A novel duplication in the HOXA13 gene in a family with atypical hand-foot-genital syndrome

L Frisén, K Lagerstedt, M Tapper-Persson, I Kockum, A Nordenskjöld

A genome wide linkage analysis showed evidence for linkage to the short arm of chromosome 7. Sequence analysis of the HOXA13 gene showed a heterozygous 18 bp duplication in the second polyalanine tract, resulting in six additional alanines.

The following mutations in HOXA13 have been found in seven HFGS families: four different nonsense mutations (W369X, S136X, Q196X, and Q365X), one missense mutation (N372H), and two in frame insertions of 24 and 18 bp respectively. In addition, an interstitial deletion removing the entire HOXA cluster was found in the family reported by Devriendt et al.

The insertions are both located in the last of three polyalanine tracts in the first exon and result in additional polyalanines. Similar polyalanine tract expansions have been described in HOXD13 in several families with synpolydactyly. The insertions in HOXA13 and HOXD13 consist of cryptic expansions (GCA, GCC, GCG, GCT) rather than trinucleotide repeats, are stable through generations, and are believed to have originated through unequal crossing over.

Three additional families with atypical features of HFGS have been described. However, there are divergences from the classical description making the diagnosis less probable, as pointed out by Utsch et al. Nevertheless, in the family reported as Guttmacher syndrome also including polydactyly, both a missense mutation in the homeobox region of the HOXA13 gene and a dinucleotide deletion in the promoter was found.

The mutations in HOXA13 and HOXD13, together with a mutation in HOX11 resulting in amegakaryocytic thrombocytopenia and radioulnar synostosis, are the only mutations in Hox genes described in man to date. Characteristically, these abnormalities are discrete and may easily escape medical attention.

We report the identification of a novel mutation in the HOXA13 gene in a six generation family originally ascertained
because of the accumulation of hypospadias, which turned out to be an atypical variant of HFGS.

**MATERIALS AND METHODS**

**Patients**

The family with autosomal dominant inheritance of hypospadias was initially ascertained through the Department of Pediatric Surgery at Astrid Lindgren Children Hospital, Karolinska Hospital as part of an effort to map genes for hypospadias. Clinodactyly and mild foot malformations were present in both sexes (fig 1A). Phenotype information was acquired as described in table 1. We collected peripheral venous blood from available family member and isolated genomic DNA according to a standard protocol. The Ethics Committee at the Karolinska Hospital approved the study.

**Linkage analysis**

A genome wide linkage analysis was performed using 360 microsatellite markers with an average distance of 9.5 cM according to standard procedures. An extended genotyping was subsequently carried out on chromosome 7 with the markers D7S2514, D7S641, D7S2464, D7S664, D7S2557, D7S2508, D7S507, D7S503, D7S488, D7S2551, D7S493, and D7S673. PCR conditions are available on request. PCR

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**Table 1** Phenotype data of affected family members

