Alternative mechanisms associated with silencing of \textit{CDKN1C} in Beckwith–Wiedemann syndrome

N Diaz-Meyer, Y Yang, S N Sait, E R Maher, M J Higgins

\textbf{Background:} Mutations in the imprinted gene \textit{CDKN1C} account for approximately 10% of Beckwith–Wiedemann syndrome (BWS) cases. Fibroblasts from BWS patients with loss of methylation (LOM) at the imprinting control region (ICR) KvDMR1 have reduced \textit{CDKN1C} expression. Another group of BWS patients with downregulated \textit{CDKN1C} expression but with normal methylation at KvDMR1 has been identified.

\textbf{Objective:} To investigate the mechanism of \textit{CDKN1C} silencing in BWS in these two classes of patients.

\textbf{Methods:} The \textit{CDKN1C} promoter region was analysed for changes in DNA methylation using bisulphite sequencing, and for alterations in chromatin structure using the chromatin immunoprecipitation (ChIP) assay.

\textbf{Results:} There was only spurious CpG methylation of the \textit{CDKN1C} promoter in fibroblast DNA from both normal individuals and patients with BWS, irrespective of the methylation status of KvDMR1. There was no detectable change in chromatin structure at the \textit{CDKN1C} promoter in patients with LOM at KvDMR1. BWS patients with downregulated \textit{CDKN1C} and normal methylation at KvDMR1 had depletion of dimethylated H3-K4 and enrichment of dimethylated H3-K9 and HP1\textsubscript{\alpha} at the \textit{CDKN1C} promoter, suggesting that in these cases gene silencing is associated with repressive chromatin changes.

\textbf{Conclusions:} \textit{CDKN1C} may be downregulated by multiple mechanisms including some that do not involve promoter methylation. In BWS patients with normal methylation at KvDMR1 and reduced expression of \textit{CDKN1C}, repressive chromatin may play a role, but the absence of methylation and repressive chromatin structure at the \textit{CDKN1C} promoter in BWS patients with LOM at KvDMR1 argues for a direct role of this epimutation in silencing \textit{CDKN1C}.

A n imbalance in the expression of imprinted genes in human chromosome band 11p15.5 (fig 1A), either by mutation or deregulation of genomic imprinting, results in Beckwith–Wiedemann syndrome (BWS), an over-growth condition where patients have a 1000-fold increased risk of developing embryonal tumours.\textit{CDKN1C} (also known as\textit{p57\textsuperscript{kip2}}) is one of the genes in human chromosome 11p15.5 that is implicated in BWS. It encodes a cyclin dependent kinase inhibitor involved in the negative regulation of the cell cycle\textsuperscript{3} and is critical during mouse embryogenesis.\textsuperscript{4,5} \textit{CDKN1C} is imprinted and primarily expressed from the maternal allele; however, in humans some expression (5–30%) is observed from the paternal chromosome.\textsuperscript{6,7} In BWS, mutations of \textit{CDKN1C} have been found in 40% of familial cases and in roughly 5% of sporadic cases.\textsuperscript{8–10}

Chromosome 11p15.5 contains at least two imprinting control regions (ICRs), which are differentially methylated in the germline and which regulate the imprinted expression of two or more genes. The \textit{H19} ICR controls the imprinted expression of the \textit{H19} and \textit{Igf2} genes (and the \textit{Im} gene in mouse) (see the paper by Arney\textsuperscript{11} and references therein), whereas KvDMR1 functions by silencing at least two maternally expressed genes on the paternal chromosome.\textsuperscript{12–14} The exact mode of action of KvDMR1 is still unknown. Enhancer blocking assays suggest that KvDMR1 may function as a histone modification sensitive silencer or insulator.\textsuperscript{15–18} KvDMR1 is normally methylated on the maternally inherited allele and unmethylated on the paternal allele.\textsuperscript{19–20} However, a large proportion (~50%) of non-UPD BWS patients suffer an epimutation at KvDMR1, namely loss of methylation (LOM) at the maternally inherited allele.\textsuperscript{19–21} These patients have a high occurrence of omphalocele similar to BWS patients with mutations in \textit{CDKN1C}.\textsuperscript{19–21} This observation suggested that LOM at the maternally inherited KvDMR1 allele in BWS may result in the downregulation of paternally expressed genes including \textit{CDKN1C}. Indeed, we have recently demonstrated a strong correlation between LOM at KvDMR1 and reduced expression of \textit{CDKN1C} in BWS patients.\textsuperscript{22} Although we postulate that the silencing of \textit{CDKN1C} in these patients is a direct consequence of this epimutation at KvDMR1, we cannot exclude the possibility that these two epigenetic phenomena are mechanistically unrelated and simply represent two manifestations of domain-wide epigenetic disruption. In this regard, we have identified some BWS patients with reduced expression of \textit{CDKN1C} but with apparently normal methylation at KvDMR1.

