Isolation of a candidate gene for Norrie disease by positional cloning

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The following revised versions of Figs 2,3,5 and 6 should have appeared in this paper.

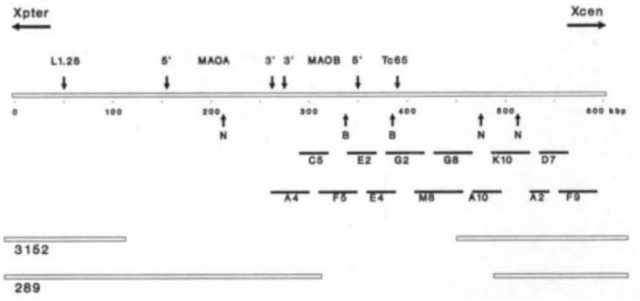
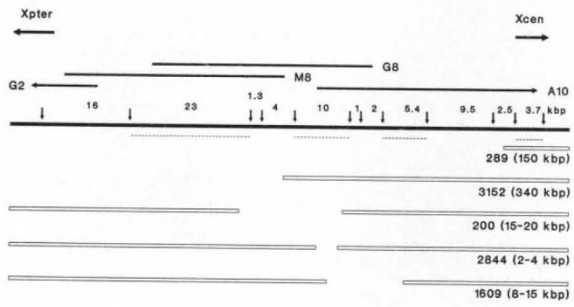


Fig. 1 Overlapping cosmid clones (dark bars) spanning the proximal half of YAC1 which encompasses the ND gene as well as two submicroscopic deletions (nos 3152 and 289). 5' and 3' ends of the MAO genes, the locations of marker sequences L1.28 (DXS7) and Tc65, as well as *BSS*HII (B) and *Not*I (N) restriction sites are indicated by arrows.

Fig.3 The ND gene region as defined by microdeletions. The location of cosmids (dark bars) and *Eco*RI restriction sites (arrows) are indicated above. Genomic fragments hybridizing to cDNA C2 are underlined.



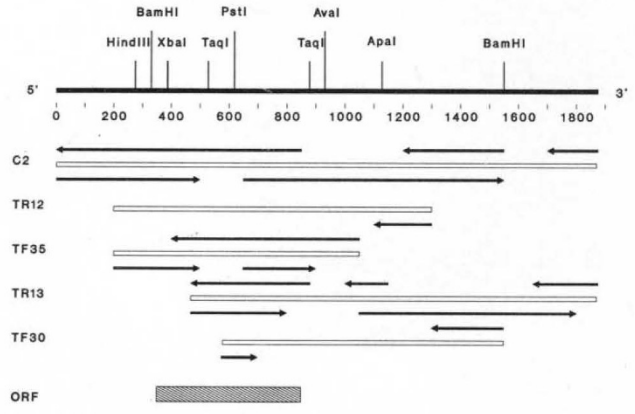


Fig. 5 Overlapping cDNA clones (open bars) spanning 1.9 kb of the putative ND gene, which were isolated from fetal (C2) and adult retinal libraries (TR12, TR13), and from a fetal brain library (TF30, TF35). Sequenced segments are indicated by arrows, and the open reading frame given as shaded box.

