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RESEARCH COMMUNICATION

The E3 ubiquitin ligase activity of RING1B is not essential for early mouse development

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Polycomb-repressive complex 1 (PRC1) and PRC2 maintain repression at many developmental genes in mouse embryonic stem cells and are required for early development. However, it is still unclear how they are targeted and how they function. We show that the ability of RING1B, a core component of PRC1, to ubiquitinate histone H2A is dispensable for early mouse embryonic development and much of the gene repression activity of PRC1. Our data support a model in which PRC1 and PRC2 reinforce each other’s binding but suggest that the key functions of PRC1 lie beyond the enzymatic capabilities of RING1B.

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There are two principal types of Polycomb group (PcG) complexes. Polycomb-repressive complex 2 (PRC2) is responsible for trimethylation of Lys27 on histone H3 (H3K27me3) via the EZH2 or EZH1 protein subunit (Di Croce and Helin 2013). Canonical PRC1 contains CBX subunits (the vertebrate homologs of Drosophila Polycomb) whose chromodomains are able to bind H3K27me3 [Kastov et al. 2011]. PRC1 also contains the heterodimeric E3 ligase RING1B/PCGF1–6, which can catalyze the ubiquitination of Lys119 on histone H2A [Illingworth et al. 2012]. PRC1 catalytically inactive RING1B protein with an alanine at position 53 in place of isoloeucine (Ring1BI53A). This amino acid change has been shown to disrupt the interaction of RING1B with the E2 UBCH5C and ablates the ability of RING1B to act as an E3 ligase in vitro [Buchwald et al. 2006]. However, I53A does not perturb the incorporation of RING1B into canonical and variant PRC1 complexes [Illingworth et al. 2012]. Using homologous recombination, we generated heterozygous (Ring1B+/−I53A) and homozygous (Ring1B+/−I53A/I53A) knock-in alleles at the endogenous Ring1B locus in E14TG2a mESCs (Fig. 1A, B). The resulting cells are distinct from those generated previously [Eskeland et al. 2010] in that the mutation is introduced within the Ring1B coding sequence rather than as a transgene and therefore better preserves endogenous Ring1B expression levels. For direct comparison, we also derived Ring1B−/− mESCs from the same parental E14TG2a mESCs, catalytically inactive Ring1B also permits development to progress much further than in Ring1B-null mice [Voncken et al. 2003]. We conclude that although Ring1B is essential for early murine embryonic development, its catalytic activity is not.

Results and Discussion

RING1B catalytic activity is dispensable for repression at most PRC1 target loci in mESCs

To determine the role of endogenous Ring1B’s E3 ligase activity, we generated a knock-in allele that expresses a mutant form of Ring1B protein with an alanine at position 53 in place of iso-leucine (Ring1B+/−I53A). This amino acid change has been shown to disrupt the interaction of Ring1B with the E2 UBCH5C and ablates the ability of Ring1B to act as an E3 ligase in vitro [Buchwald et al. 2006]. However, I53A does not perturb the incorporation of Ring1B into canonical and variant PRC1 complexes [Illingworth et al. 2012]. Using homologous recombination, we generated heterozygous (Ring1B+/−I53A) and homozygous (Ring1B+/−I53A/I53A) knock-in alleles at the endogenous Ring1B locus in E14TG2a mESCs (Fig. 1A, B). The resulting cells are distinct from those generated previously [Eskeland et al. 2010] in that the mutation is introduced within the Ring1B coding sequence rather than as a transgene and therefore better preserves endogenous Ring1B expression levels. For direct comparison, we also derived Ring1B−/− mESCs from the same parental E14TG2a mESCs, catalytically inactive Ring1B also permits development to progress much further than in Ring1B-null mice [Voncken et al. 2003]. We conclude that although Ring1B is essential for early murine embryonic development, its catalytic activity is not.

