

REVIEW

Clinical significance of copy number variations in the 11p15.5 imprinting control regions: new cases and review of the literature

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ABSTRACT

Among the clusters of imprinted genes in humans, one of the most relevant regions involved in human growth is localised in 11p15. Opposite epigenetic and genomic disturbances in this chromosomal region contribute to two distinct imprinting disorders associated with disturbed growth, Silver–Russell and Beckwith–Wiedemann syndromes. Due to the complexity of the 11p15 imprinting regions and their interactions, the interpretation of the copy number variations in that region is complicated. The clinical outcome in case of microduplications or microdeletions is therefore influenced by the size, the breakpoint positions and the parental inheritance of the imbalance as well as by the imprinting status of the affected genes. Based on their own new cases and those from the literature, the authors give an overview on the genotype–phenotype correlation in chromosomal rearrangements in 11p15 as the basis for a directed genetic counselling. The detailed characterisation of patients and families helps to further delineate risk figures for syndromes associated with 11p15 disturbances. Furthermore, these cases provide us with profound insights in the complex regulation of the (imprinted) factors localised in 11p15.

INTRODUCTION

Imprinted genes with a parent-of-origin specific expression are involved in various aspects of growth that are rooted in the prenatal period. As a result, disturbances of these genes result in aberrant growth as one key feature in nearly all known imprinting disorders (IDs). Imprinted genes tend to cluster, and thus the imprinting control is often not restricted to a single gene at an imprinted locus but affects the expression of several factors. Among these clusters of imprinted genes, one of the most relevant regions involved in human growth is localised on the short arm of chromosome 11 (11p15). Opposite epigenetic and genomic disturbances in this chromosomal region contribute to two distinct IDs associated with disturbed growth, Silver–Russell syndrome (SRS) and Beckwith–Wiedemann syndrome (BWS). Additionally, in nearly all patients with aberrant methylation at multiple loci (multilocus methylation defects), the imprinted 11p15 regions are affected (for review see Eggermann *et al*¹).

The 11p15 region contains a number of imprinted genes. Their expression is regulated by two different imprinting control regions (ICR1 and ICR2), also

called *H19* differentially methylated region (DMR) and KvDMR1 (figure 1). The telomeric ICR1 confers a differential chromatin architecture to the two parental alleles leading to reciprocal expression of *H19* and *IGF2* (insulin-like growth factor 2).

The ICR1 contains seven ccctc-binding factor (CTCF) target sites (CTCF1–CTCF7) in the DMR 2 kb upstream of *H19* and shows allele-specific methylation. The zinc-finger binding factor CTCF binds to the maternal unmethylated ICR1 copy and thereby forms a chromatin boundary. This CTCF binding mechanism blocks *IGF2* and promotes *H19* transcription of the maternal 11p15 copy.

The centromeric ICR2 is maternally methylated and controls the monoallelic silencing of the non-coding antisense transcript *KCNQ1OT1* as well as the monoallelic expression of cyclin-dependent kinase inhibitor 1c (*CDKN1C*) and potassium channel KQT-family member 1 (*KCNQ1*) in a not yet fully understood way.

As aforementioned, two IDs are known to be associated with molecular alterations in 11p15: SRS is mainly characterised by severe prenatal and postnatal growth restriction. The children are relatively macrocephalic and their faces are triangular-shaped with broad foreheads and pointed, small chins. In many cases, asymmetry of limbs and body and clinodactyly V are present. Growth failure is often accompanied by severe failure to thrive, and severe feeding difficulties in early childhood are frequent. However, the clinical diagnosis is difficult and requires an anamnestic investigation of an experienced clinician. The genetic basis of SRS is heterogeneous. In approximately 10% of SRS patients, a maternal uniparental disomy for chromosome 7 (upd(7)mat) can be observed (for review see Abu-Amro *et al*²). More than 40% of SRS patients show a hypomethylation of the ICR1 in the imprinted region 11p15. However, upd(11)mat has been reported only once.³ Nearly 7% of SRS patients carrying an ICR1 hypomethylation show aberrant methylation at additional imprinted loci, and in all cases the ICR2 in 11p15 was affected (for review see Eggermann *et al*¹). Numerous (sub-microscopic) chromosomal disturbances have been described in SRS patients; among them, 11p15 disturbances (tables 1 and 2).^{17 18}

Interestingly, the opposite 11p15 epigenetic and genetic findings can be observed in BWS. BWS was initially called EMG syndrome from its three main features of exomphalos, macroglossia and



