Tracing Dynamic Changes of DNA Methylation at Single-Cell Resolution

Citation

As Published
http://dx.doi.org/10.1016/j.cell.2015.08.046

Publisher
Elsevier

Version
Author’s final manuscript

Accessed
Sun Apr 07 00:18:50 EDT 2019

Citable Link
http://hdl.handle.net/1721.1/108812

Terms of Use
Creative Commons Attribution-NonCommercial-NoDerivs License

Detailed Terms
http://creativecommons.org/licenses/by-nc-nd/4.0/
Tracing dynamic changes of DNA methylation at single cell resolution

Yonatan Stelzer1,3, Chikdu Shakti Shivalila1,2,3, Frank Soldner1, Styliani Markoulaki1, and Rudolf Jaenisch1,2,4

1Whitehead Institute for Biomedical Research, Cambridge, MA 02142, USA
2Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02142, USA

SUMMARY

Mammalian DNA methylation plays an essential role in development. To date, only snapshots of different mouse and human cell types have been generated, providing a static view on DNA methylation. To enable monitoring of methylation status as it changes over time, we establish a Reporter of Genomic Methylation (RGM) that relies on a minimal imprinted gene promoter driving a fluorescent protein. We show that insertion of RGM proximal to promoter-associated CpG islands reports the gain and loss of DNA methylation. We further utilized RGM to report endogenous methylation dynamics of non-coding regulatory elements, such as the pluripotency-specific super enhancers of Sox2 and miR290. Loci-specific DNA methylation changes, and its correlation with transcription was visualized during cell state transition following differentiation of mouse embryonic stem cells and during reprogramming of somatic cells to pluripotency. RGM will allow the investigation of dynamic methylation changes during development and disease at single cell resolution.

INTRODUCTION

DNA methylation is recognized as a principal contributor to the stability and regulation of gene expression in development and maintenance of cellular identity (Bird, 2002; Cedar and Bergman, 2012; Jaenisch and Bird, 2003; Reik et al., 2001). Changes in DNA methylation are dynamic and it is still largely unknown how they dictate spatial and temporal gene expression programs (Smith and Meissner, 2013). Recent advancements in sequencing technologies enabled the establishment of methylation maps for multiple cell types in both human (Roadmap Epigenomics et al., 2015; Schultz et al., 2015; Smith et al., 2014; Ziller et
al., 2013) and mouse (Hon et al., 2013), thus providing a framework for identifying key lineage-specific regulators (Rivera and Ren, 2013). DNA methylation is a dynamic process and current methods are only bulk and provide a static “snapshot” view of the methylation state during cell state transitions. The difficulty in translating real-time epigenetic changes into a traceable readout, is, to date, a limiting factor in our ability to follow the dynamics of DNA methylation. Therefore a key challenge in the field is to generate tools that allow tracing changes in DNA methylation over time.

Here we set out to generate a DNA methylation reporter system that is capable of visualizing genomic methylation states at single cell resolution. The design of the reporter was based on two premises: (i) previous observations suggesting that CpG sites can serve as cis-acting signals, affecting the methylation state of adjacent CpGs (Brandeis et al., 1994; Mummaneni et al., 1995; Turker, 2002); (ii) a methylation-sensitive promoter that, when introduced in proximity to a CpG region of choice, may be utilized to report on methylation changes of the adjacent sequences. Thus, a key issue in establishing a DNA methylation reporter was identifying a methylation-sensitive promoter, which is not independently regulated by the DNA methylation machinery, but can be affected by exogenous methylation changes. Constitutively active genes usually contain hypomethylated high density CpG islands (CGIs) in their promoter regions and are not regulated by DNA methylation (Deaton and Bird, 2011) whereas gene promoters associated with low density CGI are activated and repressed in a tissue-specific manner. Because methylation of both classes of promoters is either not regulated by the DNA methylation machinery in all tissues or regulated in a tissue-dependent manner, these promoters cannot be utilized as DNA methylation reporters. In contrast, imprinted gene promoters exhibit inherent sensitivity to DNA methylation of adjacent genomic regions resulting in transcriptional activation or silencing. This mechanism has been established for a subgroup of germline-derived differentially methylated regions (DMRs) that affect in cis the methylation state of secondary regulatory promoter elements, which in turn control imprinted gene activity. Importantly, following their establishment, promoter-associated imprinted DMRs are not regulated by the DNA methylation machinery in a tissue-specific manner (Ferguson-Smith, 2011). We hypothesized that these intrinsic characteristics of imprinted gene promoters make them attractive candidates for methylation sensors. Perhaps one of the best-studied example is the Prader-Willi Angelman region, in which an imprinted DMR resides at the small nuclear ribonucleoprotein polypeptide N (Snrpn) gene promoter region controlling its parent-of-origin monoallelic expression (Buiting et al., 1995; Kantor et al., 2004). Furthermore, *Snrpn* is expressed in most of the tissues and thus serves as an attractive candidate to generate a DNA methylation reporter.

Changes in DNA methylation occur mostly at non-CGIs, some of which are associated with tissue-specific gene promoters (Jones, 2012). Nevertheless, a growing body of evidence suggests that the bulk of tissue-specific changes in DNA methylation is associated with noncoding sequences (Irizarry et al., 2009) such as distal regulatory elements, which include enhancers and transcription factor binding sites (Hon et al., 2013; Stadler et al., 2011; Ziller et al., 2013). Recent reports identified super-enhancers (SE) as clusters of TF and mediator binding sites associated with bona-fide enhancer chromatin marks to control the
expression of key cell identity genes (Dowen et al., 2014; Hnisz et al., 2013; Whyte et al., 2013). Global genomic comparisons of tissue-specific DNA methylation and transcription factor (TF) chromatin immunoprecipitation sequencing (ChIP-seq) data correlated the chromatin with the methylation state (Xie et al., 2013). Thus, many tissue-specific enhancers are hypomethylated in tissues where the target genes are expressed, but are hypermethylated in tissues where the target genes are silent (Hon et al., 2013).

