Incidence of germline hMLH1 and hMSH2 mutations (HNPCC patients) among newly diagnosed colorectal cancers in a Slovenian population

EDITOR—Hereditary non-polyposis colorectal cancer (HNPCC) syndrome is a common autosomal dominant predisposition to colorectal cancer. Clinical diagnostic features of sporadic and HNPCC associated colorectal cancer do not differ significantly and until recently the identification of HNPCC patients was based mainly on their family history. Because of the importance for relatives of HNPCC patients to be clinically examined frequently in order to detect the disease at an early, curable stage, the International Collaborative Group (ICG) on HNPCC proposed criteria for identification of HNPCC families. According to the guidelines agreed by the ICG in Amsterdam in 1990, an HNPCC family has to fulfil the following criteria: there should be at least three relatives with colorectal cancer (one of whom is a first degree relative to the other two), at least two successive generations should be affected, and one relative should be diagnosed under the age of 50.1 CRC patients with HNPCC syndrome can also develop cancer of the endometrium, stomach, ovary, and urinary and hepatobiliary tracts.2–5 In several epidemiological studies, the incidence of HNPCC has been estimated to be between 0.5%6 and 15%3 of all colorectal cancers. The identification of mismatch repair genes (MMR), of which at least five (hMLH1,7,8 hMSH2,9,10 PMS1,10 PMS2,11 and hMSH6 (GTBP)11) are associated with HNPCC, has enabled mutational analysis in families fulfilling complete or partial Amsterdam criteria. Carriers of germline MMR mutations have a higher than 80% risk for cancer by the age of 75.2 The great majority of germline mutations were found in approximately equal proportions in hMLH1 and hMSH2, while mutations in the other three MMR genes have been reported only in a limited number of cases.12 Germline hMLH1 and hMSH2 mutations were also found in a considerable proportion of colorectal cancer patients from families not fulfilling the Amsterdam criteria,13 especially if they were young,14 15 indicating that some HNPCC families might be missed if they are preselected before mutational analysis.

Mutations in MMR genes result in microsatellite instability (MSI),16 which is characteristic of more than 90% of tumours in HNPCC patients but was also found in 12-15% of sporadic colorectal tumours.17–19 In the absence of other diagnostic criteria, MSI analysis of tumours could be valuable markers in HNPCC identification.

Here we report an effective MSI analysis of CRC and subsequent mutational analysis of the hMLH1 and hMSH2 genes in tumours with considerable MSI for identification of HNPCC among randomly collected, newly diagnosed colorectal cancers. This approach allowed us to identify HNPCC families and to estimate the minimal incidence of HNPCC in a Slovenian population based solely on molecular genetic analysis.

Primary colorectal adenocarcinomas and corresponding normal tissue samples were collected from patients who gave consent for testing of their DNA. Between 1996 and 1998, 300 newly diagnosed CRC patients from clinics all over Slovenia participated in this study. The sample of CRC is thus representative for the Slovenian population. All samples were gathered in a central institution where two physicians histologically evaluated each resection for a high proportion of tumour tissue. We also confirmed a high proportion of cancer cells versus normal cells in tumour tissue in many samples that exhibited LOH during MSI analysis. Normal colorectal mucosa taken from a site distant from the tumour was used as a normal control in the study.

We isolated DNA after tissue digestion using standard phenol/chloroform extraction and ethanol precipitation from frozen colorectal tumours and corresponding normal tissue samples. For MSI analysis of tumour and control...
Table 1 Pathogenic germline hMLH1 and hMSH2 mutations identified in high MSI tumours

<table>
<thead>
<tr>
<th>Gene and patient</th>
<th>Exon</th>
<th>Nucleotide change</th>
<th>Consequence</th>
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<td>2</td>
<td>199 G→A</td>
<td>G67R</td>
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<td>15</td>
<td>1684 C→T</td>
<td>Q562X</td>
<td>This study</td>
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<td>1964 T→C</td>
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<td>hMSH2</td>
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<tr>
<td>OG/97-2426</td>
<td>3</td>
<td>561 del TGAGGCTCT</td>
<td>In frame del of codons 188-190</td>
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For mutational analysis of hMLH1 and hMSH2 mismatch repair genes (MMR), we used PCR/non-isotopic conformation analysis (article in preparation). The basic principle of this method is a combination of three analyses which are all based on changes in three dimensional DNA structures, that is, single strand conformation analysis (SSCA), heteroduplex analysis (HA), and double strand conformation analysis (DSCA). We conducted them simultaneously on the same thin polyacrylamide gel.

Altogether, of 300 randomly collected primary colorectal tumours, 29 (9.7%) were classified as high MSI tumours and 23 (7.7%) as low MSI tumours. The use of BAT26 only has been previously proposed for determination of high MSI status. Our results show that using BAT26, D2123, BAT25, and D5S346, respectively. In this case, tumour tissue was scored as high MSI if at least two of four markers were altered.

In total, we tested the majority of samples with the following markers: mononucleotides BAT26, BAT25, BAT40, dinucleotides D2S123, D5S346, TP53, D11S1294, D112179, D17S250, D18S85, and D18S69, and tetranucleotide MYCLY. Tumours were scored as high MSI if more than 40% of tested markers were positive and were scored as low MSI if less than 20% of tested markers were positive. During the analysis, it turned out that for determination of high MSI status four selected markers were sufficient, BAT26, D2123, BAT25, and D5S346. Therefore, we analysed additional samples in multiplex PCR reactions for microsatellite markers BAT26 and D2123, and BAT25 and D5S346, respectively. In this case, tumour tissue was scored as high MSI if at least two of four markers were altered.

MSI analysis was performed as previously described. Briefly, after PCR amplification products were run on a thin (0.4 mm) denaturing polyacrylamide gel matrix fixed on one of the glass plates followed by an optimised silver staining protocol that markedly improved the resolution. MSI was detected as some additional bands in tumour DNA compared to control DNA (fig 1A).

For mutational analysis of hMLH1 and hMSH2 mismatch repair genes (MMR), we used PCR/non-isotopic conformation analysis (article in preparation). The basic principle of this method is a combination of three analyses which are all based on changes in three dimensional DNA structures, that is, single strand conformation analysis (SSCA), heteroduplex analysis (HA), and double strand conformation analysis (DSCA). We conducted them simultaneously on the same thin polyacrylamide gel.

Altogether, of 300 randomly collected primary colorectal tumours, 29 (9.7%) were classified as high MSI tumours and 23 (7.7%) as low MSI tumours. The use of BAT26 only has been previously proposed for determination of high MSI status. Our results show that using only this marker we would have missed one of 29 high MSI tumours. In the other hand, no low MSI tumour was positive for BAT26 or BAT25.

Genomic DNA from 29 subjects with high microsatellite instability tumours were further analysed for the presence of germline mutations in two MMR genes. The whole coding regions as well as all exon/intron boundaries of hMLH1 and hMSH2 were tested with PCR/conformational analysis. We observed 17 different aberrant gel migrations in 29 DNA samples from patients with high MSI tumours. All 17 alterations were detected as single stranded conformational polymorphisms, one sample also showed altered double stranded conformation, and in two samples heteroduplexes were also formed. Eleven alterations were in hMLH1 and six in hMSH2. Sequencing showed four presumably pathogenic mutations, three in hMLH1 and one in hMSH2 (table 1). A new polymorphism IVS9+10A>G in hMLH1 (allele frequency 0.02) has also been detected (fig 1B, C).

Mutations G67R and I655T in hMLH1 have been previously reported in connection with hereditary bowel cancer, while Q562X has been detected for the first time among Slovenian patients with high MSI CRC tumours. We also detected a germline deletion of three consecutive amino acids from 188-190 in hMSH2 in a person with a high MSI tumour (OG/97-2426-T). The same mutation was previously found in a Slovenian patient (HNPCC-8-2B) with a family history of CRC. Although these two patients live in different parts of Slovenia and have different family names, a retrospective pedigree search showed common roots two generations back and resulted in the identification of an extensive Slovenian HNPCC pedigree (fig 2). Similarly, other patients with germline mutations were contacted for their family history. All patients with germline mutations accessed via MSI analysis had at least one first degree relative with HNPCC associated cancer.

In this study, we used a molecular genetic approach for identification of HNPCC families. Our approach was based firstly on microsatellite instability (MSI) analysis of newly diagnosed randomly collected CRC and subsequently on mutational analysis of mismatch repair genes (MMR) in MSI positive tumours. We used a solely molecular genetic approach for detecting HNPCC families because (1) a considerable proportion of germline MMR mutations were found in patients from families not fulfilling the Amsterdam criteria, and (2) access to well organised cancer registries is not available in many countries. In Slovenia, a cancer registry exists but it does not contain family data. No specialised registries for hereditary forms of cancer are available. In our first attempt to identify Slovenian HNPCC families, 600 colorectal cancer patients were questioned for their family history data. A total of 44 patients reported at least one first degree relative with CRC and 16 families agreed to contribute blood samples for DNA analysis. Germline mutation was detected in one family only. This approach...
showed some inaccuracy of data obtained directly from patients and suggested that epidemiological studies of HNPCC incidence based on patients' answers should be treated with caution.

With a molecular genetic approach, we found germline mutations in four out of 300 newly diagnosed colorectal cancers. These four alterations are unambiguously pathogenic mutations; one is a deletion, one is nonsense, and two are missense mutations. Two mutations are so far specific for Slovenian families: a deletion of codons 188-190 in exon 3 of hMSH2 (fig 2) and a C to T substitution in exon 15 of hMLH1 resulting in a stop codon at 562. A substitution of Ile to Thr at codon 655 detected in a patient OG/97-3941 was previously reported in a patient with gastric carcinoma. Interestingly, also, Slovenian patient OG/97-3941 had a metastatic gastric cancer two years after colon cancer. The Ghn to Arg substitution at codon 67 was previously described in a Swedish HNPCC family and its pathogenicity was proved in a functional assay in yeast.

