Ring1B and Suv39h1 delineate distinct chromatin states at bivalent genes during early mouse lineage commitment

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SUMMARY
Pluripotent cells develop within the inner cell mass of blastocysts, a mosaic of cells surrounded by an extra-embryonic layer, the trophectoderm. We show that a set of somatic lineage regulators (including Hox, Gata and Sox factors) that carry bivalent chromatin enriched in H3K27me3 and H3K4me2 are selectively targeted by Suv39h1-mediated H3K9me3 and de novo DNA methylation in extra-embryonic versus embryonic (pluripotent) lineages, as assessed both in blastocyst-derived stem cells and in vivo. This stably repressed state is linked with a loss of gene priming for transcription through the exclusion of PRC1 (Ring1B) and RNA polymerase II complexes at bivalent, lineage-inappropriate genes upon trophoblast lineage commitment. Collectively, our results suggest a mutually exclusive role for Ring1B and Suv39h1 in regulating distinct chromatin states at key developmental genes and propose a novel mechanism by which lineage specification can be reinforced during early development.

KEY WORDS: Bivalent chromatin, Early development, Histone methylation, Mouse, Silencing, Stem cells

INTRODUCTION
Gene expression programmes must be tightly controlled to govern cell identity and lineage choice. An inherent challenge for developing organisms is to maintain a critical balance between stable and flexible gene regulation (Reik, 2007). This is most obvious in pluripotent embryonic stem (ES) cells, which are functionally characterised by their ability to self-renew and to generate all somatic lineages when induced. Accordingly, ES cells express genes that encode self-renewal factors, while repressing many lineage-specific regulators that are ultimately required during development (Jaenisch and Young, 2008). A series of recent reports have indicated how Polycomb-mediated gene repression might provide short-term, and therefore flexible, epigenetic silencing of such developmental genes in pluripotent cell lines (Azuara et al., 2006; Bernstein et al., 2006a; Boyer et al., 2006; Lee et al., 2006; Pan et al., 2007; Zhao et al., 2007). This contrasts with long-term repression mechanisms as conferred, for example, by DNA methylation at transposons, imprinted and pluripotency-associated genes in somatic cells (Bird, 2002; Delaval and Feil, 2004; Epsztejn-Litman et al., 2008; Farthing et al., 2008; Weber and Schubeler, 2007).

Two distinct Polycomb Repressive Complexes (PRC), PRC1 and PRC2, are known to be important for the function of ES cells. PRC2 contains Ezh2, which catalyses histone H3 lysine 27 tri-methylation (H3K27me3), as well as Eed and Suz12. PRC1 contains the E3 ubiquitin ligases Ring1A (also known as Ring1) and Ring1B (Rnf2 – Mouse Genome Informatics) that mono-

ubiquitylate histone H2A lysine 119. Other PRC1 components include Bmi1, Mel18 (Pegf6 – Mouse Genome Informatics) and proteins of the Cbx family with H3K27 methylation affinity (Bantignies and Cavalli, 2006; Pietersen and van Lohuizen, 2008; Ringrose and Paro, 2007; Schuettengruber et al., 2007; Schwartz and Pirrotta, 2007; Simon and Kingston, 2009). Candidate-based (Azuara et al., 2006) and genome-wide (Bernstein et al., 2006a) studies of histone methylation in ES cells led to the remarkable finding that many PRC2-target genes not only carry the repressive H3K27me3 mark, but are also enriched for conventional indicators of active chromatin, including methylated H3K4. These so-called bivalent chromatin domains are thought to silence key developmental regulators while keeping them primed for future activation (or repression), and thus generally resolve to monovalent configurations upon differentiation, in accordance with gene expression changes (Bernstein et al., 2006a; Mikkelson et al., 2007; Pan et al., 2007). Further work showed that multipotent stem cells and some differentiated cells also possess bivalent domains, albeit perhaps fewer than in ES cells (Baksi et al., 2006; Bernstein et al., 2006a; Bracken et al., 2006; Cui et al., 2009; Mikkelson et al., 2007; Pan et al., 2007; Roh et al., 2006; Sanz et al., 2008; Wei et al., 2009), indicating that plasticity might be maintained at loci that are required for the function and differentiation of lineage-committed cells. Consistent with gene priming, bivalent genes assemble RNA polymerase II complexes preferentially phosphorylated on Ser5 residues (poised RNAP) and are transcribed at low levels (Brookes and Pombo, 2009; Guenther et al., 2007; Stock et al., 2007). Productive expression is, however, prevented by the action of PRC1 with conditional deletion of Ring1A/B, resulting in an upregulation of target gene expression in ES cells (from primed to overt transcription) (Endoh et al., 2008; Guenther et al., 2007; Jorgensen et al., 2006; Stock et al., 2007).

