ONLINE MUTATION REPORT

Partial deletion of the critical 1.5 Mb interval in Williams-Beuren syndrome

R Heller, A Rauch, S Lüttgen, B Schröder, A Winterpacht

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Williams-Beuren syndrome (WBS, OMIM 194050) is a microdeletion syndrome caused by hemizygosity for multiple genes in 7q11.23 including the elastin locus (ELN).1,2 The classical WBS phenotype comprises elastin arteriopathy (supravalvular aortic stenosis and/or peripheral pulmonary stenosis), connective tissue abnormalities (for example, abnormal joint mobility, hernia and diverticula, hoarse voice), and a particular facial appearance (supraorbital fullness, stellate pattern of the iris, short nose with long philtrum, full lips, and wide mouth). Other frequent features are growth and psychomotor retardation with muscular hypotonia, limited visuospatial cognition, and specific language as well as behavioural abnormalities (overfriendliness and anxiety disorders, hypersensitivity to sounds).3–5 Endocrine and metabolic disturbances (infantile hypercalcaemia) may occur.

Despite at least 21 genes having been identified in the common 1.5 Mb deletion interval in humans,6 their individual contribution to the multisystem phenotype of WBS is unclear. So far, only the gene coding for elastin (ELN) has been proven to be causally involved: ELN is deleted in all WBS patients with a microdeletion 7q11.23 who have been reported to date. However, hemizygosity for ELN alone does not cause WBS, but isolated supravalvular aortic stenosis (SVAS).8 Hence, haploinsufficiency for ELN is necessary but not sufficient for WBS.

Molecular dissection of the WBS phenotype is hindered by the fact that over 95% of patients with the classical phenotype carry an apparently identical ~1.5 Mb deletion interval.9–11 This constant size is explained by non allelic-homologous recombination between duplicons flanking the deletion interval.12 The presence of these direct repeats is assumed to be a predisposing factor for the WBS microdeletion that occurs with a frequency of approximately 1 in 20 000 liveborn children.12 So far, several cases of either classical WBS or SVAS with or without cognitive deficits have been found to be associated with a smaller deletion. In seven of these cases an alternative proximal breakpoint was involved, and an eighth case featured an alternative distal breakpoint13–16 (reviewed in Osborne). We present a further independent case with an atypical deletion and the classical WBS phenotype. Together, these cases indicate that the critical WBS region is smaller than 1.5 Mb.

CASE REPORT AND METHODS

The patient and his healthy twin sister were born to non-consanguineous parents (maternal age 26, paternal age 41) after an uneventful pregnancy. Birth weight, height, and head circumference were within the normal range for twins. The constellation of supravalvular aortic stenosis, pulmonary arte-
valve stenosis, developmental retardation (not talking or walking at the age of 18 months), very friendly nature, and characteristic facial features in the patient led to the clinical diagnosis of Williams-Beuren syndrome (fig 1). Serum calcium levels from repeat measurements were within the normal range with one slightly raised value. When specifically asked about any behavioural traits, the patient’s parents mentioned his hypersensitivity to environmental noise in comparison to his healthy sister.

Chromosomes were analysed by conventional GTG banding of 15 metaphases from lymphocytes at approximately 500 bphs. For FISH analysis, commercial WBS probes from Qbiogene-Alexis (catalogue No CP5155-DC) and from Vysis (catalogue No 32-190041) were used. Some of the non-commercial FISH probes were kindly provided by Dr Lucy Osborne, Department of Genetics and Genomic Biology, Hospital for Sick Children, Toronto, Canada. Labelling, hybridisation, and detection were performed according to the suppliers’ instructions and as described elsewhere.

**RESULTS**

Initial chromosomal analysis yielded a normal 46,XY karyotype. FISH analysis with the commercially available WBSCR probe from Qbiogene-Alexis (catalogue No CP5155-DC) showed two specific signals at 7q11.23 in all analysed metaphases (example shown in fig 2A). However, there was a reproducible difference in signal intensity for the cognate probe (fig 2A) that was not found in the metaphases from either of the parents (data not shown). In view of the clinical diagnosis and of the fact that the WBSCR probe represents three different regions (around FZD9, LIMK1, and CYLN2) and covers almost the complete WBS chromosome region (fig 2A), a further 25 metaphases were analysed with the commercially available FISH probe from Vysis (catalogue No 32-190041). This probe consists of an approximately 180 kb probe covering the ELN and LIMK1 genes. There was one signal only in each of the 25 metaphases (fig 2B). The result was compatible with a de novo rearrangement that has led to a deletion including the ELN locus but clearly not of all the loci within the WBSCR that are recognised by the 7q11.23 WBSCR probe from Appligene-Oncor. We concluded that the WBS phenotype in this patient was most likely caused by an atypical 7q11.23 deletion.