It is possible that we missed some tumours with MMR gene mutation, because we analysed only MSI positive tumours. Cases with MMR mutations without MSI were also reported. However, 1.3% (4/300) tumours with germline MMR gene mutations in the Slovenian population is lower than the 2% observed in a similar study in a Finnish population. If the common ancestral Finnish specific mutation, which accounts for a half of all Finnish HNPCC families, is excluded, the incidence in our country is even higher than in Finland. No comparison with other populations using a similar approach is currently available. Finnish and Slovenian molecular genetic based estimations of HNPCC incidence are considerably lower than the 5-10% estimated in the majority of epidemiological studies. However, Evans et al also reported the incidence of HNPCC to be 1.4%. Their population based study of 1137 consecutive cases of colorectal cancer showed a lower frequency of familial bowel cancer than previous studies and may reflect a lower incidence of inherited mutations in the HNPCC MMR genes than is currently accepted. Since germline mutation in MMR genes is a reliable indicator of HNPCC syndrome, the estimation of incidence of this hereditary disorder in a Slovenian population could be calculated. If we consider 19 000 newborns annually and 850 newly diagnosed colorectal cancer cases annually (of which 1.3% have germline MMR gene mutation), the HNPCC incidence in the Slovenian population is approximately 1 in 1700. However, this estimate represents the absolute minimum. It is possible that we missed some mutations because of technical limitations and because we did not analyse three minor genes (hPMS1, hPMS2, and hMSH6), which are also predisposing factors for HNPCC. Another reason for underestimation of the disease frequency might be that we only search for mutations in patients with colorectal cancer, but this cancer accounts for only approximately two thirds of cancers in HNPCC affected families.

The proportion of patients younger than 50 years in our study was the same as it is for colorectal cancer patients in the complete National Cancer Registry indicating that there was no bias in overestimation according to age.

With molecular genetic analysis of colorectal cancers, we were able to identify Slovenian families with a hereditary form of CRC. Only patients with germline MMR mutations who wished to be acquainted with the results of DNA testing were further contacted by both a gastroenterologist and a geneticist for future medical surveillance and family history data. Some extended HNPCC pedigrees have thus been detected. Through this study, we succeeded in providing more information about the role of molecular genetic analysis to general physicians and HNPCC family members. Presymptomatic DNA testing was offered to well informed and consenting non-symptomatic relatives.

A prevention programme in the sense of periodic clinical examination of relatives with a constitutional mutation has been initiated. In particular, records of young CRC patients have been re-examined for family and clinical data and additional potential HNPCC families have been identified. This enabled us to initiate building of a national HNPCC registry.

We conclude that a molecular genetic approach with evaluated genetic markers for efficient MSI analysis and subsequent MMR gene analysis of patients with MSI positive tumours is valuable for identification and surveillance of HNPCC families and may serve also as a model for detection of familial cases of CRC in other populations.
Does the survival motor neuron protein (SMN) interact with Bcl-2?

Editor—Spinal muscular atrophy (SMA) is an autosomal recessive disease resulting from mutations in the telomeric copy of the survival motor neuron gene (SMN1).\(^7\) which results in reduced expression of the survival motor neuron (SMN) protein.\(^3\) The SMN protein is ubiquitously expressed but is found at high levels in motor neurons.\(^4\)\(^5\)\(^7\) The SMN protein associates with Sm proteins,\(^9\) SIP-1 protein,\(^10\) and itself.\(^11\) SMN is found in structures termed gems that are associated with coiled bodies in the nucleus. The SMN protein is involved in RNA biogenesis\(^10\) and is important for the maturation of a functional snRNP complex that performs splicing.\(^12\) The complete loss of SMN is lethal\(^16\) whereas the low levels of SMN found in SMA cause loss of the motor neurons.\(^11\) The mechanism by which the reduction of SMN protein results in the loss of motor neurones is unknown. Some groups have suggested it occurs by apoptosis.\(^14\) Apoptosis is a conserved, highly regulated mechanism of non-chronic cell death for the removal of surplus, aged, or damaged cells.\(^15\) Apoptosis is regulated by interactions of apoptosis agonists and antagonist with the Bcl-2 protein being one of the key inhibitors of apoptosis.\(^16\) Recently Iwahashi et al.\(^7\) have suggested a direct interaction between SMN and Bcl-2 using transfected constructs. In an effort to confirm and extend their results, we have attempted to coimmunoprecipitate SMN and Bcl-2 both in a native environment and using transfected cells. The SMN protein and Bcl-2 are expressed in Jurkat cells and in spinal cord. Jurkat cells are a human lymphoblast T cell line that has been previously shown to express Bcl-2 and can be induced to undergo apoptosis.\(^16\)\(^18\)\(^20\) Immunoprecipitation experiments were performed using two different methods.\(^17\)\(^22\) Fig 1A shows a western blot of the immunoprecipitation reactions using the method of Iwahashi et al.\(^7\) Jurkat cell lysate was precipitated with anti-SMN (MANSMA2), anti-Bcl-2 (Bcl-2(100)), and anti-dystrophin (MANDYS1) monoclonal antibodies. The precipitated proteins were western blotted and probed with anti-SMN or anti-Bcl-2 polyclonal antibodies. As shown in fig 1A-1, anti-SMN polyclonal antibody MANSMA2 but not in the immunoprecipitation reactions in control individuals and in colorectal tumors with and without replication errors. Oncogene 1997; 15:713-18.


on the transfected cells using an HA epitope monoclonal antibody and the Bcl-2 antibodies described above. The HA antibodies resulted in immunoprecipitation of SMN and not Bcl-2 whereas Bcl-2 antibodies immunoprecipitated Bcl-2 alone (fig 2A). The transfection studies provided no evidence for interaction of SMN and Bcl-2.

Dual labelling of COS-7 cells cotransfected with SMN and HA tagged SIP-1 expression constructs shows SMN and SIP-1 are colocalised as previously reported (fig 2B). Dual labelling of SMN and Bcl-2 using cotransfection of a HA tagged SMN expression construct and a Bcl-2 expression construct failed to show convincing colocalisation of SMN and Bcl-2 in either COS-7 (fig 2C) or HeLa cells (not shown). As seen in fig 2C, in the cotransfected cell Bcl-2 is expressed abundantly throughout the cytoplasm. Similarly, overexpressed SMN is located in the cytoplasm. Even under these conditions of extreme overexpression, there is no clear example of colocalisation, as would be expected if they associate. The apparent association of diffuse staining of SMN and Bcl-2 in the cytoplasm most likely arises from overlapping expression distributions as supported by the immunoprecipitation results.

Although we cannot exclude the possibility that SMN and Bcl-2 interact indirectly with each other in cell death pathways, these results strongly indicate that SMN and Bcl-2 do not directly interact in vivo. It is most likely that the high expression levels in the experiments of Iwahashi et al 17 resulted in artefactual aggregation of Bcl-2 and SMN and that this interaction does not exist in vivo. In order to show clearly a synergistic effect of Bcl-2 and SMN either by direct or indirect mechanisms, it is important to eliminate the possibility that transfection of SMN increases Bcl-2 levels. It appears most likely that the reduction in SMN levels results in inefficient splicing which leads to a reduction or accumulation of a critical product that causes death of the motor neurons.
Figure 2 (A) Immunoprecipitation of transiently transfected HA tagged SMN and Bcl-2 from COS-7 cells. COS-7 cells, transiently cotransfected with Bcl-2 and HA tagged SMN expression constructs, were immunoprecipitated using rabbit anti-Bcl-2 polyclonal (lanes 1–3) and rabbit anti-HA (lanes 5–7) polyclonal antibody as indicated above the blot. As indicated below the blot, lanes 1 and 7 were probed with anti-SMN monoclonal antibody MANSMA2. Lanes 2 and 6 were probed with anti-Bcl-2(100) monoclonal antibody. As seen in lanes 1 and 2, HA-SMN is not coprecipitated when using the anti-Bcl-2 polyclonal antibody. In the reciprocal experiment (lane 5), Bcl-2 is not communoprecipitated with HA-SMN. The middle and lower panels show western blots of the proteins remaining in the supernatants following the immunoprecipitation reactions. These are included to indicate the relative levels of Bcl-2, SMN, and HA-SMN expression in the transfected cells. Additionally, neither SMN nor HA-SMN are depleted from the supernatant incubated with anti-Bcl-2 polyclonal antibody (middle panel), but Bcl-2 is depleted (bottom panel). The reciprocal experiment shows only HA-SMN is depleted by the anti-HA polyclonal antibody (middle panel), but neither SMN nor Bcl-2 (bottom panel) is depleted. (B) Immunofluorescent detection of SMN and HA tagged SIP-1 in transiently cotransfected COS-7 cells. SMN (left panel), indirectly labelled with an FITC conjugated antibody, is located in gems, cytoplasmic particles, and diffusely in the cytoplasm. HA tagged SIP-1 (middle panel), indirectly labelled with TRITC conjugated antibodies, shows a similar distribution pattern. Merging the left and middle images (right panel) clearly shows the association of SMN and SIP1 as previously reported. (C) Dual labelling of HA tagged SMN and Bcl-2 detected with anti-HA polyclonal and anti-Bcl-2 monoclonal antibodies. SMN (left panel), indirectly labelled with an FITC conjugated antibody, is located in gems, cytoplasmic particles, and faint diffuse staining (green indicated by arrows). Bcl-2 (middle panel), indirectly labelled with a TRITC conjugated secondary antibody, is expressed throughout the cytoplasm (red, diffuse fluorescence). In contrast to the SIP-1/SMN merged image above, the merged image (right panel) indicates a lack of colocalisation of SMN and Bcl-2. Methods. COS-7 cells (∼10^6) were seeded onto coverslips and prepared as described previously. Bcl-2(100) and Bcl-2(C21) (Santa Cruz Biotechnology Inc) and anti-HA polyclonal antibody (BabCO) were used at 1/500 dilution. The secondary antibodies, rabbit anti-haemagglutinin antibody conjugated to TRITC (Sigma) and donkey anti-chicken F(ab)2 antibody conjugated to FITC (Jackson Immunoresearch) were used at 1/400 dilution. SIP-1 cDNA was ligated to haemagglutinin (HA) tag and subcloned into the pcDNA3 vector. Bcl-2 was subcloned into pcDNA3 vector. DNA plasmids were prepared for transfection using Endo Free Plasmid Kit (Qiagen). COS-7 cells were transfected with lipofectamine (Life Technologies) according to the manufacturer’s instructions. Images were obtained using a Zeiss microscope equipped with an Optronics colour digital camera using FITC and TRITC/DAPI double pass filters. Total magnification of images is 945×.