<table>
<thead>
<tr>
<th>Patient</th>
<th>Sex</th>
<th>Skeletal abnormalities</th>
<th>Urogenital manifestations</th>
<th>Phenotype source</th>
</tr>
</thead>
<tbody>
<tr>
<td>III.3</td>
<td>Male</td>
<td>Clinodactyly, short thumbs, small feet</td>
<td>Glandular hypospadias</td>
<td>IV.4, IV.6, IV.11</td>
</tr>
<tr>
<td>III.4</td>
<td>Male</td>
<td>Clinodactyly, short thumbs, small feet</td>
<td>Glandular hypospadias</td>
<td>IV.4, IV.6, IV.12</td>
</tr>
<tr>
<td>IV.2*</td>
<td>Female</td>
<td>Clinodactyly</td>
<td>Chordee</td>
<td>Interview with spouse</td>
</tr>
<tr>
<td>IV.3</td>
<td>Male</td>
<td>Small feet “without heels”</td>
<td>Chordee</td>
<td>Telephone interview</td>
</tr>
<tr>
<td>IV.5*</td>
<td>Male</td>
<td>Clinodactyly, hallux varus</td>
<td>Glandular hypospadias</td>
<td>Interview with relative</td>
</tr>
<tr>
<td>IV.7</td>
<td>Female</td>
<td>Clinodactyly, hallux varus</td>
<td>Glandular hypospadias</td>
<td>Interview with relative</td>
</tr>
<tr>
<td>IV.9*</td>
<td>Male</td>
<td>Clinodactyly</td>
<td>Glandular hypospadias</td>
<td>Telephone interview</td>
</tr>
<tr>
<td>IV.11*</td>
<td>Female</td>
<td>Clinodactyly, large gap between 1st and 2nd toe</td>
<td>Incontinence</td>
<td>Medical records</td>
</tr>
<tr>
<td>IV.14*</td>
<td>Male</td>
<td>Clinodactyly, small feet</td>
<td>Penile hypospadias, chordee</td>
<td>Interview with spouse</td>
</tr>
<tr>
<td>V.6*</td>
<td>Female</td>
<td>Clinodactyly</td>
<td>Incontinence</td>
<td>Telephone interview</td>
</tr>
<tr>
<td>V.10*</td>
<td>Male</td>
<td>Clinodactyly, large gap between 1st and 2nd toe, short 2nd toe</td>
<td>Glandular hypospadias</td>
<td>Telephone interview</td>
</tr>
<tr>
<td>V.12*</td>
<td>Male</td>
<td>Small feet</td>
<td>Glandular hypospadias</td>
<td>Telephone interview</td>
</tr>
<tr>
<td>V.13*</td>
<td>Female</td>
<td>Small feet</td>
<td>Recurrent urinary tract infections</td>
<td>Telephone interview</td>
</tr>
<tr>
<td>V.22</td>
<td>Male</td>
<td>Clinodactyly, hallux varus, short 2nd toe</td>
<td>Glandular hypospadias</td>
<td>Interview with relative</td>
</tr>
<tr>
<td>V.35*</td>
<td>Male</td>
<td>Clinodactyly, large gap between 1st and 2nd toe, short 2nd toe</td>
<td>Penoscrotal hypospadias, chordee</td>
<td>Examination by authors</td>
</tr>
<tr>
<td>V.36*</td>
<td>Female</td>
<td>Clinodactyly, large gap between 1st and 2nd toe, short 2nd toe</td>
<td>Incontinence</td>
<td>Examination by authors</td>
</tr>
<tr>
<td>V.44*</td>
<td>Male</td>
<td>Clinodactyly</td>
<td>Penile hypospadias</td>
<td>Interview with parent</td>
</tr>
<tr>
<td>VI.3*</td>
<td>Male</td>
<td>Clinodactyly, small feet, large gap between 1st and 2nd toe</td>
<td>Recurrent urinary tract infections</td>
<td>Medical records</td>
</tr>
<tr>
<td>VI.5</td>
<td>Female</td>
<td>Clinodactyly, large gap between 1st and 2nd toe, short 2nd toe</td>
<td>Glandular hypospadias</td>
<td>Examination by authors</td>
</tr>
<tr>
<td>VI.12*</td>
<td>Male</td>
<td>Clinodactyly</td>
<td>Glandular hypospadias</td>
<td>Examination by authors</td>
</tr>
</tbody>
</table>

*DNA analysed from these subjects.
products were separated by electrophoresis on an ABI377 (Applied Biosystems) and genotypes were scored in the GENOTYPER software. All genotypes were checked manually.

Two point linkage analysis was performed using MLINK in the FASTLINK package through the HGMP web site (http://www.hgmp.mrc.ac.uk), assuming an autosomal dominant model with full penetrance and the gene frequency of 0.001.