Keywords: PRC1; histone ubiquitination; H3K27me3; embryonic stem cell; Polycomb

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et al. 2012; Bhatnagar et al. 2014). Ring1BI53A/I53A mESCs express RING1B protein at levels similar to wild-type (Fig. 1D) and appear to maintain levels of the canonical PRC1 component MEL18. Quantitative immunoblotting confirmed this while also showing a moderate reduction in the level of the noncanonical subunit RYBP (Supplementary Fig. 1). Conversely, Ring1B−/− cells show a marked reduction in MEL18 levels, compatible with the destabilization of core PRC1 components in cells lacking RING1B (van der Stoop et al. 2008; Eskeland et al. 2010).

Despite the proposed mechanism by which H2AK119ub facilitates the deposition of H3K27me3 (Blackledge et al. 2014; Cooper et al. 2014; Kalb et al. 2014), we found that loss of H2AK119ub in Ring1B−/− or Ring1B I53A/I53A cells did not result in global reduction in H3K27me3 levels (Fig. 1D, Supplemental Fig. 1). Moreover, we did not detect an increase in H3K36me3 despite the proposed antagonistic relationship between H2AK119ub and H3K36me3/2/3 deposition (Fig. 1D, Yuan et al. 2013).

Using microarrays, we compared the expression profiles of Ring1B−/− and Ring1B I53A/I53A mESCs with wild type (Fig. 2A, B, Supplementary Table 1). Loss of RING1B results in hundreds of genes showing both significant up-regulation (721) and down-regulation (285) by more than twofold relative to wild type. Most of these changes are likely indirect, since, for those genes that are directly bound by RING1B in wild type, only 98 are up-regulated and 18 are down-regulated in knockout cells (Supplemental Fig. 2A, B). These changes were largely rescued in Ring1B I53A/I53A cells where only 55 and 25 genes (12 and two RING1B-bound genes) showed up-regulation and down-regulation, respectively. Differentially expressed genes in Ring1B I53A/I53A overlap well (41 of 55 up-regulated and 19 of 25 down-regulated) with those also showing differential expression in Ring1B−/− mESCs. Even for this small number of “rescued” genes, the fold change in up-regulation relative to wild type is lower in Ring1B−/− than in Ring1B−/− (Fig. 2C, Supplementary Fig. 2C). Nonrescued genes were generally those with the highest level of up-regulation in Ring1B−/− cells. Gene expression changes were confirmed by real-time RT–PCR (Fig. 2D). These data suggest that many of the “rescued” genes are still misregulated in Ring1B I53A/I53A cells, but to a much lower extent, and hints that RING1B-mediated gene regulation is enhanced by, but not primarily dependent on, its catalytic activity.

RING1B and H3K27me3 deposition is impaired in I53A cells

In mammalian genomes, the placement of PRC2 has been suggested to occur primarily at CpG islands (Deaton and Bird 2011; Klose et al. 2013). The conventional model for PcG targeting to chromatin is then the hierarchical recruitment of PRC1 by the prior binding and activity of PRC2. However, it has been suggested that a reciprocal situation may occur, with PRC1-mediated H2AK119ub
that RING1B ChIP-seq signal was lost from CGI TSSs and gained within gene bodies [Supplemental Fig. 4A]. Although both RING1B- and H3K27me3-enriched regions in wild type typically had decreased signal in Ring1B\(^{+/−}\) mESCs [Fig. 3E,F], the absolute number of RING1B/H3K27me3-enriched regions identified in Ring1B\(^{+/−}\) mESCs was greater than that found in wild-type; we identified 5,200 unique RING1B-occupied sites [Fig. 3E,F, Supplemental Fig. 4B]. These ectopic “peaks” were at sites of low RING1B signal, showed a modest but significant \(P\)-value of \(< 1 \times 10^{-9}\); Wilcoxon rank sum test] increase in ChIP-seq signal in the Ring1B\(^{−/−}\) mESCs [Supplemental Fig. 4B], and occurred preferentially within gene bodies [Supplemental Fig. 4C]. To determine whether RING1B and H3K27me3 levels may be simply tracking transcription, we compared RING1B/H3K27me3 levels over rescued and nonrescued genes, and this revealed that the genes most up-regulated in Ring1B\(^{−/−}\) cells do indeed have a higher loss of H3K27me3 and RING1B ChIP signal [Supplemental Fig. 3C,D]. Despite this, the abundance of sites with reduced H3K27me3/RING1B levels in Ring1B\(^{−/−}\) cells greatly exceeds the number of differentially expressed genes, suggesting that altered expression alone is not the principal driver of these chromatin changes.