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6 Parsons DW, McAndrew PE, Monani UR, Mendell JR, Burghes AHM, Prior TW. An 11 bp duplication in exon 6 of the SMN gene produces a type 1 spinal muscular atrophy (SMA) phenotype; further evidence for SMN as the primary SMA-determining gene. Hum Mol Genet 1996;5:1727–32.
Novel mutations in the homogentisate-1,2-dioxygenase gene identified in Slovak patients with alkaptonuria

EDITOR—Alkaptonuria (AKU, McKusick No 203500), a rare autosomal recessive disorder (1:250 000), is a classical example of a specific biochemical lesion leading to degenerative disease. As a result of deficiency of homogentisic acid 1,2-dioxygenase activity (HGO, EC. 1.13.11.5), AKU patients are unable to degrade homogentisic acid (HGA), an intermediary metabolite in phenylalanine and tyrosine catabolism. Accumulated HGA is excreted into the urine in large amounts, which darkens on standing. Over the years, benzoquinonae acid, an oxidation product of HGA, is deposited in connective tissues, causing their pigmentation (ochronosis), which leads to painful and disabling arthropathy of the large joints and spine (ochronotic arthropathy).

AKU was the first disease interpreted in terms of Mendelian inheritance.1 The HGO gene in humans is located on chromosome 3q21-23.1 13 15 Fernandez-Canon et al6 cloned the human HGO gene and by identifying the first loss of function mutations also provided formal proof that AKU results from a defect in this gene. So far, 24 different mutations have been identified in the HGO gene in patients from various populations.7 Notable exceptions to the low prevalence of AKU in all ethnic groups studied are the Dominican Republic and Slovak patients with alkaptonuria.

Founder effects as the consequence of genetic isolation have been postulated to explain this observation. Here, we present results of mutation screening of the HGO gene in 32 AKU chromosomes carried by 17 Slovak AKU patients (in two families, one chromosome was shared by two patients from different generations). All 14 exons of the HGO gene were amplified from genomic DNA, using PCR primers and conditions as described by Fernandez-Canon et al. PCR products were analysed for the presence of mutations by non-radioactive single strand conformation polymorphism analysis (SSCP).13 DNA was visualised by silver staining essentially as described by Budowle et al.14 Fragments showing SSCP shifts were sequenced directly using the dye terminator cycle sequencing kit (Perkin Elmer) with Taq FS DNA polymerase. Sequences were resolved on an ABI-310 Automatic Analyser.

In our patients, we identified nine different mutations (tables 1 and 2). Four of them were novel mutations, two missense (S47L, G270R), a frameshift (P370fs), and a splice site mutation (IVS5+1G→A), increasing the total number of known AKU causing nucleotide changes within the HGO gene to 28. The remaining five mutations have been described previously: G161R and G152fs,6 P230S and V300G,6 7 and IVS1-1G→A.8 Novel mutation S47L is caused by a transition C→T at the second position of codon 47 (fig 1A). This transition abolishes a restriction site for BsrI in exon 3 PCR fragments. The presence of the S47L mutation in our patient was confirmed by BsrI digestion (fig 2A).

Mutation G270R is caused by transition G→A at the first position of codon 270, which creates a novel EcoNI restriction site (fig 1C). Therefore, its presence in our patients was confirmed by restriction digestion of exon 11 PCR fragments with EcoNI (fig 2B). Glycine at position 270, affected by this mutation, is conserved in man, mouse, and Aspergillus nidulans (fig 3).

Splice site mutation IVS5+1G→A affects the donor splice sites of intron 5 (fig 1B). Interestingly, Beltran-Valero de Bernabe et al identified in one patient from Holland a transversion G→T affecting the same position of intron 5 as our mutation IVS5+1G→A. This mutation, however, was not identified in our patients.

Mutation IVS1-1G→A abolishes restriction sites for Rsal, so the presence of this mutation on one AKU chromosome was confirmed by restriction analysis of the corresponding PCR fragment with this enzyme (fig 2A). A novel P370fs frameshift mutation, caused by a single base insertion c1273insC (fig 1D), brings about a premature translation stop four codons downstream and subsequent

<table>
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<td>S 47 L</td>
<td>Splice sites</td>
<td>c183-1G→A</td>
<td>1 (3.125%)</td>
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<tr>
<td>S 47 L</td>
<td>Splice sites</td>
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<td>1 (3.125%)</td>
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<tr>
<td>G152fs</td>
<td>Frameshift</td>
<td>c621 ins G</td>
<td>8 (25%)</td>
</tr>
<tr>
<td>G161R</td>
<td>Missense</td>
<td>c648 G→A</td>
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<td>V300G</td>
<td>Missense</td>
<td>c1273 ins C</td>
<td>5 (15.625%)</td>
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Table 2 Genotypes of all analysed AKU patients from 15 families indicating identified disease causing mutations within the HGO gene

Patient No Family code | HGO mutations | Allele 1 | Allele 2 |
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<td>ALK17</td>
<td>G152fs</td>
<td>G300G</td>
</tr>
</tbody>
</table>

shortening of translated HGO protein from 445 to 373 amino acids.

The novel mutations were not identified in any of the 50 healthy controls, supporting the evidence that they are disease causing mutations, rather than polymorphisms.

Segregation of all mutations with AKU was confirmed in all families, except for the S47L mutation, where no DNA from family members was available (fig 4). However, serine at position 47 of the HGO protein molecule is conserved in man and mouse (fig 3). In Aspergillus nidulans, threonine is found at this site, which, as well as serine, belongs to the group of hydrophilic amino acids with uncharged polar side chains that are usually on the outside of the protein. Conversely, leucine, which is introduced into the HGO protein by transition $c^{307}C \rightarrow T$, is an amino acid with non-polar side chains that tend to cluster together on the inside of proteins. This indicates that substitution S47L may influence the HGO protein conformation and therefore also affect its function.

Recently, Beltran-Valero de Bernabé et al. provided the evidence that the CCC triplet or its inverted complement (GGG) are mutational hotspots in the HGO gene, because 34.5% (10/29) of HGO nucleotide changes identified so far involve these sequence motifs. Data shown in our report further support their finding, since 55.5% (5/9) of the mutations identified in our patients lie within or are adjacent to these triplets. Taking into account the novel mutations found in Slovak patients and one identified by Felbor et al., the total number of HGO nucleotide variations involving the CCC/GGG motif identified so far can be increased to 38.2% (13/34).

In all 17 analysed Slovak AKU patients, both disease causing mutations were found (table 2). The identification of nine different mutations in this sample was not expected.
because the founder effect had been considered to be the main reason responsible for an increased incidence of AKU in Slovakia. The most frequent mutations, G161R and G152fs (previously identified in two Slovak families by Gehrig et al.), were present on 50% of 32 screened AKU chromosomes (table 1). So far, these mutations have not been identified in any other screened population. This indicates that they might be specific for Slovakia. The high proportion of these two mutations can be explained by founder effect and subsequent genetic isolation. In addition, however, there must have been at least four other founders contributing to the gene pool of the Slovak AKU population (table 1). Three further mutations were each found on only one AKU chromosome, thus indicating that this mechanism is not the only one responsible for the high incidence of this disease in Slovakia (1:19 000).

Possible common origins of chromosomes carrying the same AKU mutations can be further traced by the analysis of DNA polymorphisms in the HGO gene and construction of haplotypes. This work is now in progress.

Figure 3  Comparison of primary structure of homogentisate-1,2-dioxygenase protein from man (HGO, AF000573), mouse (MHGO, U58988), and Aspergillus nidulans (HMGA, U30797) using ClustalX 1.3b. Positions conserved in all three organisms are indicated by (*). Arrows mark sites of identified missense mutations, novel mutations are shown in bold.

Figure 4  Non-radioactive SSCP analysis of exon 13 indicating segregation of mutation P370fs in family ALK5. Arrows mark the SSCP shifts corresponding to this mutation. The presence of the mutation in heterozygous state is indicated by (*). Patients were also heterozygous for mutation G270R (exon 11) (table 2).
Clinical and molecular correlates of somatic mosaicism in neurofibromatosis 2

EDITOR—Neurofibromatosis 2 (NF2) is an autosomal dominant disorder that is characterised by benign nervous system tumours (such as vestibular schwannomas (VSs), intracranial meningiomas, and spinal tumours) and other abnormalities.1 Somatic mosaicism (the presence of a mutation, deletion, or chromosomal abnormality in a subpopulation of somatic cells) is thought to be relatively common in NF2, affecting perhaps 15% of sporadic cases.2

There can be considerable clinical variability in mosaics because somatic mutation can occur at different stages of the postzygotic cell lineage. Evans et al.3 reported the degree of mosaicism for five NF2 patients. Two patients with an estimated <10% of peripheral lymphocytes with mosaicism had ages of onset of symptoms of 41-48 years, while three patients with an estimated 21-44% of affected cells had ages of onset of symptoms of 21-28 years. This is consistent with a relationship between degree of mosaicism and disease severity, although there are too few patients to draw firm conclusions.