To gain a better understanding of the mechanisms by which \textit{CDKN1C} is silenced in BWS, we analysed DNA methylation and chromatin structure in the promoter region of \textit{CDKN1C} in fibroblasts from normal individuals and patients. We found that the promoter region of \textit{CDKN1C} was unmethylated in all the normal and BWS patient samples analysed. However, the two subgroups of BWS patients with downregulated \textit{CDKN1C} were distinguishable on the basis of their chromatin structure at the \textit{CDKN1C} promoter, indicating different silencing mechanisms.

\textbf{Abbreviations:} BWS, Beckwith–Wiedemann syndrome; ChIP, chromatin immunoprecipitation; ICR, imprinting control region; LOI, loss of imprinting; LOM, loss of methylation; MI, methylation index; RPA, ribonuclease protection assay
METHODS

Methylation analysis of KvDMR1 and the H19 ICR region by Southern hybridisation

Genomic DNA of fibroblast cell lines from normal individuals and BWS patients was digested with EcoRI and the methylation sensitive enzyme NotI. Blots were hybridised with the DMRP probe (fig 1) as described previously. Hybridisation signals were detected using a Typhoon PhosphorImager and quantitated using ImageJ software (http://rsb.info.nih.gov/ij/). The methylation status (that is, normal or LOM) of a patient was determined by comparing their methylation index (MI; intensity of methylated band/ intensity of unmethylated band) to that of normal controls. For the Southern blot in fig 2A, the mean (SD) MI of three normal samples was 0.81 (0.09). Thus methylation at KvDMR1 in BWS patients was considered normal if the MI was 0.81 ± 2SD or from 0.63 to 0.99, which is comparable to previous studies. For analysis of CTCF binding site No 6 was 0.81 (0.09). The following “touchdown” PCR program was used: one cycle of 94°C for 10 minutes; 10 “touchdown” cycles of 94°C for one minute, 53°C for one minute, and 72°C for one minute; 35 cycles of 94°C for one minute, 65°C (−1.2°C per cycle) for one minute, 72°C for one minute; 35 cycles of 94°C for one minute, 53°C for one minute, and 72°C for one minute; followed by a final extension cycle of 72°C for 10 minutes. Before cloning, amplification was confirmed by running a portion of the PCR products on a 2% agarose gel. To decrease the chance of stochastically amplified PCR products, the PCR products were cloned into the pCR4-TOPO vector following the manufacturer’s recommendations (Invitrogen, San Diego, California, USA). Plasmid DNA was isolated by miniprep using the Qiaprep Turbo BioRobot kit (Qiagen) or the High Pure Plasmid isolation kit (Roche, Indiana, USA). For every sample analysed by bisulphite sequencing, 10 clones were sequenced with T3 primers using an ABI PRISM 3700 DNA analyser (Applied Biosystems). Sequencing was done by Macrogen (Seoul, Korea). In the alignment process, vector sequences were removed and clone sequences were aligned. A compilation of individual sequenced clones was saved in FASTA format. Methylation status was determined by using the MethTools software (http://genome.imb-jena.de/methtools).