Clearly, Polycomb repressors are functionally required to prevent premature expression of primed genes and thus to stably maintain a pluripotent ES cell identity in culture (Azuara et al., 2006; Boyer et al., 2006; Chamberlain et al., 2008; Endoh et al., 2008; Leeb and Wutz, 2007; van der Stoop et al., 2008). Whether ES cell epigenetic signatures can also be seen in the developing...
embryo and when (and how) bivalent domains are established and subsequently resolved upon lineage commitment in vivo remains to be elucidated. In this study, we have focused on the earliest stages of mouse development to address whether poised chromatin structures are unique hallmarks of the founder (pluripotent) cells of the early embryo, and to investigate the kinetics of appearance and resolution of bivalent domains during the first lineage decision event (trophectoderm formation). We provide in vivo evidence that bivalent histone marking operates in the early mouse embryo from the eight-cell up to the blastocyst stage. Unexpectedly, we show that bivalent domains are retained at a subset of genes encoding key somatic lineage regulators in extra-embryonic restricted cells, as assessed both in vitro and in vivo. However, and in contrast to pluripotent cells, PRC1 (Ring1B) and poised RNAP are not engaged at these PRC2 (Suz12)-bound genes, consistent with a loss of gene priming. Instead, bivalent genes become selectively targeted by Suvs9h1-mediated repression upon trophoblast lineage commitment. Collectively, our results suggest a mutually exclusive role for Ring1B and Suvs9h1 in specifying the fate of bivalent genes in a lineage-specific manner upon blastocyst formation.

MATERIALS AND METHODS

Cell lines

The B1-TS cell line was established and maintained as described (Mak et al., 2004). ZHBTc4-ES cells were cultured on gelatinised plates with LIF 1000 U/μl (ESGRO-LIF; Millipore) (Azuara et al., 2006). Pou5Fl repression in ZHBTc4-ES was induced by addition of doxycycline (Sigma) at 1 μg/ml. TS-like (TSL) cells were derived from Dox-treated ZHBTc4-ES cells plated at low density on irradiated feeders in the presence of 37 ng/ml FGF4 (R&D Systems) and 1 μg/ml heparin (Sigma) (Niwa et al., 2000). Note that Dox treatment was sustained for approximately two weeks in these conditions; until the time at which positive staining for the trophectoderm stem cell marker Cdx2 was seen in the same proportion of ZHBTc4-derived TSL cells as B1-TS cells, while Oct4 was undetectable in either culture. TSL cells could then be serially passaged and propagated in culture for at least 6 weeks.

RNA interference

Lentivirus vector containing a short-hairpin RNA (shRNA) targeting mouse Suv39h1 mRNA was cloned in pLKO.1 (Sigma). The sequence used to successfully knockdown expression of Suv39h1 is as follows: 5'-GCTTTGATACTGAGGAAG-3' (TRCN97439). Recombinant lentiviruses were generated using a three-plasmid system in 293T cells as described (Mohn et al., 2008) and methylated DNA immunoprecipitation (MeDIP) analysis (Mohn et al., 2008) were carried out as previously described. Carrier ChIP followed by quantitative PCR (qPCR) was performed as described with minor modifications (O'Neill et al., 2006). S2 Drosophila cells (5×10^5 cells/ml) were mixed with eight-cell embryos (40n), compacted morula (20n), ICM or TE (10-12n) for immunoprecipitations. Native chromatin fragments were prepared by digestion with 5 U of micrococcal nuclease (GE Healthcare) per 2.5 μg of chromatin, and were subsequently incubated with 15 μl of commercially available antibodies against modified histones or control IgG antibodies. Protein A sepharose (GE Healthcare) was added to immobilise chromatin-antibody complexes; unbound chromatin fractions were recovered upon centrifugation and bound complexes further washed in a series of stringent buffers. Elution was carried in 1% SDS prior to proteinase K (0.2 mg/ml; Sigma) treatment of both unbound and bound fractions. DNA was subsequently purified on gel extraction columns (Qiagen) into a final volume of 50-60 μl TE buffer. DNA concentrations were determined by PicoGreen fluorimetry (Invitrogen) and unbound fractions were diluted to match bound concentrations, before qPCR analysis using mouse-specific primers. Real-time qPCR analysis was carried out on a Chromo4 DNA engine (Bio-Rad, Hercules, CA), using SYBR green jumpstart PCR master mix (Sigma) and 300 nM primers. Each qPCR reaction was performed in triplicate. Primer sequences are listed in Table S1 in the supplementary material.