While our data align with the model in which PRC1 enzymatic activity can direct PRC2 recruitment, we cannot easily discount the possibility that abrogated H3K27me3 deposition is due to an alternative deficit in the function of RING1B catalytic activity is dispensable for early mouse development

Whereas RING1A is dispensable for embryonic development [del Mar Lorente et al. 2000], RING1B is essential for gastrulation [Voncken et al. 2003]. To determine the in vivo role for the catalytic function of RING1B, we generated Ring1B\(^{−/−}\) mice from heterozygous knock-in mESCs. Correct targeting was validated in embryonic day 12.5 (E12.5) embryos using the PCR strategy illustrated in Figure 1A. Immunoblotting showed a major reduction in H2AK119ub-dependent expression of Ring1B in E12.5 embryos when compared with wild-type (Fig. 4A). Successful heterozygous matings did not yield live-born homozygous pups [98 Ring1B\(^{+/−}\), 147 Ring1B\(^{+/+}\), and 0 Ring1B\(^{−/−}\); \(\chi^2 = 88.2\), \(P < 0.0001\)], suggesting that the E3 ligase activity of RING1B is required for full murine embryonic development. However, in contrast to the reported embryonic lethality of Ring1B\(^{−/−}\) by E10.5, we found that Ring1B\(^{+/−}\) embryos could complete gastrulation and develop to E15.5, albeit at sub-Mendelian frequencies (\(\chi^2 = 3.2\), \(P = 0.20\) at E15.5; \(\chi^2 = 19.6\), \(P < 0.0001\) at E12.5; \(\chi^2 = 5.6\), \(P = 0.06\) at E10.5; Fig. 4A). This is consistent with the model that E3 ligase activity of RING1B is largely dispensable for gene repression, as mutant mESCs showed RING1B and H3K27me3 at the same sites (TSSs) with RING1B enrichment in wild-type and down-regulated (blue) if they had a log2 fold change of >1 or less than −1, respectively, and a Benjamini-Hochberg-corrected \(P\)-value of <0.05. The number of differentially expressed probes and the number of genes they represent [in parenthesis] are indicated. (\(\ast\)) Box plots of log2 fold expression changes for Ring1B\(^{−/−}\) versus wild type (KO) and Ring1B\(^{+/−}\) versus wild type (L53A) for genes with “rescued” and “nonrescued” expression levels in Ring1B\(^{+/−}\)/L53A mESCs. The number of probes [genes in parentheses] is indicated for each subset. (\(\ast\)) Candidate expression analysis by quantitative RT–PCR. Plots show the mean expression across three biological replicates, with error bars indicating standard deviation. Significant differential gene expression, as determined by a Student’s t-test, is indicated with asterisks. (\(\ast\)) \(P\)-value < 0.05 and > 0.01; (\(\ast\)\(\ast\)) \(P\)-value < 0.01.