Few NF2 somatic mosaics have been reported, and clinical and molecular differences between mosaics and sporadic non-mosaic NF2 patients have not been quantified. To examine this question, we compared somatic mosaic and sporadic non-mosaic NF2 patients selected from NF2 populations in the United Kingdom (341 patients)4,5 and Germany (118 patients).6 The study groups included 13 previously identified somatic mosaic patients3 and 86 sporadic non-mosaic NF2 patients, all of whom had head and spine gadolinium enhanced magnetic resonance imaging. Sporadic NF2 patients were defined as non-mosaic if they had identified germline NF2 mutations with normal strength gel bands. In theory, somatic mosaic patients could have near normal band strength, but in practice band strength will be reduced when <50% of peripheral lymphocytes have NF2 mutations.2 Clinical data were not available in sufficient detail to determine if the distribution of lesions was non-uniform, which could result from somatic mosaicism.

The covariates that were examined were age at onset of symptoms, age at diagnosis, number of VSs (none or unilateral versus bilateral), presence and number of intracranial meningiomas, presence of spinal tumours, and germline NF2 mutation type (frameshift or nonsense versus other identified mutations). In univariate analyses, the two tailed test was used for continuous variables and the two tailed Fisher exact test for binary variables. Multiple logistic regression was then used to examine the association between somatic mosaic status and covariates that differed between groups; interaction terms of age with number of tumours were also considered.

The characteristics of somatic mosaics and sporadic non-mosaics are compared in table 1. Age at onset of

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**Table 1 Characteristics of somatic mosaic and sporadic non-mosaic NF2 patients**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Somatic mosaic</th>
<th>Sporadic non-mosaic</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>No of patients</td>
<td>13</td>
<td>86</td>
<td></td>
</tr>
<tr>
<td>Age at onset of symptoms, years, mean (SE)</td>
<td>26.5 (2.4)</td>
<td>18.7 (1.1)</td>
<td>0.012</td>
</tr>
<tr>
<td>Age at diagnosis, years, mean (SE)</td>
<td>33.6 (2.7)</td>
<td>24.7 (1.3)</td>
<td>0.013</td>
</tr>
<tr>
<td>Germline mutation type (%)</td>
<td></td>
<td></td>
<td>0.055</td>
</tr>
<tr>
<td>Frameshift or nonsense</td>
<td>92.3</td>
<td>62.8</td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>7.7</td>
<td>37.2</td>
<td>0.391</td>
</tr>
<tr>
<td>Vestibular schwannomas (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>None or unilateral</td>
<td>30.0</td>
<td>12.9</td>
<td></td>
</tr>
<tr>
<td>Bilateral</td>
<td>70.0</td>
<td>87.1</td>
<td>0.733</td>
</tr>
<tr>
<td>Spinal tumours (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>30.8</td>
<td>24.4</td>
<td></td>
</tr>
<tr>
<td>Present</td>
<td>69.2</td>
<td>75.6</td>
<td></td>
</tr>
<tr>
<td>Intracranial meningiomas (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>46.2</td>
<td>41.9</td>
<td></td>
</tr>
<tr>
<td>Present</td>
<td>53.8</td>
<td>58.1</td>
<td></td>
</tr>
<tr>
<td>Intracranial meningiomas, number, mean (SE)</td>
<td>1.5 (1.0)</td>
<td>1.5 (0.2)</td>
<td>0.993</td>
</tr>
</tbody>
</table>

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§E KÁDAŠI*
symptoms, age at diagnosis, and the distribution of germ-line NF2 mutation types were significantly different between the two groups. On average, somatic mosaics were 7.8 years younger than non-mosaics at onset of symptoms (p=0.012) and 8.9 years younger at diagnosis (p=0.013). Nonsense or frameshift mutations were identified in 92.3% of somatic mosaics, compared to 62.8% of non-mosaics (p=0.055). The prevalence of no VSs or unilateral VSs was higher in mosaics than in non-mosaics (30.0% versus 12.9%), but this difference was not statistically significant. The prevalence and number of other central nervous system tumours were similar in the two groups.

Since age at onset of symptoms and age at diagnosis were highly correlated ($r^2=0.65$, $p=0.001$), age at diagnosis was used in the multiple logistic regression model because tumour burden was evaluated at diagnosis. In the multiple logistic regression model, age at diagnosis and germline NF2 mutation type were significantly associated with somatic mosaic status and number of VSs was of marginal statistical significance. Interaction terms were not statistically significant. Patients with frameshift or nonsense mutations had 23.1-fold greater odds of somatic mosaic than patients with other types of identified mutations (95% confidence interval 1.7-316.4, $p=0.019$). This may be a bias that results from milder disease in somatic mosaic patients and more severe disease in NF2 patients with nonsense or frameshift mutations, so that somatic mosaic NF2 patients with nonsense or frameshift mutations are more likely to be clinically detected as having NF2.

The odds of somatic mosaic increased 11.1-fold per decade increase in age at diagnosis (95% confidence interval 10.3-11.8, $p=0.004$). Patients with no VSs or unilateral VSs were 7.1-fold more likely to be mosaic (95% confidence interval 1.0-53.7, $p=0.056$). Considering two sporadic NF2 patients (one 40 years old at diagnosis with a unilateral VS and another 20 years old at diagnosis with bilateral VSs, both with no-truncating mutations), the former patient has 157.6-fold greater odds of being a somatic mosaic than the latter patient.

This study is based on relatively few mosaic patients, but if substantiated by other studies, these findings may be a useful adjunct in identifying somatic mosaics. For example, sporadic NF2 patients who are >40 years old at diagnosis with no VSs or unilateral VSs could be evaluated for somatic mosaicism. This is an unusual clinical presentation in NF2, occurring less frequently than the estimated 15% prevalence of somatic mosaicism in sporadic NF2 cases. In the United Kingdom NF2 patient series, nine of 206 sporadic patients (4.4%) meet this description. These patients include only one previously identified somatic mosaic; the rest have unidentified germline NF2 mutations. The eight patients with unidentified mutations have ages at onset of symptoms ranging from 29-45 years (median 36 years) and ages at diagnosis ranging from 42-59 years (median 48 years). We are currently analysing tumours from these patients to determine the proportion that are mosaic.

We thank the NF2 patients and their families for participating and Drs L Kluwe, V F Mautner, and J M Friedman for helpful comments.

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Many ΔF508 heterozygote neonates with transient hypertrypsininaemia have a second, mild CFTR mutation


EDITOR—Mutations of the cystic fibrosis transmembrane conductance regulator (CFTR) gene have an extremely wide phenotypic spectrum.1 The “classical” severe form of cystic fibrosis (CF) is characterised by pancreatic insufficiency and chronic endobronchial infection.2 Milder forms may show no CFTR protein, such as truncating mutations, or those, such as ΔF508, which result in mislocalisation of the protein, result in a severe phenotype with pancreatic insufficiency. Missense mutations, particularly in the transmembrane domains, result in a milder, more variable disease.3,4 11 12 The sweat test, long regarded as the gold standard diagnostic test for cystic fibrosis, may give normal results in these milder forms.

Neonatal screening for CF relies on an increased immunoreactive trypsinogen (IRT) concentration in blood of affected babies during the first two months of life.13 However, this method has low specificity, particularly with samples taken in the first week of life, so mutation analysis is increasingly being used as a second tier. In the Trent region of the United Kingdom (UK), where ΔF508 accounts for over 80% of CF mutations, we currently use a three stage IRT-DNA-IRT protocol, which has a low requirement for second blood samples and for sweat testing.14 Any initial blood sample with IRT readings above the threshold is analysed for the ΔF508 CFTR mutation. Subjects who are heterozygous for ΔF508 are resampled at 27 days; if the IRT level is again above the threshold the child is referred for sweat testing. The families of heterozygous neonates...
than in non-
transient hypertrypsinaemia born between April 1991 and
November 1996 were available for testing.15 All had exceeded the IRT cut off value for the 6th day blood sample (usually 90 ng/ml but adjusted periodically to select approximately 0.5% of tested babies) and had an IRT concentration below 80 ng/ml in the 27th day sample. Cases with meconium ileus were excluded. There was a sample available from every subject fulfilling the selection criteria with meconium ileus were excluded. There was a sample available from every subject fulfilling the selection criteria. In addition, three transiently hypertrypsinaemic babies who would otherwise have qualified for the cohort had already been identified as compound heterozygotes for AF508/R117H CF mutations through extended mutation analysis of their parents. DNA for PCR was obtained from the blood spot by elution in 100 µl of 50 mmol/l NaOH for 30 minutes at room

with a second IRT level below the threshold are referred for genetic counselling on the assumption that such neonates are unaffected carriers.

It has previously been shown that neonates with transient hypertrypsinaemia carry the AF508 mutation at a higher frequency than the general population.16 Additionally, IRT remains on average higher in the repeat blood sample in babies who are heterozygous for AF508 than in non-AF508 babies.17 Thus, it is possible that a proportion of infants with transient hypertrypsinaemia and AF508 may have a second (mild) CF mutation. We have examined this hypothesis in a cohort of infants assessed through the Trent (UK) neonatal screening programme.