In this paper we establish a Reporter of Genomic Methylation (RGM) that enables the visualization of changes in DNA methylation in live cells. We show that a minimal Snprn promoter can report on the DNA methylation state of endogenous gene promoters. We also generated reporter cell lines for the pluripotency-specific miR290 and Sox2 SEs and demonstrate that RGM can be used to capture dynamic DNA methylation changes in distal non-coding regulatory regions. An attractive aspect of RGM is its utility to visualize DNA methylation changes in development and disease at single cell resolution in the same sample.

RESULTS

A methylation-sensitive reporter system based on a minimal imprinted promoter

To establish a methylation reporter, we generated a minimal Snrpn promoter that includes the conserved elements between human and mouse and contains the endogenous imprinted DMR region (Figure S1A). The minimal promoter region driving GFP was cloned into a sleeping beauty transposon vector (Ivics et al., 1997) to facilitate stable integration into the genome. Recent studies have demonstrated that different CGI vectors, when stably inserted into mouse embryonic stem cells (mESCs), adopt a methylation pattern that corresponds to the in vivo methylation pattern of the respective endogenous sequence (Sabag et al., 2014). To test whether DNA methylation can propagate into the Snrpn promoter region in vivo, we designed an experimental system in which the CGI regions of Gapdh and Dazl were cloned upstream of our reporter (Figure 1A). The promoter of Gapdh encompasses a hypomethylated CGI consistent with constitutive expression in all tissues. In contrast, the Dazl promoter-associated CGI is hypermethylated in all tissues excluding the germ cells (Hackett et al., 2013). Given the different expression and methylation patterns of both genes, upon stable integration of the two reporter vectors into mESCs the Gapdh CGI is expected to maintain its hypomethylated state, while the Dazl CGI would be subjected to de novo methylation (Sabag et al., 2014). Figure 1B show that more than 95% of cells carrying the Gapdh reporter expressed GFP. In contrast, more than 30% of cells carrying the Dazl reporter were GFP negative, corresponding to reporter silencing. The effect of the Dazl reporter becomes more robust upon continued passage, with more than 80% of the cells silencing their reporter within 4 weeks (Figure 1B).

To assess the DNA methylation levels of the Gapdh and Dazl reporters following introduction into mESCs, we sorted Gapdh GFP positive and Dazl GFP negative cell populations (Figure 1C). The GFP expression state was stable upon continuous culture and passaging of the two sorted cell populations for over 7 weeks (Figure 1C). DNA was extracted from both Gapdh GFP positive and Dazl GFP negative cells and subjected to bisulfite conversion and PCR sequencing. Figure 1D shows that Gapdh GFP positive cells
maintained the hypomethylated state at both Gapdh CGI and the Snrpn promoter regions, whereas Dazl GFP negative cells became highly de novo methylated at the Dazl CGI region and its corresponding downstream Snrpn promoter (Figure 1E). These results are consistent with the hypothesis that DNA methylation can be propagated from the CGI into the Snrpn promoter region resulting in repression of transcriptional activity.

**RGM is a reporter for in vivo demethylation**

The experiments described above showed that RGM reports on de novo methylation imposed in vivo on the unmethylated Dazl CGI donor test sequence. Conversely, we were interested to assess whether a methylated and silent donor Snrpn promoter can be reactivated by means of demethylation acquired in vivo. For this we used the CpG methyltransferase M.SssI to in vitro methylate both Gapdh and Dazl reporter constructs. Treatment of the plasmids with M.SssI enzyme followed by bisulfite conversion, PCR amplification and sequencing, confirmed the complete hypermethylation of both the CGI and Snrpn promoter regions (Figures 2A, S1B and S1C). ESCs were transfected with either Gapdh or Dazl reporter and selected for cells carrying stably integrated vectors. Following one week of culture we identified robust activation of GFP in virtually all cells carrying the integrated Gapdh reporter, whereas cells carrying the Dazl reporter remained GFP negative (Figures 2B, C, D). To assess the DNA methylation state of the Gapdh and Dazl CGI and the respective downstream Snrpn promoter regions, DNA was extracted from the two cell lines, subjected to bisulfite conversion, PCR amplification and sequencing. Figure 2E demonstrates that, consistent with high GFP expression, the Gapdh CGI and its downstream Snrpn promoter had become fully demethylated. In contrast, the Dazl CGI and its downstream Snrpn promoter sequences maintained the hypermethylated state in agreement with complete repression of the GFP signal (Figure 2F). Thus, our data support the hypothesis that a Snrpn promoter can report on in vivo demethylation of the CGI in its proximity.