Expression analysis

Total RNA was isolated using the RNeasy Mini (cell line samples) or Micro (embryo samples) kits and DNase I treatment (Qiagen). Samples were reverse transcribed using Superscript II following the manufacturer’s recommendations (Invitrogen) and analysed by qPCR. Primer sequences are listed in Table S2 in the supplementary material.

Western blot analysis

Protein concentrations of whole cell extracts were measured using the Bradford assay (Thermo Fisher Scientific). Samples (20 μg) were loaded onto 10% acrylamide gels and blotted onto methanol-activated polyvinylidene difluoride membranes using a semi-dry transfer system. After incubation and washing, membranes were treated with enhanced chemiluminescent substrate (Thermo Fisher Scientific).

Immunofluorescence analysis

Cells were seeded on gelatinised glass coverslips and fixed in PBS with 4% paraformaldehyde. Samples were permeabilised and blocked at room temperature before incubation with antibodies. Coverslips were mounted on Vectashield with DAPI (Vector Laboratories) and examined using a Leica SP5 confocal microscope (×40 or ×63 lenses).
RESULTS

Bivalent domains mark silent, lineage-inappropriate genes in trophoblast stem cells

In pre-implantation development the transition from morula to blastocyst is the starting point for lineage segregation into the inner cell mass (ICM) and trophectoderm (TE; Fig. 1A). ES cells are derived from the ICM and are pluripotent. By contrast, TE-restricted trophoblast stem (TS) cells are multipotent and contribute solely to placenta formation in vivo (Rossant and Tam, 2009). To investigate whether bivalent signatures are unique attributes of pluripotent cells in the early embryo, we directly compared the chromatin environment of key developmental genes in ES and TS cells. In particular, we focused on previously identified bivalent, CpG-rich promoters in ES cells (Azuara et al., 2006; Bernstein et al., 2006a; Mikkelsen et al., 2007) that were described as PRC2 and PRC1 joint targets (Fig. 1) (Ku et al., 2008). We have included in this study a panel of transcriptional regulators (Atoh1, Gata4, Hoxa7, Kdr, Mixl1, Pax3, Sox1 and Sox7) covering different embryonic lineages, as well as TS-associated markers (Cdx2, Fgfr2 and Hand1). Note that the genetic inactivation of most of these genes results in embryonic lethality (see Table S3 in the supplementary material).

Chromatin immunoprecipitation (ChIP) and quantitative PCR (qPCR) were performed to initially evaluate the abundance of repressive H3K27me3 and permissive H3K4me2 histone marks at selected promoters in ES and TS cells (Fig. 1B). For these analyses, qPCR primers were designed to amplify up to 600 bp upstream of the transcriptional start site of each gene. Modified histone levels were normalised against detected H3, and expressed as relative enrichment (% over H3). As anticipated, significant enrichment for H3K27me3 and H3K4me2 marks was detected at the promoters of silent genes in ES cells (Fig. 1B, left panel). Actively transcribed actin showed, by contrast, low H3K27me3 and high H3K4me2 levels, whereas an intergenic region used as negative control was not enriched for either histone modification.