A cohort of 88 AF508 heterozygous neonates with transient hypertrypsinaemia born between April 1991 and
Intron 19 used non-denaturing electrophoresis on 8% polyacrylamide gels in 1× TBE. Any samples displaying shifts (indicative of a sequence alteration) were investigated further by direct DNA sequencing (as per manufacturer’s instructions). This methodology identified the putative intronic variant poly-T tract, IVS8-nT, which interacts with the R117H mutation. The IVS8-5T allele was present in three of the 91 neonates, none of whom were identified as being compound heterozygotes for a second CF mutation. The 7T variant from the cohort have already presented with symptoms of lung disease. An increased frequency of the IVS8-5T variant from the cohort have already presented with symptoms of lung disease. 

### Compound heterozygotes detected

<table>
<thead>
<tr>
<th>Domain and mutation type</th>
<th>Genotype</th>
<th>Exon</th>
<th>1st IRT</th>
<th>2nd IRT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transmembrane, missense</td>
<td>ΔF508/P67L</td>
<td>3</td>
<td>129</td>
<td>34*</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117H</td>
<td>4</td>
<td>110</td>
<td>21*</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117L</td>
<td>4</td>
<td>84</td>
<td>34</td>
</tr>
<tr>
<td></td>
<td>ΔF508/ΔF508</td>
<td>4</td>
<td>95</td>
<td>39</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117H</td>
<td>4</td>
<td>104</td>
<td>40</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117L</td>
<td>4</td>
<td>146</td>
<td>41</td>
</tr>
<tr>
<td></td>
<td>ΔF508/ΔF508</td>
<td>4</td>
<td>104</td>
<td>48*</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117H</td>
<td>4</td>
<td>129</td>
<td>53</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117L</td>
<td>4</td>
<td>111</td>
<td>54</td>
</tr>
<tr>
<td></td>
<td>ΔF508/ΔF508</td>
<td>4</td>
<td>175</td>
<td>72*</td>
</tr>
<tr>
<td></td>
<td>ΔF508/R117L</td>
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<td>70</td>
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<tr>
<td></td>
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<td>15</td>
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<tr>
<td></td>
<td>ΔF508/F1052V</td>
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<td>189</td>
<td>29</td>
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<tr>
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<td>17b</td>
<td>94</td>
<td>18</td>
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<tr>
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<td></td>
<td>ΔF508/R851X</td>
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<td>112</td>
<td>76</td>
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<tr>
<td>Alternate splice site</td>
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<td></td>
<td>ΔF508/3849+10KB C→T</td>
<td>19</td>
<td>99</td>
<td>26*</td>
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<td></td>
<td>ΔF508/3849+10KB C→T</td>
<td>19</td>
<td>112</td>
<td>36*</td>
</tr>
</tbody>
</table>

None of these samples had the IVS8-5T variant sequence.

*These patients have presented with symptoms of lung involvement.

Fig 1 shows the range of second IRT reading displayed by non-ΔF508 babies, the putative ΔF508 heterozygotes, and the compound heterozygotes. The IRT distributions of the putative ΔF508 heterozygotes (19) and particularly the compound heterozygotes are shifted to the right. Forty one percent of ΔF508 heterozygote neonates with >25 ng IRT/ml in the 27th day blood sample possessed a second mutation compared to ~6% for those with <25 ng/ml, an enrichment factor of 2.35.

Recent work has suggested that “polyvariant mutant CFTR genes” may, when combined, result in less functional or pathologically insufficient CFTR.21 In the light of this, we determined the incidence of the intronic poly-T tract, IVS8-nT, which interacts with the R117H mutation. The IVS8-5T allele was present in three of the 91 neonates, none of whom were identified as being compound heterozygotes for a second CF mutation. The 7T variant from the cohort have already presented with symptoms of lung disease. In addition, there are data on phenotypic presentation. In general, the severity of lung disease is less predictable than the degree of pancreatic involvement.22

Amplified fragments were screened for sequence alterations by single stranded conformational polymorphism analysis (SSCP)/heteroduplex analysis (HA) using standard conditions and procedures as in table 1 with 14% v/v (59:1 acrylamide:bisacrylamide) polyacrylamide gels and electrophoresis at 12°C in 0.5 × TBE except exon 11, which used a 14% (37:1 acrylamide:bis polyacrylamide gel. Intron 19 used non-denaturing electrophoresis on 8% (29:1 acrylamide:bis) polyacrylamide gels in 1× TBE. Any samples displaying shifts (indicative of a sequence alteration) were investigated further by direct DNA sequencing (as per manufacturer’s instructions). This methodology identifies >95% of all mutations in our laboratory.

Second mutations were identified in 20 subjects (table 2) giving a compound heterozygote frequency of 22%. R117H was the most common second mutation found, constituting 45% of the compound heterozygotes identified. In this study, we have confirmed that the combination of heterozygosity for ΔF508 and persisting mild hypertrypsinemia in the newborn period carries a substantial risk of that infant having a second CF mutation. In addition, the concentration of IRT in whole blood at 27 days is a biochemical marker to refine this risk further.

All the mutations found in our cohort have been reported previously and for the more common ones there are data on phenotypic presentation. In general, the severity of lung disease is less predictable than the degree of pancreatic involvement.22

Figure 1. Distribution of immunoreactive trypsin concentrations in 27th day blood spots. The data from the non-ΔF508 sample have been normalised to the number of ΔF508/N samples.
described to define genotype-phenotype correlations. The missense mutation F693L is located in the regulatory domain of CFTR and was first identified in a young girl with AF508 on her other allele who was diagnosed with pancreatic insufficient cystic fibrosis.28

Three subjects had nonsense mutations which are normally associated with severe disease as they introduce a stop codon, leading to truncated, usually inactive, CFTR protein being transcribed.

The 3849+10 kb C→T mutation, identified in two subjects in our cohort, activates a partially active, cryptic splice site within the intron that causes an 84 bp “exon” to be inserted, in frame, within exon 19.27 Homozygotes for this mutation usually have relatively mild lung disease, while compound heterozygotes may show pancreatic insufficiency and may have more severe lung disease.

Compared to other neonatal metabolic screening tests, that for CF has a relatively low sensitivity; the more successful programmes detect approximately 90% of severe, “classical” CF.25 With the increasing recognition of milder forms of CFTR deficiency, and the tendency to use DNA analysis rather than the sweat test as the ultimate diagnostic arbiter, the perceived effectiveness of neonatal screening is being further eroded. Nevertheless, provided that the prime aim of the programme remains the detection of classical cystic fibrosis, in the way the term was understood 10 years ago, performance using either a two stage IRT method or one of the newer IRT-DNA protocols may be regarded as acceptable.

The difficulties with DNA based protocols arise from the need to provide explicit counselling to families where the baby has been found to be heterozygous for AF508 but has given a normal sweat test or had a normal IRT concentration in a second blood sample. In most screening programmes more babies will fall into this group than will be diagnosed with classical cystic fibrosis (representative figures are given in reference 15). The present study shows that such babies, particularly the subgroup with IRT in the second blood sample >25 ng/ml, have a high likelihood of a second CFTR mutation. Should further testing of AF508 heterozygotes be restricted to mutations associated with a severe phenotype or should extended mutation analysis, at least in the higher risk group with second IRT >25 ng/ml, become part of routine investigation? Would such investigation improve the accuracy of counselling of such families?

The majority of compound heterozygotes detected in this study have mutations usually associated with milder forms of CFTR disease. However, some of our hypertrypsinaemic cohort have genotypes previously reported in severe forms of CF and may be regarded as having given false negative screening test results. Genotype-phenotype correlation is complicated by the existence of polyvariant CFTR genes and modifier polymorphisms,29 as well as possible modifiers at other loci. It is probably unsound to extrapolate data from clinically selected cases to a cohort which was selected on an entirely different basis. The clinical significance of compound heterozygosity detected through neonatal screening will only become apparent through systematic follow up. Preliminary indications are that some of the expected mild cases develop significant early symptoms, six of the compound heterozygotes in our cohort (indicated in table 2) were unblinded by being diagnosed with cystic fibrosis, enabling them to be followed forwards from their neonatal screening results. All have developed symptomatic respiratory infections associated with positive bacterial cultures. A prospective study is under way to determine the clinical spectrum present in such compound heterozygotes.

It is generally agreed that diagnosing adult onset disease during childhood is undesirable if there is no effective preventive treatment. One would not normally wish to predict fertility problems in an otherwise healthy male neonate. However, in so far as early active treatment can reduce the impact of lung disease in moderate CFTR deficiency, previous warning that a child is thus predisposed would be valuable. Thus, the increased possibility of mild CF spectrum disease should be raised during counselling for AF508 heterozygosity detected on newborn screening. There may be a case for more active clinical follow up, particularly in the persistent mild hypertrypsinaemia group. However, until we are more confident in predicting outcome from genotype, the prospective identification of “milder” mutations should not be included in routine neonatal screening protocols.

The support of the Sheffield Children’s Hospital Research and Development Fund and the Cystic Fibrosis Trust (UK) is gratefully acknowledged.

8 http://www.genet.sickkids.on.ca/cftr/.
Further evidence for genetic heterogeneity of autosomal dominant disorders with accumulation of multiple deletions of mitochondrial DNA

EDITOR—Disorders of oxidative phosphorylation are highly heterogeneous from both a clinical and a genetic point of view. The nuclear as well as the mitochondrial genomes contain genes that are necessary for respiratory chain function. Consequently, different modes of inheritance are encountered in disorders of oxidative phosphorylation.

Single large scale deletions of mitochondrial DNA (mtDNA) usually occur in sporadic cases. However, multiple deletions of mtDNA also occur in autosomal dominant disorders. These deletions are generated de novo as somatic mutations in each affected subject. The nuclear gene defects predisposing to secondary mtDNA deletions in these patients remain unknown.

