The chromatin remodeling factor Chd1l is required in the preimplantation embryo

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Summary
During preimplantation development, the embryo must establish totipotency and enact the earliest differentiation choices, processes that involve extensive chromatin modification. To identify novel developmental regulators, we screened for genes that are preferentially transcribed in the pluripotent inner cell mass (ICM) of the mouse blastocyst. Genes that encode chromatin remodeling factors were prominently represented in the ICM, including Chd1l, a member of the Snf2 gene family. Chd1l is developmentally regulated and expressed in embryonic stem (ES) cells, but its role in development has not been investigated. Here we show that inhibiting Chd1l protein production by microinjection of antisense morpholinos causes arrest prior to the blastocyst stage. Despite this important function in vivo, Chd1l is non-essential for cultured ES cell survival, pluripotency, or differentiation, suggesting that Chd1l is vital for events in embryos that are distinct from events in ES cells. Our data reveal a novel role for the chromatin remodeling factor Chd1l in the earliest cell divisions of mammalian development.

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Introduction
The first differentiation decision in the mammalian embryo is made prior to the blastocyst stage, when blastomeres must commit to becoming either part of the trophectoderm (TE) or the inner cell mass (ICM) (Rossant and Tam, 2009). Cells of the ICM possess the property of pluripotency and will contribute to the many tissues of the embryo, whereas the TE will give rise to extra-embryonic material (Rossant and Tam, 2009). We reasoned that factors compartmentalized in the ICM could be novel developmental regulators of pluripotency or early differentiation. To identify candidate preimplantation regulators, we performed an expression analysis on purified ICM and whole blastocysts and identified genes enriched in the ICM. Gene ontology clustering revealed a large group of chromatin regulatory enzymes.

The high degree of chromatin organization within the nucleus is oppressive to transcription and other processes that require DNA accessibility (Kezetic and Luse, 1986; Lorch et al., 1987). Chromatin remodeling factors (CRFs) utilize energy to alter nucleosome positioning and contain a core SNF2-like ATPase/helicase domain responsible for enzymatic activity (Hirschhorn et al., 1992; Flaus et al., 2006). CRFs participate in key chromatin-dependent processes including transcriptional activation and repression, histone exchange, cell cycling, DNA repair, and many others (Hirschhorn et al., 1992; Cairns, 2005; Morrison et al., 2004; Fyodorov and Kadonaga, 2001). CRFs assemble into multi-subunit complexes, and their functions depend in part on the composition of the complexes (Flaus and Owen-Hughes, 2004; Wang et al., 1996a; Wang et al., 1996b).
critical for early development. The protein has a Snf2-like ATPase domain but lacks any of the signature domains of the four classic Snf2 subclasses. Instead, Chd1l contains a unique C-terminal “macro” domain and therefore defines a distinct subclass (Yan et al., 2002; Mohrmann and Verrijzer, 2005). The macro domain binds poly(ADP-ribose), or PAR, a post-translational modification added to nuclear acceptor proteins. The nucleosome remodeling activity of Chd1l is dependent on PAR synthesis, indicating that the PAR-binding macro domain is central to its function as a chromatin remodeler (Ahel et al., 2009; Gottschalk et al., 2009).

Chd1l is involved in the DNA damage response. Chd1l localization to sites of induced DNA damage is dependent on a functional macro domain, and dissociation from sites of damage is dependent on a functional ATPase domain (Ahel et al., 2009; Gottschalk et al., 2009). Recent studies have also implicated Chd1l as an oncogene. The majority of hepatocellular carcinomas in humans are associated with genomic amplification of a region that includes Chd1l, and its overexpression in liver cell lines and mouse models is tumorigenic (Chen et al., 2009; Ma et al., 2008). While evidence is accumulating for a role for Chd1l as an oncogene and in DNA repair, its importance during development has not been examined.

We find that Chd1l is expressed in cultured embryonic stem (ES) cells, which are derived from the ICM and share the ability to differentiate into the three major germ layers. Our data show that Chd1l is not required for ES cell viability, pluripotency or differentiation. Using a morpholino (MO) knockdown approach in the zygote-stage embryo, we show that Chd1l is required for the very earliest stages of development.

