DNMT3L promotes quiescence in postnatal spermatogonial progenitor cells

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ABSTRACT

The ability of adult stem cells to reside in a quiescent state is crucial for preventing premature exhaustion of the stem cell pool. However, the intrinsic epigenetic factors that regulate spermatogonial stem cell quiescence are largely unknown. Here, we investigate in mice how DNA methyltransferase 3-like (DNMT3L), an epigenetic regulator important for interpreting chromatin context and facilitating de novo DNA methylation, sustains the long-term male germ cell pool. We demonstrated that stem-cell enriched THY1+ spermatogonial stem/progenitor cells (SPCs) constituted a DNMT3L-expressing population in postnatal testes. DNMT3L influenced the stability of promyelocytic leukemia zinc finger (PLZF), potentially by downregulating the cell-proliferation-promoting factor SALL4 in THY1+ SPCs and to prevent premature stem cell exhaustion. Our results indicate that DNMT3L is required to delicately balance the cycling and quiescence of SPCs. These findings reveal a novel role for DNMT3L in modulating postnatal SPC cell fate decisions.

KEY WORDS: DNMT3L, Proliferation, Spermatogonial progenitor cell, Quiescence, Mouse

INTRODUCTION

Stem cells are crucial for tissue homeostasis and regeneration (Orford and Scadden, 2008; Cheung and Rando, 2013). Spermatogenesis is a well-characterized stem cell-dependent process. Spermatogonial stem cells reside in a subpopulation of mouse male germ cells, spermatogonial stem/progenitor cells (SPCs), which include As, Apaired (Apr) and Aaligned (Aal) spermatogonia (Nakagawa et al., 2007, 2010). SPCs provide the fundamental source of cells for spermatogenesis and are responsible for the spermatogenic cycle throughout the reproductive lifespan of males. These cells can produce differentiating spermatogonia, which undergo a series of divisions to mature into differentiated spermatogonia and spermatocytes, ultimately developing into functional spermatocytes (Oatley and Brinster, 2012).

An adequate number of stem cells remain in a relatively quiescent state to avoid premature exhaustion and to allow long-term maintenance of a functional stem cell pool (Ema and Suda, 2012; Cheung and Rando, 2013). Cyclin-dependent kinase 2 (CDK2), a positive regulator of cell cycle progression, has been suggested as a regulator of the quiescence-proliferation decision in various somatic cells (Spencer et al., 2013) and functions in promyelocytic leukemia zinc finger (PLZF) stability by mediating PLZF phosphorylation, rendering it prone to ubiquitylation and subsequent degradation (Costoya et al., 2008). PLZF and Sal-like protein 4 (SALL4) are crucial regulators of cell quiescence and proliferation (Yang et al., 2008b; Hobbs et al., 2012). PLZF has been characterized as a DNA-binding transcriptional repressor of cell cycle progression, whereas SALL4 is an oncogene due to its cell growth-stimulating properties. It participates in the modulation of several signal transduction cascades, including the MAPK kinase/ERK-ERK (MEK-ERK) and AKT pathways (Yeyati et al., 1999; McConnell et al., 2003; Yang et al., 2008a; Rice et al., 2009; Aguila et al., 2011). PLZF and SALL4 are SPC-specific molecules expressed in mouse testes (Gassei and Orwig, 2013). PLZF antagonizes SALL4A activity and prevents SPC cycling; however, an increase in the SALL4-to-PLZF ratio promotes SPC differentiation (Hobbs et al., 2012).

DNMT3L is an epigenetic modifier closely associated with transcriptional repression and is crucial for genome-wide reprogramming in quiescent embryonic germ cells (Aapola et al., 2000, 2001; Bourc’his et al., 2001; Buaas et al., 2004). DNMT3L itself does not possess enzymatic activity but acts as a processive catalyst and cooperates with other DNA methyltransferases (DNMTs) via its C-terminus to promote the de novo methylation of DNA sequences, including retrotransposons, gene bodies and the regulatory sequences of imprinted genes (Bourc’his et al., 2001; Chedin et al., 2002; Mata et al., 2002; Bourc’his and Bestor, 2004; Suetake et al., 2004; Kato et al., 2007; Holz-Schietinger and Reich, 2010; Niles et al., 2011; Smallwood et al., 2011; Van Emburgh and Robertson, 2011; Arad et al., 2012; Kobayashi et al., 2012; Ichiyangai et al., 2013). In addition, DNMT3L contains a plant homeodomain (PHD)-like domain that can recruit histone
modifiers, such as histone deacetylase 1 (HDAC1), or bind to the N-terminus of histone H3 when the lysine 4 of histone H3 is unmethylated (Aapola et al., 2002; Deplus et al., 2002; Jia et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007). Moreover, DNMT3L may mediate the DNA methylation of properly chromatinized DNA templates (Wienholz et al., 2007; Ooi et al., 2007).

