ELECTRONIC LETTER

Screening of the 1 Mb *SOX9* 5' control region by array CGH identifies a large deletion in a case of campomelic dysplasia with XY sex reversal

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Campomelic dysplasia (CD; OMIM #114290) is a semi-lethal, autosomal dominant osteochondrodysplasia, characterised by congenital shortening and bowing of the long bones (campomelia) in combination with other skeletal anomalies such as hypoplasia of the scapular and pelvic bones, lack of mineralisation of thoracic pedicles, a missing pair of ribs, and clubbed feet. Severe respiratory distress resulting from Robin sequence, hypoplastic lungs with narrow airways, and a bell shaped narrow thorax are the major cause of death, which mostly occurs during the neonatal period. About two thirds of karyotypic male CD patients show XY sex reversal. As is the case for any of the symptoms, campomelia is not an obligatory feature and is absent in about 10% of the cases, referred to as the acampomelic form of CD (ACD).^{1 2}

Most CD cases have heterozygous de novo mutations in the coding region of the transcription factor gene *SOX9* on 17q.^{3 4} The mutations cause loss of DNA binding or of the transactivation function of *SOX9*, implying that CD results from haploinsufficiency for *SOX9*. In accordance with the human phenotype caused by *SOX9* mutations, studies in the mouse have shown that *Sox9* functions as an essential developmental regulator at various steps of chondrogenesis^{5 6} and during the initial phase of testis determination and differentiation.⁷⁻⁹ Furthermore, heterozygous *Sox9* knockout mice recapitulate essentially all the symptoms seen in CD patients but for the sex reversal.^{3 10}

Some CD cases have two intact copies of the *SOX9* structural gene but a chromosomal rearrangement in the vicinity of one *SOX9* allele. These rearrangements, which include translocations and inversions, occur de novo, and their breakpoints are always 5' to *SOX9*. In 11 of these cases, the breakpoints have been mapped from 50 kb up to 950 kb upstream of *SOX9*.^{3 4 11-13} Detailed analysis of the genomic sequence of this 1 Mb region showed it to be devoid of any protein coding gene, suggesting that the chromosomal rearrangements remove one or more *cis* regulatory elements from an extended *SOX9* control region.¹³ In support of this, mice transgenic for human *SOX9* spanning YACs showed expression patterns (except in gonads) for the transgene similar to endogenous *Sox9* only when the YAC transgene contained a 350 kb sequence upstream of *SOX9*, but not with a truncated YAC containing only 75 kb of *SOX9* 5' flanking sequence.¹² By phylogenetic footprinting comparing the genomic sequences of the *SOX9* regions of human, mouse, and puffer fish (*Takifugu rubripes*), we recently identified five conserved sequence elements up to 290 kb 5' of human *SOX9* and showed that 8 of 10 CD translocation breakpoints separate part or all of these elements from *SOX9*.¹⁴

Our mutation detection rate, performed by sequencing of the *SOX9* open reading frame (ORF) and of the four exon-intron junctions, is about 90–95% in classical CD/ACD non-translocation/inversion cases. The remaining cases could have

Key points

- Campomelic dysplasia (CD), an autosomal dominant skeletal malformation syndrome with XY sex reversal, is caused by heterozygous de novo mutations in and around the *SOX9* gene on 17q. *SOX9* has an extended control region as indicated by CD translocation breakpoints that scatter over 1 Mb 5' to the gene.
- We screened a sample of 11 CD or CD-like cases without *SOX9* coding region mutations or translocations for deletions in the *SOX9* 5' flanking region by comparative genomic hybridisation (CGH) on a DNA microarray, using large insert clones covering a 2.5 Mb region around *SOX9*. The array CGH was validated with DNA from a male CD patient reported here with a de novo deletion of at least 4.0 Mb including the *SOX9* locus.
- A 1.5 Mb de novo deletion was detected by array CGH in a 46,XY sex reversed patient with the acampomelic form of CD. The proximal and distal ends of the deletion could be placed at 380 kb and 1.869 Mb 5' to *SOX9*, respectively. The deletion does not remove the five evolutionarily conserved sequence elements we previously identified, which are up to 290 kb 5' to *SOX9*, but removes two such elements, newly identified.
- This study provides strong evidence for the existence of *cis* acting regulatory elements more than 380 kb upstream of *SOX9* and demonstrates the usefulness of array CGH for the detection of deletions in an extended control region.

a mutation within the proximal promoter, the 5' or 3' UTR, or the introns, regions not routinely analysed. They could also have a submicroscopic deletion within the 1 Mb 5' control region of *SOX9*. We reasoned that comparative genomic hybridisation (CGH) on a DNA microarray, using large insert clones from the *SOX9* locus, might be an effective and simple procedure to search for a deletion in such an extended genomic region.