**Results**

Chromatin remodeling factors are compartmentalized in the blastocyst

The decision to become inner cell mass (ICM) or trophoderm (TE) is the first lineage commitment a totipotent blastomere must make. The ICM retains pluripotency, the ability to give rise to the three primary germ layers, whereas the TE will give rise to extra-embryonic tissue. We reasoned that mRNAs enriched in the ICM would encode proteins that contribute to the development of the blastocyst and/or the establishment of pluripotency. An alternative model would be that repression of these mRNAs in the TE marks an important step in the differentiation of TE and that continued expression in the ICM restricts TE differentiation. To screen for ICM-enriched mRNAs, we purified the ICM by immunosurgery (Solter and Knowles, 1975), taking advantage of the structural organization of the blastocyst (Fig. 1A). Outer TE cells of the blastocyst were labeled with IgG by incubation with rabbit anti-mouse serum and specifically lysed by the complement cascade, leaving behind purified ICMs.

RNA

![Fig. 1. Chromatin remodeling factors are enriched in the ICM.](image)

(A) Schematic of immunosurgery followed by whole-genome expression analysis. Inner cell masses (ICMs) were separated by lysing outer trophoderm (TE) cells. Expression levels of transcripts in purified ICMs were compared to transcripts from whole blastocysts. (B) Compartmentalization of mRNAs encoding known ICM and TE factors and mRNAs of ubiquitously expressed genes. The number above the bars represents the ratio of expression in ICM relative to whole blastocyst. Transcripts for ubiquitously expressed genes are represented with approximately equivalent levels in ICM and whole blastocyst. Relative expression levels of selected markers of pluripotency are higher in the ICM (green) than in the whole blastocyst (yellow); relative expression levels for selected markers of the differentiated TE are higher in the whole blastocysts than in the purified ICM. (C) Enrichment of selected classes of chromatin factors in ICM. Relative expression levels of selected transcripts encoding chromatin factors in the ICM (green) and whole blastocyst (yellow) are shown. TF: transcription factor; DNMT: DNA methyltransferase; Pcg: Polycomb group; ETP: Enhancers of Trithorax and Polycomb; TrxG: Trithorax group; KMT: lysine (histone) methyltransferase; KDM: lysine (histone) demethylase; HDAC: histone deacetylase.
extracted from the ICM was compared with total blastocyst RNA using genome-wide expression analysis. Transcripts encoding Oct4 and Nanog, factors known to be critical for pluripotency, were enriched in the ICM 1.9- and 2.4-fold, respectively, providing proof of sound methodology (Fig. 1B). In addition, mRNAs encoding Cdx2 and Eomes, markers of extra-embryonic material, were under-represented 4.5-fold and 2.4-fold, respectively, in ICM compared to the whole blastocyst (Fig. 1B). Ubiquitously expressed transcripts encoding β-actin and β-tubulin demonstrate roughly equivalent levels in ICM and whole blastocyst (Fig. 1B). Clustering of genes whose transcripts are enriched in ICM revealed three major GO-term classes: cell signaling molecules, transcription factors, and chromatin-modifying enzymes. Some of the chromatin factors identified have known enzymatic activity and/or developmental roles, including the DNA methyltransferases, the polycomb group proteins, and the Snf2 family of chromatin remodeling enzymes (Fig. 1C).

Chromatin remodeling factors are often found in large, multi-subunit complexes (Wang et al., 1996a). Subtle changes in the composition of a complex can have dramatic effects on its function, and on the differentiation status of a cell (Ho and Crabtree, 2010; Lessard et al., 2007; Ho et al., 2009). Enrichment (or repression) of one or more subunits of a complex is one way in which the composition of a complex can be regulated (Peng et al., 2009). In general, our data support a model in which, compared to the trophectoderm, the ICM is characterized as having a chromatin state with tight transcriptional control and an abundance of chromatin proteins that mediate transcription and differentiation.

Chd1l expression patterns suggest a developmental role

Among the Snf2 family of chromatin enzymes whose mRNAs were enriched in the ICM was the CRF called Chd1l. Its enrichment score of 4.28-fold was higher than that of the “master regulator” of pluripotency, Oct4 (1.8-fold) (Fig. 2A). The Snf2 family of chromatin remodeling factors has powerful and diverse roles in development and transcriptional regulation (Ho and Crabtree, 2010; Eisen et al., 1995), and Chd1l is a member of this family by virtue of the split DNA-dependent ATPase/helicase domain (Flaus et al., 2006). Chd1l is the only member of the Snf2 family that contains a poly(ADP-ribosyl)ation binding macro domain (Fig. 2B) (Yan et al., 2002). Chd1l protein expression was confirmed in ES cells using a Chd1l-specific antibody (Fig. 3B).