RESULTS

Abnormal distribution of SPCs in Dnmt3l KO postnatal testes

The complete germ cell exhaustion in adult Dnmt3l KO testes suggests that DNMT3L may be important for SPC maintenance in postnatal testes (Bourc’his and Bestor, 2004; Webster et al., 2005; Hata et al., 2006). We examined the SPC distribution in postnatal testes using PLZF staining because PLZF is strongly expressed in all types of SPCs (Sada et al., 2009; Gassei and Orwig, 2013). Immunostaining of whole-mount dispersed seminiferous tubules from mice between 4 dpp and 4 weeks of age indicated that the Dnmt3l KO testes began to display an uneven distribution of PLZF+ cells at 7 dpp (data not shown). By 8 dpp, a clearly uneven distribution of PLZF+ cells was observed in the Dnmt3l KO testes compared with wild-type testes (Fig. 1A, top lane). Some segments of seminiferous tubules contained many PLZF+ cells (Fig. 1A, middle lane), whereas other segments had very few PLZF+ cells (Fig. 1A, bottom lane). Additional immunostaining of 8 dpp testis sections confirmed the aberrant distribution of PLZF+ cells in Dnmt3l KO testes (Fig. 1B). The average number of PLZF+ cells per tubule cross-section in the mutant testes was not significantly different from that in wild-type testes at 8 dpp (Fig. 1C). However, while the wild-type testes indicated a bell-shaped distribution of the number of PLZF+ cells in each cross-section, the mutant testes followed a distorted distribution; a large proportion of the cross-sections contained either very few or many PLZF+ cells (Fig. 1D). Thus, the progressive loss of germ cells in Dnmt3l KO postnatal testes may be caused by dysregulated SPCs.

Significant expression of DNMT3L in postnatal THY1+ cells

To determine whether DNMT3L is expressed and functions in postnatal germline stem/progenitor cells, we used an anti-THY1 antibody with magnetic beads to isolate the stem cell-enriched THY1+ cell populations (THY1+ cells) from mouse testes at several postnatal stages. Thy1 mRNA exhibited an approximate 25-fold enrichment in 8 dpp THY1+ cells compared with THY1− cell populations (Fig. 2A). Furthermore, 98±0.9% and 98±0.5% of the THY1+ cell...
populations isolated from 8 dpp wild-type and Dnmt3l KO testes, respectively, were positive for an SPC marker, CD49f (Fig. 2B), indicating that the isolated populations were enriched for SPCs. qPCR analyses revealed that wild-type THY1+ cells, but not wild-type THY1− cells or Dnmt3l KO THY1+ cells, expressed a significant level of Dnmt3l mRNA (Fig. 2C). Furthermore, we analyzed DNMT3L expression in 4 dpp to 4-week-old wild-type THY1+ cells and found that THY1+ cells expressed significant levels of DNMT3L from 8 dpp onwards (Fig. 2D,E). Compared with entire 8 dpp testes, the isolated 8 dpp THY1+ cells displayed a significantly higher level of DNMT3L expression (Fig. 2D), suggesting the role of DNMT3L in SPC maintenance after birth.

Increased cell proliferation and elevated CDK2 expression in Dnmt3l KO THY1+ SPCs

At 8 dpp, the isolated THY1+ cells represented approximately 4.31±0.23% and 6.05±0.46% of the total cells in the wild-type and Dnmt3l KO testes, respectively. This finding was consistent with the qPCR results indicating that the Dnmt3l KO testes displayed a higher level of Thy1 mRNA than the wild-type testes (Fig. 2A). To determine the proliferative potential of postnatal THY1+ SPCs, we performed immunostaining of Ki67, which is a protein strictly associated with cycling cells. The percentages of non-quiescent SPCs in these prepubertal Dnmt3l KO populations were significantly higher than those in the wild-type populations, which displayed significant DNMT3L expression (Fig. 2D and Fig. 3A, and see supplementary material Fig. S1).

We then studied the expression of cell cycling regulators, such as CDKs and cyclins, to explain the over-representation of proliferating cells among Dnmt3l KO THY1+ cells (Fig. 3B). Compared with wild-type cells, 8 dpp Dnmt3l KO THY1+ cells showed significantly increased Cdk2 expression (Fig. 3B). Subsequent western blotting confirmed elevated CDK2 protein expression in Dnmt3l KO THY1+ cells (Fig. 3C). The mouse Cdk2 promoter region contains two CpG islands (−188 to +63 and −677 to −536) with several binding sites for transcription factors, including SP1, AP1 and ETS1 (Fig. 3D) (Heinemeyer et al., 1998; Sun et al., 2011). The bisulfite sequencing results revealed that compared with wild-type cells, the Dnmt3l KO THY1+ cells displayed hypomethylation of the distal CpG island, particularly at a putative ETS1-binding-site (EBS) (Fig. 3D). We did not find obvious differences in the cytosine methylation of the proximal CpG island (see supplementary material Fig. S2).