CASES AND METHODS

Case reports

Patient 1 (Neuburg) was the first child of unrelated, healthy parents. At birth, maternal age was 22 years, and paternal

Abbreviations: ACD, acampomelic form of campomelic dysplasia; CD, campomelic dysplasia; CGH, comparative genomic hybridisation; ORF, open reading frame

Figure 1 Radiographic features of the two CD patients. (A–C) Patient 1. (A) Chest 3 days after birth, showing bell shaped thorax, 11 pairs of ribs, and hypoplastic scapula. (B) Chest at 7.5 months of age, showing severe scoliosis. (C) Pelvis and lower extremities 1 day after birth, showing vertically narrow iliac bones, hypoplastic ischial and pubic bones, bent femur and slightly bowed tibia and fibula. (D–F) Patient 2. (D) Chest at 13 months of age. Note only mild hypoplasia of the scapula. (E) Lateral cervical spine at 5 years of age, showing kyphosis and partial non-mineralisation of pedicle C2. (F) Pelvis and lower extremities at 5 months of age, showing hypoplastic parts of the ischial and pubic bones, no narrow iliac wings, and no overt bending of the long bones.

age 26 years. The mother previously had a termination of pregnancy with another partner. Birth weight was 2720 g, length was 49 cm, and occipitofrontal circumference was 37 cm. Apgar scores were 9/3/6. The child had to be intubated directly after birth, and presented with radiological signs typical of CD such as hypoplastic scapulae, narrow bell

shaped thorax, 11 pairs of ribs (fig 1A), vertically narrow iliac bones, hypoplastic ischial and pubic bones, and bent femur, but only slightly bowed tibia and fibula (fig 1C). Clinical signs included macrocephaly, flat nasal bridge, low set ears, Robin sequence, and clubbed feet. External genitalia were normal male, karyotype was 46,XY. By the age of 7.5 months,

he had developed a severe scoliosis (fig 1B), and had to be tube fed continuously. He had severe respiratory problems, which required repeated hospitalisation and from which he died at 10 months of age. His final weight was 4790 g, length 59.5 cm, head circumference 44.7 cm.

Patient 2 (Tours) was born at 39 weeks gestation to healthy, unrelated parents, a 21 year old G1P1 mother and a 22 year old father. Pregnancy was uneventful. Birthweight was 3540 g, and occipitofrontal circumference was 37.5 cm. The child presented at birth with macrocephaly, epicanthic folds, flat nasal bridge, shallow orbits, anteverted nostrils, Robin sequence, bilateral clubfoot, and tracheobronchomalacia that initially required tracheotomy. Radiological findings included a mild, non-characteristic hypoplasia of the scapula (fig 1D), and an unusual kyphosis of the cervical spine with partial non-mineralisation of the pedicle C2 (fig 1E). The pelvis and lower extremities showed hypoplastic ischial (ramus) and pubic (inferior ramus) bones, but no narrow iliac wings and no overt bending of the long bones (fig 1F). Ischial and pubic rami were still insufficiently mineralised at 5 years of age. Metacarpophalangeal pattern profile analysis of hand radiographs demonstrated some shortness of metacarpal I (−2.4 SD), moderately short middle phalanges II (−5.6 SD) and V (−2.6 SD), and mild shortness of distal phalanges I, IV, and V, a pattern similar to that described for other CD cases.¹⁵ At 5 years of age, her height was 106 cm (−1 SD), weight 16.5 kg (−0.6 SD), and head circumference 51.5 cm (+1 SD). Retrognathia had improved and hearing was normal. She has normal female external genitalia and a 46,XY karyotype. At the last follow up, at 5 years and 8 months of age, she was found to be a hyperactive, cheerful girl, attending a regular kindergarten where she showed good social integration. She was still having some problems with pronunciation, but was able to make herself understood.

Somatic cell hybridisation and FISH analysis

Mouse–human somatic cell hybrids were established by fusion of a lymphoblastoid cell line from patient 1 with mouse RAG cells (Hprt[−]), and of skin fibroblasts from patient 2 with mouse RAG (Hprt[−]) and B82 cells (Tk[−]), as described previously.¹⁶ FISH analysis was performed as previously described.¹³

PCR typing of microsatellite and STS markers

Microsatellite markers amplified by PCR with unlabelled primers were analysed on 6% denaturing polyacrylamide gels followed by silver staining. Microsatellite markers amplified by PCR with dye labelled primers were analysed on an ABI Prism 310 automated DNA sequencer using Genotyper software (version 3.7) (both Applied Biosystems). Paternity was tested using the ProfilerPlus kit (Applied Biosystems). Marker content of somatic cell hybrids was determined using primers for microsatellite and previously published STS markers.¹³ For fine mapping of the deletion breakpoint for patient 2, new primer pairs were developed from the genomic sequence and are available on request (RP markers). Primers used for deletion spanning PCR were RP17F-Long (5'-ACCCTCCAGGAGAACATGCATCCAG-3'), and RP14R-Long (5'-CTTGAGACTTGGGCCCTAGTGCTG-3'). Standard PCR was performed as previously described.¹³ Long range PCR was conducted with the Expand Long Template PCR system (Roche).