Sequence analysis of the HOXA13 gene

We used primers described by Kosaki et al., with the exception that primer HOXA13-A67 was shortened with two nucleotides in the 3’ end to eliminate the large difference in annealing temperature between primers HOXA13-A67 and HOXA13-A68. Exon 2 of the HOXA13 gene was amplified using primers HOXA13-ex2fwd (5’-CAGATCGAGCTGTCGCCTA-3’) and HOXA13-ex2rev (5’-TATCTGGGCAAAGCAACGA-3’). PCR reactions were performed in 10 mmol/l Tris-HCl pH 8.3, 50 mmol/l KCl, 2.0 mmol/l MgCl₂, 1.25 U AmpliTaq Gold (Applied Biosystems), 100 µmol/l dNTP (GibcoBRL), 0.1 µmol/l of each primer, and approximately 200 ng of genomic DNA in a total volume of 25 µl. We used the PCRx Enhancer System with 1X Enhancer solution (Invitrogen) when amplifying primers HOXA13-A65 and HOXA13-A66. PCR reactions were cycled in a 10 minute 96°C heat shock step followed by 35 cycles of a 30 second 96°C denaturation step, a 30 second 55-64°C annealing step, depending on the fragment to be amplified, and a two minute 72°C extension step.

DNA sequence analysis was performed on both strands of amplified and purified PCR products using the ABI PRISM BigDye Terminator Cycle Sequencing kit 2.0 (Applied Biosystems). The sequencing reactions were carried out according to the manufacturer’s recommendations and analysed on an ABI310 DNA sequencer.

Nomenclature

Gene symbols used in this article follow the recommendation of the HUGO Gene Nomenclature Committee. Mutations are described according to recommendations by den Dunnen and Antonarakis.

RESULTS

Phenotype in affected family members

The family was originally identified because of the accumulation of hypospadias cases. Several phenotypic features distinguished this family from previously described families with HFGS (see table 1 for phenotype data and figs 2, 3, and 4 for photographs of affected family members). The limb abnormalities in this family were much milder and restricted to clinodactyly of the fifth finger and also several family members showed a varying degree of short thumbs. They also exhibited brachydactyly of the first, second, and fifth toe and a large gap between the first and second toe (a feature not previously described in HFGS). Affected family members had small feet with male shoe size less than 6.

X-ray of the hands of three family members showed varying degrees of a malformed middle phalanx in the little finger.
with a shortened radial length causing clinodactyly. The most prominent findings in the feet were a fusion of the middle and distal phalanges of the fifth and sometimes also the fourth toe as well as a distinctly shortened end phalanx of the second toe (figs 5 and 6).

The urogenital abnormalities in affected females were restricted to urinary incontinence and recurrent urinary tract infections. Cystoscopy and voiding urethrocystography in VI.5 showed double kidneys on the right side and ectopic ureters ending in the bladder neck bilaterally. Two females (IV.11 and VI.5) had “short urethra” according to the medical case history. There were no reports of bicornuate uterus, vaginal septum, or female infertility. However, gynaecology records were only available for IV.11. Interestingly, there was a high penetrance of hypospadias in this family. All but two affected males had hypospadias. They were mildly affected with the urethra opening on the ventral side of glans, with the exception of three cases with proximal variants of hypospadias.

**Mutation analysis**

The genome wide linkage analysis showed evidence in favour of linkage to chromosome 7p. With additional markers we obtained a maximum lod score of 6.70 at θ=0 for marker D7S503.

HOXA13 is located in this region at chromosome 7p15 (http://www.ncbi.nlm.nih.gov) and was therefore subject to mutation analysis. We used PCR primers amplifying the whole coding region of HOXA13. PCR and electrophoresis with the primers HOXA13-A65 and HOXA13-A66, amplifying part of exon 1, showed two alleles of different sizes in affected patients. Sequence analysis showed a duplication of 18 bp in the second polyalanine stretch in the first exon (234_251dup TGGGCGGCGGCCGCGGCGG). This duplication was observed in all affected available family members (fig 1B). In addition, it was also found in V.18, who is apparently unaffected. The mutation was not found in 100 healthy subjects originating from Sweden, thus confirming that the mutation does not represent a polymorphism.