In TS cells, all of the silent promoters analysed (including Atoh1, Sox1, Hoxa7, Mixl1, Gata4 and Sox7) also showed high levels of H3K27me3 together with H3K4me2, suggesting these genes remain bivalent despite the fact that they are not normally expressed upon placental development (see Fig. S1 in the supplementary material). By contrast, the active Cdx2, Fgfr2, Hand1, Kdr and Pax3 promoters were only marked by H3K4me2 in TS cells, as expected (Fig. 1B, right panel).

The retention of bivalent domains in trophoblast-restricted cells at genes that are not required in this lineage was unexpected. To verify that methylated H3K27 and H3K4 co-exist on the same allele in TS cells, we performed a series of sequential ChIP experiments in which chromatin was immunoprecipitated firstly with H3K27me3 and secondly with H3K4me2 antibodies (Fig. 1C), and vice versa (data not shown). Results confirmed that all genes with bivalent domains were simultaneously enriched for both marks in ES cells, as well as in ES cells, in comparison with expressed genes and controls. Remarkably, substantial enrichment for both H3K4me2 and H3K4me3 was still detected at bivalently marked genes when TS cells were induced to differentiate into spongiotrophoblasts and trophoblast giant cells, even though these genes were not activated (see Fig. S2 in the supplementary material). Taken together, these data show that the restriction of developmental potency in TE-derived stem cells and differentiated progeny is not necessarily accompanied by a loss of activating marks at silent, lineage-inappropriate genes.
Bivalent histone marking operates in vivo at silent genes in the early mouse embryo

To address whether bivalent domains are also present in vivo, we examined the histone profile of key developmental genes in the ICM and TE of newly formed blastocysts as well as in early eight-cell and morula-stage embryos. Individual ICMs were isolated by immunosurgery of early-stage blastocysts, whereas mural TE samples were prepared by manual dissection (Fig. 2A). Typically, 10-12 ICM or TE preparations were combined per immunoprecipitation. Eight-cell embryos (40n) and compacted morula (20n) were freshly collected and pooled for subsequent analyses. Histone modifications were analysed using carrier ChIP (C-ChIP) followed by qPCR (O’Neill et al., 2006; VerMilyea et al., 2009). C-ChIP allows small pools of ex vivo populations to be analysed by mixing with excess carrier Drosophila S2 cells, before preparation of nuclei and chromatin (see protocol outlined in Fig. 2B). Using this approach, we assessed the relative enrichment for H3K27me3 and H3K4me2 at the promoters of Sox1 and Gata4 – two examples of bivalently marked genes in both ES and TS cells – as well as of Pou5f1 and Cdx2, which show differential gene expression patterns upon pre-implantation development (Dietrich and Hiiragi, 2007; Jedrusik et al., 2008). Pou5f1 transcripts were detected in eight-cell and morula embryos and remained present in both ICM and TE tissues of newly formed blastocysts, whereas Cdx2 was predominantly expressed in the TE, as expected (see Fig. S3 in the supplementary material).

Sox1 and Gata4 were undetectable in eight-cell embryos onwards (see Fig. S3 in the supplementary material). In agreement with the lack of expression, these promoters displayed high levels of the repressive H3K27me3 marks in all four populations analysed, in contrast to actively transcribed Pou5f1, which shows low H3K27me3 and high H3K4me2 levels (Fig. 2C). H3K4me2 was also detected alongside H3K27me3 at Sox1 and Gata4, demonstrating the occurrence of bivalent domains in vivo. These domains were seen from the eight-cell embryo up to the blastocyst stage at silent loci, suggesting that they are established early during pre-implantation development and are stably retained upon blastocyst formation in both ICM and TE lineages. Cdx2 showed, by contrast, a more dynamic histone profile, being enriched for both marks in early eight-cell embryos and ICM cells where this gene is expressed at low or variable levels, but depleted of H3K27me3 marks in TE-committed cells (Fig. 2C, bottom panel). Together, these results corroborate our in vitro data in ES and TS cells, and further reveal that bivalent histone signatures associated with gene silencing exist in the early mouse embryo, prior to blastocyst formation and during the blastocyst stage.