Sequence analysis

The Vectorette protocol¹⁷ was used to obtain the human insert end sequence of YAC 946E12. The PCR product from the deletion junction of patient 2 was cloned into pCRII-TOPO (Invitrogen) prior to sequencing. Sequence reactions were

performed with the Thermosequenase II Dye Terminator Cycle Sequencing kit (Amersham Pharmacia) and analysed on an ABI Prism 310. Conserved sequence elements were identified by BLAST searches of human sequences against the *Takifugu* sequence release 3 on the (Taki)Fugu website (<http://fugu.hgmp.mrc.ac.uk>), and against mouse sequences at the NCBI BLAST site (<http://www.ncbi.nlm.nih.gov/BLAST>). PipMaker analyses were performed at <http://bio.cse.psu.edu/pipmaker>.

Microarray printing, hybridisation and data analysis

BACs and PACs from chromosome 17¹³ and reference BACs from the X chromosome were grown in selective media in an overnight culture and DNA was extracted with the Qiagen Plasmid Midi kit using the manufacturer's protocol for very low copy plasmids. DNA was eluted from the columns with deionised water and spotted onto Corning CMT-GAPSTM coated slides according to the manufacturer's recommendations. The dot spacing was 500 µm. Each clone was spotted twice in one array and arrays printed in duplicate. Washing and coupling steps were also performed as per the manufacturer's (Corning) instructions. After a denaturation step in boiling water, the slides were rinsed in 100% ethanol and dried by centrifugation.

The labelling and hybridisation steps were performed according to the protocol of Pollack *et al* (http://cng.stanford.edu/pbrown/protocols/4_genomic.html). In brief, 2 µg test and 2 µg reference DNA were labelled with Cy3 and Cy5 dCTP (Amersham Pharmacia) using the BioPrime DNA labelling kit (Invitrogen). Labelled probes were purified using the PCR purification kit from Qiagen. Probes were pooled, and 60 µg Cot1 DNA and 100 µg tRNA were added. This mixture was then concentrated in a speed vacuum and adjusted to a volume of 15 µl containing 3.4×SSC with 0.3% SDS final concentration. After a short denaturation step, the mixture was prehybridised for 4 h at 37°C to block repetitive sequences. The prehybridised DNA was then transferred to the chip and hybridised for 16 h under a coverslip in a humidity chamber (Genemachine). Slides were washed for 5 minutes in 2×SSC with 0.03% SDS at 65°C, 5 minutes in 1×SSC at 65°C, and 5 minutes in 0.2×SSC. The slides were then dried by centrifugation.

Following hybridisation, arrays were scanned in the Cy3 and Cy5 channels (595 nm and 685 nm, respectively) using an Arrayworx reader and software (Applied Precision). Using the DataBridge software (GeneScan Europe AG), the ratios of the Cy3 and Cy5 signals were normalised relative to the signals from the reference BAC clones from the X chromosome, with the average ratio of all reference clones set to 1, as described previously.¹⁸

RESULTS

Validation of the array CGH with a 4 Mb SOX9 deletion case

To validate the sensitivity and reproducibility of our CGH and microarraying protocols, we used DNA from patient 1 with a large *SOX9* deletion previously identified by us, who had been described only in preliminary form¹⁹. FISH analysis with the 2.4 Mb *SOX9* spanning YAC 946E12¹³ revealed a complete absence of the corresponding region on one of the two chromosomes 17 in this patient (fig 2A). The centromeric end of the human insert in this YAC was sequenced and maps to position 70 869 708 (November 2002 freeze, human genome browser at UCSC; <http://genome.ucsc.edu>); its telomeric end is 250 kb distal to *SOX9*¹² (fig 2C). Haplotype analysis in the family (fig 2B) showed that the deletion had arisen de novo on the paternal chromosome and extends from the proximal informative microsatellite marker D17S1797 down to D17S1829. Taken together, these data indicate a minimum size for the deletion of 4.0 Mb (fig 2C).

Figure 2 A large interstitial deletion spanning SOX9 in patient 1 (A) FISH with YAC 946 E12 on metaphase spread showing complete absence of signal on the del(17) chromosome. (B) Haplotype analysis of the family of patient 1, showing hemizygozity for paternal alleles of microsatellite markers either side of SOX9 in the patient. (C) Relative positions of polymorphic markers used, with their physical distances from the tip of the short arm of chromosome 17 (November 2002 freeze, human genome browser at UCSC). All markers were used for somatic cell hybrid analysis (see text); markers informative for the haplotype analysis shown in B are underlined. YAC-CEN and YAC-TEL denote the centromeric and telomeric insert end, respectively, of YAC 946E12, used in (A). The minimum and maximum extent of the patient 1 deletion is indicated on the right.