Bisulphite sequencing

Genomic DNA was digested with BamHI (Fermentas), which flanks the region analysed by bisulphite sequencing. Following digestion, DNA was purified by phenol-chloroform extraction and resuspended in 50 μl of H2O. Two micrograms of digested genomic DNA were denatured with 5.5 μl of fresh 2M NaOH and incubated at 37°C for 10 minutes. Bisulphite treatment was carried out at 50°C under mineral oil for 16 hours with 30 μl of 10 mM hydroquinone (Sigma, St Louis, Missouri, USA) and 520 μl of sodium (meta)bisulphite (Sigma) at pH 5.0. Reactions were desalted using the Qiagen Gel Extraction kit (Qiagen, Valencia, California, USA). Bisulphite treated DNA was eluted in 50 μl of water, desulphonated with 5.5 μl of 3M NaOH for five minutes at room temperature, followed by ethanol precipitation and resuspension in 40 μl of water.

Ribonuclease protection assay (RPA)

RPA was carried out as described previously. Briefly, radioactive RNA probes were synthesised using the MaxiScript T7/T3 kit (Ambion, Austin, Texas, USA) and 32P-UTP (800Ci/mmol) (Perkin-Elmer Life Sciences, Norwalk, Connecticut, USA). The probe used for CDKN1C was from Pharmingen (San Diego, California, USA) and the human
and from normal individuals (N) was digested with precast Ready Gels (BioRad, Hercules, California, USA). Protected fragments were electrophoresed in 5% TBE-urea mix. Conditions were such that both probes were in excess. digestion was done with a 1/100 dilution of the RNaseA/T1 m was eluted in 500 buffers (Upstate Biotechnology), and the bound chromatin was collected by gentle centrifugation and washed three times with ChIP dilution buffer (200 μl), pre-cleared with 80 μl salmon sperm DNA/protein A agarose for one hour at 4˚C with rotation. A portion of the protein A purified chromatin (20 μl) was used to prepare DNA for the “input” sample. Antibodies (2–5 μl) were added to the clarified chromatin (180 μl) and incubated overnight with rotation. Sixty microliters of protein A-agarose were added to the antibody–chromatin mix and incubated at 4˚C for one hour with rotation. The complex was collected by centrifugation and the supernatant was collected.

Chromatin immunoprecipitation (ChIP)

We used the ChIP assay kit from Upstate Biotechnology (Santa Cruz, California, USA). Between one million and five million cells were fixed with 1% formaldehyde for 10 minutes at 37˚C in cell culture media. The formaldehyde cross linked cells in 0.6 ml sodium dodecyl sulphate lysis buffer were sonicated for 180 seconds (10 seconds on, and five seconds off) on ice using a Branson sonicator with a 2 mm microtip, and sonicated for 180 seconds (10 seconds on, and five seconds off) on ice using a Branson sonicator with a 2 mm microtip, and sonicated for 180 seconds (10 seconds on, and five seconds off) on ice using a Branson sonicator with a 2 mm microtip, and sonicated for 180 seconds (10 seconds on, and five seconds off) on ice using a Branson sonicator with a 2 mm microtip. Sonicated chromatin was diluted 10-fold in ChIP dilution buffer (200 μl), pre-cleared with 80 μl salmon sperm DNA/protein A agarose for one hour at 4˚C with rotation. A portion of the protein A purified chromatin (20 μl) was used to prepare DNA for the “input” sample. Antibodies (2–5 μl) were added to the clarified chromatin (180 μl) and incubated overnight with rotation. Sixty microliters of protein A-agarose were added to the antibody–chromatin mix and incubated at 4˚C for one hour with rotation. The complex was collected by centrifugation and the supernatant was collected.