Ring1B and poised RNAP are not recruited to genes that retain bivalent signatures in TE-derived stem cells

To further explore the chromatin status of bivalent, lineage-inappropriate genes in trophoblast-committed cells, we assessed the patterns of PRC2 and PRC1 binding at selected promoters in TS cells as compared with ES cells. As anticipated from the presence of H3K27me3, the PRC2 component Suz12 was found at all bivalent promoters analysed in both populations, although relatively lower levels were seen in TS cells (Fig. 1D). However, in striking contrast to ES cells, silent, Suz12-bound genes showed only low (or undetectable) enrichment for the PRC1 component Ring1B in TS cells, as seen at their active counterparts. These altered profiles of Suz12 and Ring1B binding did not correlate with overall changes in protein levels in the two cell types (Fig. 1E). The presence of Ring1B proteins in TS cells was also verified by immunofluorescence, confirming the colocalisation of Ring1B and Suz12 components on the inactive X chromosome of female trophoblast stem cells, as expected (Fig. 1F) (de Napoles et al., 2004; Fang et al., 2004).
PRC1 and RNAP act together in ES cells to maintain a poised chromatin state at bivalent genes. To investigate whether bivalently marked genes in TS cells are also primed by RNAP, we next examined the recruitment and conformation of these complexes by ChIP assay using previously validated antibodies against hypophosphorylated (8WG16) or Ser5-phosphorylated (Ser5P; 4H8) RNAP (Stock et al., 2007). As shown in Fig. 3, bivalent genes and active (actin and Hprt) controls were found to be highly enriched for Ser5P RNAP at their promoter regions in ES cells. A poised RNAP conformation was discriminated by measuring the level of 8WG16 binding, which was low at bivalent promoters but abundant at actively transcribed controls, as previously reported (Guenther et al., 2007; Stock et al., 2007). In TS cells, Ser5P and 8WG16 RNAP both marked expressed Cdx2, Fgf2, Hand1, Kdr and Pax3 genes and active controls, as expected (Fig. 3, right panel). RNAP complexes were, by contrast, virtually absent from the promoters of Atoh1, Sox1, Hoxa7, Mix11, Gata4 and Sox7, which is consistent with a loss of gene priming for transcription at these loci in TS cells.

**Selective induction of the H3K9 tri-methyltransferase Suv39h1 upon trophoblast lineage commitment**

The loss of Ring1B and RNAP recruitment at bivalently marked promoters in TS cells, as compared with ES cells, suggests that alternative repressive pathways might operate to regulate these loci in extra-embryonic and embryonic tissues. To further investigate the relationship between lineage identity and targeted chromatin changes, we exploited the potential to convert ES cells into TS-like cells, using a previously established ES cell line that carries a Doxycycline (Dox)-regulated Pou5f1 transgene (ZHBTc4) (Niwa et al., 2000) (Fig. 4A). In this system, Dox-treated ES cell colonies gradually acquire a TS-like (TSL) morphology upon Pou5f1 shutdown and provision of permissive conditions (Fig. 4B), whereas established TSL cell cultures show uniform staining for the TE-associated marker Cdx2, as seen in TS cells (Fig. 4C). Here, we surveyed by qRT-PCR the relative mRNA levels for a cohort of developmental regulators and control (actin and Hprt) transgenes, including PRC components, histone lysine methylases (KMTs) and demethylases (KDMs) as well as DNA methyltransferases (DNMTs), in ES and TS cells, and looked at dynamic gene expression alterations upon Pou5f1 shutdown and TSL cell derivation (Fig. 4D).

In agreement with previous reports (Mak et al., 2004; Matoba et al., 2006), we verified that Eed expression is rapidly and significantly reduced, in contrast to that of its partners Ezh2 and SuZ12, in Dox-treated ES, TSL and TS cells, as compared with ES cells. Surprisingly, we identified a pronounced imbalance in mRNA levels for several H3K9 KMTs [Ehmt1, G9a (Ehmt2), Suv39h1 and Suv39h2] and H3K9 KDMs (JmjD1a and JmjD2c; also known as Kdm3a and Kdm4c, respectively) between ES and TS cell populations. In particular, H3K9 tri-/di-demethylase JmjD2c (Cloos et al., 2006; Wissmann et al., 2007), which is highly expressed in undifferentiated ES cells (Loh et al., 2008) was promptly downregulated upon Pou5f1 shutdown (Fig. 4E). Conversely, H3K9 tri-methyltransferase Suv39h1 was dramatically upregulated upon TSL cell derivation and Cdx2 induction with a 30-fold increase in TSL and TS cells relative to ES cells (Fig. 4E). By comparison, Suv39h2, G9a or Ehmt1 showed a relatively modest induction (from 4- to 6-fold) upon ES cell differentiation, whereas Eset (also known as Setdb1) remained expressed at similar levels in all populations analysed (Fig. 4E, bottom panel). These results point to a key role for Suv39h1 in the establishment or maintenance of a TS cell fate; an observation that is consistent with the selective induction of Suv39h1 (in contrast to Suv39h2, G9a, Ehmt1 or Eset) in TE relative to ICM or morula cells in vivo (Fig. 4F).