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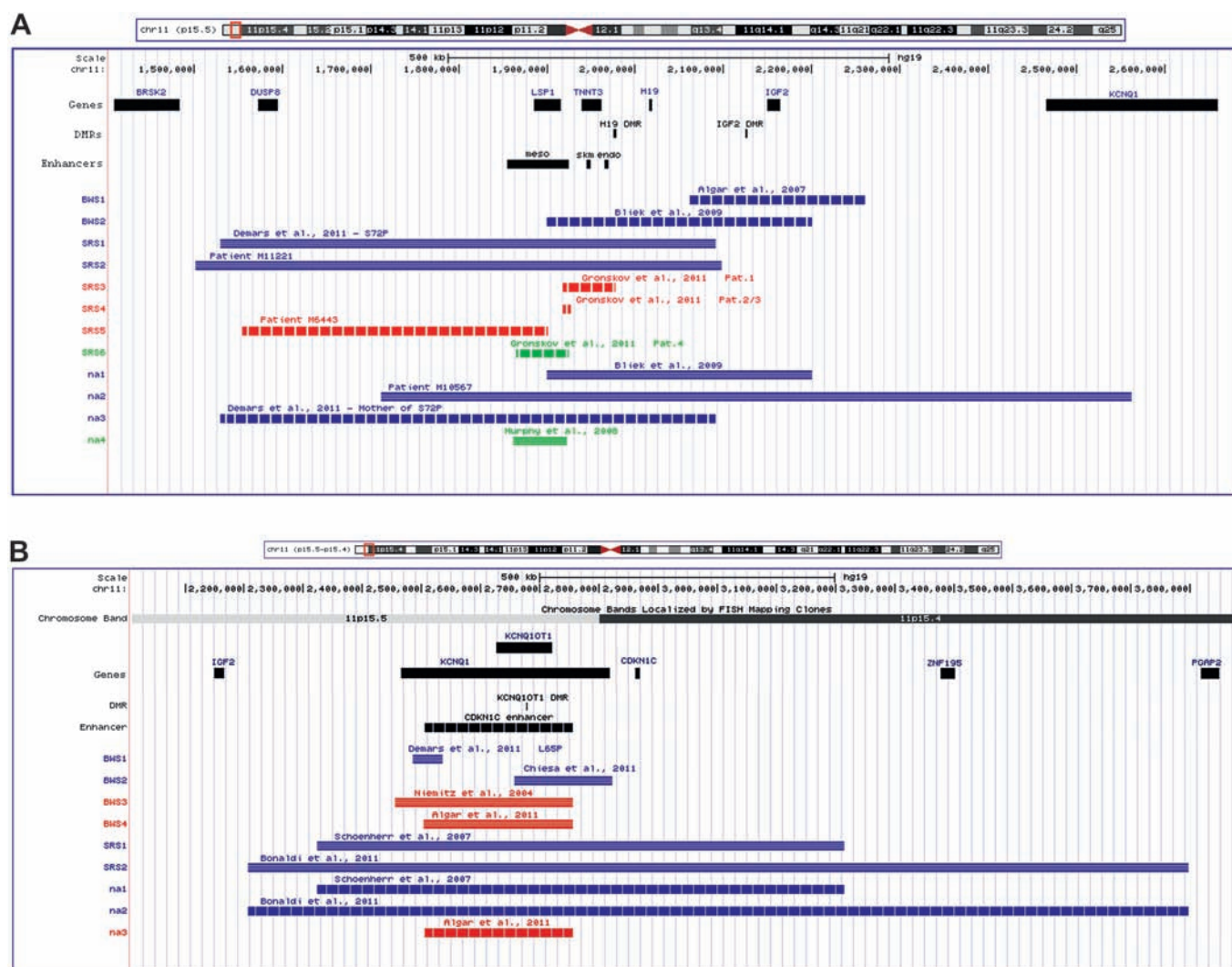


Figure 1 UCSC genome browser custom tracks for the 11p15 region for the cases in this study and for the cases from the literature. (A) ICR1. (B) ICR2. (Blue: duplication; red: deletion; green: translocation; horizontal striping: paternal allele; vertical striping: maternal allele; BWS, Beckwith–Wiedemann syndrome phenotype; SRS, Silver–Russell syndrome phenotype; na, non-affected carrier; meso, mesodermal; endo, endodermal; skm, skeletal muscle enhancers.)