RESULTS

CDKN1C expression is reduced in some BWS patients with apparently normal methylation at KvDMR1

We have previously observed complete concordance between LOM at KvDMR1 and the reduction of CDKN1C expression in fibroblasts from BWS patients. From an expression analysis of six BWS patients with normal methylation at KvDMR1 (fig 2A and data not shown), three samples (BWS3, BWS7, BWS11) were identified with decreased expression of CDKN1C using either a ribonuclease protection assay (RPA) (fig 2B) or real time reverse transcriptase PCR (RT-PCR, data not shown). The degree of CDKN1C repression was similar to that observed in BWS patients with LOM at KvDMR1 (fig 2B, fig 2B, fig 2B, fig 2B), real time reverse transcriptase PCR (RT-PCR, data not shown). The degree of CDKN1C repression was similar to that observed in BWS patients with LOM at KvDMR1 (fig 2B, fig 2B, fig 2B, fig 2B), real time reverse transcriptase PCR (RT-PCR, data not shown). The degree of CDKN1C repression was similar to that observed in BWS patients with LOM at KvDMR1 (fig 2B, fig 2B, fig 2B, fig 2B), real time reverse transcriptase PCR (RT-PCR, data not shown). The degree of CDKN1C repression was similar to that observed in BWS patients with LOM at KvDMR1 (fig 2B, fig 2B, fig 2B, fig 2B), real time reverse transcriptase PCR (RT-PCR, data not shown).

Silencing of CDKN1C in BWS is not associated with hypermethylation at the promoter region

A large CpG island containing the promoter region and most of the gene body of CDKN1C is differentially methylated in mouse but not in humans. However, it has been shown that CDKN1C becomes biallelically methylated in several human cancers and that this correlates with downregulation of CDKN1C expression. In our earlier study, we showed by Southern blot that methylation is absent at two SacII sites in the promoter region of CDKN1C (fig 1) in BWS patients with loss of methylation at KvDMR1 and downregulation of CDKN1C.
CDKN1C.\textsuperscript{22} To rule out the possibility that downregulation of CDKN1C observed in BWS patients simply reflects methylation elsewhere at the CDKN1C promoter, we carried out a comprehensive methylation analysis of the promoter using bisulphite sequencing.

PCR primers were chosen that amplified a 155 bp fragment containing 14 CpG dinucleotides spanning the proximal promoter and transcription start site of CDKN1C, and which is consistently methylated in tumour cell lines where the CDKN1C gene is silenced (fragment C in Kikuchi \textit{et al} \textsuperscript{22}). PCR products were cloned and 10 clones were sequenced for each sample. As a positive control, the same region of PCR products were cloned and 10 clones were sequenced for the CDKN1C promoter, we carried out a bisulphite sequencing.

Considering that we observed primarily unmethylated alleles in the normal and BWS samples, silencing mechanisms other than the hypermethylation observed in some cancers\textsuperscript{27–30} appear to be operating in BWS.

Repressive chromatin in BWS patients with downregulation of CDKN1C but normal methylation at KvDMR1

As BWS patients with loss of methylation at KvDMR1, and some with normal methylation at KvDMR1, both show downregulation of CDKN1C in a promoter methylation independent fashion, we postulated that chromatin modifications associated with gene silencing might be involved. We first sought to determine whether allele specific differences in chromatin structure were detectable at the CDKN1C promoter by carrying out chromatin immunoprecipitation (ChIP) experiments on somatic cell hybrids containing a single human chromosome 11 of known parental origin. We have previously shown that these hybrids maintain both allele specific gene expression and methylation.\textsuperscript{33} The advantage of these cell lines is that one can examine the chromatin structure of each parental allele independently, even in the absence of a polymorphism. As internal controls, we used the promoter regions of the housekeeping gene LDHA and the erythroid specific \(\beta\) globin gene, two chromosome 11 genes assumed to be active and silent, respectively, in the somatic cell hybrids. Figure 4 shows that, compared with the hybrid carrying the paternal chromosome, the CDKN1C promoter in the maternal hybrid was highly enriched in dimethyl H3-K4, a histone modification associated with active genes,\textsuperscript{35} and depleted in HP1\(\gamma\), a protein associated with the chromatin of inactive promoters.\textsuperscript{36} In contrast, the hybrid containing the paternally derived chromosome 11 had a threefold lower level of H3-K4 dimethylation, but was enriched for HP1\(\gamma\) at the CDKN1C promoter. These results are consistent with the imprinted expression of CDKN1C, which is expressed predominantly from the maternal allele.\textsuperscript{6} Somewhat
surprisingly, we found little difference between the maternal and paternal CDKN1C promoters with respect to dimethyl H3-K9 levels, a histone modification associated with silent chromatin.\(^{23}\) (fig 4A and 4B).