To assess the importance of the distal CpG island for Cdk2 promoter activity, CD49f+ GSCs were transfected with reporter plasmids containing different components of the Cdk2 promoter and analyzed for luciferase activity. Compared with the plasmid containing both the proximal and distal CpG islands, an EBS mutation or the removal of the distal CpG island resulted in significantly decreased luciferase activity (Fig. 3E), suggesting that the EBS and the distal CpG island are important for Cdk2 transcriptional activity. We also performed chromatin immunoprecipitation (ChIP) using an anti-ETS1 antibody. Whereas there was no significant difference in ETS1 protein expression between wild-type and Dnmt3l KO THY1+ cells (Fig. 3G), significantly increased ETS1 was bound to the DNA hypomethylated, H3K4me3-overaccumulated Cdk2 promoter in 8 dpp Dnmt3l KO THY1+ cells (Fig. 3F). These data suggest that DNMT3L mediates CDK2 expression through transcriptional regulation and support a role for DNMT3L in influencing the cycling/quiescent fates of SPCs.

Decreased quiescence among Dnmt3l KO THY1+ SPCs

Previous studies have shown that SPCs display PLZF/H3K9me3 colocalization (Payne and Braun, 2006) and exhibit two major PLZF nuclear distribution patterns: perinuclear distribution is associated with quiescent and non-differentiated SPCs, whereas a punctate distribution pattern characterizes active/differentiating SPCs (Hobbs...
Fig. 3. Increased proliferation, Cdk2/CDK2 elevation and ETS1 accumulation at the Cdk2 promoter in Dnmt3l KO THY1+ cells. (A) Percentages of Ki67+ cells in isolated 8 dpp THY1+ cells, analyzed by immunocytochemistry. Randomly selected groups of 400 cells from four independent experiments were analyzed. (B) Relative mRNA expression levels of cyclins and Cdns in 8 dpp THY1+ cells. The means and s.e.m. were calculated from three independent experiments performed in triplicate. (C) Relative CDK2 protein expression levels of 8 dpp THY1+ cells (n=6, P=0.012). (D) The mouse Cdk2 promoter and the bisulfite sequencing analysis of the Cdk2 promoter in isolated 8 dpp THY1+ cells. The black boxes denote CpG islands in the Cdk2 promoter and the gray line represents the sequenced region. The batch numbers are indicated on the left. Five postnatal mice of the same genotype were used for each batch. The white and black circles indicate unmethylated CpGs and methylated CpGs, respectively. The asterisks mark putative ETS1-binding sites predicted using the TFSEARCH program. (E) Luciferase reporter assays of the mouse Cdk2 promoter in the presence or absence of the distal CpG island. Different lengths of the Cdk2 promoter were fused to a luciferase reporter (pGL4.17), and the luciferase activity was measured in CD49f+ GSCs transfected with these reporter constructs. Data are mean±s.e.m. (n=8) and are representative of two independent experiments. (F) Real-time PCR analysis of ChIP products. Antibodies against ETS1, H3K4me3, H3K27me3 and IgG were used to immunoprecipitate fragmented chromatin from 8 dpp THY1+ cells. Primer pairs A and B were used for the quantitative real-time PCR analysis and the fold enrichment was normalized to the input. Data are mean±s.e.m. (G) ETS1 expression in 8 dpp wild-type and Dnmt3l KO THY1+ cells (n≥3). n, the number of independently performed experiments; WT, wild type. Data are mean±s.e.m.; **P<0.01, respectively (Student’s t-test).
et al., 2012). Wild-type and Dnmt3l KO THY1+ cells at 8 dpp contained 98.3±0.9% and 96.6±1.2% PLZF+ cells, respectively (Fig. 4A). However, compared with their wild-type counterparts, some Dnmt3l KO THY1+ cells displayed weaker PLZF signals (Fig. 4B, arrow). In addition to punctate and perinuclear localizations, a small fraction of THY1+ cells displayed a diffuse PLZF/H3K9me3 staining pattern (Fig. 4C,D). These cells represented As and Apr spermatogonia based on the germ cell arrangement in whole-mount seminiferous tubules (Fig. 4E). The percentages of cells with diffuse PLZF/H3K9me3 staining were similar in the wild-type and Dnmt3l KO populations (Fig. 4D). Most of the H3K9me3 staining was colocalized with DAPI, suggesting that H3K9me3 were enriched in heterochromatin in both 8 dpp wild-type and Dnmt3l KO THY1+ cells (Fig. 4C). Of particular interest was a switch from a predominantly perinuclear staining pattern of PLZF and H3K9me3 in the wild-type THY1+ cells and the predominantly punctate staining pattern in the Dnmt3l KO THY1+ cells (Fig. 4D), indicating an enhanced tendency towards proliferation in the THY1+ population in the absence of DNMT3L. Fewer than 10% of the wild-type and Dnmt3l KO PLZF+THY1+ cells exhibited both nuclear and cytoplasmic PLZF staining. The appearance of cytoplasmic PLZF was mostly associated with perinuclear PLZF staining. The intensity of the cytoplasmic PLZF in the wild-type cells was considerably stronger than in the Dnmt3l KO cells (see supplementary material Fig. S3). We subsequently isolated the nuclear/cytoplasmic fractions and quantified the PLZF in different subcellular locations. In 8 dpp wild-type THY1+ cells, 78±0.6% and 21.3±0.6% of the PLZF protein levels were in the nucleus and cytoplasm, respectively. PLZF was predominantly localized in the nuclei of Dnmt3l KO THY1+ cells.