**DISCUSSION**

While searching for genes involved in hypospadias, we identified this family with atypical HFGS carrying a novel mutation in the HOXA13 gene. The mutation consists of a duplication of 18 bp resulting in six additional alanines in the second polyalanine tract in the first exon of HOXA13.

This is the largest HFGS family reported so far, with 27 affected subjects in six generations. However, it appears to be an atypical variant of the syndrome since many phenotypic features distinguish this family from previously described HFGS families. The skeletal anomalies are less severe, in particular regarding the feet. Affected subjects have small feet, brachydactyly of the second and fifth toes, and a large gap between the first and second toes. The latter two features have not been described in any previously reported HFGS families; however, short or uniphalangeal second toes with absent nails are found in Guttmanch syndrome in which a mutation in the HOXA13 gene was recently reported. Hallux varus has only been reported in three subjects. Hypoplasia of the big toe, a
hallmark feature of HFGS found in all previously described families, is not present at all in this family. Moreover, there is no evidence of any Mullerian duct fusion defects in women, whereas in affected males there is a high penetrance of hypospadias. Interestingly, there is no obvious reduced fertility in this large pedigree. Since low birth weight is known to affect the risk for hypospadias, we checked the birth weight of four affected males and they were all within normal limits. There is a striking variation in phenotype between affected subjects in this family, as reported previously in HFGS families. In the family described here, the skeletal as well as the urogenital abnormalities show variable expression. Interestingly, V16 carries a mutation but claims to be unaffected. However, phenotype information could only be acquired by telephone interview and she declined further examination.

The polyalanine tract expansion in this family is stable through the generations (fig 1B). This is in line with the concept that cryptic polyalanine expansions may derive from unequal crossing over. In the N-terminal region of HOXA13, there are three alanine repeats of 14, 12, and 18 respectively. The insertion described here results in six additional alanines in the second polyalanine tract in the first exon, in contrast to the two previously reported polyalanine expansions (resulting in eight and six additional alanines, respectively) localised in the third tract. It is likely that the discrepancies in phenotype between this and the previously reported families are caused by the different localisation of the insertion.

There are several reasons to question whether the malformations seen in patients heterozygous for the different mutations in HOXA13 are the result of haploinsufficiency. The patient with a heterozygous deletion of the entire HOXA4 cluster has a relatively mild HFGS phenotype, in particular with regards to the genital malformations that are limited to cryptorchidism and chordee, whereas the patient with a missense mutation has an unusually severe phenotype. Mice heterozygous for a minor deletion within the HOXA3 gene have a more severe limb phenotype than mice homozygous for a HOXA3 null mutation. The fact that heterozygous mutations in HOXA3 result in a phenotype more severe than anticipated from haploinsufficiency suggests that the mutant protein may not only be dysfunctional. It may instead have other deleterious effects, acting in a dominant negative way. The mutations described in HOXD13 may render a dominant negative protein as well, since the severity of synpolydactyly has been shown to correlate with the size of the polyalanine expansion. Interestingly, in the family with the largest expansion (14 additional alanines) affected males have hypoplasias. Urogenital manifestations (that is, lack of preputial glands in males) are also found in mice homozygous for a spontaneous polyalanine expansion (expanding the stretch from 15 to 22 alanines) in the HOXd13 gene. Genetic complementation studies in this mouse model confirms that the mutated protein exerts a “super” dominant negative effect, by interfering with the function of the remaining wild type HOxd13 and other 5’HOx proteins. Moreover, these mice have a much more severe phenotype than mice with complete absence of HOxd13 function. Further evidence for dominant negative effects is derived from mice with homozygous deletions of HOxd11, HOxd12, and HOxd13 which have a less severe phenotype than mice and humans with polyalanine tract expansions in HOXD13. The above observations are especially interesting in light of the suggested synergistic roles of HOXA13 and HOXD13.

In conclusion, we have described here a family with limb and urogenital malformations reminiscent, but yet distinct from those previously described in families with HFGS. The genetic basis for the phenotype in this family is a mutation in HOXA13. This finding illustrates the easily overlooked mild abnormalities resulting from mutations in human HOX genes.

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