**Figure 2.** The E3 ligase activity of RING1B is largely dispensable for gene repression. (\(\mathbf{A}, \mathbf{B}\)) Log2 expression values in wild-type (WT) versus Ring1B\(^{−/−}\) mESCs (\(\mathbf{A}\)) and Ring1B\(^{+/−}\)/L53A mESCs (\(\mathbf{B}\)) from expression microarrays. Probes were considered to be up-regulated [orange] or down-regulated [blue] if they had a log2 fold change of >1 or less than −1, respectively, and a Benjamini-Hochberg-corrected \(P\)-value of <0.05. The number of differentially expressed probes and the number of genes they represent [in parenthesis] are indicated. (\(\mathbf{C}\)) Box plots of log2 fold expression changes for Ring1B\(^{−/−}\) versus wild type (KO) and Ring1B\(^{+/−}\) versus wild type (L53A) for genes with “rescued” and “nonrescued” expression levels in Ring1B\(^{+/−}\)/L53A mESCs. The number of probes [genes in parentheses] is indicated for each subset. (\(\mathbf{D}\)) Candidate expression analysis by quantitative RT–PCR. Plots show the mean expression across three biological replicates, with error bars indicating standard deviation. Significant differential gene expression, as determined by a Student’s t-test, is indicated with asterisks. (\(\ast\)) \(P\)-value < 0.05 and > 0.01; (\(\ast\)\(\ast\)) \(P\)-value < 0.01.
E9.5] (Fig. 4C–E). No gross morphological abnormalities or anterior–posterior patterning defects were seen at E9.5 or E12.5. At E15.5, two of the five Ring1BI53A/I53A embryos that we recovered were developmentally retarded, but the morphology of the remaining three Ring1BI53A/I53A embryos was largely normal [exemplified in Fig. 4E]. All three of these E15.5 Ring1BI53A/I53A embryos exhibited edema [Fig. 4E, arrows], which was never seen in any of the 27 control littermate embryos at this stage [Fisher’s test, \( P < 0.01 \)], suggesting some defects in development of the cardiovascular system. One of these three E15.5 Ring1BI53A/I53A embryos exhibited exencephaly [Fig. 4E, asterisk]. Interestingly, the co-occurrence of these two phenotypes is also seen in embryos deficient for the H3K27me3 demethylase KDM6A (Shpargel et al. 2012).

We showed that catalytically inactive RING1B disrupts H3K27me3 deposition at target loci in ESCs, consistent with a model in which PRC1 and PRC2 co-operatively reinforce each other’s binding, with the loss of PRC1 activity prompting some loss of H3K27me3, which in turn reduces PRC1 binding. We cannot exclude that reduced levels of H3K27me3 are not just a consequence of increased transcription in mutant cells (Rissig et al. 2014). Despite this disruption of the epigenetic landscape, catalytically inactive RING1B is able to maintain near wild-type levels of gene expression compared with Ring1B-null ESCs and support embryonic development to an extent much greater than that reported for Ring1B knockout. Our findings support the notion that loss of RING1B E3 ligase activity and the consequent loss of most H2AK119ub only partially disrupt polycomb recruitment and function, consistent with the ability of ectopically expressed catalytically inactive RING1B to maintain chromatin compaction at polycomb target loci (Eskeland et al. 2010). Together with the importance of other PRC1 sub-units in modulating higher-order chromatin structure.

Figure 3. Mouse ESCs expressing catalytically inactive RING1B display impaired RING1B and H3K27me3 deposition. (A) RING1B and H3K27me3 levels (percentage input bound) for selected loci measured by ChIP-qPCR. (B) Genome browser screenshots showing normalized read depth for RING1B and H3K27me3 ChIP-seq in wild-type [WT] and Ring1BI53A/I53A mESCs. (C,D) Heat maps depicting normalized ChIP-seq signal across RING1B-enriched TSSs [+5 kb] for Ring1B [C] and H3K27me3 [D], ranked from highest to lowest ChIP-seq signal in wild-type mESCs. Peaks were considered increased or decreased (red and blue spots, respectively; numbers given in parenthesis) if both replicates of Ring1BI53A/I53A showed an at least twofold differential signal compared with that observed in both wild-type replicates. The right panels show the genomic size occupied by each category of enriched region.
Materials and methods

**Generation of Ring1B ^iS3A/iS3A^ and Ring1B ^−/−^ mice**

The targeting vector to knock in the iS3A mutation into exon 3 of Ring1B (Rn02) was generated by BAC recombineering (Liu et al. 2003). Briefly, a 129S7/AB2.2-derived BAC, BmQ291b2 (Adams et al. 2005), was modified using galk-positive/negative selection to introduce the iS3A mutation and two silent restriction sites (SacI and XbaI) into exon 3 of Ring1B and a 10.1-kb region of the BAC (chromosome 1: 153,321,960–153,332,059; mm9) cloned into PL253 by gap repair. A floxed neomycin resistance cassette was then integrated into intron 3 (position chromosome 1: 153,323,749; mm9) in this gap-repaired plasmid using a mini targeting vector. The resulting plasmid was linearized and electroporated into E14TG2a ESCs (Joyner 2000), and G418-resistant clones were screened by PCR to identify correct targeting events. The neomycin resistance cassette was removed from correctly targeted clones by transient transfection of a Cre-expressing plasmid. Ring1B ^iS3A/iS3A^ mESCs were injected into blastocysts to generate chimeric mice and backcrossed three times to C57BL/6 (Joyner 2000). A second round of targeting in Ring1B ^−/−^ mESCs generated Ring1B ^iS3A/iS3A^ mESCs.

