A frameshift mutation in the gene for PAX3 in a girl with spina bifida and mild signs of Waardenburg syndrome


Abstract
Neural tube defects (NTD) are among the most prevalent congenital malformations in man. Based on the molecular defect of Splotch, an established mouse model for NTD, and on the clinical association between NTD and Waardenburg syndrome (WS), mutations in the PAX3 gene can be expected to act as factors predisposing to human NTD. To test this hypothesis, 39 patients with familial NTD were screened by SSC analysis for mutations in exons 2 to 6 of the human PAX3 gene. One patient with lumbosacral meningomyelocele was identified with a 5 bp deletion in exon 5 approximately 55 bp upstream of the conserved homeodomain. The deletion causes a frameshift with a stop codon almost immediately after the mutated site. Clinical investigation of the index patient indicated mild signs of WS type I. Varying signs of this syndrome were found to cosegregate with the mutation in the family. Our results support the hypothesis that mutations in the gene for PAX3 can predispose to NTD, but also show that, in general, mutations within or near the conserved domains of the PAX3 protein are only very infrequently involved in familial NTD.

SSC ANALYSIS
DNA fragments overlapping exons 2 to 6 of the human PAX3 gene were amplified by the polymerase chain reaction (PCR) from genomic DNA together with 5' and 3' flanking intron sequences. Amplification was carried out in a total volume of 25 μl containing 50 ng of genomic DNA, 0.45 mmol/l of each primer, 0.1 mmol/l dCTP, 0.4 mmol/l dATP, 0.4 mmol/l dGTP, 0.4 mmol/l dTTP, 0.1 μl [α32P]dCTP (Amersham) in PCR buffer (50 mmol/l KCl, 10 mmol/l Tris-HCl, pH 8.3, 1 mmol/l DTE, 0.001% gelatine, 1–5–6 mmol/l MgCl2) with 0.5 U Taq DNA polymerase (Boehringer Mannheim). Samples were denatured at 92°C for five minutes and then subjected to 35 cycles of amplification: 92°C for 30 seconds, 55°C for 50 seconds, 72°C for one minute 30 seconds. Exon 2 was analysed as two partly overlapping fragments. The following primers were used for amplification (fig 1), some of which are identical to those reported by Tassabehji et
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DIRECT SEQUENCING OF NORMAL MUTANT ALLELES

To determine the nature of the shifted bands in the SSC analysis, 4 μl of amplification product was loaded on a 6-6% denaturing polyacrylamide gel. The gel was electrophoresed at 60 W for three hours at room temperature, dried, and exposed overnight to Kodak X-omat S film to visualise the bands. Bands representing wild type and mutant alleles were cut out of the gel. DNA was eluted from each of the gel slices in 50 μl distilled water for one hour at 37°C and reamplified under the conditions described above. Subsequently, the amplified DNA fragments were purified by electrophoresis on a 1% agarose gel (one hour, 10 V/cm), allowed to migrate into ultra low gelling temperature agarose (Sigma), and sliced out of the gel. This material served as substrate for direct sequencing using the Cycle Sequence Kit (BRL) according to the protocol of the manufacturer. Sequences were determined in two directions with the forward and reverse amplification primers after 5' end labelling with 32P.

Results

A PAX3 GENE MUTATION IN A PATIENT WITH SPINA BIFIDA

PAX3 belongs to a family of embryonic transcription factors, which are related by pos-
Figure 2. Molecular analysis of exon 5 of the PAX3 gene. Autoradiographs show the allelic band patterns obtained with (A) SSC analysis and (B) denaturing gel analysis of genomic DNA from two control persons (lanes 1 and 2) and from a patient with spina bifida (lane 3). With DNA from the patient, SSC analysis shows bands with abnormal mobility in addition to the wild type bands, indicating the presence of a heterogeneous mutation in exon 5. On denaturing gel electrophoresis the aberrant allele appears to be of reduced length owing to a deletion.

poplastic nasal alae, a round nasal tip, and smooth philtrum. There is a naevus above the right eye. The palate is high arched and there is dental crowding. Below the spina bifida she has a deep sacral pit. She has no heterochromia irides, no pigmentary disturbances, and no hearing loss.

The mother of the index patient (II.4) has a similar appearance with dystopia canthorum (ICD 41 mm, +97th centile; OCD 85 mm, 25th–50th centile), leading to blepharophimosis, brushy eyebrows, a high nasal root, hypoplastic nasal alae, and a round nasal tip. She has vitiligo of the left hand and wrist. She has no heterochromia irides and no hearing loss.

The maternal grandfather of the index patient (I.2) has heterochromia irides and dystopia canthorum, but no pigmentary abnormalities and no long standing hearing loss. No abnormalities were seen on a photograph of the maternal grandmother (I.1).