Our lab previously reported genome-wide gene expression profiles during preimplantation development from the zygote through the blastocyst stage (Wang et al., 2004). In these studies, Chd1l expression was found to increase through the first several cell divisions of development, peaking at the late morula stage (Fig. 2C). Upon formation of the blastocyst, total Chd1l expression decreases slightly; our ICM data indicate it then becomes preferentially expressed in the ICM. Compartmentalization in the ICM, expression in ES cells, and developmental regulation support a potential role for Chd1l in pluripotency and during early embryogenesis. We chose to investigate the developmental function of this novel CRF of the Snf2 family (Fig. 2D).

Chd1l is dispensable for ES cell pluripotency and proliferation

Mouse ES cells are derived from the ICM of blastocyst stage embryos and maintain the property of pluripotency indefinitely. Because Chd1l mRNA is enriched in the ICM and abundant in ES cells, we asked whether Chd1l is essential for ES cell survival and pluripotency. To knock down Chd1l in ES cells, we introduced shRNA-encoding sequence into the EBRTcH3 ES cell line (Masui et al., 2005). These cells are engineered to allow stable, Cre-mediated integration and inducible transgene expression under the control of a CMV promoter (Tet-Off) (Fig. 3A). First, we created a control ES cell line, NS-shRNA EBRTcH3, by integrating DNA encoding shRNA that does not target any transcript in the mouse genome (“Non-Silencing”).
Fig. 3. See next page for legend.
Chd1l does not regulate gene expression in ES cells
A primary function of the SNF2 family of DNA-dependent ATPases is transcriptional regulation (Fry and Peterson, 2001; Flaus and Owen-Hughes, 2001). The four major subfamilies, SWI/SNF, CHD, ISWI, and INO80 all regulate gene expression during development (Ho and Crabtree, 2010). Chd1l contains a seven-motif, DNA-dependent ATPase module that defines the SNF2 family of chromatin remodeling factors as well as a macro domain that recognizes PAR-modified nuclear proteins, including PAR-modified histones. Chd1l might also regulate transcription, and ES cells lacking Chd1l could have transcription changes even in the absence of obvious morphological changes. We took a whole-genome approach and obtained the expression profiles of induced (-Tet) EBRTcH3 ES cells expressing Chd1l-shRNA or NS-shRNA and uninduced (+Tet) ES cells that did not express shRNA. Expression indices confirm the reduction of Chd1l expression in ES cells expressing Chd1l-shRNA as compared to NS-shRNA (Fig. 3E). Only a small number of other transcripts that changed more than 1.4-fold between induced ES cells expressing Chd1l-shRNA and uninduced ES cells (~30), and these transcripts were also differentially expressed between induced ES cells expressing NS-shRNA and uninduced ES cells, indicating the expression changes were a byproduct of inducing shRNA expression. We found no statistically significant changes in expression of pluripotency markers, differentiation markers, or cell cycling genes (Fig. 3E). Our data suggest that Chd1l does not regulate transcription in ES cells.

Chd1l is not required for differentiation of ES cells
Like the ICM, ES cells are capable of differentiating into the three germ layers. While ES cells maintain this property indefinitely in vitro, the ICM is only transiently pluripotent as cells rapidly differentiate during embryogenesis. In the absence of the pluripotency cytokine LIF, ES cells can be grown into embryoid bodies (EBs), differentiating cellular aggregates that mimic in vivo post-implantation development. We reasoned that Chd1l may regulate gene expression in differentiating cells, when new gene expression patterns are being established. To ask whether Chd1l is required for the formation of the germ layers, Chd1l was reduced in Chd1l-shRNA ES cells, which were then differentiated into EBs. We measured the expression of a panel of lineage markers by q-RT-PCR over time. For comparison, we measured gene expression in EBs made from induced and uninduced NS-shRNA ES cells.