ChIP analysis using the same antibodies detected no differences at the CDKN1C promoter between fibroblasts from normal individuals and BWS patients with loss of methylation at KvDMR1 (fig 4A and 4B). The same analysis was carried out on two of the three BWS samples with reduced CDKN1C expression but normal methylation at KvDMR1 (the third sample was not available for analysis). Strikingly, cells from these patients showed both decreased levels of H3-K4 dimethylation and enrichment of dimethyl H3-K9 and HP1\(^{\gamma}\) (fig 4A and 4B). These data suggest that, compared with normal controls and BWS patients with LOM at KvDMR1, a repressive chromatin structure exists at the CDKN1C promoter in this BWS subgroup which is probably associated with gene silencing. Raji, the Burkitt’s lymphoma cell line that is hypermethylated at the CDKN1C promoter (fig 4),\(^{27}\) shows a ChIP profile similar to the fibroblast cell lines from normal individuals for all three antibodies analysed. This indicates that even though there is a reduction in CDKN1C expression levels, no change in histone modification was identified. More importantly, this suggests that DNA methylation alone (or in combination with DNA methylation binding proteins) is capable of downregulating CDKN1C without accompanying chromatin changes typically of repressed chromatin. Furthermore, Raji shows normal methylation at the Nott site in KvDMR1 as determined by Southern blot (not shown), suggesting that KvDMR1 is not associated with the silencing of CDKN1C by hypermethylation.

**Downregulation of CDKN1C is not associated with hypermethylation at H19**

Several mouse models have been constructed that partially recapitulate the complex phenotype of BWS, the most complete being a mouse line having both a null mutation of Cdkn1c and loss of imprinting for Igf2 (see Caspary et al\(^{16}\) and references therein). Analysis of this double mutant suggested that Cdkn1c and Igf2 function in the same developmental pathway and are antagonistic. A corollary of this, which is consistent with the high degree of similarity between the mutant mouse phenotype and BWS, is that CDKN1C and Igf2 may synergise to produce some characteristics of this condition. In BWS, loss of imprinting (LOI) at