Fig. 4. Decrease in quiescent cells among the Dnmt3l KO THY1+ SPC population. (A) Percentages of PLZF+ cells in THY1+ cells isolated from 8 dpp wild-type and Dnmt3l KO testes. Data are mean±s.e.m. of six independent experiments. (B) Immunostaining of PLZF in 8 dpp THY1+ cells. Arrows indicate the THY1+ cells with weaker PLZF signals. Green, PLZF; blue, Hoechst 33342. Scale bars: 50 µm. (C) Immunostaining patterns of PLZF (green) and H3K9me3 (red) in 8 dpp wild-type and Dnmt3l KO THY1+ cells. Blue, Hoechst 33342. Scale bars: 2.5 µm. (D) Distribution of cells with perinuclear (quiescent), punctate (active) and diffuse H3K9me3 staining patterns in the various THY1+PLZF+ cell populations. The results were compiled from approximately 600 randomly selected cells from six independent experiments. WT, wild type. (E) Whole-mount staining was performed on 3-week-old seminiferous tubules using an anti-PLZF antibody. The white arrows indicate Apr spermatogonia with diffuse PLZF staining. Green, PLZF; blue, Hoechst 33342. Scale bars: 25 µm. Data are mean±s.e.m.; **P<0.01 (Student’s t-test).
showed significantly reduced PLZF protein levels compared with wild-type cells (Fig. 5B,C), suggesting a potential post-translational regulatory role of DNMT3L in PLZF. Dnmt3l KO THY1+ cells exhibited increased CDK2 expression (Fig. 3C). CDK2 may phosphorylate PLZF, making it vulnerable to ubiquitylation-induced degradation (Costoya et al., 2008). After confirming the CDK2-PLZF interaction in THY1+ cells (Fig. 5D), we analyzed the post-translational modification of PLZF. PLZF was excessively post-translationally modified (Fig. 5E) and ubiquitylated (Fig. 5F) in 8 dpp Dnmt3l KO THY1+ cells, indicating that DNMT3L is involved in the regulation of PLZF stability in postnatal germ cells.

We further compared the PLZF expression levels of perinatal wild-type and Dnmt3l KO testes to clarify whether DNMT3L affects PLZF stability before the formation of the SPC pool. However, there was no clear difference of the low PLZF expression between wild-type and Dnmt3l KO testes at embryonic E18.5 or on the day of birth (see supplementary material Fig. S4). This was in contrast to the significant reduction in PLZF in postnatal Dnmt3l KO THY1+ SPCs (Fig. 5B,C), suggesting that DNMT3L significantly affects PLZF stability only at postnatal stages.

Increased SALL4B levels and the SALL4A/PLZF ratio in Dnmt3l KO THY1+ cells

Next we quantified two cell proliferation-promoting factors, SALL4A and SALL4B (Aguila et al., 2011; Oikawa et al., 2013), in wild-type and Dnmt3l KO germ cells. We observed strong SALL4B protein expression in wild-type testes from E17.5 to 8 dpp (Fig. 6A). However, in the prepubertal wild-type THY1+ cell population, the SALL4B protein levels were dramatically downregulated (Fig. 6B,D and see supplementary material Fig. S5A,B), consistent with the reduced proliferative ability of this cell population. However, SALL4B expression was not suppressed in Dnmt3l KO THY1+ SPCs, suggesting that the suppression of SALL4B in SPCs may be DNMT3L dependent (Fig. 6B vs 6A).