Figure 3 Large deletion in the *SOX9* 5' control region identified by microarray CGH. (A) Map of the *SOX9* region with positions of the BACs and PACs used, and with the extent of the patient 1 (P1) and 2 (P2) deletions shown on top. The coordinates of sequenced BACs are from the November 2002 freeze, human genome browser at UCSC; those from BAC 328J17 and PACs 18K10 and 297P01 are from Pfeifer *et al.*¹³ (B) Control hybridisation with normal genomic DNA used as test DNA, showing Cy5/Cy3 ratios of ~1.0. (C) Hybridisation with patient 1's DNA as test DNA, showing Cy5/Cy3 ratios ~0.5 for BACs within the deletion. (D) Hybridisation with patient 2's DNA as test DNA, showing a reduced Cy5/Cy3 ratio for seven BACs or PACs. (B–D) The ordinates show the ratios of Cy5 to Cy3 labelled reference DNA; the normal genomic DNA used as test DNA in B served as reference DNA throughout. The values shown are the means (SD) for three, three, and four independent hybridisations for (B), (C), and (D), respectively.

To independently determine the size of the deletion, we isolated the deleted chromosome 17 from the normal chromosome 17 in a mouse/human somatic cell hybrid. By STS content mapping of the del(17) containing hybrid using the markers shown in fig 2C, the centromeric and telomeric end of the deletion could be assigned to the intervals D17S940/D17S949 and D17S1829/D17S1352, respectively, in agreement with the FISH and haplotype data (data not shown).

The DNA of patient 1 was then used for array CGH. The positions of the chromosome 17 BAC and PAC clones used for the microarray are shown in fig 3A. Whereas the Cy5/Cy3 ratios for the 17 BAC/PAC clones were all ~1.0 in control hybridisations with normal DNA used as test DNA (fig 3B), the ratios for the 12 BAC/PAC clones from the patient 1 deletion were consistently reduced to ~0.5 if patient 1's DNA was used as test DNA (fig 3C).

Array CGH detects a large deletion in the *SOX9* 5' control region in patient 2

Having established the CGH DNA chip protocol with the deletion case (patient 1), we used this protocol to screen a sample of 11 non-translocation campomelic cases, six of which were classified as typical CD/ACD cases according to the criteria of Mansour *et al.*² the other five presenting only

with some of the features. For all cases, we had excluded a *SOX9* coding region mutation by sequencing, and a *SOX9* deletion by Southern dosage blots or quantitative PCR. A single sample gave a CGH result indicative of a deletion 5' to *SOX9*, showing a reduced signal for seven contiguous clones, with all Cy5/Cy3 ratios <0.8 (fig 3D). This indicates a minimum size for the deletion of 0.9 Mb (fig 3A). This DNA sample derived from patient 2, a 46,XY sex reversed patient with the acampomelic form of CD.

The patient 2 deletion is 1.5 Mb in size

To define the extent of the deletion more precisely, the two copies of chromosome 17 of patient 2 were separated in mouse/human somatic cell hybrids. Fragment analysis using microsatellite marker D17S808, which lies centromeric to the deletion (fig 2C) showed that of the two alleles of 145 bp and 159 bp present in patient 2's DNA (fig 4A, lane 3), hybrid 1 (H1) showed only the 145 bp allele (lane 1), while hybrid 19 (H19) showed only the 159 bp allele (lane 2). As shown below, hybrid 1 contains the del(17) chromosome, hybrid 19 the normal chromosome 17. Genotyping of this patient's mother (fig 4A, lane 4) revealed that the deleted chromosome in hybrid 1 is of maternal origin (DNA from the father was not available). As the mother was heterozygous and patient 2 hemizygous for the marker D17S949 that lies within the deletion (fig 2C), the deletion must have arisen de novo (data not shown).

STS markers, developed from the available genomic sequence, were then used for STS content mapping of DNA from hybrid 1, using DNA from hybrid 19 as positive and mouse DNA as negative controls. Starting from the information provided by the CGH data (fig 3D), the centromeric end could be narrowed down to a 3 kb interval flanked by STS markers RP17 and RP18, which typed positive and negative for hybrid 1, respectively (fig 4B, top left). The telomeric end of the deletion could similarly be assigned to a 2.5 kb interval defined by STS markers RP13 and RP14, which again typed negative and positive for hybrid 1, respectively (fig 4B, top right). Subsequently, the forward primer for RP17 and the reverse primer for RP14 were extended to a length of 25 nucleotides each and were used in long range PCR, yielding a 4.2 kb fragment with DNA from hybrid 1 and from the total genomic DNA of patient 2, but not from a control DNA or with mouse DNA (fig 4B, bottom). This junction fragment enabled us to sequence directly across the deletion (fig 5B). The centromeric end of the deletion lies within BAC 118F13 (not used for CGH), between bases 139 568 and 139 572 (GenBank accession no. AC005242), 1 869 431–33 bp upstream of the *SOX9* transcription start site. The telomeric deletion breakpoint lies between bases 4054 and 4058 of BAC 423M11 (GenBank accession no. AC 006448), 379 769–71 bp upstream of *SOX9*. (The central CAA nucleotides in fig 5B could derive from either clone; see fig 5A). The patient 2 deletion is thus 1 489 662 bp in size.