The disorder discovered by Zeviani et al was later found in several families and was called autosomal dominant progressive external ophthalmoplegia (ADPEO), as ptosis and external ophthalmoplegia are the major clinical findings. More generalised weakness of the skeletal muscles and sudden unexpected death are also common clinical features. Additional features vary among different families.

Linkage analysis provided direct evidence for genetic heterogeneity of ADPEO. One locus predisposing to ADPEO in a Finnish family was assigned to chromosome 10q23.3-q24.3. Another locus was assigned to chromosome 3p14.1-p21.2 in three Italian families. In another Italian ADPEO family the disorder is linked to chromosome 4q34-q35.

Figure 1 Pedigree of the autosomal dominant Belgian PEO family. Filled symbols indicate affected subjects. Subjects III.5 and III.7 had multiple mtDNA deletions on Southern blots of DNA isolated from skeletal muscle biopsies. Open symbols indicate healthy subjects. A plus sign (+) denotes subjects from whom DNA samples were available for genetic analysis. The proband is indicated by an arrow.

We previously reported three unrelated Belgian families with progressive external ophthalmoplegia and multiple deletions of mtDNA. Only one of these families was of sufficient size to examine cosegregation of PEO with the known loci on chromosomes 10q, 3p, and 4q.

Fig 1 shows the updated pedigree of the Belgian PEO family. Several male to male transmissions indicate clear autosomal dominant inheritance. The diagnosis of ADPEO was based on the clinical symptoms and the presence of multiple mtDNA deletions on Southern blots of muscle biopsy specimens in two patients. The detailed clinical features and the muscle biopsy findings with mtDNA analysis have been described elsewhere.

Blood samples were obtained after informed consent. The primer sequences for the polymorphic DNA markers on chromosomes 3, 4, and 10 were obtained from the Genome Database (http://gdbwww.gdb.org). The linkage analysis was carried out by MLINK 5.1 using a disease gene frequency of 1/10 000. Since variable penetrance of the disease was shown in the 10q linked Finnish family, only affected subjects were included in our linkage analyses. Subjects were considered affected when clinical examination showed PEO and absent Achilles tendon reflexes (fig 1). Dead, but not clinically examined subjects were considered affected if there was a positive family history obtained from relatives and the appearance of PEO in photographs.

The average expected maximum lod score in computer simulation analysis was 1.5, assuming a 80% informative linked marker at 5% recombination distance from the PEO gene. In 500 simulated replicates, the maximum lod score obtained was 3.60. Linkage analysis excluded all three known loci (table 1). Few markers generated minor positive lod scores (Z) of 0.5 to 1 at large recombination distances (0), but flanking markers and haplotype analysis clearly excluded the candidate regions.

Our data provide further evidence for the genetic heterogeneity of autosomal dominant PEO, indicating that
Liebenberg syndrome: brachydactyly with joint dysplasia (MIM 186550): a second family

Editor—In 1973, Liebenberg described a five generation pedigree with unusual anomalies of the elbows, wrists, and hands and autosomal dominant inheritance (MIM 186550). The same family was re-examined in 1985 by Beighton with corroboration of the distinctive phenotype. The most prominent features were dysplasia of all the bony components of the elbow joint, abnormally shaped carpal bones, and brachydactyly. Since then, no other families have been described.

We report on a mother and two sons whose clinical and radiological features closely resemble those of Liebenberg syndrome.

The pedigree of our patients is showed in fig 1. When last examined, the two affected children, III.4 and III.5, were 3 years and 1 year old, respectively. Their older sister, III.3, was aged 6 and was thought to be unaffected. The affected mother, II.2, was 33 and her husband, II.3, 36 years old and were healthy and non-consanguineous. The mother’s parents, I.1 and I.2, were said to be unaffected.

Patient III.5 was born at term. Pregnancy and delivery were uneventful. Birth weight was 3800 g, length 50 cm, and head circumference 35 cm. His development...
stones were normal. At 1 year he was able to sit alone and spoke his first words. There were no health problems. His joint anomalies were noticed at birth.

We examined the patient at the ages of 6 months and 1 year. At 1 year weight was 12 kg (>90th centile), height 80.6 cm (>97th centile), and OFC 47 cm (>50th centile). In the “anatomical position”, the elbow joints were slightly flexed and active extension from that position was not possible. Pronosupination was slightly limited. The wrist joints were radially deviated. Flexion, extension, abduction, and adduction at the wrists were somewhat stiff but almost normal in range. The fingers were short and bilateral camptodactyly of the fifth finger was present.

X-rays of the arms, forearms, and hands showed enlarged and poorly modelled distal humeral, proximal radial, and proximal ulnar metaphyses, abnormally long radius and ulna, a very large triquetrum the size of that of a 3 1/2 year old child, and shortness of all the components of the digital rays, but especially marked in the distal phalanges (fig 2). No synostoses were noted. X-rays of the whole skeleton showed no other relevant anomalies.

Patient III.4 was born at term. Pregnancy and delivery were uneventful. Birth weight was 3400 g, length 45 cm, and head circumference 35 cm. Development milestones were normal. He was able to sit alone at 9 months and to walk at 12 months. He spoke his first words at 12 months and the first sentences at 2 years. He had no health problems. His joint anomalies were noticed at birth.

We examined the patient at the ages of 2 1/2 and 3 years. At 3 years weight was 18.5 kg (>97th centile), height was 106 cm (>97th centile), and OFC was 49.6 (>25th centile). Flexion at the elbow joints, radial deviation of the wrists, and limitation in the range of movement at the elbow and wrist joints were slightly more marked than in his younger brother. Brachydactyly, bilateral camptodactyly of the fifth fingers and partial bilateral syndactyly between the second and third fingers were evident. The x-ray features were very similar to those of III.5. The size of the triquetrum was that of an 8 year old child (fig 3). His symptoms improved after one year of physiotherapy.

The mother, II.2, was 33 years old at the time of examination. Weight was 60 kg (>50th centile), height was 165 cm (>50th centile), and OFC was 53 cm (>25th centile). She denied any health problems and was of normal intelligence. Her joint anomalies had been present since birth and she had not noticed any worsening of her symptoms. She had never received any rehabilitation therapy.
In the anatomical position, flexion at the elbow joints was 10° and active extension from that position was impossible (fig 4). Pronosupination was slightly limited. The wrist joints were radially deviated. At the wrist, flexion was limited to about 60° while extension, abduction, and adduction were almost normal. The hands showed brachydactyly and bilateral camptodactyly of the fifth finger (fig 5).

X rays of the arms, forearms, and hands showed enlarged and poorly modelled distal humeral, proximal radial, and proximal ulnar metaphyses, abnormally shaped carpal bones, scaphoid-lunate fusion, large triquetrum, and shortness of all the components of the digital rays, especially marked at the distal phalanges (figs 6 and 7). No synostoses were present. X rays of the whole skeleton showed no other relevant anomalies.

The unusual association of brachydactyly, abnormally shaped carpal bones, and elbow dysplasia in our family and...
that described by Liebenberg in 1973 could be ascribed to the same autosomal dominant clinical condition. Our patients showed only some slight differences from Liebenberg’s family.

In our family, the bony components of the elbow joints were consistently enlarged and poorly modelled. In Liebenberg’s patients the radial head had a “bulbous appearance” while the humeral condyles and the ulnar olecranon and coronoid processes were “underdeveloped”. The large triquetrum and camptodactyly of the fifth fingers, which were described only in the 7 year old child of the family of Liebenberg, were constant findings in our patients. Moreover, patient III.4 had bilateral partial syndactyly between the second and third fingers. Triqueto-pisiform fusion, which was present in all Liebenberg’s patients, was not found in our family. However, since the ossification centre of the pisiform appears at about 10 years, triqueto-pisiform fusion would not be expected to be seen in the children III.4 and III.5. Yet, in the mother, II.2, the fusion is between the scaphoid and lunate.

The differential diagnosis between Liebenberg syndrome and the other skeletal disorders involving elbow dysplasia/carpal synostoses and brachydactyly, such as the syndrome and the other skeletal disorders involving elbow II.2, the fusion is between the scaphoid and lunate.

Prenatal detection of trisomy for the entire long arm of chromosome 7

The patient was delivered by caesarean section at 34 weeks’ gestation to a G1, P0, 15 year old female. She was first seen at 33 weeks’ gestation when a sonogram showed multiple congenital anomalies including severe hydrocephalus, a two vessel umbilical cord, bowed femur, clubbed feet, and dilated kidneys. At birth, the infant was cyanotic with Apgar scores of 3 and 4 at one and five minutes, respectively. She weighed 3000 g and was 41 cm long. Head circumference was 44 cm (average at 34 weeks’ gestation is 31.5 cm). Multiple congenital anomalies were noted in addition to those seen on sonogram and included contractures of both hands and feet, missing digits from the left hand, contorted right hand, bilateral hip dislocation, low set, malformed ears, micrognathia, hypertelorism, and skeletal abnormalities. The extent of the duplication and verification of breakpoints were determined using FISH probes.
At necropsy, additional congenital anomalies were noted, including a dilated, tortuous right ureter with kinking (fig 2). The lungs were markedly hypoplastic with dilated airways and apical blebs. The hydrocephalic brain contained about 500 ml of CSF in markedly dilated ventricles. The mesencephalic aqueduct was markedly stenotic.

Cytogenetic studies on percutaneous umbilical blood sampling (PUBS) obtained at 33 weeks' gestation and cultured fibroblasts obtained from the umbilical cord at birth showed a duplication of the entire long arm of chromosome 7. This was confirmed by a FISH probe for the elastin gene at 7q11.2 (Oncor). Three copies of the FISH probes for the elastin gene and markers at 7q36 were present in each metaphase analysed, indicating that the patient was trisomic for chromosome 7q.