The SALL4A/PLZF expression ratio is important for SPC cell fate determination (Hobbs et al., 2012). Compared with wild-type THY1+ cells, we observed a statistically significant upregulation of
the SALL4A protein in 8 dpp but not in 2-week-old Dnmt3l KO
THY1+ SPCs (Fig. 6B,C and see supplementary material Fig. S5A).
Along with the significant PLZF reduction in this mutant cell type
(Fig. 5B,C), the SALL4/PLZF ratio was significantly increased in
both 8 dpp and 2-week-old Dnmt3l KO THY1+ SPCs at the
prepubertal stage (Fig. 6E and see supplementary material Fig. S5D),
consistent with the increased non-quiescent THY1+ SPCs in
prepubertal Dnmt3l KO testes.

We further investigated whether the increased SALL4 in
Dnmt3l KO SPCs was associated with enhanced MEK-ERK and PTEN-
AKT signaling cascades because the overexpression of SALL4 enhances
the proliferation-stimulating AKT and ERK signal intensities (Yang et al.,
2008b; Oikawa et al., 2009). PTEN protein levels were not significantly
increased, but we observed a significant increase in PTEN phosphorylation (S380/T382/T383)
(Fig. 7A,B), which restricts PTEN activity and results in increased
AKT expression (Vazquez et al., 2000, 2001). We also observed
increased AKT activation and excessive MEK-ERK activation in
8 dpp Dnmt3l KO THY1+ cells (Fig. 7A,B). The elevated
phosphorylation of ERK and AKT proteins persisted in Dnmt3l
KO SALL4A cells isolated from older mice (data not shown).

Thus, DNMT3L is required for the protection of PLZF from
excessive ubiquitylation and for the appropriate SALL4-regulated
signaling pathways.

**Aberrant expression of proliferation- and differentiation-
associated factors in Dnmt3l KO THY1+ cells**

To further characterize the function of DNMT3L in SPC maintenance,
we analyzed the expression of factors crucial for SPC cell cycling and
differentiation. Compared with wild-type cells, 8 dpp Dnmt3l KO
THY1+ cells displayed increased expression of ERK- and AKT-
activated factors (Gfra1, Ret, Nanos2 and Etv5) and of Epcam, an SPC
differentiation-associated molecule. We also observed significantly
decreased expression of Ngn3, Pou3f1 and Sohlh2, which are essential
for precise SPC differentiation (Fig. 7C). Thus, DNMT3L may be
important for SPC cycling and may also be involved in their
differentiation.

**DISCUSSION**

Many adult stem cells remain in a quiescent state as they wait to self-
renew or to differentiate, suggesting a delicate balance between
quiescence and cycling ensures tissue homeostasis (Kippin et al.,
2005; Horsley et al., 2008; Gan et al., 2010; Matsumoto et al., 2011).
A large proportion of SPCs are found in the quiescent phase of the cell
cycle (Costoya et al., 2004; Sada et al., 2009). Recent findings indicate
that quiescence is essential for preventing premature activation of
SPCs and stem cell depletion (Bruccoli et al., 2012; Hobbs et al., 2012;
Hu et al., 2013). We demonstrated that postnatal Dnmt3l KO GFP*
SPCs failed to repopulate busulfan-treated wild-type recipient testes
(see supplementary material Fig. S6), suggesting that autonomous
defects in these cells contribute to the germ cell exhaustion phenotype
observed in Dnmt3l KO animals (Liao et al., 2012). The newly
identified significant DNMT3L expression in THY1+ cells in this
study suggested that DNMT3L may function directly at the postnatal
stage. We further revealed that DNMT3L participates in the
maintenance of THY1+ SPC quiescence at least partly through
modulating Cdk2 expression and PLZF stability, as well as through
silencing proliferation-promoting SALL4B expression.

Stem cell maintenance is modulated by the appropriate extrinsic
stimulation by the niche and intrinsic gene expression. We
compared the transcriptome profiles of 8 dpp wild-type and
Dnmt3l KO THY1+ SPCs and identified cell proliferation-related
cascades, including the PI3K-AKT, RAS and MAPK signaling
pathways that were among the most significantly differentially
regulated pathways based on a KEGG analysis (see supplementary
material Fig. S7A). We also selected 53 genes involved in SPC
proliferation and differentiation to perform a classical gene set
enrichment analysis (GSEA). The results revealed significant
enrichment (P<0.0002) of these genes, further indicating that
DNMT3L plays a role in SPC maintenance (see supplementary
material Fig. S7B). Our transcriptome profiles revealed that, apart
from cell proliferation-related molecules, receptor-ligand interaction
and cell adhesion molecules were clearly affected in Dnmt3l KO
THY1+ SPCs compared with wild-type SPCs. The uneven
distribution of SPCs in prepubertal Dnmt3l KO testes implies that
DNMT3L may contribute to the maintenance of an adequate niche microenvironment. This dysregulated niche might be associated with a regulatory feedback loop through germ cell and niche cell communications (Zamudio et al., 2011), although further research into the contributions of DNMT3L to niche homeostasis at the prepubertal stage is needed.