Chd1l transcripts are abrogated in MO-injected embryos
Next, we addressed the question of whether Chd1l plays a role in development prior to differentiation of the ICM. The preimplantation embryo can be cultured in vitro through the blastocyst and hatching stages. We took a rapid knockdown approach, utilizing synthetic antisense oligos called morpholinos (MOs) that inhibit translation and splicing machinery. This approach has been used extensively to study the early development of diverse organisms (Gore et al., 2005; Imai et al., 2006; Sumanas and Larson, 2002; Yamada et al., 2003). In the mouse preimplantation embryo, MOs have been employed to show that Oct4 has a critical role prior to the blastocyst stage (Foygel et al., 2008). MOs are stable oligos and effectively reduce production of specific proteins in the preimplantation blastocyst.
embryo, with minimal toxicity or off-target effects because they function through steric hindrance rather than through activation of the RNAi pathway (Foygel et al., 2008).

Splice-blocking MOs were designed to target Chd1l pre-mRNA. The predicted splice mutants produce truncated proteins due to stop codons within the intron (Fig. 4A). Chd1l MO-1 was microinjected into the cytoplasm of one-cell stage mouse embryos collected from superovulated and mated females. To confirm that MO-1 was functioning as predicted, we used microfluidic q-rtPCR on RNA collected from single MO-injected and control embryos. We used a TaqMan primer-probe assay that targeted the junction between exons 2 and 3 (ex2–3). This junction would be present in the wild-type Chd1l transcript but absent if the MO blocks its targeted splicing event. Microfluidic qPCR confirmed abrogation of the wild-type transcript. Ct values showed that amplification of the ex2–3 splice junction was efficient in control embryos but nearly absent in injected embryos (a difference in Ct values of ~20, reflecting >99% reduction of transcripts containing the normal splice junction in injected embryos) (Fig. 4B,C). Wild-type transcripts were similarly abrogated by injection of a second splice-blocking MO (MO-2), which targeted the ex4–5 splice junction (a difference in Ct values of ~10, reflecting a >99% reduction of normal transcripts) (Fig. 4C). Changes in Oct4 gene expression in embryos injected with Chd1l MO were not statistically significant (α=0.05).

Using either MO, the altered splicing would lead to the introduction of a stop codon within the intron. The effect of impaired splicing on the transcript as a whole is unknown, and whether or not nonsense mediated decay (NMD) will be initiated cannot be predicted. The Chd1l transcript is not significantly reduced in embryos injected with MO-1 compared to uninjected embryos, as demonstrated by the lack of any significant change in amplification of the 3’ sequences (ex20–21). This suggests that the transcript is stable despite abrogation of splicing between exons 2 and 3. On the other hand, the Chd1l transcript (ex20–21) is somewhat reduced in embryos injected with MO-2, indicating that the transcript resulting from the abrogation of splicing between exons 4 and 5 may be more unstable or may trigger NMD. Regardless of transcript stability, the only protein products translated would be truncated near the N-terminus and devoid of any of the known functional protein domains.

**Fig. 4. Efficiency of Chd1l MO knockdown.** (A) Mechanism of splice-blocking morpholinos (MOs). Splice-blocking MOs were designed targeting exon–intron boundaries. The schematic depicts “MO-1” disrupting the junction between exon 2 and exon 3. Disruption of this junction is predicted to produce a mutant protein truncated prior to the ATPase domain, thus lacking any functional activity. “MO-2” is designed in a similar manner, except that the disrupted splice junction is between exon 4 and exon 5. (B–D). Validation of Chd1l MO activity. Heat map (B) and quantitation (C,D) of microfluidic q-rtPCR of Chd1l transcripts. The “Ex20–21” probe targets the 3’ end of the Chd1l transcript and will amplify any Chd1l transcripts, regardless of splicing aberrations. The “Ex2–3” and “Ex4–5” probes target exon–exon junctions and will only amplify if that splicing event has occurred. MO-1 disrupts exon2–exon3 splicing (B,C). MO-2 disrupts exon4–exon5 splicing (D). Each embryo sample was run nine times. Black represents no amplification above the threshold and an “x” indicates a reaction automatically excluded from Ct value calculations. Ct values for each PCR reaction were subtracted from a value of 40 to reflect a positive correlation with expression levels. P-values were calculated using one-tailed, heteroscedastic Student’s t-test to compare Ct values of embryos injected with morpholino to Ct values of control embryos.
Embryos injected with Chd1l-targeting MOs arrest prior to blastocyst stage

