A Beckwith-Wiedemann Syndrome Case with de novo 24 Mb Duplication of Chromosome 11p15.5-14.3

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Research

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Abstract

Background

Molecular genetic testing for the 11p15-associated imprinting disorder Beckwith-Wiedemann syndrome(BWS) is challenging because of the molecular heterogeneity and complexity of the affected imprinted regions. An accurate diagnosis of BWS requires a complete molecular method to analyze epigenetic changes.

Case presentation

We reported a Chinese case with BWS detected by SNP array analysis and methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA). The genetic analysis showed a de nove duplication of 24 Mb at 11p15.5-14.3 is much longer than ever reported. MS-MLPA showed copy number changes with a peak height ratio value of 1.5(three copies) at 11p15. The duplication of paternal origin with

increase of methylation index of 0.68 at H19 and decreased methylation index of 0.37 at KCNQ1OT1.

Conclusion

Combined chromosome microarray analysis and methylation profiling provided reliable diagnosis for this paternally derived duplication of BWS. The phenotype associated with 11p15 duplications depends on the size, genetic content, parental inheritance and imprinting status. Identification of these rare duplications is crucial for genetic counselling.

Full Text

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Figures

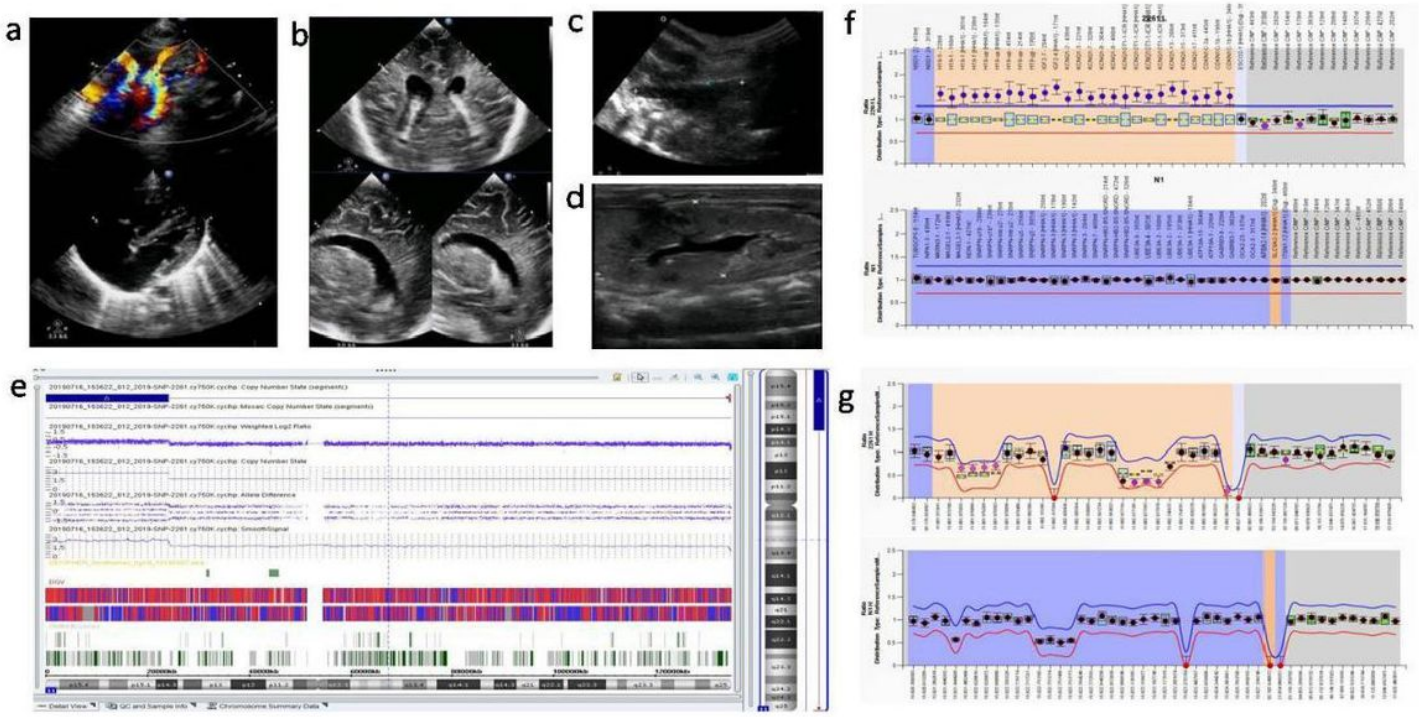

Figure 1

Ultrasound images, SNP array analysis and MS-MLPA results of this patient. (a) Ultrasound examinations demonstrated cardiac ultrasound results. (b) Cranial ultrasound showed bilateral ventricular dilatation. (c) Abdominal ultrasound showed abdominal hydrocele. (d) Renal ultrasound showed that both kidneys were larger. (e) The SNP array revealed a 24,170 kb duplication at (arr[hg19] 21q11.2q22.3(15,016,486-48,093,361) x3). (f) MS-MLPA result of copy number change. (g) MS-MLPA result of methylation index.