**Dnmt1, 3a and 3b mediate methylation and reporter activity**

We used ESCs deficient for the DNA methyltransferases Dnmt1, Dnmt3a and Dnmt3b to gain mechanistic insights into demethylation and de novo methylation imposed on the Snrpn promoter in transfected ESCs. Figure 2G shows that introduction of an in vitro methylated Dazl Snrpn vector into Dnmt1 mutant cells resulted in about 80% GFP positive cells by passage five, in contrast to no GFP positive cells when inserted into wt cells. In agreement with the role of Dnmt1 as being the maintenance DNA methyltransferase (Li et al., 1992), bisulfite sequencing analysis on the sorted GFP positive cells confirmed that reactivation of the methylated Dazl reporter occurred by passive demethylation (Figure 2H). To clarify the mechanism of de novo methylation, we introduced an unmethylated version of both vectors into mESCs deficient for both de novo DNA methyltransferases Dnmt3a and Dnmt3b (Pawlak and Jaenisch, 2011). Figure 2I shows that the vast majority of cells carrying the Dazl or the Gapdh reporters were positive for GFP unlike Dazl reporter expression in control V6.5 cells (Figure 2I), which is consistent with Dnmt3a/b mediating de novo methylation and reporter silencing.
Recent studies have shown that culturing mESCs in 2i medium (inhibitors of MEK and GSK3), and leukemia inhibitory factor (LIF) results in downregulation of *Dnmt3a* and *Dnmt3b*, consequently leading to global hypomethylation (Lee et al., 2014). To assess whether these culture conditions affect reporter activity, we transfected the unmethylated *Gapdh* and *Dazl* reporters into wt mESCs cultured in 2i and LIF. Figure 2I shows that the great majority of the stably transfected cells were GFP positive, consistent with 2i-mediated downregulation of the *Dnmt3a* and *3b*.

RGM can report on methylation associated with endogenous gene promoters

To test whether the *Snrpn* promoter could also report on DNA methylation levels associated with endogenous gene promoters, we utilized CRISP/Cas-mediated gene editing to target the endogenous CGI's located at the promoter regions of *Gapdh* and *Dazl* (Figures 3A, S2A and S2B). Figure 3B shows 35/36 *Dazl* targeted clones were GFP negative indicating robust silencing of the *Dazl* reporter whereas 20/21 *Gapdh* targeted clones were GFP positive (Figure 3B). FACS analysis of correctly targeted clones confirmed that *Gapdh* reporter cells were all GFP positive with the CGI and *Snrpn* promoter unmethylated (Figure 3C,D) in contrast to *Dazl* GFP negative clones with the corresponding sequences methylated (Figure 3E,F). Our results demonstrate that *Snrpn* reporter activity reports on the methylation state of its surrounding sequences and does not alter their methylation state. Furthermore, the endogenous targeting results suggested that the partial repression of the *Dazl* reporter (Figure 1B), observed at early passages of the transgene experiment, may be due to multiple genome integration and position effects.

RGM can report on methylation of pluripotency specific super-enhancers

Methylation of super enhancers (SEs) has been shown to change during differentiation. We tested whether RGM would report on the active and hypomethylated state of the pluripotency-specific SEs associated with the *miR290* and *Sox2* genes in mESCs and their methylated and inactive state in somatic cells (Figure 4A and Figure S3A). In contrast to the CGIs located at gene promoters (*Gapdh* and *Dazl*), the SE regions of both *Sox2* and *miR290* represents low-density CpG sequences. Utilizing CRISP/Cas mediated gene editing, we inserted a *Snrpn* tdTomato reporter into the endogenous *miR290* and *Sox2* enhancer (Figure 4B and Figure S3B, respectively). As recipient cells, we used the previously established *Oct4, Sox2, Klf4* and *c-Myc* (OSKM) polycistronic dox-inducible secondary reprogrammable mESCs (Carey et al., 2011), which also carried a GFP reporter knocked into the endogenous *Nanog* locus. Correct integration of the vector was validated by PCR and Southern analysis (Figure S3C). Figure 4C shows that both targeted ESC lines (*miR290 #21 and Sox2 #2*) expressed tdTomato as well as *Nanog*-GFP. To assess whether the tdTomato expression correlated with hypomethylation of the inserted RGM, DNA extracted from the bulk mESCs population was bisulfite converted, amplified by PCR and sequenced with the PCR amplification including both the SE CpG region and the downstream *Snrpn* promoter. As predicted from the methylation maps (Figure 4A and Figure S3A), both endogenous *miR290* and *Sox2* CpG regions were mostly hypomethylated (Figure 4D). Importantly, the *Snrpn* promoter was also hypomethylated consistent with reporter expression. Of note, a few highly methylated alleles were detected (Figure 4D), possibly reflecting an inherent variation in the bulk population due to the presence of cells that carry
an inactive reporter. To test this possibility, we analyzed the Sox2 SE region in the untargeted parental cell, which identified the presence of both methylated and unmethylated alleles at the same frequency as the targeted reporter cell line (Figure S3D). We conclude that RGM can report on the methylation state of distal genomic regulatory regions.

**Dynamic de novo DNA methylation during differentiation**

To monitor real-time changes in genomic DNA methylation during *in vitro* differentiation, mESCs carrying the tdTomato reporters reflecting DNA methylation levels at the SE regions, were exposed to Retinoic Acid (RA), which induces a rapid exit from pluripotency, and cellular differentiation (Rhinn and Dolle, 2012). The presence of the Nanog-GFP reporter allowed monitoring exit from pluripotency by loss of GFP expression. Sorted double positive (tdTomato+/GFP+) miR290 and Sox2 cells were plated on feeder-free gelatin coated plates, treated with 0.25μM RA the following day (Figure 5A) and analyzed at different times after addition of RA (Figure 5A and B). As expected, undifferentiated cells were double positive (tdTomato+/GFP+). However, upon induction of differentiation a gradual reduction in the fraction of double positive cells was observed with most disappearing over the time course of 7 days, resulting in a largely double negative cell population (Figures 5B and 5C). This is in contrast to control Gapdh reporter cells which, as expected, appeared completely GFP positive following 7 days of RA differentiation (Figure S4A). tdTomato and Nanog-GFP positive cells disappeared with different kinetics: while singly tdTomato positive cells (tdTomato+/GFP−) appeared after 2 days, only a few single Nanog-GFP positive cells (tdTomato−/GFP+) were detected during differentiation (Figure 5B and 5C) suggesting that Nanog was silenced prior to methylation and silencing of the miR290 and Sox2 SEs.