**H3K9 tri-methylation specifies epigenetic asymmetry at bivalent genes between ICM and TE lineages**

To address whether Suv39h1 could directly target bivalent genes upon trophoblast lineage commitment and to assess its functional implication, we compared the levels of Suv39h1 occupancy, H3K9 tri-methylation and associated DNA methylation (Fuks et al., 2003) at the same panel of developmental regulators and control (actin and -satellite) loci in ES, Dox-treated ES (ESDox48h), TSL and TS cells (Fig. 5; see also Fig. S4 in the supplementary material). As anticipated, Cdx2, Fgf2r, Hand1, Flk1 and Pax3 expression was upregulated to levels seen in TS cells upon Dox treatment and TSL cell derivation (see Fig. S5 in the supplementary material). Thus, little H3K9me3 (Fig. 5A) or DNA methylation (Fig. 5B) associated with gene silencing was detected at these induced promoters that were marked by H3K4me2 only in TS cells, as previously seen in TS cells (see Fig. S4 in the supplementary material). By contrast,
Fig. 4. Developmentally regulated changes in gene expression profiles of chromatin regulators upon Pou5f1 repression and TS-like cell derivation. (A) Schematic of Pou5f1 shutdown and Cdx2 activation induced upon Doxycyline (Dox) treatment of ZHBTc4-ES cells. Differentiation into TS-like (TSL) cells was accomplished by culture on inactivated primary embryonic fibroblasts and in the presence of FGF4 and heparin. (B) Light microscope images comparing the morphology of ZHBTc4-derived TS-like (TSL) and B1-TS (TS) colonies. (C) Immunofluorescence analysis showing homogeneous expression of the TS-associated marker Cdx2 in TSL and TS cells. Note that no Cdx2 signal was detected in untreated ZHBTc4-ES cells, as expected (data not shown). (D) The expression of selected chromatin regulators was compared in ZHBTc4-ES cells after 24 and 48 hours of Dox treatment (ES-Dox) in the presence of LIF, and in ZHBTc4-derived TSL (TSL) cells and B1-TS (TS) cells, using quantitative RT-PCR (qRT-PCR). Values shown are normalised to actin and L19 and are expressed relative to untreated ZHBTc4-ES cells (ES=1). Upregulation (mean±s.d.>2) and downregulation (mean±s.d.<0.5) are coloured in red and blue, respectively. (E) Histograms showing the expression pattern of Cdx2, Pou5f1, Suv39h1, Jmjdc, Suvinh2, Ehmt1, G9a and Eset upon Pou5f1 shutdown and TSL cell derivation. Error bars represent s.d. of three independent experiments. (F) Expression levels of Cdx2, Suv39h1, Suv39h2 and G9a, as assessed by qRT-PCR, in morula (grey), dissected ICM (green) and TE (orange) sample preparations. Values shown are normalised to S17 and L19 mRNA levels and are expressed relative to morula samples (morula=1). Error bars represent s.d. of three independent experiments. Note that Ehmt1 and Eset transcript levels were below detection in all three samples under the same experimental conditions (data not shown). N.D., not detectable.