Dual labelled centromere probes for 7 (Oncor) and 15 (Vysis) identified two centromeres each, with the 15 centromere on the derivative chromosome, confirming 7q and 15p breakpoints. The patient's karyotype was 46,XX,der(15)t(7;15)(q11.2;p11.2) (fig 3). The mother's karyotype was normal, 46,XX; however, no sample was available from the father for analysis. A fibroblast cell line established from umbilical cord on the patient is available through Coriell Cell Repositories (Camden, NJ).

Of all previously reported cases of trisomy 7q, there has been only one reported case involving duplication of the entire long arm of chromosome 7; we report the second case. Trisomy 7q produces abnormalities affecting virtually every system in the body including the central nervous system, the face, the musculoskeletal system, the heart, and the genitourinary system, but the combination of specific malformations may vary among patients. Our case showed a number of features similar to the previously reported case of duplication of the whole of 7q by Wahrman et al., including frontal bossing, hypertelorism, low set, malformed ears, short neck, downward slanting palpebral fissures, and skeletal and kidney abnormalities. The features in our case not reported by Wahrman et al. include hydrocephalus, bilateral clubbing fingers, and the combination of specific malformations may vary among patients.

Figure 1 The patient showing the physical features including hydrocephalus, low set ears, micrognathia, deformed hands and feet, hypertelorism, and small mouth.

Figure 2 Dilated, tortuous right ureter with kinking noted at necropsy.

Figure 3 Cytogenetics. (A) Partial karyotype of the patient chromosomes 7 and 15, with the duplicated 7q translocated onto the short arm of chromosome 15 (on far right). (B) FISH confirmation of 7q duplication with three sets of signals for elastin and marker probes, and (C) FISH centromeric probes for 15 (long arrow) and 7 (short arrow). The der(15) is on the far left (long arrow).
of the hands and feet, micrognathia, increased intermammary distance, and pulmonary hypoplasia.

The features in our case were also similar to those described in partial trisomies of 7q. The majority of reports of partial trisomy 7 result from a parental balanced translocation (reciprocal or insertion) or inversion 7. Clinical findings for duplications for 7q22q31, 7q21qter, and 7q32qter have been well accepted as having characteristic abnormalities. Because trisomies of other regions usually involve deletion of another chromosome region owing to missegregation of a balanced translocation or crossing over of an inverted 7, review of cases included those that only contained duplicated 7q material (table 1). Kidney abnormalities and lung hypoplasia have been reported in trisomy 7 and mosaic trisomy 7 cases. We wish to thank Mrs Cindy Cutaneous for her technical expertise.

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Table 1 Clinical characteristics of duplication 7q and trisomy 7

Cockayne syndrome associated with low CSF 5-hydroxyindole acetic acid levels

**Editor**—Cockayne syndrome is a rare, clinically heterogeneous disorder, characterised by severe growth failure, cognitive impairment, characteristic facies, and photosensitivity. In the older patient the face has a characteristic aged appearance with sunken orbits, a relatively large, “beak-like” nose, and narrow mouth and chin. Both the central and peripheral nervous systems are involved in this neurodegenerative disorder with pigmentary retinopathy, delayed nerve conduction velocities, sensorineural hearing loss, progressive spasticity, and cerebellar involvement with dysarthria, tremor, and ataxia. The cerebral histopathological changes most commonly seen are patchy demyelination of the subcortical white matter and microscopic calcifications throughout the central nervous system. Calcification of the basal ganglia may be visible on CT scan. The diagnosis of Cockayne syndrome is made on clinical grounds in association with the failure of RNA synthesis in cultured fibroblasts or lymphoblastoid cells to recover to normal rates after UV-C irradiation. Inheritance is presumed to be autosomal recessive.

Here we report a patient with Cockayne syndrome in whom cerebrospinal fluid 5-hydroxyindole acetic acid was markedly reduced. To date there are no reports of abnormalities of the cerebrospinal fluid neurotransmitters in association with Cockayne syndrome. This finding may provide insight into the pathogenesis of the central nervous system abnormalities. Furthermore we have described the

12 Verma RS, Conte RA, Pitter JH. Tandem duplication of the terminal band of the long arm of chromosome 7 (dir dup(7)(q36→qter)). **J Med Genet** 1992;29:344-5.
patient’s body composition in terms of resting energy expenditure, total body protein, fat, and bone mineral density which are relevant to management of the progressive cachexia associated with this disorder.

The proband, a 16 year old male, is the third child of consanguineous Sri Lankan parents and was born at term with a birth weight of 2722 g. His early expressive speech development was delayed, but gross and fine motor development were within normal limits. He initially presented at 8 years of age with tremor and poor motor coordination. A cerebral CT scan at that time was normal. He was re-evaluated at the age of 14 years. At this time he had an obvious intention tremor, gait ataxia, mild cognitive impairment, bilateral high tone sensorineural hearing loss, and poor growth. His parents reported extreme sun sensitivity, dry skin, and poor sweating in hot conditions.

On physical examination at 14 years, the proband had slightly sunken eyes, thin hair, and dry skin. His speech was slow and mildly dysarthric. His height, 136 cm, and weight, 32 kg, were both below the 3rd centile (50th centile for 9 years) and head circumference, 52.5 cm, was on the 2nd centile (50th centile for 8 years). He had normal secondary sexual characteristics. Neurological examination showed cerebellar dysfunction with a marked, coarse, irregular intention tremor with overshooting, slow fine finger movements, and heel-shin incoordination. His gait was broad based and unsteady with flexed posture and toe walking. Dystonic posturing of his left arm and fingers were noted intermittently. There was minimal involuntary movement at rest. Muscle tone and power were within normal limits. Deep tendon reflexes were brisk, but his plantar reflexes were downward. There was no clinical evidence of peripheral neuropathy. Examination of his cranial nerves showed saccadic hypermetria, but no nystagmus. The pupils were poorly reactive to light and he was unable to converge. On neuropsychological testing there were specific deficits in...
short term memory, abstract reasoning, skills of generativity, and mental flexibility.

A repeat CT scan at 14 years of age showed generalised cerebral atrophy and calcification of the globus pallidus, which on MRI scan presented as decreased signal intensity of the globus pallidus (fig 1). In addition, there was atrophy of the cerebellum, temporal lobe structures, hippocampal formation, and brain stem. The pattern of myelination approximated that of a 12 month old child. Nerve conduction studies showed absent sensory action potentials and moderately slowed motor conduction (29 m/sec at the right common peroneal nerve). There was segmental demyelination and onion bulb formation on sural nerve biopsy.

Other investigations at this time included a full blood count, serum electrolytes, liver function tests, calcium, phosphorus, glucose, parathyroid hormone, copper, caeruloplasmin, 25-hydroxycalciferol, uric acid, cholesterol, triglycerides, thyroid function tests, vitamin A, vitamin D, folate, ferritin, transferrin, lactate, pyruvate, alanine aminotransferase, aspartate aminotransferase, alkaline phosphatase, γ-glutamyl transpeptidase, total bilirubin, direct bilirubin, prothrombin time, activated partial thromboplastin time, fibrinogen, platelet count, serum protein electrophoresis with immunofixation, cryoglobulins, protein electrophoresis, immunoglobulins, lymphocyte subset analysis, CD 4 and CD 8 lymphocyte count, bone marrow examination, lymph node biopsy, gall bladder ultrasound, gall bladder aspiration, renal ultrasound, endocrine assessment, DEXA scan, thyroid ultrasound, parathyroid hormone, calcitonin, and blood gases.

Because of progressive weight loss, the proband was referred for nutritional assessment. The resting energy expenditure measured by indirect calorimetry was 75% of the predicted value, 3856 kJ/24 h, with a predicted resting energy expenditure based on age, sex, height, and weight of 5470 kJ/24 h. The respiratory quotient was 0.89, indicative of appropriate nutritional intake.

Cerebrospinal fluid protein was raised above the normal range on two occasions, 0.76 g/l and 0.65 g/l (normal range <0.3 g/l). Cerebrospinal fluid and plasma lactates were normal. On analysis of cerebrospinal fluid neurotransmitter metabolites, there was a low 5-hydroxyindole acetic acid level, 0.03 µmol/l (normal range 0.13-0.21 µmol/l) and a normal homovanillic acid level with a ratio of 5-hydroxyindole acetic acid:homovanillic acid of 0.1 (normal 0.3-0.8).

Cerebrospinal fluid amino acid levels including tryptophan were normal. Peripheral serotonin levels, urinary 5-hydroxyindole acetic acid, and platelet serotonin were also normal, as were plasma phenylalanine levels and dihydropteridine reductase activity. In view of these findings a primary disorder of central serotonin metabolism was considered and the proband started treatment with 5-hydroxytryptophan, 1 mg/kg/day.

Over a two year period the dose of 5-hydroxytryptophan was gradually increased to 5 mg/kg/day. There was no obvious clinical improvement, but on the other hand, his cognitive function, tremor, and gait have not deteriorated and cerebral MRI scan showed no change. During this period, however, he developed a pigmentary retinopathy, lost 3 kg in weight, and his facial appearance came to resemble a “cachectic bird-nose dwarf” with sunken eyes (fig 2). Despite continued treatment with 5-hydroxytryptophan, cerebrospinal fluid levels of 5-hydroxyindole acetic acid on two further occasions have remained markedly low (0.02 and 0.03 µmol/l).

The clinical diagnosis of Cockayne syndrome was confirmed by survival studies of Epstein-Barr virus transformed B cells after irradiation with UVB (fig 3). These studies show that the proband’s cells were very sensitive to irradiation, with only 1% of cells surviving a dose of 100 J/sq m UVB. In comparison, the normal controls’ cells did not approach 1% survival until irradiated with doses of 250 J/sq m and over. To confirm the Cockayne phenotype further, the rate of RNA polymerase II transcription in the lymphoblastoid cells was compared with control lymphoblastoid cells. The constitutive incorporation of 14C-uridine over 90 minutes was found to be 64 ±2% (n=4) of the control lymphoblastoid cells (after normalisation against thymidine incorporation). This is within the 40-70% range for Cockayne syndrome lines reported by Balaji et al., who also found that xeroderma pigmentosus cells had the same rate of RNA synthesis as controls.