To ask whether Chd1l is required during early development we microinjected the zygote-stage embryo with MO-1 targeting Chd1l and observed embryos for a period of four days. MO-injected embryos did not reach the blastocyst stage and instead arrested at the compaction stage (Fig. 5A,B). Cells of arrested embryos do not fragment and instead appear morphologically normal. An arrest prior to blastocyst formation is consistent with the peak in Chd1l expression at the late morula stage and enrichment in the ICM. In contrast, the majority of embryos microinjected with MO targeting the Snf2l transcript, encoding

Fig. 5. Chd1l knockdown results in developmental arrest in early embryos. (A) Uninjected embryos and embryos injected with no MOs (uninjected), Snf2l MO (negative control), Chd1l MO-1 and Chd1l MO-2, at 4 days after microinjection. (B) Quantification of development to blastocyst stage in uninjected embryos and embryos injected with different MOs. (C) Partial rescue of developmental arrest phenotype with co-injection of Chd1l mRNA. Error bars were calculated using weighted standard deviations. The difference between embryos injected with MO-2 and Chd1l mRNA and embryos injected with MO-2 and a control mRNA was significant at the α=0.01 level (P=0.009) when analyzed using a one-tailed, heteroscedastic Student’s t-test.

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another Snf2-like chromatin remodeling factor, reached the blastocyst stage (Fig. 5A,B). This result demonstrates that embryonic arrest is not a general effect of microinjection of a CRF MO. To further test our finding we microinjected MO-2 targeting ex4–5 splice junction. These embryos also arrested prior to the blastocyst stage (Fig. 5A,B). The precise timing of the arrest varied between the MOs, perhaps due to different binding affinities of the MO sequences.

The Chd1l phenotype is partially rescued by co-injection of Chd1l mRNA
To confirm that the embryonic arrest phenotype is a result of disrupting Chd1l protein production, mRNA encoding Chd1l was co-injected along with Chd1l MO. We reasoned that embryos arrested at an earlier stage would be more able to progress to later developmental stages with addition of mRNA than embryos arrested at later stages, so we used MO-2 for co-injection. MO-2 targets a splicing junction and therefore could not target the injected mRNA, which was synthesized from cDNA lacking intron sequences. Embryos injected with MO-2 alone did not progress to the morula stage, nor did embryos co-injected with MO-2 plus GFP mRNA. About 50% of the embryos co-injected with MO-2 plus Chd1l mRNA progressed to the morula stage or further (Fig. 5C). Mitigation of the developmental arrest phenotype by Chd1l mRNA confirmed that loss of Chd1l was responsible for the embryonic arrest.

Discussion
Chromatin remodeling activities are abundant in preimplantation embryos and in ES cells, and many of these activities are geared toward initiating pluripotent transcriptional competence and ensuring that differentiation programs are locked in epigenetically (Corry et al., 2009; Albert and Peters, 2009). Although Chd1l is part of the Snf2 family of DNA-dependent ATPases (Flaus et al., 2006), many of which are potent transcriptional regulators, Chd1l itself does not seem to regulate gene expression, at least in ES cells. It remains a formal possibility that Chd1l regulates gene expression in the preimplantation embryo, where a prominent developmental arrest phenotype was observed, but subsequently ceases to have gene regulation activity in ES cells. Despite being abundantly expressed, Chd1l is not required for normal proliferation, pluripotency, or differentiation of ES cells. Chd1l might have no function at all in ES cells, its function may be masked by the function of a redundant ES cell protein, its function may only become apparent when some trigger or insult presents itself, or the ES cell protein may represent a store of protein that will be important later in development. Chd1l is likely function differently in the transiently pluripotent ICM than in ES cells that have undergone artificial epigenetic changes to adapt to immortal growth in culture.

