were almost equally represented, with a small preponderance of heterozygous females. Among 267 F1 animals, 135 were female; of these, 78 were heterozygous ($\chi^2 = 3.267, P = 0.089$). A total of 65 hemizygous mutant mice were identified by PCR on DNA from tail tips removed 14 days after birth.

Initial ophthalmological examinations were performed with a slit-lamp, 3 weeks after birth. In three of six hemizygous mutant mice examined, conspicuous precipitate-like retrolental structures were seen in the vitreous body. Slit-lamp examination of older mutant mice (10–20 weeks) revealed pathological signs in nine of nine cases. These differences point to a variable age of onset. In contrast, the variation in number and size of the precipitates was age independent. The control group, consisting of 10 wt animals, was found to be completely normal upon slit-lamp examination. Apart from these precipitate-like structures, depigmented bundles or stripes were present in some of the eyes of hemizygous mutant mice, which were interpreted as retinal folding or detachment.

Table 1. Ophthalmologic examination of hemizygous mutant mice by slit-lamp biomicroscopy and morphohistological analysis

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From each mouse the left (L) and the right (R) eye were examined. Pathological changes within the outer segments (os) of the photoreceptor layer, the outer and inner nuclear layer (onl, inl), the ganglion cell layer (gcl), and the vitreous body (vb) are indicated by +. Morphological analysis was performed on sections of 5 µm, obtained every 100 µm.
First, morphological and biochemical data were obtained from embryonic stem cells. Upon differentiation, a variety of cell types were observed, including neural progenitors, neuronal precursor cells, and astrocytes. These results indicate that the embryonic stem cells can be induced to differentiate along multiple lineages.

Next, the expression of genes involved in neural development was examined. This was done by analyzing the expression patterns of various neural genes in the differentiated cells. The results showed that the expression of these genes was consistent with the expected patterns of neural development.

Finally, the functional significance of these results was discussed. The expression of neural genes in the differentiated cells suggests that the embryonic stem cells have the potential to differentiate into neural cells and that these cells may be useful for studying neural development and disease models.
polypeptide sequences were used for database screening (EMBL as well as SwissProt).

Genomic fragments of the mND gene were cloned preparative-ly from EcoRI or BamHI digested liver DNA from mouse strain 129/SvJ. Restriction fragments were separated in a preparative 0.8% low melting temperature agarose gel at 40 V in 40 mM Tris-acetate pH 7.5 and 1 mM Na2 EDTA for 16 h. The gel was sliced into 2 mm fractions, aliquots of 75 ml each were incubated at 65°C and dot-blotted on GeneScreenPlus membrane, hybridized with pmnc2 and the DNA of positive fractions was purified by making use of the GeneClean protocol (Bio101). The fragments were cloned into λZAP and λZAPEXPRESS for EcoRI and BamHI fragments, respectively. The exon containing EcoRI fragments of 2.5 (exon1), 6.5 kbp (exon2) and 4 kbp (exon3) were used to establish the intron–exon boundaries of the mND gene by sequencing with cDNA-derived primers.

The two preaparatively isolated BamHI fragments of 6.5 and 4 kbp were used for the isolation of the 5' and 3' probes, respectively, which are represented by a 1.8 kbp EcoRI and a 1.7 kbp EcoRI–BamHI fragment and situated external with respect to the targeted 6.5 kbp EcoRI fragment.

Expression studies
Northern blots containing poly(A)+ RNA from adult tissues (Clontech) were hybridized with the mouse cDNA pmnc2 according to the manufacturers instructions. Northern blots of fetal RNA samples were made by separating 10–20 μg total RNA from different tissues, isolated by the guanidinum isothiocyanate method (28), in a 1% agarose gel containing 8% formamide and subsequent blotting on to GeneScreenPlus membranes. Hybridization was performed according to standard methods (29).

For RNA in situ hybridization whole embryos or single organs of mice were fixed overnight with 4% paraformaldehyde in PBS at 4°C and prepared from cryostat sections and in situ hybridization was carried out as described (30). Briefly, antisense and sense probes were generated by in vitro transcription with α-35S-dUTP using the EcoRI and XhoI linearized plasmid pmnc2 and the T7 or T3 RNA polymerase, respectively. The probe length was reduced to 150–200 nucleotides by alkaline hydrolysis. The slides containing tissue sections were prehybridized at 54°C in a solution containing 50% formamide, 10% dextrane sulfate, 0.3 M NaCl, 10 mM Tris, 10 mM sodium phosphate pH 6.8, 20 mM DTT, 0.2xDenhardt’s, 0.1% Triton-X-100, 0.1 mg/ml E.coli RNA, and 0.1 mM αS-UTP. For hybridization, 80 000 d.p.m./μl labelled RNA probe was added to the hybridization mix, incubated for 16 h at 54°C in a humid chamber, and washed in hybridization solution. After RNase A digestion the slides were washed 30 min 37°C in 2xSSC; 0.1% SDS, 30 min in 0.1xSSC and dehydrated by increasing concentrations of ethanol. The slides were coated with Ilford K5 photoemulsion for autoradiography. After 2–3 weeks of exposure at 4°C, developing was performed in Kodak D19b. Slides were subsequently stained with Giemsa and embedded. The sections were analysed with bright- and dark-field illumination using a Zeiss SV8 stereomicroscope and an Axioptiphot microscope.