CDK2 may be a key factor in the quiescence-proliferation decision (Spencer et al., 2013). A higher density of methylated DNA prevents ETS1-DNA binding and inhibits transcriptional activation (Maier et al., 2003; Chan et al., 2004). The upregulation of Cdk2 in Dnmt3l KO THY1+ cells results from reduced DNMT3L-dependent CpG methylation at the distal CpG island of the Cdk2 promoter. However, we cannot exclude the possibility that the hypomethylation of the Cdk2 promoter in Dnmt3l KO THY1+ cells is partially a result of passive DNA demethylation due to excessive cell proliferation. In addition, the PHD-like domain in DNMT3L, which is responsible for recruiting histone modifiers, may also influence transcriptional control at the chromatin level (Apola et al., 2002; Deplus et al., 2002).

PLZF can be regulated by CDK2-mediated PLZF degradation, by cytokine-induced PLZF inactivation or by stress-induced PLZF degradation (Namba et al., 2003; Costoya et al., 2008; Kang et al., 2008; Doulatabov et al., 2009). Among these processes, only CDK2-mediated degradation does not lead to cytoplasmic PLZF accumulation. The lack of cytoplasmic PLZF accumulation in Dnmt3l KO THY1+ cells suggests that CDK2-mediated PLZF degradation occurs in these mutant cells.

Recent studies have demonstrated that extended AKT activity enhances SPC differentiation (Lee et al., 2007; Hasegawa et al., 2013) and that increases in both the ERK and AKT signaling cascades are associated with the premature exhaustion of SPCs (Bruscoli et al., 2012). In addition to increased proliferation, elevated AKT and ERK activities have been linked to deregulated spermatogenesis (Goertz et al., 2011; Ishii et al., 2012). PLZF may antagonize SALL4 activity in postnatal SPCs (Hobbs et al., 2012). SALL4 has been linked to the AKT and ERK signaling cascades, and has been implicated in the proliferation and differentiation of several types of stem cells (Ma et al., 2006; Sakaki-Yumoto et al., 2006; Zhang et al., 2006; Yang et al., 2008a; Oikawa et al., 2009; Oikawa et al., 2013). For example, SALL4A or SALL4B overexpression in hematopoietic stem cells results in enhanced proliferation, but also in ineffective differentiation and excessive cell death (Ma et al., 2006; Aguila et al., 2011; Yang et al., 2011). Thus, the excessive PLZF ubiquitylation, dysregulated SALL4A and elevated SALL4B expression in Dnmt3l KO THY1+ cells suggest that DNMT3L affects PLZF stability and the ability of SALL4-mediated signaling cascades, including the AKT and ERK cascades, to regulate cell fate determination in mouse SPCs. In Dnmt3l KO SPCs, the aberrant expression of proliferation- and differentiation-related molecules leads to abnormally differentiated spermatogonia, followed by germ cell apoptosis at the spermatocyte stage (see supplementary material Fig. S8).

SALL4 interacts with DNMT3s, and SALL4 overexpression induces the DNA hypermethylation of its own promoter in the in vitro system (Yang et al., 2012b). However, there was no significant difference in Sall4a or Sall4b mRNA expression between 8 dpp wild-type and Dnmt3l KO THY1+ cells, which excludes the possibility of DNMT3L-mediated DNA methylation of the Sall4 promoter and suggests that DNMT3L is crucial for the inhibition of SALL4 protein expression/accumulation in postnatal THY1+ cells. Moreover, SALL4A and SALL4B have distinct but overlapping functions; the two splice isoforms can bind to unique promoter and overlapping promoter regions (Lu et al., 2009; Rao et al., 2010), which may account for the variable expression of SALL4 in Dnmt3l KO THY1+ cells. Recently, SALL4B stability was reported to be regulated through post-translational modifications (Yang et al., 2012a). Future investigations of DNMT3L-mediated cell type-specific SALL4 suppression should improve our understanding of mouse postnatal germine maintenance.

Redd1 (Ddit4 – Mouse Genome Informatics), a negative regulator of mammalian TOR complex 1 (mTORC1), is crucial for maintaining the undifferentiated state of SPCs (Hobbs et al., 2010). The downregulation of Redd1 results in increased mTORC1 activity, the decreased expression of ERK-stimulated molecules (Gfra1 and
Rasgrf1 methylated imprinting control regions (including IG-DMR, 2410 dosage and PLZF stability. These findings suggest that DNMT3L may be dispensable for quiescence establishment/maintenance at the embryonic stage. Our results revealed that, compared with 8 dpp wild-type THY1+ cells, the expression levels of Cdk2 were very low in both embryonic wild-type and Dnmt3l KO prospermatogonia (data not shown), indicating that DNMT3L does not participate in cyclin/CDK-mediated cell cycle modulation in quiescent embryonic prospermatogonia. In contrast, beginning at 8 dpp, our results revealed clearly dysregulated SPC proliferation in Dnmt3l KO testes, indicating that postnatal DNMT3L contributes to the cell fate determination of SPCs when they have matured from prospermatogonia. DNMT3L may also be involved in different complexes and participate in different mechanisms for proper germ cell development at different stages. Our results show that PLZF interacts with DNMT3L and CDK2 in 8 dpp wild-type THY1+ cells; however, PLZF and CDK2 were weakly expressed in the perinatal germ cells. The lack of a significant difference in the expressions of these molecules between perinatal wild-type and Dnmt3l KO germ cell implies that DNMT3L may not be responsible for their expression or function throughout embryonic germ cell development.