The critical developmental role of Chd1l in preimplantation embryos may stem from the ADP-ribose-binding macro module that distinguishes Chd1l from the other members of its family (Ahel et al., 2009; Gottschalk et al., 2009; Karrais et al., 2005). ADP-ribose is a post-translational modification that is added to acceptor proteins by several enzymes including the PARPs, which catalyze poly-ADP-ribosylation, and the sirtuins, which catalyze mono-ADP-ribosylation in addition to histone deacetylation (Landry et al., 2000; Imai et al., 2000; Frye, 1999). Chd1l may bind to ADP-ribose catalyzed by these enzymes and act as an effector protein for sirtuin- and/or PARP-mediated processes. The sirtuins have diverse cellular roles, including gene regulation and DNA repair, and have been shown to be critical during embryogenesis (Wang et al., 2006; Rine and Herskowitz, 1987; McBurney et al., 2003; Mao et al., 2011). However, mono-ADP-ribosylation by the sirtuins appears to be weak compared to histone deacetylation, and the physiological significance this activity remains somewhat controversial (Du et al., 2009).

Poly-ADP-ribose (PAR) is synthesized by the PARP family of PAR polymerases and has important roles in diverse chromatin-dependent processes. Evidence is accumulating for the importance of PAR regulation in the embryo. Double knockout of PAR polymerases Parp-1 and the partially redundant Parp-2 in mice is embryonic lethal at the onset of gastrulation (Ménissier de Murcia et al., 2003), whereas knockout of the non-redundant PAR depolymerase PARG is lethal at E3.5 (Koh et al., 2004). These data suggest that PAR levels are tightly regulated in the embryo and that fluctuations are highly deleterious. Chd1l contains a macro module responsible for binding PAR. Thus Chd1l could contribute to PAR regulation, and the Chd1l embryonic arrest phenotype may be due to aberrant PAR levels or downstream PAR signaling.

Two independent groups recently demonstrated the ability of Chd1l to respond to DNA damage by interacting with PAR (Ahel et al., 2009; Gottschalk et al., 2009). DNA damage is one of the most prominent triggers of PAR modification and signaling. Parp-1 is activated by DNA damage and synthesizes PAR onto itself in an auto-modification reaction, which initiates DNA repair mechanisms (Berger, 1985; Benjamin and Gill, 1980). Blocking Parp-1 activity with specific inhibitors, or through null mutations, results in cellular hypersensitivity to DNA damaging agents and defects in DNA repair (Herceg and Wang, 2001). Repair of damaged DNA is critical in the early embryo. Damage to DNA occurs frequently as a result of normal cellular metabolism, and the repair of resulting errors is critical in the early embryo as it must maintain genomic integrity for the future organism. Consistent with this requirement, genes involved in all of the major DNA repair pathways are expressed in the preimplantation embryo (Jaroudi and SenGupta, 2007). Therefore, because Chd1l responds to DNA damage through its interaction with PAR, and because DNA repair is crucial during embryogenesis, defects in DNA repair could underlie the Chd1l early embryonic arrest.

Large number of double-stranded break repair proteins are embryonic lethal when deleted (Hakem, 2008). Double-stranded breaks are the most toxic form of DNA damage and can be repaired through either non-homologous end-joining (NHEJ) or homologous recombination (HR). NHEJ can function throughout the cell cycle, whereas HR is restricted to S/G2 phase (Rothkamm et al., 2003). In the zygote, repair of the paternal genome is especially crucial because double-stranded breaks and other errors are introduced during spermatogenesis, and the extreme chromatin compaction of the sperm is inhibitory to repair (Generoso et al., 1979; Matsuda et al., 1985). The zygote spends ~20 hours in G1 prior to the first cell division, and much of the paternal DNA is repaired through NHEJ (Fiorelza et al., 2001; Hagmann et al., 1996; Hagmann et al., 1998; Lee et al., 1997). The ability of Chd1l to function in NHEJ is suggested by its PARP-dependent association with a major NHEJ component, DNA-PKcs, upon induced DNA damage (Ahel et al., 2009).
An intriguing question is why is Chd1l essential in the earliest stages of embryogenesis but not in ES cells? In contrast to the zygote, ES cells have rapid cell cycles with abbreviated G1 and G2 phases and rely heavily on HR to repair lesions during S phase (Savatier et al., 2002). Therefore, one explanation for why reduced Chd1l causes preimplantation arrest but is dispensable for ES cells is that Chd1l plays a role in NHEJ, which is acutely essential during early embryogenesis but not in ES cells.