The maternal aunt of the index patient (II.1) has no signs of WS. Another sister of the mother (II.3) was born with a lumbar meningocele and hydrocephalus, but died at the age of 6 months without having left the hospital. It is unknown whether she had any sign of WS. No material was saved for genetic analysis.

Several sibs of the index patient III.4, III.8, III.9, and III.10, show the facial characteristics of WS. III.9 was born with a white forelock, which subsequently disappeared, and has unilateral hearing loss. III.8 had poliosis.

These observations show that WS is indeed segregating in this family and that the index patient has a mild expression of this syndrome in combination with spina bifida. Based on the presence/absence of specific symptoms, three subtypes of Waardenburg syndrome are distinguished. WS-I (MIM 193500) and WS-II (MIM 193510) are characterised by the presence or absence of dystopia canthorum, respectively, whereas the disorder is diagnosed as WS-III (MIM 148820) if limb deformities are among the symptoms. Accordingly, the present family can be categorised as having WS-I. So far, WS with NTD patients have only been reported in families with WS type I.

CORRELATION BETWEEN MUTATION AND PHENOTYPE

The pattern of inheritance of WS is compatible with that of an autosomal dominant disorder. To investigate further the relationship between the clinical signs and the mutation discovered in the index patient, exon 5 was amplified from the DNA of all available persons and analysed by denaturing gel electrophoresis. As can be seen in fig 5, there is an exact correlation between the presence/absence of the abnormal allele and the phenotype (Z = +2.40 at θ = 0:0).

Discussion

The association between NTD and WS is well documented. Interestingly, of the 11 patients with NTD and WS reported since 1988, eight represent familial cases of NTD.19-24 This includes the index patient of the present study, who had a maternal aunt with spina bifida. Apparently, there is an increased recurrence risk of NTD in families with WS, which corroborates the common aetiology of both disorders. The molecular defect in two other patients with WS and NTD has previously been reported.12,15 Both cases concern missense mutations in exon 2 changing an amino acid within the paired domain of the PAX3 protein.
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Figure 4 Pedigree of the family with two closely related patients with lumbar meningomyelocoele and hydrocephalus: the index patient II.5 and her maternal aunt II.3. All members were clinically examined for symptoms of WS. Those with a positive diagnosis of WS in addition to the index patient are indicated by shaded symbols.

Figure 5 Co-segregation of the exon 5 deletion with symptoms of WS. All available members of the family were analysed for the presence of the mutant allele by PCR amplification of exon 5 and subsequent denaturing gel separation of amplified fragments. All members diagnosed as having WS symptoms appear to carry the mutant allele.

Here we show that mutations disrupting the open reading frame of the PAX3 gene may also be found in patients with WS and NTD.

Despite the fact that carriers of a PAX3 mutation probably have an increased risk for NTD, in the present study only one of 39 patients with familial NTD was found to have such a mutation indicating that, in general, PAX3 mutations are an infrequent cause of familial NTD. However, SSC analysis is not completely sensitive, leaving the possibility that some mutations have not been detected by this method. Further, mutations could be present in exons 1, 7, or 8, which have not yet been examined in detail. Nevertheless, mutations within or near the conserved domains of the PAX3 protein are not likely to play a major role in familial NTD.

Because of the findings in Splotch mice, it is not surprising that NTD may be present in humans carrying a mutation in the PAX3 gene. Homozygous Splotch embryos die on day 13 of gestation and 50% have lumbosacral spina bifida. Heterozygous animals display pigmentedary disturbances, but have a normally closed neural tube, yet breeding experiments have shown that a heterozygous PAX3 mutation influences the incidence of NTD in animals already committed to NTD development.6, 10 Apparently, in those animals the occurrence of NTD depends on a combination of pre-determining factors. A similar situation may exist in humans, where additional factors may modify the phenotypic expression of the same PAX3 mutation in different persons. Spina bifida is not the only malformation of homozygous Splotch embryos. In 50% exencephaly is observed and congenital heart defects also occur, which are regarded as the major cause of death. In humans, exencephaly and congenital heart defects do not seem to be associated with WS but, considering the influence of other genetic factors on the phenotype, it may be worth looking for PAX3 mutations in patients with NTD and congenital heart defects.

The pathophysiological processes leading to NTD in Splotch have not yet been elucidated. Suggested mechanisms include delayed migration of neural crest cells and an abnormal curvature of the caudal region. More likely, these phenomena are secondary to a defect of the neuroepithelium, where the PAX3 gene is expressed before neural tube closure.10 The detection and functional characterisation of PAX3 gene mutations in patients with NTD may help to clarify the pathogenesis of NTD further.

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