Because of progressive weight loss, the proband was referred for nutritional assessment. The resting energy expenditure measured by indirect calorimetry was 75% of the predicted value, 3856 kJ/24 h, with a predicted resting energy expenditure based on age, sex, height, and weight for healthy children of 5135 kJ/24 h. The respiratory quotient was 0.89, indicative of appropriate nutritional intake.
Figure 4  Synthetic and catabolic pathways of serotonin and dopamine. 5-hydroxyindole acetic acid is formed initially from tryptophan in a reaction catalysed by tryptophan hydroxylase $\alpha$ to form 5-hydroxytryptophan (5HTP), which requires molecular oxygen and tetrahydrobiopterin (BH4) for its activity. 5-hydroxytryptophan is decarboxylated by pyridoxine dependent aromatic L-amino acid decarboxylase $\beta$ to form the active neurotransmitter serotonin. Serotonin is catabolised by monoamine oxidase $\gamma$ to form 5-hydroxyindole acetic acid (5HIAA). Tyrosine is metabolised by tyrosine hydroxylase $\delta$ to L-dopa. Aromatic L-amino acid decarboxylase $\epsilon$ is also required for the decarboxylation of L-dopa to dopamine, which is then catabolised to homovanillic acid by monoamine oxidase and catechol $\beta$-methyltransferase $\zeta$.

Total body protein measured by neutron capture analysis was low for age (65%) but above predicted for weight (112%), height (112%), and lean body mass (108%). Total body bone mineral density measured by dual energy x ray absorptiometry was on the 50th centile for age, 1.141 g/cm$^2$. Total body fat tissue measured by dual energy x ray absorptiometry was 31.2%.

Our patient’s clinical features are consistent with the diagnosis of Cockayne syndrome (table 1). Diagnostic criteria include growth failure after normal or slightly low birth weight, neurological dysfunction with cerebral white matter involvement plus at least three of the following features: cutaneous photosensitivity, progressive pigmentary retinopathy/cataracts, optic disc atrophy, miotic pupils or decreased lacrimation, sensorineural hearing loss, dental caries, short stature, and a characteristic physical appearance of “cachectic dwarfism”. Atypical features in our patient include later age of onset of neurological signs, absence of dental caries, and only mild cognitive impairment. The diagnosis of Cockayne syndrome was supported by finding hypersensitivity to UV light in Epstein-Barr virus transformed lymphoblasts. The pathogenesis of Cockayne syndrome is poorly understood. The cells of patients with Cockayne syndrome are hypersensitive to the lethal effects of UV light because they have a defective subpathway of nucleotide excision repair known as “transcription coupled repair”. Cockayne syndrome is genetically heterogeneous. Two disease genes have been identified, CSB on chromosome 10q11 and the CSA gene maps to chromosome 5. Both proteins play an essential role in preferential repair of transcription blocking lesions from active genes. The CSB protein is a member of the SW12/SNF2 family of ATPases whose function is thought to involve remodelling of protein-DNA interactions, such as chromatin structure in different situations. The CSA gene encodes a “WD repeat” protein.

A unique finding in our patient was very low cerebrospinal fluid 5-hydroxytryptophan (5HTP), normal homovanillic acid levels on three separate occasions. The peripheral serotonin levels were normal. The metabolic pathways of 5-hydroxyindole acetic acid and homovanillic acid are shown in fig 4. The concentrations of 5-hydroxyindole acetic acid and homovanillic acid in the cerebrospinal fluid are thought accurately to reflect the turnover of catecholamine neurotransmitters. The low 5-hydroxyindole acetic acid, in association with normal tryptophan and homovanillic acid in the cerebrospinal fluid and normal peripheral serotonin, is suggestive of low brain serotonin turnover with normal dopamine turnover and may suggest a primary central serotonin deficiency, a selective serotonergic tract degeneration, or an isolated central nervous system tryptophan hydroxylase deficiency. This finding in our patient may provide some insight into the mechanism of the neurological complications and the initiation of Cockayne syndrome given the putative roles of serotonin in control of movement and appetite. We treated our patient with 5-hydroxytryptophan (5 mg/kg/day) in an attempt to increase his cerebrospinal fluid 5-hydroxyindole acetic acid levels, with no change in levels observed. However, from a clinical point of view, he has had no further deterioration in cognitive or neurological function.

The cause of death in the majority of cases of Cockayne syndrome has been secondary to inanition and thus attention to nutrition is essential to patient care and well being. Although our patient was always small for his age, he recently showed accelerated weight loss. In the setting of premature ageing we predicted an increased metabolic rate, but, surprisingly, detailed energy expenditure studies indicated a lowered metabolic rate. This is similar in subjects with anorexia nervosa, whose resting energy expenditure is reduced when compared to healthy, aged matched controls. With re-feeding, however, the resting energy expenditure in anorexia nervosa subjects normalises, with concomitant increases in body weight. It would therefore appear possible to manage Cockayne syndrome patients with programmes that correct the energy deficits, documented by energy expenditure studies. Whether such strategies will prevent deterioration in nutritional status remains to be shown.

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Unilateral lobar pulmonary agenesis in sibs

EDITOR—Pulmonary agenesis is an extremely rare congenital malformation which has been classified morphologically by the extent to which bronchopulmonary tissue is absent. Spencer1 divided pulmonary agenesis into (1) complete bilateral agenesis, (2) unilateral agenesis with (a) complete absence of bronchi, (b) rudimentary bronchus present but no pulmonary tissue, or (c) poorly developed main bronchi with poorly organised parenchyma, and (3) lobar agenesis. The incidence of this rare condition is not established; however, in a review of the paediatric literature, Pulmonary agenesis was documented in less than 50 cases.2


as shown in our patient 1 or in a case with agenesis of the left lung detected at necropsy in a 72 year old woman. Most cases present in the neonatal period with non-specific respiratory symptoms such as cyanosis, tachypnoea, dyspnoea, stridor, or feeding difficulties. Physical examination may be normal, but can show diminished breath sounds on the affected side with the heart and mediastinum shifted to the ipsilateral side. Chest x rays which show a homogeneous density in one hemithorax suggest the diagnosis, but endoscopic, bronchographic, and echocardiographic studies, as well as computerised tomography are necessary for confirmation.

The aetiology of lung agenesis remains unknown. According to the possible associated anomalies, this rare malformation has been discussed as part of the VACTERL association and Goldenhar syndrome. Warkany et al. induced pulmonary agenesis of one lung, but also other major malformations of the eyes and cardiovascular and urogenital systems by maternal gestational vitamin A deficiency in rats. Chromosomes were not studied in the older reports. However, Say et al. described a patient with agenesis of the left lung who had a duplication of the region 2p21→p24 resulting in a partial trisomy 2p and Schober et al. reported a case with left pulmonary agenesis and associated malformations in partial trisomy 2p (p21→pter) and 21q (pter→q21) owing to an unbalanced segregation of a maternal reciprocal translocation t(2;21). The minimal overlapping region of duplication includes the segment 2p21→p24. Therefore, Say and Carpenter suggested studying patients with pulmonary agenesis for the presence of such a duplication. Unilateral agenesis has also been documented in trisomy 18 and in trisomy of a C group chromosome.

Pulmonary agenesis in twins was reviewed by Lehmann. In female monozygotic twins, one sister had agenesis of the left and the other agenesis of the right lung. Yount documented agenesis of the right lung in concordantly affected monozygotic twins, while others found pulmonary agenesis in only one of monozygotic twins. Concordant occurrence of congenital malformations in monozygotic twins does not necessarily imply a genetic cause and vice versa.

The only clear indication of possible autosomal recessive inheritance of unilateral pulmonary agenesis so far was the family reported by Brimblecombe. The healthy parents were first cousins and had two normal children and two affected girls with agenesis of the right upper and middle lobes. Our report is the second case of unilateral lobar pulmonary agenesis in sibs and supports the hypothesis of an autosomal recessively inherited disease. Alternatively, our observation could be explained by an extrinsic origin (infection during pregnancy, drugs, environmental substances, etc), for which, however, we do not have the slightest proof. Further support for the presence of a rare autosomal recessive gene for unilateral pulmonary agenesis comes from the observation of Mardini and Nyhan, who documented parental consanguinity in four patients; two patients had right upper and middle lobe agenesis and two presented with left sided pulmonary agenesis. All had associated congenital heart defects and three infants presented with abnormalities of the thumb. Podlech et al., who observed a family with one healthy and two affected children with bilateral agenesis of the lungs, concluded that an autosomal recessive mode of inheritance could also be valid for bilateral pulmonary agenesis. Embryogenesis of human lung development is poorly understood, but in mice Fgf10 (fibroblast growth factor 10) is an important regulator of limb and lung formation. Homozygous Fgf10 deficient mice die at birth owing to lack of lung development.

In conclusion, our report suggests an autosomal recessive gene or genes which cause pulmonary agenesis with optional heart, kidney, and other defects. In such cases, a 25% recurrence risk should be considered in genetic counselling.

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9 Heerup L. Case of absence of left lung. Hospitalstidende 1927;70:1165.

**Correction**

In the paper by Carroll et al in the February 1999 issue of the journal (J Med Genet 1999;36:94-6), the intronic polymorphism in PTEN was reported as IVS4+109InsACTAA. The correct sequence should be IVS4+109InsATCTT. The authors would like to apologise for any confusion caused by this error.