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**Figure 4** Analysis of chromatin structure at the promoter region of CDKN1C by chromatin immunoprecipitation (ChIP). (A) ChIP polymerase chain reaction (PCR) results obtained using antidimethyl H3-K4, antidimethyl H3-K9, and anti HP1\(^{\gamma}\) antibodies. Samples analysed correspond to: (1) fibroblast cell lines from Beckwith–Wiedemann syndrome (BWS) patients (BWS6 and BWS9) with loss of methylation at KvDMR1 and with low expression of CDKN1C (LOM Kv/low p57); (2) fibroblast cell lines from normal individuals (N3 and N6); (3) fibroblast cell lines from BWS patients (BWS7 and BWS11) with normal methylation at KvDMR1 and low expression of CDKN1C (normal Kv/lowp57); (4) human–mouse somatic cell hybrids containing either a maternally derived human chromosome 11 (M) or a paternally derived human chromosome 11 (P). The Burkitt’s lymphoma cell line, Raji, was also analysed. Input (I) corresponds to PCR of DNA isolated from chromatin before immunoprecipitation. (B) Histograms show the relative enrichment (left vertical axis values) of dimethyl H3-K4 (green), dimethyl H3-K9 (purple), and HP1\(^{\gamma}\) (yellow) in the different samples analysed. The relative enrichment for each chromatin modification was determined by comparing the normalised intensity (relative to input) of the bands for CDKN1C dimethyl H3-K4 with that of LDHA, and dimethyl H3-K9, or HP1\(^{\gamma}\), with that of \(\beta\) globin. Lines in the graph show the enrichment (right vertical axis values) of silencing associated factors, HP1\(^{\gamma}\) (red) and dimethyl H3-K9 (green) relative to dimethyl H3-K4. No substantial enrichment of HP1\(^{\gamma}\) and dimethyl H3-K9 with respect to dimethyl H3-K4 in the paternal chromosome hybrid and in BWS patients with normal methylation at KvDMR1 and downregulation of CDKN1C.
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Figure 5  Methylation analysis of the region upstream of the H19 gene. (A) Map of the upstream region of the human H19 gene showing the locations of the seven CTCF binding sites and the positions of the two regions analysed for methylation; enlargements of these regions are shown below the map indicating the position of the methylation sensitive restriction enzymes (HhaI and Smal) used in the analysis. The heavy black lines below the enlargements represent the location of the hybridisation probes. (B) DNA from the indicated cell lines was digested with Sau96I and HhaI, electrophoresed and hybridised with a probe encompassing CTCF binding site No 6. The HhaI site was cleaved (unmethylated) in DNA from the somatic cell hybrid containing a maternally derived human chromosome 11 giving rise to a unresolved doublet of 178/154 base pairs. The same site was resistant to cleavage (methylated) in DNA from a hybrid carrying a paternally derived chromosome 11 resulting in a 332 bp Sau96I fragment. All normal and patient samples showed both alleles suggestive of normal differential methylation at this site. (C) DNA from the indicated cell lines was digested with PstI and Smal, electrophoresed, and hybridised with a probe encompassing the promoter region and part of exon 1 of the H19 gene. In each sample, the uncut 1.8 kb paternal allele as well as the cleavage products (1.0 and 0.8 kb) of the maternal allele were visible, with no indication of hypermethylation. The band marked with an asterisk represents hybridisation of the probe to an adjacent region.

IGF2 is usually associated with hypermethylation upstream of the H19 gene. Therefore we determined whether BWS patients with downregulated expression of CDKN1C also suffered an epimutation at the H19/IGF2 locus. Of the seven potential binding sites for the insulator protein CTCF in the human H19/IGF2 ICR (fig 5A), only site No 6 appears to be differentially methylated in normal tissue, and methylation at this site largely correlates with expression of IGF2 in somatic cell hybrids treated with 5-aza-2′-deoxycytidine. Consistent with these results, we found that a single site for the methylation sensitive restriction enzyme HhaI next to CTCF binding site No 6 was unmethylated (cleaved) in a somatic cell hybrid carrying a maternally derived human chromosome 11, but methylated (uncut) in a hybrid containing a paternally derived chromosome 11 (fig 5B). Both digested and undigested alleles were observed in fibroblast DNA from normal individuals and BWS patients, including both subgroups with downregulation of CDKN1C, with no evidence of hypermethylation in any case (fig 5B). Also consistent with the lack of an epimutation in the H19 ICR in these patients was the finding of normal differential methylation at a SmaI site just upstream of the H19 start site (fig 5C), hypermethylation of which is associated with loss of imprinting at IGF2.