The patient 2 deletion removes two sequence elements conserved between human, mouse, and fish

The patient 2 deletion spares the five potential regulatory sequence elements E1–E5, which are highly conserved between human, mouse, and *Takifugu*, located from 28 kb to 290 kb upstream of *SOX9* (fig 5C). These elements are all about 100 bp in size and show sequence identities of 67–80% and 81–95% between human and *Takifugu*, and between human and mouse, respectively.¹⁴ A BLAST search of the 1.5 Mb sequence deleted in patient 2 against the recent *Takifugu* sequence release 3 disclosed two conserved sequence stretches, each with a highly conserved core of ~120 bp with 76–79% identity. These sequence elements, designated Eb1 and Eb2, are 395 kb and 611 kb, respectively, from human

Figure 4 Somatic cell hybrid analysis of the patient 2 deletion. (A) Microsatellite analysis. The electropherogram displays allele sizes for microsatellite marker D17S808 from dye labelled nucleic acid fragments of somatic cell hybrid 1 with the maternal chromosome 17 of patient 2 (lane 1), hybrid 19 with the paternal chromosome 17 of patient 2 (lane 2), patient 2 (lane 3), and patient 2's mother (lane 4), separated on an ABI Prism 310 genetic analyser and analysed by the Genotyper software (version 3.7). (B) Typing of STS markers flanking the deletion breakpoints and deletion spanning long range PCR. Top, agarose gels showing PCR products obtained from hybrids for STS markers flanking the centromeric and telomeric deletion breakpoint. Note that STS markers RP18 and RP13 within the deleted region resulted in no amplification for hybrid 1. Bottom, deletion spanning long range PCR with primer pair RP17 F-Long and RP14 R-Long showed amplification of a 4.2 kb-fragment for hybrid 1 and patient 2, but not for a normal control DNA and for mouse DNA. P2, patient 2; C, normal human control; H1, hybrid 1; H19, hybrid 19; M, size marker; Mo, mouse.

SOX9 (fig 5C), and 38 kb and 56 kb from a second *Takifugu* *SOX9* paralogue that had not been available at our previous analysis, but are absent from the previously characterised *Takifugu* *SOX9* locus.¹⁴ Eb1 and Eb2 are also conserved in mouse. BLAST and PipMaker analyses of the deleted human sequence with the corresponding mouse sequence, using a minimum size of 100 bp and a minimum sequence identity of 90%, identified an additional 10 conserved sequence blocks (R1–R10 in fig 5C) (sequences available on request).

DISCUSSION

Two patients with large deletions in the *SOX9* region are described in the present report. One deletion, found in patient 1, extends to both sides of the *SOX9* gene. Patient 1 is only the second case with a molecularly confirmed complete deletion of *SOX9*; the first case has been described in an XX female infant with an interstitial deletion 17q23.3–q24.3, who died 4 days after birth.²⁰ The fact that no symptoms other than those typically seen in CD were observed in patient 1 may be attributable to the fact that only 10 genes are located within the 4.0 Mb minimum, and 15 genes within the 5.1 Mb maximum deletion interval. Both *SOX9* deletion cases provide the strongest evidence so far that CD is a *SOX9* haploinsufficiency disorder.

The second deletion, found in patient 2, is 1.5 Mb in size and lies entirely within the 2 Mb region 5' to *SOX9* that is devoid of any protein coding gene.^{13 14} Analysis of the patient 2 deletion reveals that the centromeric breakpoint lies within a partial LINE-1 repeat (L1, fig 5C). Unequal homologous recombination between LINE-1 elements has been described as a mutational mechanism generating interstitial deletions.²¹ However, the telomeric breakpoint of the patient 2 deletion lies 400 bp from another partial LINE-1 element. Several interstitial deletions have been described where a LINE-1 repeat is present on one side and an unrelated sequence on the other side of the deletion breakpoint, as in the present

case.^{22–24} The involvement of LINE-1 is probably fortuitous in all these cases.

An indication as to which mechanism might have created the patient 2 deletion is given by the 3 bp homology, CAA, at the deletion junction (fig 5A). Short homologies of 2–6 bp have been observed at the junctions of both small and larger sized deletions in the human genome (Woods-Samuels *et al.*²⁵ and references therein). Bullock *et al.*²⁶ observed 2–3 bp homologies at the excision points for SV40 in cultured rat cells and showed that the sequences at these crossover points were associated with eukaryotic topoisomerase I cleavage sites *in vitro*. In fact, one of the crossover points had a CAA homology, followed by a T and an A residue, respectively, as in fig 5A, and was shown to be cut at each site by topoisomerase I after the T residue opposite the central A in the CAA sequence. As topoisomerase I is known to also catalyse the ligation of nonhomologous DNA *in vitro*,^{27 28} this enzyme might have been involved in the creation of the patient 2 deletion by mechanisms similar to those described.^{25 26} Whether the nearly identical sequences either side of the centromeric and telomeric deletion junction (underlined in fig 5A) contributed to the recombination event remains unclear.