To confirm that loss of the tdTomato signal correlated with accumulation of *de novo* methylation in both SE regions, we sorted the main populations at different time points during RA differentiation (Figure 5C). DNA was extracted from the different cell populations and subjected to bisulfite sequencing, thus allowing a comprehensive analysis of the methylation state in both the endogenous miR290 and Sox2 SE and their respective Snrpn promoter regions (Figures 5D,E, S4B, C). In contrast to the bulk population of mESCs (Figure 4D), the sorted double positive cells did not harbor completely methylated alleles, consistent with the notion that methylated alleles in the bulk population represent intrinsic variation. The methylation of both miR290 and Sox2 in single positive cells (tdTomato+/GFP−) was low, consistent with tdTomato expression. The overall increased *de novo* methylation in the single positive cells, compared with the double positive cells, may suggest that DNA methylation mediated silencing was already initiated in this intermediate cell population. Notably, our analysis identified completely methylated genomes in the Sox2 single positive (tdTomato+/GFP−) cell population (Figure 5E). This suggest that during rapid changes of *de novo* methylation the half-life of the fluorescent protein (FP) may lead to an over-estimation of cells that are still hypomethylated during cell state transitions.

Finally, in agreement with the silencing of tdTomato expression, the double negative cells (tdTomato−/GFP+) exhibited robust hypermethylation on both endogenous SE regions and their respective Snrpn promoters (Figures 5D, E, S4B, C). To test whether the targeted reporter allele correlated with the methylation levels of the untargeted allele (wt), we
analyzed the wt allele in Sox2 reporter cells at different time points during differentiation. Figure S4D shows that similar to the reporter allele, the wt allele exhibited low levels of methylation in the sorted double positive cells, and high levels of methylation following seven days of differentiation. We conclude that RGM allows dynamic monitoring de novo methylation events that are imposed on genomic sequences upon exiting from pluripotency. Our data suggest that the differentiation of ESCs induces silencing of Nanog prior to de novo methylation of the two miR290 and Sox2 SEs.

To test whether in vivo differentiation resulted in silencing of the tdTomato reporter in both miR290 and Sox2 SE regions, we analyzed 13.5 dpi chimeric embryos. As control, we injected ESCs harboring the Gapdh CGI reporter driving a GFP sequence, which had also been infected with lentiviruses resulting in constitutive expression of tdTomato. The robust expression of GFP in the Gapdh control embryos, demonstrated the widespread expression signature of the Snrpn promoter throughout mouse tissues (Figure 6A). Unlike the Gapdh control, both miR290 and Sox2 embryos were completely negative for both GFP and tdTomato, demonstrating robust repression of Nanog and the Snrpn promoter during in vivo differentiation (Figure 6A).

DNA demethylation during cellular reprogramming

Reprogramming of somatic cells to iPSCs involves demethylation and activation of the pluripotency SEs Sox2 and miR290 (see Figures 4A and S3A). We investigated whether RGM could be used to capture demethylation events that are gradually acquired during cellular reprogramming. For this we used secondary Dox-inducible reprogrammable mouse embryonic fibroblasts (MEFs) isolated from 13.5 dpi chimeric embryos that had been injected at the blastocyst stage with the OSKM DOX inducible ESCs (Carey et al., 2011) carrying Nanog-GFP and the tdTomato reporter reflecting DNA methylation levels at the Sox2 or miR290 SE alleles (see Figure 6B). Culture of these MEFs in DOX induces the reprogramming factors while Nanog-GFP activation allows monitoring the course of reprogramming in the bulk somatic cell population (Buganim et al., 2012). As expected, MEFs isolated from 13.5 dpi embryos were negative for both GFP and tdTomato expression, as measured by fluorescent microscopy and FACS analysis (Figures 6C and S5A). Importantly, consistent with tdTomato repression, both endogenous miR290 and Sox2 SE regions as well as their corresponding downstream Snrpn promoter regions were hypermethylated (Figure 6D). Further analysis of the wt allele in Sox2 MEF showed high correlation with the targeted reporter allele, demonstrating robust repression of the SE region in vivo (Figure S5B).

To test whether reprogramming-induced demethylation can be visualized by RGM, we treated the secondary MEFs with serum and LIF medium supplemented with 2 ug/ml doxycycline (Dox). Both miR290 and Sox2 MEFs were successfully reprogrammed, resulting in double positive cells (tdTomato+ / GFP+, data not shown). It was recently shown that a combination of three chemicals, TGF-β antagonist ALK5 inhibitor II; GSK3b antagonist CHIR99021 and Ascorbic Acid, an enzymatic cofactor (from here on referred to as 3C), results in more efficient and synchronous reprogramming (Vidal et al., 2014). To achieve more synchronized and efficient reprogramming, both miR290 and Sox2 MEFs were
subjected to 3C culture conditions and the dynamics of reporter activation was monitored by flow cytometry. While the first expression of tdTomato$^+$ and GFP$^+$ cells emerged at day 16 (Figure 6E), reporter activation of both miR290 and Sox2 occurred with different kinetics. Figure 6E shows accumulation of miR290 reporter cells that activated both GFP and tdTomato (tdTomato$^+$ / GFP$^+$) over time. A small population of single positive GFP cells appeared in late stages of reprogramming consistent with a stochastic sequence of events in the reprogramming of the miR290 SE region. Unlike miR290 reporter cells, however, Sox2 cells showed a more robust and defined dynamics of activation of both reporters. By day 16 a population of single positive GFP cells (tdTomato$^-$ / GFP$^+$) had accumulated, which gradually shifted to become double positive (tdTomato$^+$ / GFP$^+$) over time (Figures 6E and S5C). To test whether the single positive GFP cells give rise to double positive cells, we sorted the single positive GFP cells and replated them on feeders using Dox independent culture conditions. Consistent with the repression of the tdTomato signal, bisulfite sequencing confirmed that the single positive GFP cells exhibit high levels of methylation in the SE region, as well as in the downstream Snrpn promoter region (Figure S5D). Upon further culture tdTomato positive cells appeared demonstrating that single positive GFP cells give rise to double positive cells (Figure S5E).