(neonatal) gigantism. Additional signs include neonatal hypoglycaemia, hemihypertrophy, organomegaly, earlobe creases, polyhydramnion, haemangioma and cardiomyopathy. In 5%–7% of children, embryonal tumours (most commonly Wilms' tumour) are diagnosed. The clinical diagnosis of BWS is often difficult due to its variable presentation and the phenotypic overlap with other overgrowth syndromes (for review see Enklaar *et al*¹⁹). In nearly 70% of BWS patients, an altered expression or mutations of 11p15.5 encoded factors can be observed with a preponderance of an ICR2 hypomethylation accounting for nearly 50% of cases. Also, upd(11p15)pat is the second important alteration, while ICR1 hypermethylation is rare. In single cases, duplications or deletions in 11p15 have been reported (tables 1 and 2, figure 1). Most BWS cases are sporadic but familial inheritance is observed in 15% of all cases. In BWS families without aberrant 11p15 methylation, *CDKN1C* point mutations are frequent.

Whereas large duplications affecting both ICRs in 11p15 are known to be associated with growth retardation/SRS or overgrowth/BWS depending on the parental origin of the imbalance (table 1), the characterisation of carriers of rare small disturbances within either the ICR1 or the ICR2 allows the identi-

cation of key elements in 11p15.5 responsible for the clinical course. On the basis of three own cases and data from the literature, we review the role of submicroscopic imbalances in 11p15.5 in the aetiology of growth disturbances.

PATIENTS

Two of the patients were initially referred as SRS for routine diagnostic testing (M11221, M6443), and the third patient (M10567) was molecularly karyotyped because of mental retardation but she did not show any aberrant growth phenotype. Appropriate informed consent was obtained from all participating patients or their legal representatives.

The 5.5-month-old girl **M11221** was the third child of healthy non-consanguineous German parents (figure 2). The father's height was 180 cm (0.28 SD), and the mother's height of 160 cm was within the lower range (−0.78 SD). The maternal brother was of normal height (180 cm/0.28 SD), the maternal grandmother's height was within the lower range (157 cm/−1.29 SD), and the grandfather was of normal height (173 cm/−0.73 SD). The propositus' elder sisters were also small at birth, and persisted at the lower range (8 years old sister: 123 cm (−1.03 SD), 3.5 years old sister: 94 cm (−2.42 SD)). Further

Table 1 List of cases with rearrangements in 11p15 and their (putative) functional consequences