The 1.5 Mb patient 2 deletion provides the first strong evidence for the existence of *cis* regulatory elements more than 380 kb 5' to human *SOX9*. The presence of such distantly upstream elements is also supported by the CD translocation breakpoints t(5;17) and t(17;22), respectively located 324–346 kb and 932–966 kb 5' to *SOX9*¹³ (corrected coordinates), which retain elements E1–E5 in front of *SOX9* (fig 5C). The effect of these two translocation breakpoints, the most distant from *SOX9* presently known, may also be explained, however, by position effects due to juxtaposition of silencers or of heterochromatin.¹³ They are therefore no solid evidence for such long distance *cis* regulatory elements. On the other hand, there is some evidence for a very distant

Figure 5 Sequence of the deletion junction and precise extent of the patient 2 deletion. (A) The normal centromeric (Cen) and telomeric (Tel) sequences are shown aligned with the deletion junction sequence (DJ). Homology between the normal and junction sequence is indicated by **bold** lettering. The junctional CAA homology is set off from the rest of the sequence. Nearly identical sequences 5' (12/15 identities) and 3' (8/11 identities) of the centromeric and telomeric deletion junction are underlined by straight and dashed lines, respectively. (B) The electropherogram shows the sequence across the deletion breakpoint. The sequences terminate within BAC clones RP11-118F13 and RP11-423M11 as indicated. (C) Details of the deleted region, drawn to scale. The centromeric deletion breakpoint is within a partial LINE-1 (L1) repeat, while the telomeric breakpoint is close to a partial L1 repeat (L1 and other elements not drawn to scale). Sequence elements conserved between human, mouse, and puffer fish identified previously (E1–E5;¹⁴) or newly (Eb1 and Eb2) are represented by black and striped boxes, respectively, while elements R1–R10, conserved between human and mouse only, are shown as white boxes. The positions of the two most distal CD translocation breakpoints are shown,¹³ as is the region corresponding to the *Ods* deletion in the mouse.²⁹ *KCNJ2*, the 5' flanking gene to *SOX9*, is 105 kb from the centromeric deletion breakpoint.

cis acting element for *Sox9* expression in the mouse. The dominant mouse mutant *Ods* carries a 150 kb deletion 1 Mb 5' to *Sox9* that leads to upregulated *Sox9* expression in fetal gonads of XX mice, causing XX sex reversal.²⁹ This deletion is thought to remove a regulatory element that mediates repression of *Sox9* expression in XX fetal gonads, a repression antagonised by SRY in XY embryos, according to the repressor model of sex determination in mammals.³⁰ The human sequence corresponding to the *Ods* deletion is located 1.2–1.4 Mb upstream of *SOX9* (fig 5C). Because the 1.5 Mb deletion in patient 2 occurred on an XY background and caused male to female sex reversal, the deletion is, unfortunately, not informative with respect to XX—that is, female to male sex reversal.

Within the patient 2 deletion, two sequence elements, Eb1 and Eb2, conserved between human, mouse, and fish, and an additional 10 sequence elements, R1–R10, conserved only between human and mouse, were identified (fig 5C). One or more of these sequence elements may function as general or tissue specific regulators for *SOX9*. It is tempting to speculate that one of these elements is actually responsible for expression of *SOX9* in testis, as a human YAC transgene containing 350 kb of *SOX9* 5' flanking sequence failed to show expression in the testes of transgenic mice,¹² and as testis development did not occur in patient 2. Functional tests in transgenic mice will show which, if any, of the elements are involved in regulating *SOX9* expression.

Patient 2 is the only case from the sample studied in which a deletion was detected. The other 10 cases may have a deletion below the detection limit of the array CGH protocol

used, which we estimate to be about half a clone size. As the sizes of the BAC and PAC clones used range from 85 kb to 203 kb, we would have detected a deletion ≥ 50 –100 kb in size in the other campomelic cases studied. These cases, therefore, have either a smaller sized deletion in the *SOX9* 5' flanking 1 Mb region, a point mutation or microdeletion in a control element, or a mutation elsewhere in the *SOX9* region. Alternatively, as some of the cases did not fulfil the minimum set of criteria for a classical CD or ACD case,² the causative mutation may lie in a gene other than *SOX9*.

The two deletion cases presented here, both of which have a 46,XY karyotype, highlight the aspect of variable expressivity with regard to XY sex reversal seen in CD. Whereas patient 1 with deletion of the entire *SOX9* region was born as a boy with normal male external genitalia, patient 2 with the upstream deletion that leaves the *SOX9* ORF intact is a completely sex reversed girl with normal female external genitalia (no gonad histologies are available for either patient). Likewise, identical point mutations in the *SOX9* coding region can cause XY sex reversal in one case, and no sex reversal in another.^{31–32} Contributions from the genetic background and/or environmental factors, or stochastic fluctuation of *SOX9* transcription levels, can be invoked to explain how reduced *SOX9* dosage can lead to such highly divergent sexual phenotypes.