**Ring1B ^−/−^ mESCs** were generated using a similar strategy, except that a gap-repaired PL253 plasmid containing chromosome 1: 153,321,960–153,332,059; mm9) and a wild-type version of Ring1B exon 3 was modified so that a lone LoxP site was introduced into intron 2 (chromosome 1: 153,324,264; mm9), and a floxed neomycin resistance cassette was introduced into intron 3 (chromosome 1: 153,323,749; mm9) using mini targeting vectors. Cre-mediated removal of the neomycin resistance cassette generated either a conditional knockout Ring1B allele with exon 3 flanked by LoxP sites or a Ring1B-null allele deleted for exon 3 that produces a transcript containing a premature STOP codon encoding a 42-amino-acid N-terminally truncated protein. Details of genotyping by PCR and cDNA sequencing are provided in Supplemental Table 2.

Generation and analysis of Ring1B mutant mice were performed under a UK Home Office project license (PPL 60/4424) with approval from an institutional ethics committee.

**Expression analysis**

The Amino Allyl MessageAmp II with Cy3 kit (Ambion, AM1795) was used to produce cRNA using the manufacturer's protocol. Six-hundred nanograms of cRNA was fragmented and hybridized to a SurePrint G3 Mouse GE 8x60K microarray (Agilent, G4852A). After washing, the arrays were scanned using a NimbleGen scanner, and images were analyzed using Agilent Feature Extraction software. The resulting values were processed and analyzed using custom R scripts. Expression data were deposited in the Gene Expression Omnibus (GEO) repository [http://www.ncbi.nlm.nih.gov/geo] under accession number GSE69978. Details of qRT–PCR for verification of expression changes are in Supplemental Table 2. A full protocol is in the Supplemental Material.

**ChIP-seq**

Libraries were prepared as previously described (Bowman et al. 2013) with modifications outlined in the Supplemental Material.

Sequence reads were trimmed [TrimGalore! version 0.2.7] to remove adapters with the “−q 30” option used to remove low-quality bases with a PHRED score of <30 using Cutadapt version 1.2.1] and mapped to the mouse genome [mm10] using Bowtie 2.1.0 with the following arguments: “–local –D 20 -R 3 -N 1 -L 20 -s 1,1,0.50” SAM files were processed using HOMER version 4.3. HOMER tag directories were created using the make TagDirectory tool with the options “–unique” and “–fragLength 150” and were used to create BedGraphs for visualization. All data output from HOMER analysis was normalized to 10 million mapped reads. BedGraphs were created using HOMER’s makeBed tool with default options. Enriched regions were identified using the findPeaks tool from HOMER with the options “–style histone” and “–minDist 500” with the input sequences as controls. High-confidence enriched regions of at least 500 base pairs enriched in both replicates were identified. The HOMER analyzeRNA tool with the “–rpmk” option was used to quantify regions of interest. To generate heat maps, HOMER’s annotatePeaks tool was used (options “–hist” and “–hist 50”) to generate a matrix of RPKM (reads per kilobase per million mapped reads) values, which was processed using custom R scripts. Illumina sequencing data were deposited in the GEO repository [http://www.ncbi.nlm.nih.gov/geo] under accession number GSE69978.

Details of cell culture conditions, RNA extraction, cDNA synthesis, protein extractions, ChIP, and immunoblotting are provided in the Supplemental Material.
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Note added in proof

Pengelly et al. (2015) recently reported similar findings for a point mutation in the PRCP subunit Sce in Drosophila melanogaster.

References


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**Supplemental Material**

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