Our results suggest that reprogramming of both miR290 and Sox2 SE regions are late events, with the Sox2 SE region being reprogrammed subsequently to the activation of endogenous Nanog. miR290 and Sox2 double positive (tdTomato$^+$ / GFP$^+$) cells invariably proceed to a Dox independent iPS cell state (Figure 6F). To assess the methylation state of the Sox2 and miR290 SEs, we performed bisulfite sequencing on DNA extracted from sorted double positive (tdTomato$^+$ / GFP$^+$) iPS cells. As shown in Figure 6G, both miR290 and Sox2 SE regions, and their corresponding downstream Snrpn promoters were demethylated. These results confirmed that RGM can visualize demethylation of regulatory genomic regions during reprogramming with single cell resolution.

Discussion

In this work we have generated a DNA methylation reporter (RGM) that allows imaging of DNA methylation with single cell resolution. The design of the reporter system took advantage of the intrinsic characteristics of imprinted gene promoters, for which the transcriptional activity reflects the DNA methylation state of adjacent sequences. Importantly, imprinted promoters are neutral to developmental or tissue specific DNA methylation changes, with their activity strictly dependent on the methylation state of the adjacent regulatory elements. This is in contrast to CGI sequences such as Gapdh or tissue-specific elements such as the Dazl promoter associated sequences, which become demethylated or de novo methylated, respectively, when inserted into the genome of ESCs (Brandeis et al., 1994; Sabag et al., 2014). This indicates that methylation of these elements as opposed to imprinted promoters is sequence – dependent and subject to trans-acting signals and cell state-dependent regulation.

The RGM reporter system described here is based on the Snrpn minimal promoter that is not subjected to methylation changes by itself, and therefore GFP expression is solely dependent on the methylation state of surrounding sequences. Consistent with this premise, ES cells

Cell. Author manuscript; available in PMC 2016 September 24.
appeared GFP positive when stably transfected with the methylated or unmethylated Gapdh/ 
Snrpn-GFP vector, but were GFP negative when transfected with the methylated or 
unmethylated Dazl/Snrpn-GFP reporter. This indicates that the Snrpn promoter region can 
be used as a faithful sensor for regional methylation changes of adjacent sequences.

To investigate whether RGM can report on the methylation state of endogenous loci we 
targeted CGIs located at Gapdh and Dazl promoter regions, resulting in differential 
methylation and activity of the Snrpn reporter. Thus, the Snrpn promoter effectively reflects 
local methylation patterns without affecting the endogenous epigenetic state. As most of the 
tissue-specific DNA methylation changes occur in low-density CpG regulatory regions, we 
asked whether RGM could report on the methylation state of non-coding low-density CpG 
regions. We chose two pluripotency-specific SEs that are associated with the miR290 and 
Sox2 genes and are known to be active and unmethylated in ESCs but become methylated 
and inactive upon cellular differentiation. CRISPR/Cas mediated insertion of the Snrpn-
tdTomato reporter into ESCs resulted in tdTomato positive clones but tdTomato expression 
was silenced in mid-gestation chimeric embryos, which reflects the demethylation state of 
the SEs in pluripotent cells and their de novo methylation upon induction of differentiation. 
Conversely, MEFs isolated from chimeric embryos were tdTomato negative with both 
elements highly methylated. Upon conversion of the MEFs into iPSCs, however, the cells 
became tdTomato positive reflecting demethylation of the SEs during reprogramming to 
pluripotency. Our results establish that RGM reporter activity mirrors the changes of DNA 
methylation imposed on endogenous CGI and low-density CpG genomic elements during 
development, upon cellular differentiation and during reprogramming. Extensive 
epigenomic analyses of multiple tissues and cell types in both human and mice, suggest that 
embryonic development and cell-type specification are associated with massive epigenomic 
remodeling at discrete enhancers (Hon et al., 2013; Roadmap Epigenomics et al., 2015; 
Schultz et al., 2015; Ziller et al., 2013). It will thus be of interest to test whether RGM can 
be utilized to report on the DNA methylation state associated with more discrete regulatory 
regions. Implementing the methylation reporter to tissue-specific DMRs holds the promise 
to further elucidate the link between DNA methylation and other epigenetic mechanisms, 
with cell fate regulation.

Reprogramming of somatic cells into iPSCs involves extensive resetting of the epigenome 
(Buganim et al., 2013; Hanna et al., 2010), and coinciding with this notion, recent studies 
identified key role for epigenetic modifiers during this process (Mansour et al., 2012; Rais et 
al., 2013; Soufi et al., 2012). However, the exact kinetics of these epigenetic changes during 
the reprogramming process are difficult to define because of cell heterogeneity and the 
stochastic nature of the reprogramming process. Here we followed the methylation changes 
of two SEs associated with Sox2 and miR290, demonstrating that demethylation of both 
regions are late events in the reprogramming process. Simultaneous activation of 
endogenous Nanog and miR290 SE demethylation is consistent with Nanog directly 
regulating the expression of miR290 cluster during reprogramming to iPS cells (Gingold et 
al., 2014). The gradual activation of the Sox2 tdTomato reporter followed expression of 
endogenous Nanog, consistent with demethylation of Sox2 SE being a late event in the 
process (Buganim et al., 2012). Systematic deletions of Sox2 upstream SE region was
recently shown to dramatically affect Sox2 expression in ESCs (Li et al., 2014; Zhou et al., 2014). Thus, the Sox2 SE methylation reporter cells provide a rigorous experimental system to investigate how DNA methylation changes at distal regulatory region influence the expression of downstream target genes.