Whereas no correlation exists between *SOX9* dosage and XY sex reversal, there appears to be some correlation between severity of the skeletal phenotype and survival time. We have previously noted that CD patients with translocations tend to have a longer life expectancy than patients with mutations in

the *SOX9* coding region, and that these two classes of CD mutations also differ with respect to the eponymous feature, campomelia, which is present in only half of the translocation cases but in over 90% of the *SOX9* ORF mutation cases.¹³ A recent study also shows that surviving cases of CD are frequently translocation cases.³³ Patient 2 resembles the majority of translocation cases in both aspects; she is a surviving case, and she has acampomelia. The milder phenotype in all these cases most probably results from residual activity of the *SOX9* allele on the affected chromosome. The translocations and the 5' deletion in patient 2 thus represent hypomorphic alleles of *SOX9* rather than complete loss of function alleles.

In conclusion, the present study provides strong evidence for the existence of *cis* acting regulatory elements more than 380 kb upstream of *SOX9*. It also demonstrates the usefulness of array CGH for the detection of deletions in a large genomic region such as the 5' control region of *SOX9*. The deletion detection limit could be reduced to 40 kb or less, if cosmid sized rather than BAC sized clones were used for the array. Such a sensitive method is particularly attractive in situations where only limited amounts of DNA and no cells for FISH analysis are available, as is frequently the case in severe disorders such as CD.