Imbalance	Affected region/gene	Allele	Phenotype	Breakpoints (hg18)	Size	(Putative) functional result	Reference
ICR1 and ICR2 affected							
Duplication	ICR1 and ICR2	Maternal	SRS	chr11:170,000-4,100,000 chr11:1,760,993-2,983,146 chr11:188,509-9,053,369	~ 3.9 Mb 1.22 Mb 8.86 Mb	CDKN1C ↑	Bliek <i>et al</i> , 2009 ⁴ Chiesa <i>et al</i> , 2011 ⁵ M4953
Duplication	ICR1 and ICR2	Paternal	BWS	chr11:170,000-4,100,000 chr11:188,509-2,883,134	~ 3.9 Mb 2.69 Mb	IGF2 ↑	Bliek <i>et al</i> , 2009 ⁴ ; M9316
Imbalances in ICR1							
Duplication	Total ICR1	Paternal	BWS/WT BWS	chr11:2,061,361-2,261,639 chr11:1,900,000-2,200,000	200 kb ~ 300 kb	IGF2 ↑	Algar <i>et al</i> , 2007 ⁶ ; Bliek <i>et al</i> , 2009 ⁴
Duplication	Total ICR1	Maternal	Not affected	chr11:1,900,000-2,200,000 chr11:1712385-2562224	~ 300 kb 850 kb	IGF2 →	Bliek <i>et al</i> , 2009 ⁴ ; M10567
Duplication	H19	Maternal	SRS	chr11:1,522,259/1,530,602-2,092,578/2,097,357 chr11:1,501,757-2,098,162	562 kb 596 kb	H19 ↑ >>trans IGF2 ↓	Demars <i>et al</i> , 2011 ⁷ (S72P), M11221
Duplication	H19	Paternal	Not affected	chr11:1,522,259/1,530,602-2,092,578/2,097,357	562 kb	H19 →	Demars <i>et al</i> , 2011 ⁷ (S72P mother)
Deletion	CTCF-BS 2-3	Paternal	Not affected	CTCF BS 2-3	1.8 kb	Binding of CTCF at maternal allele	Sparago <i>et al</i> , 2004 ⁸ ; Demars <i>et al</i> , 2010 ⁹
Deletion	CTCF-BS 2-3	Maternal	BWS with GOM of ICR1	CTCF BS 2-3	1.8 kb	Insulator model	Sparago <i>et al</i> , 2004 ⁸ ; Demars <i>et al</i> , 2010 ⁹
Deletion	CTCF-BS 3-5	Maternal	Not affected	CTCF BS 3-5	2.2 kb	Insulator model	Prawitt <i>et al</i> , 2005 ¹⁰
Deletion + duplication	CTCF-BS 3-5 + IGF2	Maternal	BWS with GOM of ICR1	CTCF BS 3-5	del.: 2.2 kb dup: ?	Insulator model	Prawitt <i>et al</i> , 2005 ¹⁰
Deletion/inversion/translocation	Breakpoints in the H19/IGF2 enhancer region	Paternal	SRS	Pat. 1: chr11:1,918,222-1,977,026 Pat. 2/3: chr11:1,918,312-1,927,132	58.8 kb 8.8 kb	Disturbed interaction of H19/IGF2 enhancer with IGF2 promotor >> IGF2 ↓; IGF2P0 LOM	Gronskov <i>et al</i> , 2011 ¹¹
			IUGR	Pat. 4 (~ breakpoint): chr11:1,865,000-1,925,000			Murphy <i>et al</i> , 2008 ¹²
			SRS	chr11:1,554,705-1,900,779	346 kb		M6443
Deletions/point mutations	OCT2/SOX2-BS/OCT1	Maternal	BWS with GOM of ICR1	A2 repeat (5930-6141: AF125183) B3 repeat (7277-7284: AF125183) A2 repeat (6153: AF125183)	212 bp 8 bp SNP	Disturbed binding of transcription factors OCT2, SOX2, OCT1 >> ICR1 GOM	Demars <i>et al</i> , 2010 ⁹
Translocation	Breakpoints in the H19/IGF2 enhancer region	Maternal	Not affected	184 kb upstream of IGF2 (~1,862,000-1,922,000)	~ 60 kb	Disturbed interaction of H19/IGF2 enhancer with IGF2 promotor >> IGF2 ↓; IGF2P0 LOM	Murphy <i>et al</i> , 2008 ¹²
Imbalances in ICR2							
Duplication	Total ICR2	Maternal	SRS	chr11:2,323,952-3,215,381 chr11:2,196,379 / 2,206,866-3,796,585 / 3,809,132	891 kb 1.59 Mb	CDKN1C ↑	Schönherr <i>et al</i> , 2007 ¹³ ; Bonaldi <i>et al</i> , 2011 ¹⁴
Duplication	Total ICR2	Paternal	Not affected	chr11:2,323,952-3,215,381 chr11:2,196,379 / 2,206,866-3,796,585 / 3,809,132	891 kb 1.59 Mb	CDKN1C →	Schönherr <i>et al</i> , 2007 ¹³ ; Bonaldi <i>et al</i> , 2011 ¹⁴
Duplication	KCNQ1: introns 1-2	Maternal	BWS with LOM of ICR2	chr11:2,485,000-2,535,000	50 kb	Duplication in cis >> altered chromatin conformation >> LOM >> KCNQ1OT1 ↑; CDKN1C ↓	Demars <i>et al</i> , 2011 ⁷ (L65P)
Duplication	KCNQ1: exons 12-15 and KCNQ1OT1: 5' 20 kb	Maternal	BWS with LOM of ICR2	chr11:2,656,737-2,822,824	166 kb	Duplication in cis >> altered chromatin conformation >> LOM >> truncated KCNQ1OT1 >> CDKN1C ↓	Chiesa <i>et al</i> , 2011 ⁵
Deletion	KCNQ1OT1	Maternal	BWS	KCNQ1 Exon 1b/c – Exon 11/14 (~chr11:2,455,053-2,646,057/2,755,112) KCNQ1 Exon 3-Exon 15 (MLPA: ~chr11:2,505,740-2,755,809)	250 kb 330 kb	KCNQ1OT1 →; CDKN1C enhancer deleted >> CDKN1C ↓	Niemitz <i>et al</i> , 2004 ¹⁵ ; Algar <i>et al</i> , 2011 ¹⁶
				KCNQ1 Exon 3-Exon 15 (MLPA: ~chr11:2,505,740-2,755,809)	330 kb	CDKN1C enhancer deleted, but CDKN1C is maternally expressed	Algar <i>et al</i> , 2011 ¹⁶

The functional result has either been reported or suggested in the specific reference, or has been delineated from the general knowledge about gene regulation and expression in 11p15. (↑ expression increased, ↓ expression decreased, → expression is not altered.)

BWS, Beckwith–Wiedemann syndrome phenotype; SRS, Silver–Russell syndrome phenotype; GOM, gain of methylation; WT, Wilms tumour; IUGR, intra uterine growth retardation.

features were not observed. Family history was normal. One spontaneous abortion of the maternal grandmother was reported.