In addition to germ cells and preimplantation embryos, DNMT3L has recently been shown to be expressed in hematopoietic stem/progenitor cells (HSCs) and may be involved in SALL4-mediated transcriptional regulation of HSC differentiation (Liu et al., 2013). However, the potential function of DNMT3L in regulating HSC quiescence and maintenance remains unclear. Recent studies have revealed that PLZF and SALL4 are expressed in HSCs, in which PLZF contributes to tumor suppression (He et al., 2000; Ono et al., 2013), and that SALL4 overexpression leads to HSC over-proliferation (Yang et al., 2011). In this study, a lack of DNMT3L in the relatively quiescent THY1+ SPCs resulted in increased proliferation, which was associated with PLZF instability and upregulated SALL4-mediated proliferation cascades. The functions of DNMT3L in SPC quiescence and potentially niche homeostasis may be applicable to other somatic stem cells.

In conclusion, our results suggest that DNMT3L has a crucial function in modulating the cell fate of quiescent THY1+ SPCs in postnatal testes. Our findings support a novel role for DNMT3L in SPCs to ensure the lifelong maintenance of the germline pool.

MATERIALS AND METHODS

Germ cell isolation and flow cytometry

Mice heterozygous for the Dnmt3l<sup>tm1Enls</sup> mutant allele (Hata et al., 2002) were intercrossed to generate Dnmt3l KO pups and littermate controls. Five postnatal mice of the same genotype were used for each experiment. Seminiferous tubules were treated with collagenase IV and DNase I to remove interstitial Leydig cells and peritubular myoid cells, followed by trypsin digestion to generate cell suspensions (Ogawa et al., 1997). THY1+ cells were isolated by magnetic-activated cell sorting (MACS) (Miltenyi Biotec), following the manufacturer’s instructions. Briefly, the dispersed testicular cells were placed in the MACS buffer and incubated with a biotin-conjugated anti-CD90.2 (THY1) antibody (Lot 25136 and Lot 80806, 553011, BD Pharmingen) at 4°C for 10 min. After being washed, the cells were resuspended, labeled with anti-biotin microbeads (Miltenyi Biotec) at 4°C for 15 min and placed in collection tubes for isolation. The isolation process was carried out within 5 h to maximize the amount of living cells. A PE-Cy5-conjugated anti-CD49F antibody (551129, BD Pharmingen) was used for the SPC population analysis. The date of birth for timed postnatal mice was defined as 0 dpp.

Quantitative reverse transcription PCR

Reverse transcription reactions and qPCR were performed using a SuperScript First-Strand Synthesis System (Invitrogen) and Roche LightCycler 480II. Primers are listed in Table S1 of the supplementary material.
Immunohistochemistry and immunocytochemistry
Mouse testes were fixed with 4% paraformaldehyde (PFA), transferred into sucrose gradients for dehydration, embedded in OCT compound (Tissue-Tek O.C.T. Compound) and cut into 8 μm sections. The sections were blocked with 10% goat serum before incubation with primary antibodies (a dilution of 1:1000), anti-PLZF (sc-22839, Santa Cruz Biotechnology) and anti-H3K9me3 (ab8898, Abcam). For whole-mount staining, seminiferous tubules were digested with collagenase IV and fixed in 4% PFA. For immunocytochemistry, the isolated THY1+ cells were placed onto poly-E-lysine slides (Thermo Scientific) and fixed in 4% PFA. Samples (testis qPCR-amplified and analyzed.

At 4°C with rotation. The immunoprecipitated DNA was isolated using DNA anti-H3K27me3 (07-449, Millipore) or control IgGs (Diagenode) overnight and the genomic DNA was sheared to lengths of approximately 500 bp by luxoid (PLZF antibody was evaluated using testes from wild-type and homozygous 549, Jackson Immunoresearch), stained with Hoechst 33342 (Sigma) and (a dilution of 1:500, 715-485-150, DyLight 488 and 211-505-109 DyLight 549, Jackson ImmunoResearch), stained with Hochest 33342 (Sigma) and mounted with a mounting medium (P36934, Invitrogen). The specificity of the PLZF antibody was evaluated using testes from wild-type and homozygous luxoid (P/;L) mice at 8 dpp (Buaas et al., 2004) (see supplementary material Fig. S10).