Construction of the replacement vector
The 6.5 kbp genomic EcoRI fragment from mouse strain 129/SvJ, which contains exon 2 of the mND gene, was cloned into a BamHI deficient pBluescript SK– vector. Additionally, to the natural present BamHI site in front of the ATG start codon, a second BamHI recognition sequence was introduced by in vitro mutagenesis employing the following primer: 5' ggagagaagg-gattctccaa 3' (Isogen Biosience, The Netherlands). Briefly, uridine containing single stranded DNA was isolated by using the helper phage VCSM13 (Stratagene, #200251), annealed to the above mentioned 5’ phosphorylated oligonucleotide, and the second strand was synthesized with Klenow DNA polymerase. After ligation with T4-DNA-ligase the dsDNA was transformed into E.coli XL-Blue and the plasmids were analysed by BamHI digestion.

From the resulting plasmid vector the 283 bp BamHI fragment spanning the coding portion of exon 2 was excised and replaced by a 1.1 kbp BamHI–BglII neomycin or a 2.2 kbp BamHI hygromycin cassette in both orientations. A pilot electroporation with the four different constructs showed that the highest number of stably transformed ES cells was obtained with the neomycin construct inserted in opposite direction to the ND gene transcription direction (pNEOMNDG). The negative selection marker HSVtk was cloned as 1.8 kbp XbaI fragment 5’ to the EcoRI site of the homologous 6.5 kbp EcoRI fragment (Fig. 4a) within the XbaI site of the multiple cloning site of pNEOMNDG (see Fig. 4a), again in antiparallel orientation. Electroporation was carried out with the KpnI linearized replacement vector, enabling the protection of the tk gene by 2.9 kbp pBluescript sequence. The neomycin, hygromycin as well as the tk cassette that were used have been described previously (22,31).

Gene targeting and tissue culture
Embryonic stem cells derived from mouse strain 129/Ola (line E14, kindly provided by A. Berns, Amsterdam) and feeder cells SNLH9 (22) were cultured in Dulbecco’s modified Eagle’s medium (DMEM) with 15 and 10% FCS, respectively, supplemented with 2 mM glutamine, 1 mM sodium pyruvate and 0.1 mM β-mercaptoethanol. For an initial pilot experiment, 5 μg linearized targeting construct were introduced by electroporation of 4 million ES cells in 800 μl supplemented DMEM with 15% FCS employing the Gene Pulser (Bio Rad, conditions: voltage 250 V, capacity 500 μF, pulse time 6–8 ms). Electroporated cells were resuspended in 20 ml supplemented DMEM + 15% FCS and plated in two 9 cm tissue culture dishes containing radiated SNLH9 feeder cells. Twenty-four h after plating selective medium was added, containing 350 μg/ml G418 or 300 μg/ml hygromycin B. Selective medium was refreshed every 2 days and after 10 days colonies became visible.

As the neo construct in opposite direction yielded highest efficiencies, this construct was used after introduction of the HSVtk gene for preparative electroporation. 20 μg linearized replacement vector DNA were electroporated into 20 million ES cells in 800 μl DMEM with 15% FCS. Electroporation and culturing was carried out as above, excepting the presence of 0.2 μM FIAU (1-[2-deoxy, 2-fluoro-β-D-arabinofuranosyl] additionally to G418 in the cell culture medium. After 10 days, 192 G418-resistant colonies were picked and transferred to 96-well plates. Colonies were expanded and splitted in two parts. One part was stored at -80°C in supplemented medium containing 10% DMSO. Of the other part DNA was isolated according to standard procedures, cleaved with BamHI and resulting blots were hybridized with the 3’ probe, a 1.7 kbp
EcoRI-BamHI fragment. Subsequently, the DNA of seven targeted ES cell lines was digested with BglII and analysed with the 5' probe (1.8 kbp EcoRI fragment) and correct targeting was confirmed for six of them. Furthermore, metaphase spreads were analysed from each targeted cell line prior to injection. All of the six cell lines revealed the normal 40(X,Y) karyotype.

Generation and analysis of knockout mice

Targeted clones were injected into 3.5 days blastocysts of C57B1/6 mice and transferred into uterine horns of pseudopregnant foster mothers (C57B1/6xCBA/Ca)F1 as described (32). Chimerism of resulting offspring was determined by coat colour, and males with more than 50% agouti coat colour were crossed with C57B1/6 females. Resulting heterozygous F1 females were bred with C57B1/6 males. Germ-line transmission was scored and genotypes were analysed by PCR assay on tail biopsies. PCR was performed with 2 mM gene intron primers (forward: 5' gttgacattcctattcttg 3', reverse: 5' cttctcacctcctgacggaa 3') in combination with two neo primers (neo5: 5' ggcgttggggtgatttctt 3', neo3: 5' ctgcatcctcaggtcctg 3'). PCR amplifications were carried out in 10 mM Tris pH 8.5, 50 mM KCl, 5 mM MgCl2, 0.5 mM dTTP, 0.25 mM each dNTP, 250 μM primer, 50–100 ng template and 0.8 units Taq DNA polymerase (Boehringer), for 35 cycles involving 1 min 94°C, 1 min 62°C and 1.5 min 72°C. The targeted locus will yield two fragments of 271 and 214 bp, and the wild-type locus results in a single 486 bp fragment. The progeny was again genotyped by PCR analysis of tail DNA.

Initial ophthalmological analysis was performed by direct slit-lamp biomicroscopy after dilatation of the pupils with 0.17% tropicamide. Prior to morphohistological analysis the eyes were analysed by PCR assay on tail biopsies. PCR was performed to identify two fragments of 271 and 214 bp, and the wild-type locus results in a single 486 bp fragment. Subsequently, the DNA was digested with the 5' probe (1.8 kbp EcoRI fragment) and correct targeting was confirmed for six of them. Furthermore, metaphase spreads were analysed from each targeted cell line prior to injection. All of the six cell lines revealed the normal 40(X,Y) karyotype.

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