During pregnancy low fetal movements were reported. The patient was born at 34 gestational weeks by primary caesarean

section due to oligohydramnios, severe intrauterine growth retardation and pathological Doppler and cardiotocography. Birth length was 39 cm (−2.28 SD), weight 1030 g (−2.89 SD) and head circumference 28 cm (−2.18 SD). APGAR was 9-10-10.

Table 2 Clinical outcomes in carriers of 11p15 imbalances as they can be delineated from some 'key' cases/families

Phenotype	Origin	Imbalance	ICR1				ICR2			Key cases
			IGF2 enh. (1,855,000– 1,970,000)*	H19 (1,972,982– 1,975,641)	H19 DMR (1,975,008– 1,978,367)*	IGF2 (2,106,923– 2,118,917)	CDKN1C enh. (2,546,981– 2,755,900)*	KCNQ1OT1-DMR (2,676,499–2,678,897)*	CDKN1C (2,861,024– 2,863,571)	
BWS	Pat	Dup								General
										Bliek <i>et al</i> , 2009 ⁴
										Algar <i>et al</i> , 2007 ⁶
	Mat	Dup								Demars <i>et al</i> , 2011 ⁷ : patient L65P
										Chiesa <i>et al</i> , 2011 ⁵
		Del								Niemitz <i>et al</i> , 2004 ¹⁵ ; Algar <i>et al</i> , 2011 ¹⁶
SRS	Pat	Del								M6443; Gronskov <i>et al</i> , 2011 ¹¹ : patients 2+3
										Gronskov <i>et al</i> , 2011 ¹¹ : patients 1
	Mat	Dup								General
										Schönherr <i>et al</i> , 2007 ¹³ ; Bonaldi <i>et al</i> , 2011 ¹⁴
										Demars <i>et al</i> , 2011 ⁷ : patient 72P; M11221
Not affected	Pat	Dup								Schönherr <i>et al</i> , 2007 ¹³ ; Bonaldi <i>et al</i> , 2011 ¹⁴
		Del								Demars <i>et al</i> , 2011 ⁷ : patient S72P mother
	Mat	Dup								Algar <i>et al</i> , 2011 ¹⁶
										M10567; Bliek <i>et al</i> 2009 ⁴

The phenotype is associated with (a) origin—the parent contributing the variant, (b) type of imbalance (duplication/deletion), (c) the affected regions in both ICR1 and ICR2 and (d) the size of the aberration (grey: duplication, black: deletion; horizontal striping: this region is partially affected).

*Coordinates of the CDKN1C enhancer are from Algar *et al* 2011; the exact physical positions of the CDKN1C enhancer, the H19 DMR and the KCNQ1OT1 DMR are currently unclear.

BWS, Beckwith–Wiedemann syndrome phenotype; DMR, differentially methylated region; mat, maternal; pat, paternal; SRS, Silver–Russell syndrome phenotype.

A small midface and a prominent forehead were reported. The placenta weight was remarkably reduced and corresponded to that of 20–25 weeks of gestation (P50 and P10, respectively).

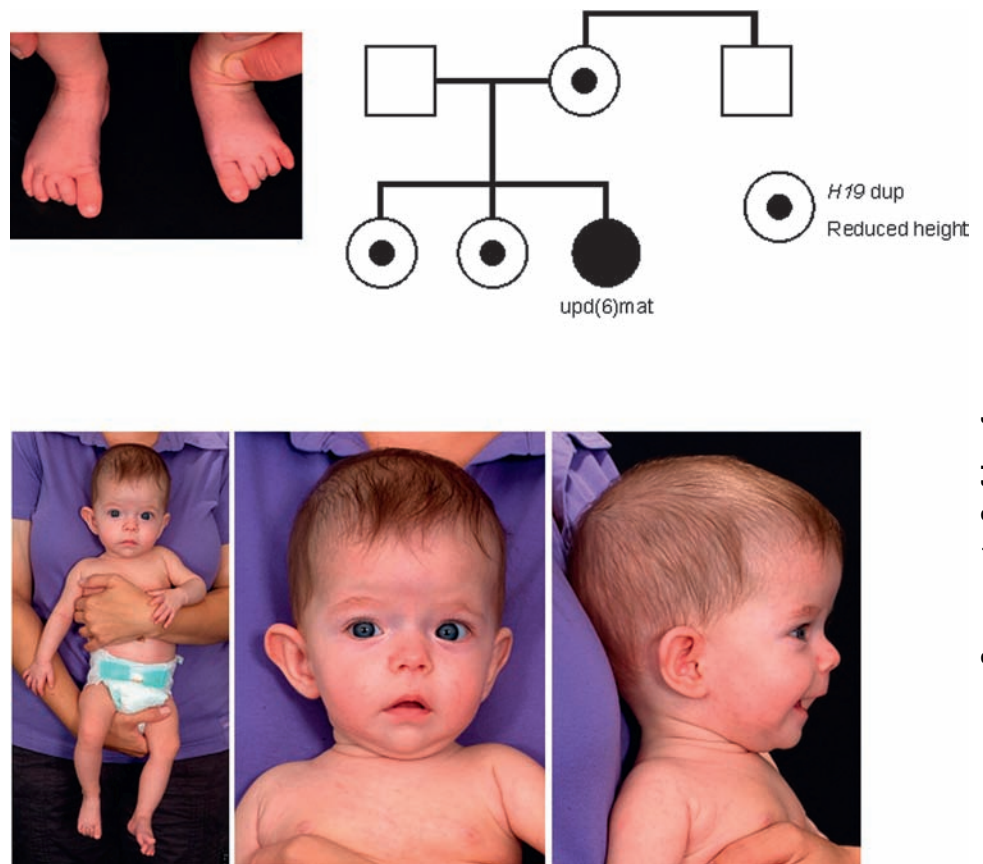
At the age of 7.5 months, the girl was severely growth retarded (length 59 cm (−3.47 SD), weight 4.5 kg (−7.0 SD)). The head circumference of 42 cm (−0.68 SD) was in the normal range and thus corresponded to a relative macrocephaly. She showed a failure to thrive, had muscular hypotonia and motor development was slightly delayed. A mild asymmetry of the face was visible, whereas other parts of the body were not asymmetric. She had an umbilical hernia.