In summary, numerous mRNAs encoding chromatin remodeling enzymes are enriched in the ICM, which will differentiate into all the cellular lineages of the adult organism. Chd1l, a candidate regulator of pluripotency studied here, is essential for preimplantation embryonic development even prior to the formation of the ICM. Despite its requirement for the earliest cell divisions in the embryo and its expression in ES cells, Chd1l appears to be dispensable for ES cell viability, pluripotency, differentiation, and gene expression. The function of Chd1l could be in PAR signaling via the PAR-binding macro domain and in downstream DNA repair. Recent studies have demonstrated a role for Chd1l as a DNA damage response protein that interacts with members of the NHEJ pathway in a PARP-dependent manner. Impaired NHEJ repair could explain why Chd1l deficiency results in developmental arrest of preimplantation embryos that rely heavily on NHEJ but causes no detectable abnormalities in ES cells. The differential requirement of Chd1l in the preimplantation embryo and in ES cells exemplifies the limitations of extrapolating conclusions from experiments using in vitro-derived ES cells and highlights the importance of studying early development directly in mouse embryos.

Materials and Methods

Immunosurgery and expression profiling

E3.5 blastocysts were collected from timed-pregnant mothers and washed in M2 medium. The zona pellucida was removed by incubation in Acid Tyrode solution for 3 minutes. Outer TE cells were labeled with IgGs by incubation with 10% rabbit anti-mouse serum for 60 minutes. Embryos were washed three times in M2 medium, and then TE cells were lysed through the complement cascade by incubation with 50% guinea pig complement for 15–30 minutes, or until lysis was visible. Remaining TGs were washed three times in M2 medium with a fine pipette to remove residual TE cells. Total RNA was extracted from purified ICm and whole blastocysts with Trizol reagent. Purified RNA was amplified using an Affymetrix kit, labeled, and hybridized to one Affymetrix mouse 430 2.0 Expression Array per sample. Chip analyses were performed with Dchip, a model-based method for expression analysis (http://www.dchip.org). Normalization of data was performed by the InvarSet Normalization method (Li and Wong, 2001).

ES cell lines

The EBRTcH3 cell line contains a cassette acceptor utilizing loxP and loxPV sites at the Rosa locus to allow efficient and directional integration of a transgene by Cre-mediated recombination. ShRNA-mir cDNAs were subcloned from pGIPZ vectors (OpenBiosystems, Chd1l shRNA Oligo ID: V2LMM_18041 and non-silencing “shRNA-mir”) into the pPHc exchange vector for recombination into the EBRTcH3 ES cell line. The parental EBRTcH3 ES cells and the pPHc exchange vector were gifts from the lab of Dr Hitoshi Niwa of Japan.

The exchange vector containing the shRNA-mir sequence was cotransfected with a Cre expression plasmid using lipofectamine. Transfected cells were plated at single-cell density and cultured with Puromycin (1.5 μg/ml) to select for successful recombinants and with Tetracycline (1.0 μg/ml) to repress transgene expression. Clones were confirmed by PCR genotyping of the 5′ and 3′ recombinant sites. To induce shRNA expression, the derived ES cell lines were cultured without Tetracycline but with high Puromycin (7.5 μg/ml). Control, uninduced ES cells were cultured in high Tetracycline (1.5 μg/ml) and high Puromycin (7.5 μg/ml).

ES cell expression profiling

Total RNA was extracted from Chd1l-shRNA and NS-shRNA ES cells three days after inducing the expression of Chd1l-shRNA or NS-shRNA by Tetracycline removal (7.5 μg/ml Puromycin), and from uninduced Chd1l-shRNA and NS-shRNA ES cells that do not express shRNA (7.5 μg/ml Puromycin, 1.5 μg/ml Tetracycline). Three different Chd1l-shRNA EBRTcH3 clones and one NS-shRNA EBRTcH3 clone were used. RNA was amplified from the eight samples, labeled using an Affymetrix kit, and hybridized to mouse 430 2.0 Expression Arrays. Fold changes in expression indices were calculated for shRNA-induced ES cells versus shRNA-uninduced ES cells. The statistical significance of fold-changes between Chd1l-shRNA induced and uninduced samples was determined using a paired t-test, a minimum fold change of 1.4, and a delta value of 1.9 (SAM Analysis) (Tusher et al., 2001).