Changes in DNA methylation during development, lineage commitment and disease are dynamic and studies of epigenetic changes are hampered by two experimental constraints that limit mechanistic studies of methylation and gene regulation. (i) Current methodology provides only a static “snapshot” view of the methylation state during cell state transitions and (ii) that current methylation analyses require the examination of multiple cells precluding assessment of epigenetic changes in single cells. Given the overwhelming evidence of cell-cell heterogeneity in embryos, cultured cells or disease states such as cancer (Junker and van Oudenaarden, 2014), this is a serious limitation for a mechanistic understanding of the epigenetic state and gene expression during these complex processes. For example, monitoring the course of differentiation in both miR290 and Sox2 reporter cells confirmed the co-existence of cell populations that harbor distinct epigenetic states. In contrast, commonly used bulk methodologies would not allow isolating and distinguishing the different cell populations. Thus, sorting and isolating different cell types according to their methylation states, can be achieved only by using readout for methylation state at single-cell resolution. The RGM reporter system overcomes some of the limitations of conventional methylation analyses by providing real time visualization of DNA methylation at single cell resolution. As with any fluorescent protein-based reporter system, the accuracy to trace real-time changes depends on the half-life of the respective FP. Because the current version of the methylation reporter does not use a destabilized FP, silencing of the reporter after de novo methylation-induced repression of the Snrpn promoter is likely delayed. To generate a reporter that more rapidly reports on DNA methylation changes would require the use of a destabilized FP. Targeting additional loci in future studies will allow to further elucidate other possible limitations of the RGM reporter system, such as inhibition of the Snrpn transcriptional activity by chromatin conformation.

As RGM allows measuring dynamics of DNA methylation at single-cell resolution, it provides a framework for understanding epigenetic changes during cell state transition in heterogeneous cell populations. For example, replacing the fluorescent-based reporter system with Cre-Lox, will enable the generation of epigenetic lineage tracing maps. Furthermore, utilizing RGM together with conventional gene expression reporters may offer detailed insights into the interplay between epigenetic cues and the execution of tissue-specific gene expression programs. The use of fluorescent reporters as readout for locus-specific methylation changes may also provide an effective screening platform for the isolation of small molecule compounds that affect the methylation state of specific genomic regions.

**Experimental Procedures**

**mESCs Cell Culture**

V6.5 mouse embryonic stem cells (mESCs) were cultured on irradiated mouse embryonic fibroblasts (MEFs) with standard ESCs medium: (500 ml) DMEM supplemented with 10%
FBS (Hyclone), 10 μg recombinant leukemia inhibitory factor (LIF), 0.1 mM beta-mercaptoethanol (Sigma-Aldrich), penicillin/streptomycin, 1mM L-glutamine and 1% nonessential amino acids (all from Invitrogen). For experiments in 2i culture conditions, mESCs were cultured on gelatin-coated plates with N2B27 + 2i + LIF medium containing: (500 ml), 240 ml DMEM/F12 (Invitrogen; 11320), 240 ml Neurobasal media (Invitrogen; 21103), 5 ml N2 supplement (Invitrogen; 17502048), 10 ml B27 supplement (Invitrogen; 17504044), 10 μg recombinant LIF, 0.1 mM beta-mercaptoethanol (Sigma-Aldrich), penicillin/streptomycin, 1mM L-glutamine and 1% nonessential amino acids (all from Invitrogen), 50 μg/ml BSA (Sigma), PD0325901 (Stemgent, 1 μM), CHIR99021 (Stemgent, 3 μM).

**Reporter Cell lines**

To generate stably integrated Gapdh and Dazl transgene reporter cell lines, either Gapdh- or Dazl- modified PiggyBac transposon (see Extended Experimental Procedures), and a helper plasmid expressing transposase, were transfected into mESCs cells using Xfect mESC Transfection Reagent (Clontech), according to the provider’s protocol. Stably integrated reporter cells were selected with puromycin (2mg/ml) for four days.

To generate Dazl, Gapdh, miR290 and Sox2 SE reporter cell lines, targeting vectors and CRISPR/Cas9 were transfected into mESCs using Xfect mESC Transfection Reagent (Clontech), according to the provider’s protocol. 48 hours following transfection, cells were FACS sorted for GFP or tdTomato expression (respectively), and plated on MEF feeder plates. Single colonies were further analyzed for proper and single integration by southern blot and PCR analysis.

**Flow Cytometry**

To assess the proportion of GFP and tdTomato in the established reporter cell lines, a single cell suspension was filtered, and assessed on the LSR II SORP, LSRFortessa SORP or FACSCanto II.

**Retinoic acid-induced differentiation**

mESCs carrying the reporter for both miR290 and Sox2 SE region, were sorted for double positive GFP and tdTomato expression, and plated on gelatin coated plates in ES cell medium (+LIF). The next day, cells were washed with PBS and resuspended in basal N2B27 medium (2i medium without LIF, Insulin and the two inhibitors), supplemented with 0.25 μM RA. Medium was replaced every other day.