Microsatellite analysis of DNA from peripheral blood lymphocytes of both parents and the patient showed biparental pattern for D7S2476 and D5489B, but was not informative.

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**Figure 2** Fluorescence in situ hybridisation with commercial microdeletion probe sets for 7q11.23 on metaphases from peripheral lymphocytes of our patient. Sequence contents as given by the manufacturers (Qbiogene-Alexis, Vysis). (A) No apparent deletion with the WBSCR probe, but different strength of signal for the cognate probe (white arrows). (B) Hemizygous microdeletion with ELN probe (missing signal marked by curved arrow).
for D7S613 and D7S1870 (data not shown, for location of markers see fig 3).

To map the 7q11.23 breakpoints in our patient more accurately, PAC and cosmid probes for FISH analysis were used in dual colour analysis together with chromosome 7 specific centromeric alphoid DNA as control. The FISH results (fig 3) proved a partial deletion, caused by a distal recombination event at the common telomeric breakpoint, as suggested by the hybridisation signals for the PAC clones RP5-1186P10. Representative microscopic images are given at the top. The control probe in (A-D) contains chromosome 7 specific centromeric alphoid DNA and is labelled with rhodamine (red signals). The experimental probe is FITC labelled (green signals). In (E) the control probe at 7pter is labelled with FluorX (green signals) while the experimental probe is labelled with Cy3 (red signals). Note that the signal intensities for PAC clones H_DJ0953F13 and RP5-1186P10 differ in strength between the two homologous chromosomes 7, suggesting partial hybridisation on one chromosome 7 (marked by white arrows). The proximal and distal breakpoints in our patient are therefore assumed within the regions spanned by these two PACs. At the bottom, the extent of the partial deletions of the WBSCR that have been published is summarised. Cases 1-3: this report and Botta et al.13 Cases 4-8: refs 14-16. Case 9: refs 16 and 27.

DISCUSSION

Williams-Beuren syndrome belongs to a group of genomic disorders that result from regional genomic architecture predisposing to recombination events. In the case of WBS, non-allelic homologous recombination between segmental DNA duplications flanking the WBS region in 7q11.23 leads to a ~1.5 Mb deletion. The finding that the relatively well defined WBS phenotype is associated with an apparently identical deletion interval in >95% of cases raised hopes that a molecular dissection of the phenotype would be feasible. The number of genes identified within the deletion interval has increased steadily and has now reached at least 21 (UCSC Genome Browser on Human November 2002 Freeze at http://genome.cse.ucsc.edu/). However, the understanding of their role in the WBS phenotype has remained unchanged since the ELN gene has been identified as the cause of the vascular malformations in WBS, mainly because of the invariant deletion size in WBS.

Naturally, but rarely occurring 7q11.23 deletion variants in humans may help to identify the genes involved by phenotype-genotype correlation studies (fig 3). The first such atypical deletions were reported by Botta et al.13 Two patients out of 50 with the classical WBS phenotype had an uncommon centromeric breakpoint between the STX1A and ELN gene, hence questioning the role of the proximal WBSCR in the WBS phenotype. The patient reported here is the third case and thus supports the idea that the dysmorphic, cardiovascular, and at least some of the behavioural features of the WBS phenotype are caused by haploinsufficiency for genes.
in the part of the 1.5 Mb interval that is telomeric to the STX1A gene (fig 3). These genes do not only seem to be sufficient but also necessary for the WBS phenotype as illustrated by six partial deletions involving either just the ELN ± LIMKI genes or the two-thirds of the 1.5 Mb interval centromeric to the RFC2 gene (cases 5–9). In none of the six cases was there a full WBS phenotype. Rather, these patients had either an isolated SVAS or an SVAS in combination with some degree of cognitive deficits.1 Our conclusion is that the true WBSCR is more likely an ~950 kb interval containing possibly 12 genes from WBCS21 to the centromeric side to GTF2I on the telomeric side. This hypothesis is important as it limits the number of genes that potentially determine the WBS phenotype and excludes STX1A as a possible candidate gene. The lack of STX1A mutations in five patients, who have WBS but no detectable microdeletions, supports this idea.2

Nevertheless, we cannot completely exclude that the partial telomeric deletions cause a position effect on the neighbouring chromosome region and may mimic haploinsufficiency for the complete set of genes in the 1.5 Mb WBSCR. The idea of a position effect is discussed in the recent publication of a spontaneously occurring familial translocation with disruption of the ELN gene in intron 5. Several members of this family who carried an identical translocation presented variably with WBS, SVAS, or no recognisable phenotype.10 The analysis of the mouse genomic sequence that is orthologous to the WBS, SV AS, or no recognisable phenotype.

The authors wish to thank the family of the patient for their cooperation, Michaela Kirsch for technical assistance, and Dr L R Osborne (Toronto) for providing several FISH probes.

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