Differentiation of embryoid bodies

Expression of shRNA was induced by Tetracycline withdrawal in Chd1l-shRNA and NS-shRNA EBRTcH3 ES cells for three days prior to differentiation into embryoid bodies (EBs) to ensure complete Chd1l knockdown. RNA was collected at Day 0 of differentiation from induced and uninduced Chd1l-shRNA and NS-shRNA EBRTcH3 ES cells. ES cells were suspended at a density of 2×10⁶ cells/ml of medium without LIF, and EBs were made using hanging droplets of 500 cells in 25 μl. After two days, embryoid bodies were collected into 10-cm UltraLure Attachment plates (Corning) and cultured for an additional seven days in the absence of LIF. RNA was collected every three days after LIF removal. cDNA was synthesized from each sample and subjected to qPCR. Relative quantities for each cDNA were calculated using Gapdh as the internal control and shRNA-uninduced, Day 0 samples as references.

TaqMan gene expression assays used in these experiments were presynthesized and ordered from Applied Biosystems: Gdh: Mm99999915_g1; Oct4: Mm00658129_gH; Gata4: Mm00438919_m1; Fgf5: Mm00135348_g1; Lhx1: Mm00521776_m1; Otx2: Mm0046859_m1; Chd1l: Mm00471579_m1.

Embryo culture and microinjection

Three to five-week-old wild-type F1 (C57BL6 × DBA/2) females (Charles Rivers) were superovulated by intraperitoneal injections of 5 IU of pregnant mare’s serum gonadotropin (Sigma) followed by 5 IU of human chorion gonadotropin (Sigma) 48 hours later and mated with wild-type males. Mice were sacrificed by cervical dislocation 17 hours after hCG injection, and 1-cell embryos were dissected and released from oviducts. Cumulus cells were removed using hyaluronidase digestion, and single-cell zygotes at the two-pronuclei stage were recovered and immediately micro-injected cytoplasmically with 5–10 pl of 0.6 mM antisense morpholino. Prior to injection, the MO was heated at 65 ℃ for 15 minutes to remove any secondary structure.

Preimplantation embryos were cultured in vitro in 20 μl droplets of Quinn’s Advantage Cleavage Medium (Sage) supplemented with 10% SP serum and covered with mineral oil. Dishes were placed in a desiccator filled with mixed gas (90% nitrogen, 5% oxygen, 5% carbon dioxide) in a 37 ℃ incubator. Embryos were observed every 24 hours for a period of four days, about the time of hatching.

Morpholinos were obtained from GeneTools: Chd1l MO-1: tacCTGGCAG (in2-EX2); Chd1l MO-2: ttggagagaagcagagggctaCCTC (in4-EX4); Sox17: Mm01351988_m1; AP2: Mm00438919_m1;AFP: Mm00135348_g1; Lhx1: Mm00521776_m1; Otx2: Mm0046859_m1; Chd1l: Mm00471579_m1.

Microfluidic qPCR

Single embryos were collected 48 hours after injection and lysed by one freeze thaw cycle. cDNA was synthesized using the CellsDirect One-Step rtPCR kit (Invitrogen) and subjected to 18 rounds of gene-specific amplification using TaqMan primer/probe assays (Applied Biosystems). TaqMan primer/probe assays and cDNA from single embryos were loaded onto a Fluidigm 48.48 microfluidic array for qPCR analysis using a Biomark thermal cycler.

TaqMan gene expression assays used in these experiments were presynthesized and ordered from Applied Biosystems: Gdh: Mm99999915_g1; Chd1l Ex4-2: Mm00471561_m1; Chd1l Ex4-5: Mm01257091_m1; Chd1l Ex20-21: Mm00471578_m1.

α-Chd1l antibody

A hydrophilic sequence of 122 aa corresponding to amino acid numbers 557–678 of the Chd1l protein was selected for the antigenic region. The antigen was produced as a TrpE fusion protein with the pATH11 vector in BL21 E. coli, solubilized, and subjected to SDS-PAGE. The gel slice was excised and submitted to Josman, LLC for injection into two rabbits and two rats. The antisera was also purified using a GIST-Chd1l-bound Sepharose column and eluted with low pH buffer. Both the rabbit and the rat antibodies recognize a ~100 kDa band on Western blot. Rabbit α-Chd1l antibody was used in all experiments reported here.

Statement regarding animal use

The animal experiments were performed in the labs of M.W.M.Y. and M.P.S. under ethical protocols approved by the Stanford Institutional Animal Care and Use Committee.
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