**Blastocyst Injections for the Generation of Chimeras and secondary MEFs**

Blastocyst injections were performed using (C57Bl/6xDBA) B6D2F2 host embryos. In brief, B6D2F1 females were hormone primed by an i.p. injection of PMS (Pregnant Mare Serum Gonadotropin, EMD Millipore) followed 46h later by an injection of hCG (human Chorionic Gonadotropin, VWR). Embryos were harvested at the morula stage and cultured in a CO2 incubator overnight. On the day of the injection, groups of embryos were placed in drops of M2 medium and using a 16 um diameter injection pipet (Origio, Inc.) approximately 10 cells were injected into the blastocoel cavity of each embryo using a Piezo
micromanipulator (Prime Tech, Ltd). About 20 blastocysts were subsequently transferred to each recipient female; the day of injection was considered as 2.5 dpc. Fetuses were collected at 13.5 dpc for the extraction of embryonic fibroblasts as described before (Buganim et al., 2012).

Southern Blots

10–15 ug of genomic DNA was digested with appropriate restriction enzymes overnight. Subsequently, Genomic DNA was separated on a 0.7% agarose gel, transferred to a nylon membrane (Amersham) and hybridized with 32P random primer (Stratagene) labeled probes.

Reprogramming to iPSCs

MEFs isolated from miR290 and Sox2 fetuses, were plated at density of 50,000 cells per 6-well in gelatin coated plates with standard MEF medium (mESCs media without LIF). The following day MEF medium was replaced with mESCs medium containing 2mg/ml doxycycline (Sigma). Alternatively, cells were grown in mESCs medium containing 2mg/ml doxycycline and a combination 3 compounds: TGF-β antagonist ALK5 inhibitor II; GSK3b antagonist CHIR99021 and Ascorbic Acid, as described before (Vidal et al., 2014). Medium was replaced every other day during the course of reprogramming.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgements

We thank Thorold W. Theunissen, Patti Wisniewski and Colin Zollo for FACS analyses and cell sorting, Denes Hnisz for providing ChIP-seq tracks, Kibibi Ganz for mouse injections, Huijing Yu for help in cloning, and Stefan Semrau for help with the RA differentiation and comments on the manuscript. This study was supported by NIH grant HD 045022. Y.S. is supported by a Human Frontier Postdoctoral Fellowship and. R.J. is co-founder of Fate Therapeutics and an adviser to Stemgent.

References


Highlights

- A Reporter for endogenous genomic DNA Methylation (RGM) is established
- RGM can capture endogenous methylation state of promoters and non coding regions
- RGM allows tracing of methylation changes both in-vitro and in-vivo
- RGM allows monitoring dynamics at single cell resolution during cell fate changes
Figure 1. An active minimal Snrpn promoter can be repressed in cis by means of spreading of DNA methylation into the promoter region

(A) Schematic representation of the sleeping-beauty based vectors. Endogenous CpG Islands (CGI) of Dazl and Gapdh genes were cloned upstream of a minimal Snrpn promoter region - driving GFP. Open circle lollipops schematically represent individual unmethylated CpG.

(B) Flow cytometric analysis of V6.5 mESCs cultured in serum + LIF, following stable integration of unmethylated Gapdh and Dazl reporter vectors, demonstrating robust repression of GFP signal in the Dazl reporter cells over time. Shown are the mean percentages of GFP negative cells ± STD of two biological replicates.

(C) Phase and fluorescence images of the sorted V6.5 mESCs, comprising stable integration of the Gapdh (left) and Dazl (right) vectors following prolonged culturing for 7 weeks.

(D and E) Bisulfite sequencing analysis of the stably transfected Gapdh (D) and Dazl (E) reporter cell lines was performed on the gene promoter-associated CGI (left) and the downstream Snrpn promoter region (right). Open circles represent unmethylated CpGs; Filled circles - methylated CpGs.
See also Figure S1.
Figure 2. An *in vitro* repressed *Snrpn* promoter can be reactivated in *cis* by means of spreading of DNA demethylation into the promoter region

(A) Schematic representation of an *in vitro* methylated sleeping-beauty based vectors. Closed circle lollipops schematically represent individual methylated CpG.

(B) Phase and fluorescence images of the stably integrated V6.5 mESCs, harboring *Gapdh* (left) and *Dazl* (right) *in vitro* methylated vectors, following one week of antibiotics selection.

(C and D) Flow cytometric analysis of the proportion of GFP positive cells in V6.5 mESCs, stably integrated with either *Gapdh* (C) or *Dazl* (D) *in vitro* methylated vectors, following 2 weeks in culture.

(E and F) Bisulfite sequencing analysis of the stably transfected *Gapdh* (E) and *Dazl* (F) reporter cell lines, was performed on the gene promoter-associated CGI (left) and the downstream *Snrpn* promoter region (right).

(G) Flow cytometric analysis of the proportion of GFP positive cells in V6.5 mESCs and *Dnmt1* KO mESCs, stably integrated with *in vitro* methylated *Dazl* reporter vector.

(H) Bisulfite sequencing analysis of sorted GFP positive *Dnmt1* KO mESCs, stably integrated with *in vitro* methylated *Dazl* reporter vector.
Flow cytometric analysis of the proportion of GFP negative cells in control V6.5 mESCs, mESCs deficient for both Dnmt3a and Dnmt3b (Dnmt3ab KO) and V6.5 mESCs cultured in 2i + LIF, which were stably integrated with unmethylated Gapdh (upper panel) and Dazl (lower panel) reporter vectors.

See also Figure S1.
Figure 3. Generation of DNA methylation reporter cell lines for endogenous gene promoters

(A) CRISPR/Cas-based strategy used to integrate the DNA methylation reporter into the endogenous promoter region of *Gapdh* and *Dazl* genes. TSS - transcription start site. Green sequence - endogenous CGI region; Black sequence - targeting CRISPR; Red sequence PAM recognition site.

(B) Flow cytometric analysis depicting the mean GFP intensity of randomly picked clones following antibiotic selection of both *Gapdh* (upper panel) and *Dazl* (lower panel) targeted V6.5 mESCs.