Atoh1, Sox1, Hoxa7, Mixl1, Gata4 and Sox7 genes remained inactive (see Fig. S5 in the supplementary material) and bivalently marked (see Fig. S4 in the supplementary material) in Dox-treated ES and TSL cells. These genes, however, became selectively targeted by Suv39h1 and rapidly acquired substantial levels of H3K9me3 upon loss of pluripotency and trophoblast lineage commitment (Fig. 5A; see also Fig. S4 in the supplementary material). Conversely, Suv39h1 knockdown by RNAi in TS cells (Fig. 5C) led to a reduction of H3K9me3 levels at bivalently marked genes, thereby confirming Suv39h1-dependent H3K9 methylation (Fig. 5D; see also Fig. S6 in the supplementary material). This establishes an unusual trivalent (H3K9me3-H3K27me3-H3K4me2) histone profile at silent, lineage-inappropriate genes in TS cells, as further verified by sequential ChIP assays (Fig. 5E). Interestingly, PRC1 (Ring1B) together with Ser5P RNAP forms were transiently retained at un-induced loci, as opposed to at activated genes in Dox-treated ES cells, yet were released in TSL and TS cells, suggesting that the loss of gene priming and the acquisition of Suv39h1-mediated H3K9me3 at bivalent genes are likely to be coordinated (see Fig. S4 in the supplementary material). Note, however, that Suv39h1 is not required to prevent transcriptional activation of Atoh1, Sox1, Hoxa7, Mixl1, Gata4 and Sox7 in Dox-treated ES cells (data not shown) or TS cells (see Fig. S6 in the supplementary material), but might rather stabilise a repressed state at silent, bivalent genes in synergy with other epigenetic marks, including H3K27me3. Consistently, chromatin changes from primed to repressed states at Suv39h1-bound genes were reinforced by de novo DNA methylation associated with stable silencing (Lande-Diner and Cedar, 2005) in TSL and TS cells in the absence of Ring1B (Fig. 5B; see also Fig. S4 in the supplementary material).

To further verify that bivalent, lineage-inappropriate genes are selectively targeted by Suv39h1-mediated H3K9 methylation upon TE formation in vivo, we examined the levels of H3K9me3 at Sox1, Gata4 and Cdx2 promoters prior to (morula) and after (ICM and TE) blastocyst formation, by C-ChIP and qPCR (Fig. 5F). The results showed that Sox1 and Gata4 genes harboured high levels of H3K9me3 in addition to H3K27me3 and H3K4me2 in the TE, but not in the ICM; an epigenetic signature also maintained in the developing placenta in vivo (data not shown). Moreover, H3K9me3 levels were low in compacted morula, which further suggested that the acquisition of the repressive H3K9me3 marks might be a late event linked with trophoblast cell fate consolidation and loss of lineage plasticity. By contrast, actively transcribed Cdx2 remained depleted of H3K9me3 in the TE, as expected (Fig. 5F; bottom panel). Together, our results indicate that alternative silencing strategies operate in a lineage-specific manner at key developmental regulators in the early embryo.
DISCUSSION

In eukaryotes, H3K9 tri-methyltransferases Suv39h1 and Suv39h2 are commonly associated with constitutive heterochromatin formation and function. In the zygote, however, paternal constitutive heterochromatin lacks Suv39h-mediated H3K9me3, and is instead targeted by PRC1 components, including Ring1B (Arney et al., 2002; Probst et al., 2007; Puschendorf et al., 2008; Santos et al., 2005). This differential loading of Ring1B and Suv39h1 onto heterochromatin underlies parental genome asymmetry in the zygote and is subsequently maintained through cell divisions up to the eight-cell stage (Puschendorf et al., 2008).

In this study, we find that Ring1B and Suv39h1 selectively target...
key developmental genes in a lineage-specific manner at the blastocyst stage, suggesting that Ring1B and Suvs91h1 mutual exclusion could occur throughout pre-implantation development.

In particular, we propose that PRC1 (Ring1B) and poised RNAP – two hallmarks of gene priming in pluripotent cells, are dynamically removed from the promoters of bivalent genes upon TE cell fate acquisition and Suvs91h1 recruitment (see model in Fig. 6). In this model, H3K9me3 and downstream repressive activities (e.g. DNA methylation) would reinforce the repressed state of Suvs91h1-bound genes upon loss of Ring1B. Absence of Ring1B enrichment at these loci does not, however, exclude the possible recruitment of other PRC1-like complexes in TE-restricted cells, as compared with pluripotent cells, owing to the dynamic composition of Polycmb complexes during development (Otto and Kwaks, 2003; Schuettengruber and Cavalli, 2009). This is exemplified by the reverse expression pattern of Phc1 and Phc2 in ES and TS cells (Fig. 4D) and the differential recruitment of these proteins on the inactive X chromosome in the two cell types (de Napoles et al., 2004). The distribution and density of methylated H3K27 and H3K9 marks in the vicinity of bivalent promoters could also alter the affinity of Cbx members, as has been previously suggested (Bernstein et al., 2006b).