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REFERENCES

- Houston CS, Opitz JM, Spranger JW, Macpherson RI, Reed MH, Gilbert EF, Herrmann J, Schinzel A. The campomelic syndrome: review, report of 17 cases, and follow-up on the currently 17-year-old boy first reported by Maroteaux *et al* in 1971. *Am J Med Genet* 1983;**15**:3–28.
- Mansour S, Hall CM, Pembrey ME, Young ID. A clinical and genetic study of campomelic dysplasia. *J Med Genet* 1995;**32**:415–20.
- Foster JW, Dominguez-Steglich MA, Guioli S, Kwok C, Weller PA, Stevanovic M, Weissenbach J, Mansour S, Young ID, Goodfellow PN, Brook JD, Schafer AJ. Campomelic dysplasia and autosomal sex reversal caused by mutations in an *SRY*-related gene. *Nature* 1994;**372**:525–30.
- Wagner T, Wirth J, Meyer J, Zabel B, Held M, Zimmer J, Pasantes J, Bricarelli FD, Keutel J, Huster E, Wolf U, Tommerup N, Schempp W, Scherer G. Autosomal sex reversal and campomelic dysplasia are caused by mutations in and around the *SRY*-related gene *SOX9*. *Cell* 1994;**79**:1111–20.
- Bi W, Huang W, Whitworth DJ, Deng JM, Zhang Z, Behringer RR, de Crombrughe B. Haploinsufficiency of *Sox9* results in defective cartilage primordia and premature skeletal mineralization. *Proc Natl Acad Sci USA* 2001;**98**:6698–703.
- Akiyama H, Chaboissier M, Martin JF, Schedl A, de Crombrughe B. The transcription factor *Sox9* has essential roles in successive steps of the chondrocyte differentiation pathway and is required for expression of *Sox5* and *Sox6*. *Genes Dev* 2002;**16**:2813–28.
- Kent J, Wheatley SC, Andrews JE, Sinclair AH, Koopman P. A male-specific role for *SOX9* in vertebrate sex determination. *Development* 1996;**122**:2813–22.
- Morais da Silva S, Hacker A, Harley V, Goodfellow P, Swain A, Lovell-Badge R. *Sox9* expression during gonadal development implies a conserved role for the gene in testis differentiation in mammals and birds. *Nat Genet* 1996;**14**:62–8.
- Arango NA, Lovell-Badge R, Behringer RR. Targeted mutagenesis of the endogenous mouse *Mis* gene promoter: in vivo definition of genetic pathways of vertebrate sexual development. *Cell* 1999;**99**:409–19.
- Kist R, Schrewe H, Balling R, Scherer G. Conditional inactivation of *Sox9*: a mouse model for campomelic dysplasia. *Genesis* 2002;**32**:121–23.
- Ninomiya S, Isomura M, Narahara K, Seino Y, Nakamura Y. Isolation of a testis-specific cDNA on chromosome 17q from a region adjacent to the breakpoint of t(12;17) observed in a patient with acampomelic campomelic dysplasia and sex reversal. *Hum Mol Genet* 1996;**5**:69–72.
- Wunderle VM, Critcher R, Hastie N, Goodfellow PN, Schedl A. Deletion of long-range regulatory elements upstream of *SOX9* causes campomelic dysplasia. *Proc Natl Acad Sci USA* 1998;**95**:10649–54.
- Pfeifer D, Kist R, Dewar K, Devon K, Lander ES, Birren B, Korniszewski L, Back E, Scherer G. Campomelic dysplasia translocation breakpoints are scattered over 1 Mb proximal to *SOX9*: evidence for an extended control region. *Am J Hum Genet* 1999;**65**:111–24.
- Bagheri-Fam S, Ferraz C, Demaille J, Scherer G, Pfeifer D. Comparative genomics of the *SOX9* region in human and *Fugu rubripes*: conservation of short regulatory sequence elements within large intergenic regions. *Genomics* 2001;**78**:73–82.
- Poznanski AK. *The hand in radiologic diagnosis*, 2nd edn. Philadelphia: WB Saunders, 1984.
- Wagner T, Tommerup N, Wirth J, Leffers H, Zimmer J, Back E, Weissenbach J, Scherer G. A somatic cell hybrid panel for distal 17q: GDIA1 maps to 17q25.3. *Cytogenet Cell Genet* 1997;**76**:172–5.
- Riley J, Butler R, Ogilvie D, Finnear R, Jenner D, Powell S, Anand R, Smith JC, Markham AF. A novel, rapid method for the isolation of terminal sequences from yeast artificial chromosome (YAC) clones. *Nucleic Acids Res* 1990;**18**:2887–90.
- Solinas-Toldo S, Lampel S, Stilgenbauer S, Nickolenko J, Benner A, Döhner H, Cremer T, Lichter P. Matrix-based comparative genomic hybridisation: Biochips to screen for genomic imbalances. *Genes Chromosomes Cancer* 1997;**20**:399–407.
- Scherer G, Lindenberg K, Zimmer J, Schmalenberger B, Pfeifer D. A *de novo* deletion of more than 2 Mb including the *SOX9* locus in a case of campomelic dysplasia (CD) proves that CD is a haploinsufficiency syndrome. *Am J Hum Genet* 1999;**65**(Suppl):A342.
- Olney PN, Kean LS, Graham D, Elsas LJ, May KM. Campomelic syndrome and deletion of *SOX9*. *Am J Med Genet* 1999;**84**:20–4.
- Burwinkel B, Kilimann MW. Unequal homologous recombination between LINE-1 elements as a mutational mechanism in human genetic disease. *J Mol Biol* 1998;**277**:513–17.
- Drechsler M, Royer-Pokora B. A LINE element is present at the site of a 300 kb-deletion starting in intron 10 of the *PAX6* gene in a case of familial aniridia. *Hum Genet* 1996;**98**:297–303.
- Kumatori A, Faizunessa NN, Suzuki S, Moriuchi T, Kurozumi H, Nakamura M. Nonhomologous recombination between the cytochrome b₅₅₈ heavy chain gene (*CYBB*) and LINE-1 causes an X-linked chronic granulomatous disease. *Genomics* 1998;**53**:123–8.
- Goodman FR, Majewski F, Collins AL, Scambler PJ. A 117-kb microdeletion removing *HOXD9*-*HOXD13* and *EVX2* causes synpolydactyly. *Am J Hum Genet* 2002;**70**:547–55.
- Woods-Samuels P, Kazazian HH, Antonarakis SE. Nonhomologous recombination in the human genome: deletions in the human factor VIII gene. *Genomics* 1991;**10**:94–101.
- Bullock P, Champoux JJ, Botchan M. Association of crossover points with topoisomerase I cleavage sites: a model for nonhomologous recombination. *Science* 1985;**230**:954–8.
- Halligan BD, Davis JL, Edwards KA, Liu LF. Intra- and intermolecular strand transfer by HeLa topoisomerase I. *J Biol Chem* 1982;**257**:3995–4000.
- Been MD, Burgess RR, Champoux JJ. Nucleotide sequence preference at rat liver and wheat germ type I DNA topoisomerase breakage sites in duplex SV40 DNA. *Nucleic Acids Res* 1984;**12**:3097–115.
- Bishop CE, Whitworth DJ, Qin Y, Agoulnik AI, Agoulnik IU, Harrison WR, Behringer RR, Overbeek PA. A transgenic insertion upstream of *Sox9* is associated with dominant XX sex reversal in the mouse. *Nat Genet* 2000;**26**:490–4.
- McElreavey K, Vilain E, Abbas N, Herskowitz I, Fellous M. A regulatory cascade hypothesis for mammalian sex determination: *SRY* represses a negative regulator of male development. *Proc Natl Acad Sci USA* 1993;**90**:3368–72.
- Kwok C, Weller PA, Guioli S, Foster JW, Mansour S, Zuffardi O, Punnett HH, Dominguez-Steglich MA, Brook JD, Young ID, Goodfellow PN, Schafer AJ. Mutations in *SOX9*, the gene responsible for campomelic dysplasia and autosomal sex reversal. *Am J Hum Genet* 1995;**57**:1028–36.
- Hageman RM, Cameron FJ, Sinclair AH. Mutation analysis of the *SOX9* gene in a patient with campomelic dysplasia. *Hum Mutat* 1997;Suppl 1:S112–13.
- Mansour S, Offiah AC, McDowall S, Sim P, Tolmie J, Hall C. The phenotype of survivors of campomelic dysplasia. *J Med Genet* 2002;**39**:597–602.