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   1  GGCACAAGCC TCTCTCTCTC TCCCTCTCTC TCTCCCTCTC TCTCTCTCCC TGTGTCGCTT
  61  AAACAACAGT CCTAACTTTT GTGTGTTGCA AATATAAAAG GCAAGCCATG TGACAGAGGG
 121  ACAGAAGAAC AAAAGCATTT GGAAGTAACA GGACCTCTTT CTAGCTCTCA GAAAAGTCTG
 181  AGAAGAAAGG AGCCCTGCGT TCCCCTAAGC TGTGCAGCAG ATACTGTGAT GATGGATTGC
 241  AAGTGCAAAG AGTAAGACAA AACTCCAGCA CATAAAGGAC AATGACAACC AGAAAGCTTC
 301  AGCCCGATCC TGCCCTTTCC TTGAACGGGA CTGGATCCTA GGAGGTGAAG CCATTTCCAA
 361  TTTTTTGTCC TCTGCCTCCC TCTGCTGTTC TTCTAGAGAA GTTTTTCCTT ACAACAATGA
                                                          M  R
 421  GAAAACATGT ACTAGCTGCA TCCTTTTCTA TGCTCTCCCT GCTGGTGATA ATGGGGGATA
        K  H  V     L  A  A     S  F  S  M     L  S  L     L  V  I     M  G  D  T
 481  CAGACAGTAA AACGGACAGC TCATTCATAA TGGACTCGGA CCCTCGACGC TGCATGAGGC
        D  S  K     T  D  S     S  F  I  M     D  S  D     P  R  R     C  M  R  H
 541  ACCACTATGT GGATTCTATC AGTCACCCAT TGTACAAGTG TAGCTCAAAG ATGGTGCTCC
        H  Y  V     D  S  I     S  H  P  L     Y  K  C     S  S  K     M  V  L  L
 601  TGGCCAGGTG CGAGGGGCAC TGCAGCCAGG CGTCACGCTC CGAGCCTTTG GTGTCGTTCA
        A  R  C     E  G  H     C  S  Q  A     S  R  S     E  P  L     V  S  F  S
 661  GCACTGTCCT CAAGCAACCC TTCCGTTCCT CCTGTCACTG CTGCCGGCCC CAGACTTCCA
        T  V  L     K  Q  P     F  R  S     C  H  C     C  R  P     Q  T  S  K
 721  AGCTGAAGGC ACTGCGGCTG CGATGCTCAG GGGGCATGCG ACTCACTGCC ACCTACCGGT
        L  K  A     L  R  L     R  C  S  G     G  M  R     L  T  A     T  Y  R  Y
 781  ACATCCTCTC CTGTCACTGC GAGGAATGCA ATTCCTGAGG CCCGCTGCTG TGTGTGGCTT
        I  L  S     C  H  C     E  E  C  N     S  -
 841  CTGGATGGGA CAACTGTAGA GGCAGTTCGA CCAGCCAGGG AAAGACTGGC AAGAAAAGAG
 901  TTAAGGCAAA AAAGGATGCA ACAATTCTCC CGGGACTCTG CATATTCTAG TAATAAAGAC
 961  TCTACATGCT TGTTGACAGA GAGAGATACT CTGGGAACTT CTTTGCAGTT CCCATCTCCT
1021  TTCTCTGGTA CAATTTCTTT TGGTTCATTT TCAGATTCAG GCATTTTCCC CCTTGGCTCT
1081  CAATGCTGTT TGGGTTTCCA ACAATTCAGC ATTAGTGGGA AAAAGTGGGC CCTCATACAC
1141  AAGCGTGTCA GGCTGTCAGT GTTTGGTGCA CGCTGGGGAA GAATTTACTT TGGAAAGTAG
1201  AAAAGCCCAG CTTTTCCTGG GACATCTTCT GTTATTGTTG ATGTTTTTTT TTACCTTGTC
1261  ATTTTGGTCT AAGGTTGCCA TTGCTGCTAA AGGTTACCGA TTTCAAAGTC CAGATACCAA
1321  GCATGTGGAT ATGTTTAGCT ACGTTTACTC ACAGCCAGCG AAACTGACAT TAAAATAACT
1381  AACAAACAGA TTCTTTTATG TGATGCTGGA ACTCTTGACA GCTATAATTA TTATTCAGAA
1441  ATGACTTTTT GAAAGTAAAA GCAGCATAAA GAATTTGTCA CAGGAAGGCT GTCTCAGATA
1501  AATTATGGTA AAATTTTGTA AGGGAGCAGA CTTTTAAAGA CTTGCACAAA TACGGATCCT
1561  GCACTGACTC TGGAAAAGGC ATATATGTAC TAGTGGCATG GAGAATGCAC CATACTCATG
1621  CATGCAAATT AGACAACCAA GTATGAATCT ATTTGTGGGT GTGCTATAGC TTTAGCCGTG
1681  TCACGGGCAT CATTCTCTAA TATCCACTTG TCCATGTGAA ACATGTTGCC AAAATGGTCC
1741  TGGCTTGTCT TCTGAACGTT TGGGTCAAAT GTGTTTTGGT CCTGGAGGCT CAAATTTTGA
1801  GTTATTCCCA CGTTTTGAAA TAAAAAGAGT ATATTCAAAA AAAAAAAAAA AAAAAAAAAA
1861  AAAAAAAAAA AA
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Fig. 6 Nucleotide sequence (EMBL accession number X65724) of the consensus cDNA, and deduced amino acid sequence starting with the putative translation initiation codon at position 417.

The peripheral myelin protein gene *PMP-22* is contained within the Charcot-Marie-Tooth disease type 1A duplication

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In Fig. 1, part *b* should have been represented by the figure reproduced below.

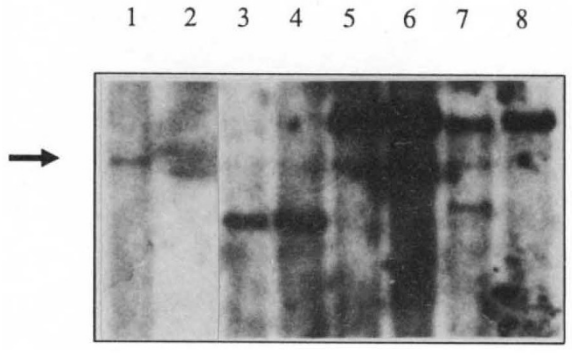

Fig. 1 Cell hybrid mapping of *PMP-22* to human chromosome 17p11.2. *b*, Southern blot of TaqI digested DNA hybridized with *pmp-22* cDNA CD25: lane 1 human; lane 2 hamster; lanes 3–4 somatic cell hybrid FTH(17)L4; lanes 5–7 somatic cell hybrids GM10889, GM10501 and GM10331, lane 8 mouse B82. The 5.5 kb human *TaqI* fragment is indicated by the arrow. The lower weight *TaqI* band seen in FHTB(17)L4 corresponds to the hybridization signal obtained with *TaqI* digested DNA from the parent rat line FT02B of FTHB9(17)L4 with the PMP-22 cDNA CD25.