Patient **M6443** is the second child of healthy German parents (father: 28 years old, 180 cm (0.28 SD); mother: 24 years old, 163 cm (−0.27 SD)). The elder sister was of normal growth. Pregnancy was uneventful but terminated at 38 weeks of gestation by caesarean section due to intrauterine growth retardation. Birth weight was 1390 g (−4.4 SD), length 40 cm (−4.83 SD) and head circumference 32 cm (−2.07 SD). Severe feeding difficulties led to gastric tube feeding at the age of 3 months and lasted for 5 weeks.

At the age of 1 1/12 years, the boy presented a short stature (height 65.5 cm/−4.42 SD; weight 5.3 kg/BMI: 12.35 SD) but with relative macrocephaly (head circumference: 44.5 cm/−2.04 SD). Further features suggestive of SRS were a triangular shaped face with a prominent forehead, a micrognathia and a clinodactyly V. Additionally, a cleft palate was reported.

Patient **M10567** is the first child of healthy non-consanguineous German parents (father: 24 years old, 183 cm; mother: 20 years old, 158 cm). Family history was normal. Pregnancy was uneventful; however, the calculated due day was advanced by 4 weeks during pregnancy. She was born spontaneously at 40+3 weeks of gestation. Birth weight was reported as 2770 g (−1.67 SD), length 53 cm (0.59 SD) and head circumference 36 cm (0.85 SD). Motor development was delayed with free walking at 2 years of age, and language development was normal. At the age of 7 years, she attended a special school due to motor and mental delay. She was hypotonic, with no special neurological deficits. During the first years of life, growth and weight were slightly below the third centile, with catch-up growth at 7 5/12 years of age (weight 20.7 kg (P10), length 113.8 cm (0.5 cm, <P3), BMI 16.0 (P50), head circumference 50.9 cm (P25)). Average growth velocity between age 4 and 7 years was 6.2 cm/year (P54). IGF I was slightly low (53 ng/ml, <P5), and IGFBP3 was in the normal range (2958 ng/ml, >P5). She presented with discrete phenotypic features including a long narrow facial appearance, slightly upslanting palpebral fissures, a small mouth, a transverse groove of the chin, relatively large ears, a symmetric clinodactyly digit V with Dubois sign, simian crease on the right and bilateral syndactyly toes II/III. Early second dentition was observed. Asymmetry was not present. Fragile X-syndrome testing was negative.

Figure 2 Clinical features (age 7.5 months) and pedigree of patient M11221 with familial 598 kb duplication affecting 11p15.5 and uphd(6)mat.



MATERIALS AND METHODS

Genomic DNA was isolated from peripheral lymphocyte cells by a simple salting-out procedure.

Methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA) was performed using the SALSA MLPA kit ME030 from MRC Holland (Amsterdam, The Netherlands) according to the manufacturer's protocol.