DISCUSSION

Our results suggest the existence of at least three silencing mechanisms for CDKN1C. These alternative methods of inactivation of CDKN1C could all be functionally equivalent to loss of function mutations of CDKN1C. Regardless of the mechanism, downregulation of CDKN1C appears to be a common occurrence that may lead to BWS or, in some cases, contribute to cancer. It should be noted, however, that reduced expression of CDKN1C in BWS patients does not generally appear to be associated with predisposition to cancer. Although one report suggests that LOM at KvDMR1, and presumably downregulation of CDKN1C, may be related to the incidence of non-Wilms’ embryonal tumours in BWS patients, several other studies suggest that biallelic expression of IGF2 associated with hypermethylation at the H19 ICR tracks with tumour development. It is silenced in association with promoter methylation in several tumour types. This represents one mechanism for epigenetic silencing of CDKN1C. Although it is a possible mechanism for silencing CDKN1C in BWS, we did not observe hypermethylation of CDKN1C in any of the BWS patient samples available; however, a larger BWS patient sample size should be analysed to extend these results. Together, our results suggest the presence of distinct mechanisms in cancer and BWS for silencing of CDKN1C. It is evident that neither DNA methylation nor chromatin structure (at least as studied here) at the CDKN1C promoter region is altered in patients with LOM at KvDMR1 and reduced expression of CDKN1C. Evidence complementing our results was recently provided by Soejima et al, who showed that downregulation of CDKN1C expression in some oesophageal cancers correlates with loss of CpG methylation and loss of histone H3 lysine 9 methylation at KvDMR1, but does

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not correlate with methylation or with histone modification at CDKN1C. Together, these results strongly support the view that LOM at KvDMR1 is mechanistically related to the silencing of CDKN1C in these patients, and that these two epigenetic alterations are not simply independent manifestations of a domain-wide epimutation in 11p15.5.

The molecular mechanisms whereby KvDMR1 regulates imprinting, in particular CDKN1C imprinted expression, are not yet understood. It has been shown previously that loss of methylation at KvDMR1 leads to biallelic expression of KCNQ1OT1, an antisense (with respect to KCNQ1) non-coding RNA transcript (fig 1A).10 It is possible that KCNQ1OT1 may function in a manner analogous to the Air transcript in the Igf2r locus, perhaps by facilitating the establishment and spreading of a domain-wide repressive chromatin structure.49

Indeed, Thakur et al have shown that, at least in an experimental context, the Kcnq1ot1 RNA may play a role in gene silencing.43 Enhancer blocking assays suggest that KvDMR1 may function as a methylation sensitive insulator or as a bidirectional silencer, or both.15–16 Our finding that the chromatin structure of the CDKN1C promoter does not appear to be altered in BWS patients with LOM at KvDMR1 and downregulation of CDKN1C argues against the establishment of domain-wide repressive chromatin on the maternal chromosome caused by the epimutation at KvDMR1. One could therefore speculate that, at least in some instances, KvDMR1 may function like the H19 ICR (that is, as a chromatin insulator).

On the other hand, CDKN1C can be silenced by a KvDMR1-independent mechanism. We identified three patients with normal methylation at KvDMR1 but with low levels of CDKN1C expression. In the two patients analysed, we observed repressive chromatin modifications at the CDKN1C promoter region. Our analysis included antibodies for only three chromatin modifications, namely dimethyl H3-K4, dimethyl H3-K9, and HP1γ; nevertheless, enrichment of dimethyl H3-K9 and HP1γ, and depletion of dimethyl H3-K4 were clearly seen in this class of BWS patients. We therefore propose that the altered chromatin structure at the CDKN1C promoter region is associated with the downregulation of CDKN1C levels in these two patients. Whether reduced expression is caused by the acquisition of repressive chromatin at the promoter, or if the altered chromatin is a result of silencing by another mechanism, remains to be determined. Although studies both in cell culture and in the mouse indicate that reduction in the expression level of CDKN1C can be associated with excess IGF2 levels,50–51 real time RT-PCR analyses do not show increased levels of IGF2 expression in these patients, nor in BWS patients with LOM at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1 (data not shown). Furthermore, Southern analysis at two loci known to be associated with LOI at KvDMR1.

The aetiology of BWS is complex, with several different genetic and epigenetic mechanisms.1 However, the molecular defect in 10–20% of patients has yet to be established. Although the sample size is small, our finding of reduced levels of CDKN1C expression in three of six non-UPD BWS patients with normal methylation at KvDMR1 suggests that a substantial proportion of these cases may show an aberrant chromatin structure at the CDKN1C promoter. Further studies are necessary to fully understand the mechanisms responsible for the change in histone modification in the CDKN1C promoter region and the impact of these modifications on chromatin structure and transcriptional regulation.

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