Chromatin immunoprecipitation (ChIP)
ChIP assays were performed using a LowCell# ChIP kit (Diagenode). Briefly, 1×10⁶ freshly isolated THY1+ cells were cross-linked using 1% formaldehyde for 10 min at room temperature; the cross-linking was arrested with glycine. After centrifugation, the cells were resuspended in a lysis buffer and the genomic DNA was sheared to lengths of approximately 500 bp by ultrasound. The sheared chromatin was incubated with 4 μg of anti-ETS1 (sc-350, Santa Cruz Biotechnology), anti-H3K4me3 (ab8580, Abcam), anti-H3K27me3 (07-449, Millipore) or control IgGs (Diagenode) overnight at 4°C with rotation. The immunoprecipitated DNA was isolated using DNA isolation buffer (Diagenode). Specific genes in the purified DNA were qPCR-amplified and analyzed.

Immunoprecipitation and western blotting
Isolated THY1+ cells and testes were lysed in RIPA buffer (Millipore) supplemented with 1× protease inhibitor cocktail (R1321, Fermentas), 1× phosphatase inhibitor cocktail (524629, Millipore), and 1 mM PMSF. Immunoprecipitation was performed using a Dynabeads kit (Invitrogen) following the manufacturer’s protocol. The anti-PLZF- and anti-CDK2-coated Dynabead/protein mixture was gently rotated overnight at 4°C. For immunoprecipitation, 50 μg of total protein from wild-type and Dnmt3l KO THY1+ cells were used for each experiment. Western blotting was performed according to a standard protocol (Sambrook and Russell, 2001) using PVDF membranes (Millipore). Cell or tissue extracts (10-15 μg per lane) were prepared for analysis. The membranes were blocked with a blocker (Bløk-PO or Bløk-CH, Millipore) or 5% BSA (Sigma), except for the membrane incubated with the anti-DNMT3L antibody, which was blocked with Bløk-PO and then switched to 5% milk in 1× PBST. Please note that an extended protocol is necessary for detecting DNMT3L from the membrane incubated with the anti-DNMT3L antibody. The proteins were detected using a chemiluminescent reagent (Millipore), and the images were quantified using ImageJ software (http://rsweb.nih.gov/ij/) and a BioSpectrum Imaging System (UVP). The antibodies used are listed in supplementary material Table S2.

DNA extraction and bisulfite sequencing
Genomic DNA was extracted from THY1+ cells and treated using an EZ DNA methylation kit (Zymo Research). The PCR products were purified and cloned for subsequent sequencing.

CD49f+GSC culture, transfection and luciferase assay
DNA segments of the Cd2c2 promoter were amplified, purified and cloned to generate promoter reporter plasmids. Mouse AP+ GSCs were derived from newborn testes as previously described (Huang et al., 2009). Cells were electroporated, seeded onto a laminin-coated plate and cultured using a serum-free basic system for 48 h. The luciferase activity was determined and recorded with a Berthold LB 960 Centro microplate luminometer (Berthold Technologies).

RNA Sequencing and bioinformatics analysis
Total RNA for the library preparation, sequencing and RNA-Seq analysis was extracted using TRI Reagent (Ambion). Poly-T oligo-attached magnetic beads were used to purify RNA. The mRNA was fragmented into small pieces and copied into first-strand cDNA, followed by second-strand cDNA synthesis. These cDNA fragments underwent end-repair, a single A base addition and adapter ligation to create the final cDNA library. Paired-end 100-nucleotide reads were obtained using HiScanSQ (Illumina). The sequences have been deposited in the NCBI GEO database under the accession number GSE54411.

Detailed experimental protocols are provided in the supplementary materials and methods.

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Competing interests
The authors declare no competing financial interests.

Author contributions
H.-F.L., W.S.C.C., P.Y., Y.-H.H. and S.-P.L. conceived and designed the experiments; K.H., H.S. and Y.-H. Ching provided study materials; H.-F.L., Y.-H. Chen, W.S.C.C., P.-L.L., C.-Y.L., Y.-C.C., G.-J.L., Y.-T.T., M.-H.T. and T.-H.K. performed the experiments and assembled and analyzed the data; H.-F.L., W.S.C.C., W.T.K.C., P.Y., Y.-H.H., S.-C.W. and S.-P.L. interpreted the data; and H.-F.L., W.S.C.C., P.Y. and S.-P.L. wrote the manuscript with support from H.-N.H., Y.-H. Ching and Y.-H.H. All authors were involved in discussions and approved the final manuscript.

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