An important aspect of our findings is the addition of the key repressive marks, H3K9me3 alongside DNA hypermethylation at promoters that retain high levels of methylated H3K4; an epigenetic state also reported in embryonic carcinoma cells (Ohm et al., 2007). This contrasts with prevailing views that loss of H3K4 methylation is a prerequisite for ‘locking-in’ a repressed state at bivalent genes that are not activated upon differentiation (Bernstein et al., 2006a; Meissner et al., 2008; Mohn et al., 2008). Our study reveals a novel mechanism by which ‘bivalency’ (and gene priming) can be resolved in extra-embryonic restricted cells through Suvs91h1 recruitment and the formation of a trivalent (H3K9me3-H3K27me3-H3K4me2) histone conformation at silent, somatic-associated genes. Interestingly, trivalent histone configurations were recently uncovered using a genome-wide approach at a limited set of genes encoding trophectoderm and early differentiation markers in ES cells (Bilodeau et al., 2009; Yuan et al., 2009). This indicates that ‘trivalency’ might not be particular to the trophectoderm lineage. In pluripotent cells, however, many of these genes are occupied by a different member of the H3K9 KMT family, Eset (also known as Setdb1), highlighting the distinct roles and/or target specificity of these chromatin regulators in early development and stem cells. However, whether Ring1B and poised RNAP are also excluded from Eset-bound promoters remains to be elucidated.

Importantly, we provide in vivo evidence that bivalent chromatin domains exist at silent developmental regulators in the early mouse embryo. These domains are present in eight-cell embryos and persist throughout pre-implantation development, providing a platform for further protein recruitment that would, in turn, dictate the fate of bivalent genes (repressed versus primed) upon lineage commitment. Although trophoblast lineage ‘fixation’ is shown to involve Suvs91h1 recruitment at bivalent, lineage-inappropriate genes, it is equally possible that transcriptional priming and pluripotency is retained through active protection from H3K9 and/or DNA methylation. Interestingly, and in keeping with this idea, Suvs91h1 and Jmd2c, which mediate H3K9 tri-methylation and demethylation, respectively, display dynamic and opposite gene expression patterns in vivo. Whereas Jmd2c is highly expressed in early cleavage-stage embryos (Wang et al., 2009), Suvs91h1 mRNA levels gradually increase during pre-implantation development with a peak at the transition from morula to blastocyst (Puschendorf et al., 2008). In our study, these two epigenetic factors are also shown to be differentially expressed in blastocyst-derived stem cells (Fig. 4D). As previously reported, Jmd2c is instrumental in stably maintaining ES cell identity in vitro (Loh et al., 2008). Similarly, we find that RNAP depletion of Suvs91h1 in TS cells causes a loss of TS cell markers (Cd cx2, Eomes, Fgfr2 and Gata3) and induction of differentiation-associated markers (Ptfl and Tph2), suggesting that Suvs91h1 might also be required for TS cell self-renewal (see Fig. 7 in the supplemental material).

In summary, we show that Ring1B and Suvs91h1 delineate distinct chromatin states at bivalent genes in a lineage-specific manner during early mouse lineage commitment. A key function for Ring1B in the epigenetic gene regulation of early embryos is consistent with the embryonic lethality of Ring1B-mutant mice (Voncken et al., 2003). By contrast, Suvs91h1/h2 mutant mice show a relatively mild phenotype, which probably reflects the synergy of Atrx, H3K4me3, Cdx2, Eomes, Fgfr2 and Gata3 and induction of differentiation-associated markers (Ptfl and Tph2), suggesting that Suvs91h1 might also be required for TS cell self-renewal (see Fig. 7 in the supplemental material).

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Competing interests statement

The authors declare no competing financial interests.

Supplementary material

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