(C) Flow cytometric analysis of the proportion of GFP positive cells in two representative clones correctly targeted with the methylation reporter at the promoter region of *Gapdh*

(D) Bisulfite sequencing analysis was performed on mESCs harboring the DNA methylation reporter in *Gapdh* promoter region. For each cell line, the PCR amplicon (marked with dashed line) includes both the endogenous CGI (left) and the downstream integrated *Snrpn* promoter region (right).
(E) Flow cytometric analysis of the proportion of GFP positive cells in two representative clones correctly targeted with the methylation reporter at the promoter region of *Dazl*.

(F) Bisulfite sequencing analysis was performed on mESCs harboring the DNA methylation reporter in *Dazl* promoter region. For each cell line, the PCR amplicon (marked with dashed line) includes both the endogenous CGI (left) and the downstream integrated *Snrpn* promoter region (right).

See also Figure S2.
Figure 4. Generation of DNA methylation reporter cell lines for the pluripotent-specific miR290 and Sox2 SE regions

(A) Regional view depicting the DNA methylation (upper panel) and chromatin (lower panel) landscape of miR290 upstream pluripotent-specific SE. Shown are average methylation levels and enrichment of chromatin marks in mouse undifferentiated cells (green) and in adult tissues (gold), with respect to the genomic organization of the genes. DNA methylation varies from 1-hypermethylated to 0- hypomethylated; Characteristic clusters of typical enhancer marks and binding of tissue-specific TF determine the SE region (light blue).

(B) CRISPR/Cas-based strategy used to integrate the DNA methylation reporter into the endogenous SE region. HR - homologous recombination. Green sequence - endogenous miR290 CpG region; Black sequence - targeting CRISPR; Red sequence PAM recognition site.

(C) Phase and fluorescence images of correctly integrated DNA methylation reporter cell lines for miR290 (upper panel) and Sox2 (lower panel) endogenous SE regions. GFP marks endogenous expression levels of Nanog, whereas tdTomato reflects the endogenous DNA methylation levels at both miR290 and Sox2 SE regions.
(D) Bisulfite sequencing analysis was performed on undifferentiated mESCs harboring the DNA methylation reporter in either miR290 SE region (upper panel) or Sox2 SE region (lower panel). For each cell line, the PCR amplicon (marked with dashed line) includes both the endogenous CGI (left) and the downstream integrated Snrpn promoter region (right). See also Figure S3.
Figure 5. Dynamics of de novo DNA methylation of miR290 and Sox2 SE regions upon in vitro differentiation

(A) Schematic representation of the RA-based differentiation protocol used on miR290 and Sox2 reporter cell lines. GFP marks endogenous expression levels of Nanog, whereas tdTomato reflects the endogenous DNA methylation levels at both miR290 and Sox2 SE regions.

(B) Flow cytometric analysis of the proportion of Nanog-GFP positive cells (X axis) and tdTomato positive cells (Y axis) during 7 days of differentiation of miR290 #21 (upper panel) and Sox2 #2 (lower panel) reporter cell lines.

(C) Bar graph summarizing the proportion of the different cell populations during the course of 7 days RA differentiation for both miR290 #21 (upper panel) and Sox2 #2 (lower panel) reporter cell lines. Data represents two biological replicates. R - tdTomato; G - GFP.

(D and E) Bisulfite sequencing analysis on the three main cell populations - sorted at 48 hours following initial treatment with RA. For both miR290 #21 (D) and Sox2 #2 (E) cell lines, the PCR amplicon (marked with dashed line) includes the endogenous CGI (left) and the downstream integrated Snrpn promoter region (right). R - tdTomato; G - GFP.

See also Figure S4.
Figure 6. Dynamics of DNA demethylation of miR290 and Sox2 SE regions during cellular reprogramming

(A) miR290 (upper panel) and Sox2 (lower panel) reporter chimeric experimental embryos (right embryo in each panel). As controls, Gapdh CGI reporter mESCs driving GFP and constitutively expressing tdTomato (Control Gapdh-GFP and tdTomato, respectively) were injected into host blastocysts (left embryo in each panel).

(B) Schematic representation of the experimental procedure to monitor the dynamics of demethylation during reprogramming of miR290 and Sox2 reporter cell lines. GFP marks
endogenous expression levels of Nanog, whereas tdTomato reflects the endogenous DNA methylation levels at both miR290 and Sox2 SE regions.

(C) Flow cytometric analysis of the proportion of GFP positive cells (X axis) and tdTomato positive cells (Y axis) in P0 MEFs derived from miR290 #21 (left) and Sox2 #2 (right) chimeric embryos.

(D) Bisulfite sequencing analysis was performed on P0 MEFs derived from miR290 #21 (upper panel) and Sox2 #2 (lower panel) chimeras. For each cell line, the PCR amplicon (marked with dashed line) includes both the endogenous CGI (left) and the downstream integrated Snrpn promoter region (right).

(E) Analysis of the proportion of GFP positive cells (X axis) and tdTomato positive cells (Y axis) during the course of reprogramming of MEFs derived from miR290 #21 (upper panel) and Sox2 #2 (lower panel) chimeras. Shown are flow cytometric data from different time points following addition of dox supplemented with 3C culture condition.

(F) Representative images of established miR290 and Sox2 iPSC lines, derived from sorted double positive (tdTomato+/GFP+) colonies.

(G) Bisulfite sequencing analysis was performed on P2 iPSCs derived from miR290 #21 (upper panel) and Sox2 #2 (lower panel) MEFs. For each cell line, the PCR amplicon (marked with dashed line) includes both the endogenous CGI (left) and the downstream integrated Snrpn promoter region (right).

See also Figure S5.