For rapid screening of aberrant methylation of several DMRs which have been reported to be frequently affected in multilocus methylation defects patients (ie, *PLAGL1* (6q24), *IGF2R* (6q25), *GRB10* (7p13), *MEST* (7q32), *H19* (11p15), *KCNQ1OT1* (11p15), *IGF2P0* (11p15), *MEG3* (14q32)), we applied multilocus quantitative methylation-sensitive single-nucleotide primer extension (MS-SNuPE) tests.²⁰

For the detection of submicroscopic genomic imbalances (<5 Mb), we typed genomic DNA of the patients by using the Affymetrix GeneChip®Genome-Wide Human SNP 6.0-Array (High Wycombe, UK) including 1.8M oligonucleotide markers. After PCR amplification and labelling of the patients' DNA the samples were hybridised to the arrays according to the manufacturer's instructions. Scanning was performed with an Affymetrix GeneChip®Scanner 3000 7G, and bioinformatics was done with the Affymetrix Genotyping Console 4.0 and the Chromosome Analysis Suite 1.1 software using annotation files version NA30 (hg18/NCBI build 36). For analysis and interpretation only copy number variations >100 kb with a mean marker distance <5 kb were considered.

To determine the inheritance of the 11p15 copy number variations in the families of patients M11221 and M10567 and to confirm the uniparental disomy of chromosome 6 in patient M11221, short tandem repeat typing with markers within 11p15 and on chromosome 6 was performed according to standard protocols.

RESULTS

Three patients with rare submicroscopic imbalances in the telomeric ICR1 in 11p15 were recruited either because of their phenotype resembling to SRS (patients M11221 and M6443) or because of molecular karyotyping results (patient M10567).

In patient **M11221** initial conventional cytogenetic analysis (500 bands) was normal. By MS-MLPA, increased hybridisation signals as well as aberrant methylation of the *H19*-specific probes could be determined, whereas the *IGF2* probes as well as those for the ICR2 factors and the control probes showed normal copy numbers. The duplication of *H19* in the ICR1 in 11p15.5 was then confirmed by molecular karyotyping and microsatellite analysis, indicating a 596 kb duplication in 11p15.5 (NCBI36/hg18: chr11:1.501.757-2.098.162) which affected the *H19* but not the *IGF2* gene (figure 1A). The duplication was inherited from the mother, and the two sisters also carried the disturbance. The maternal brother was not a carrier of the familial duplication.

Multilocus analysis by MS-SNuPE confirmed the 11p15 duplication; additionally, an increased methylation of both chromosome 6 loci *PLAGL1* and *IGF2R* was observed. Further imprinted loci showed normal results except the *H19* locus. Analyses of DNA samples of the mother and the two sisters revealed normal methylation patterns for the chromosome 6 loci. Microsatellite analysis of chromosome 6 markers confirmed a complete maternal uniparental heterodisomy of the whole chromosome 6 (uphd(6)mat) which was not detectable by SNP array typing.

In patient **M6443**, conventional karyotyping was performed after birth and showed a normal male karyotype. Further 11p15.5-specific MS-MLPA and testing for upd(7)mat did not reveal any irregularities. Subsequent SNP array analysis revealed a 346 kb deletion in 11p15.5 (NCBI36/hg18: chr11:1.554.705-

1.900.779) which was inherited from the healthy father. Unfortunately, paternal grandparents were not available (figure 1A). This copy number variation affected the mesodermal enhancer of *IGF2* but not the *H19* DMR or other sequences analysed by the MS MLPA approach. By MS-SNuPE, a hypomethylation at the *IGF2P0* DMR was visible.

Patient **M10567** as well as her healthy mother carried a 849 kb duplication in 11p15.5 (NCBI36/hg18: chr11:1.712.385-2.562.224), affecting both *H19* and *IGF2* (figure 1A). In the mother, the duplication had originated de novo but affected the grandmaternal chromosome 11. We therefore assume that the patients' phenotype is not caused by the 11p15 duplication but another, so far unknown cause.

DISCUSSION

The phenotype of carriers of duplications including both the telomeric ICR1 and the centromeric ICR2 in 11p15.5 is meanwhile well established: whereas duplication of maternal 11p15.5 material is generally associated with growth retardation and features suggestive for SRS, duplication of the paternal 11p15.5 copy results in overgrowth and BWS symptoms.

However, this strict association is at least in part derestricted in carriers of imbalances affecting only parts of the two ICRs. Here at a first glance unexpected clinical outcomes can be observed (figure 1, tables 1 and 2).

Duplications of the total paternal **ICR1** including *H19* and *IGF2* result in overgrowth (and BWS), whereas duplication of the maternal ICR1 copy are not associated with an aberrant phenotype as our patient M10567 and his family as well as the family published by Blik *et al*⁴ show (figure 1A). The situation changes if the duplication is restricted to the *H19* region (our patient M11221 and her family; patient S72P of Demars *et al*⁷): carriers of microduplication affecting the maternal allele present a SRS phenotype whereas duplications of the paternal *H19* copy are not associated with an unusual phenotype. In agreement with these observations, deletions within the maternal *H19* DMR result in BWS^{7 8 10} whereas deletions within the paternal *H19* gene/DMR do not cause a specific phenotype.^{7–10} In contrast, carriers of deletions of the paternal allele show a SRS phenotype if the deletion is localised telomeric from the *H19* DMR and affects the *IGF2* telomeric enhancer (our patient M6443¹¹). In these patients with deletions within the telomeric *IGF2* enhancers, a hypomethylation of the *IGF2P0* DMR can be observed. This prompted Grønskov *et al*¹¹ to speculate that *IGF2P0* methylation is established by the interaction with its telomeric enhancers and therefore reflects the *IGF2* promoter activity.

Duplications of the total **ICR2** region result in a SRS-like phenotype in case the maternal 11p15 copy is affected, whereas the duplication of paternal material is not associated with clinical symptoms (figure 1B).^{13 14} In contrast, a BWS phenotype can be observed in case the duplication of maternal material is restricted to the *KCNQ1OT1* DMR or the putative *CDKN1C* enhancer region.^{5 7} Interestingly, the deletion of the maternal copy of both the *KCNQ1OT1* DMR and the putative *CDKN1C* enhancer results in BWS, whereas the phenotype is normal if the paternal allele is deleted.^{6 15}

The growing number of genomic imbalances within the two ICRs of paternal or maternal origin considerably helps us to understand the complex regulation mechanisms of the imprinting regions in 11p15 (table 1). These disturbances do not simply result in an increase or decrease of expression caused by an altered copy number, but they can also affect methylation patterns and chromatin organisation and thereby indirectly affect the regulation of imprinted genes.

In addition to the complex genotype–phenotype correlations in carriers of imbalances in 11p15.5, our patient M11221 and her family is furthermore remarkable as the index patients phenotype severely differs from that of her mother and sisters also carrying the ICR1 duplication: whereas her relatives are at the lower end of normal growth centiles, the patient is severely growth retarded. Further features were suggestive for the diagnosis of SRS. Indeed, we observed that the patient is a carrier of a uphd(6)mat, whereas the other 11p15.5 duplication carriers in her family were not. Homozygosity for a recessive mutation as the cause for the phenotype in our patient can nearly be excluded as SNP array typing did not reveal any evidence for isodisomic regions. One might rather speculate that the uphd(6)mat is responsible for the phenotype: indeed, at least two upd(6)mat patients have been reported to be associated with a severe IUGR, but generally upd(6)mat has not yet been reported to be associated with a specific clinical phenotype (for review see Salahshourifar *et al*²¹).

From the diagnostic point of view, the advantages and limitations of the different applicable techniques for mutation detection have to be carefully considered.

For routine diagnostic of BWS and SRS, methylation-specific approaches are widely used. In particular, MS-MLPA is a well accepted testing procedure as it detects the majority of the currently known aberrations in the ICR1 and the ICR2 in 11p15 in both SRS and BWS patients. However, the currently available test discovers only aberrant methylation of the DMRs of *H19* and *KCNQ1OT1* as well as copy number variations of the coding sequences in *IGF2*, *H19*, *CDKN1C* and *KCNQ1*. As our cases and those from the literature show, patients might also carry copy number variations and methylation defects in other regulative regions within 11p15.5 (our patient M6443¹¹). In case of exclusion of the typical ICR1 and ICR2 alterations, further molecular characterisation is therefore needed to identify unusual mutations and epimutations. In carriers of copy number variations of 11p15, a precise breakpoint characterisation is essential to elucidate a genotype–phenotype correlation. Testing for aberrant methylation of further imprinted loci additional to the 11p15 DMRs should also be considered to identify patients with multilocus methylation defects, which might either carry genomic mutations like ZFP57 or genomic imbalances.^{22 23} Both findings can influence recurrence risks and have to be discussed in genetic counselling.

In summary, duplications or deletions affecting the ICR1 and/or ICR2 in 11p15 have been reported for both SRS and BWS as well as in clinically normal carriers. The clinical outcome in carriers of these microduplications or microdeletions is influenced by the size, the breakpoint positions and the parental inheritance of the imbalance reflecting the imprinting status of the affected genes (table 2). Due to the complexity of the 11p15 imprinting regions and their interactions, the interpretation of the copy number variations in that region is complicated and needs careful investigation.

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