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Osaka University
**Mili, a mammalian member of piwi family gene, is essential for spermatogenesis**

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**Summary**

The piwi family genes, which are defined by conserved PAZ and Piwi domains, play important roles in stem cell self-renewal, RNA silencing, and translational regulation in various organisms. To reveal the function of the mammalian homolog of piwi, we produced and analyzed mice with targeted mutations in the Mili gene, which is one of three mouse homologs of piwi. Spermatogenesis in the MILI-null mice was blocked completely at the early prophase of the first meiosis, from the zygotene to early pachytene, and the mice were sterile. However, primordial germ cell development and female germ cell production were not disturbed. Furthermore, MILI bound to MVH, which is an essential factor during the early spermatocyte stage. The similarities in the phenotypes of the MILI- and MVH-deficient mice and in the physical binding properties of MILI and MVH indicate a functional association of these proteins in post-transcriptional regulation. These data indicate that MILI is essential for the differentiation of spermatocytes.

Key words: Mili, Miwi, piwi, Mvh, Spermatogenesis

**Introduction**

Germ cells, which are highly specialized cells that transmit genetic information from generation to generation, are segregated from somatic lineages very early in embryonic life. Primordial germ cells (PGCs), which are the first germ cells specified during embryogenesis. They eventually differentiate into gametes in the adult gonad (Wylie, 1993). In Drosophila, gametes of both sexes are produced continuously from germline stem cells in the adult gonad. In mammals, the continuous production of germ cells by the stem cell system proceeds only in the male gonad via spermatogenesis. Genetic studies in Drosophila have identified several genes that are involved in germ cell development and germline stem cell division. The former include the oskar, vasa, nanos, tudor and germ cell-less genes (Rongo and Lehmann, 1996), and the latter include the piwi (Cox et al., 1998) and Yb (King et al., 2001) genes. However, the homologs of these gene products are not necessarily functional in the mammalian germ cell system. One reason is that the molecular mechanisms in Drosophila germ cell development and differentiation are quite different from those in mammals. Gene targeting analyses of Mvh (mouse vasa homolog: Ddx4 – Mouse Genome Informatics), Mgcl-1 (mouse germ cell-less-1; Gcl – Mouse Genome Informatics) and Miwi (mouse piwi; Piwil1 – Mouse Genome Informatics) have shown that although these genes are dispensable for PGC formation, they are essential for spermatogenesis (Deng and Lin, 2002; Kimura et al., 2003; Tanaka et al., 2000).

Spermatogenesis is one of the most dramatic examples of cell proliferation, differentiation and morphogenesis. The mouse spermatogenic cycle can be divided into 12 stages, with each stage consisting of a specific complement of male germ cells (Russell et al., 1990). The entire process occurs in three phases: mitosis (spermatocytogenesis), meiosis and spermiogenesis. A cascade of mitoses, which are initiated by the self-renewing division of germline stem cells (a subset of type A spermatogonia), gives rise to the primary spermatocytes. Subsequently, meiosis of primary spermatocytes leads to the production of haploid round spermatids. The prophase of the first meiotic division progresses in the following order: leptotene, zygotene, pachytene, diplotene and diakinesis. Various genes that are involved in cell cycling, DNA replication and RNA processing are essential for this process.
One of the germ cell determinant genes in Drosophila, vasa encodes an ATP-dependent RNA helicase of the DEAD-box protein family that is essential for the assembly and function of the germ plasm (Hay et al., 1988; Hay et al., 1990; Lasko and Ashburner, 1988). Based on structural conservation data, homologs of vasa have been identified in many animal species, such as C. elegans, Xenopus, zebrafish, chicken and mouse (Fujisawa et al., 1994; Komiya et al., 1994; Olsen et al., 1997; Roussel and Bennett, 1993; Tsunekawa et al., 2000; Yoon et al., 1997). All of these vasa homologs are expressed exclusively in the germ lineage. The expression and function of the Mvh gene were analyzed by immunostaining and gene-targeting analysis, respectively (Tanaka et al., 2000; Toyooka et al., 2000). The MVH protein appears initially in PGCs that colonize the embryonic gonads at 10.5-11.5 dpc, and is maintained in both male and female germ cells until the development of postmeiotic spermatids and primary oocytes, respectively. Sperm are absent from the testes of Mvh-null male mice, in which premeiotic germ cells cease differentiation by the zygotene stage and undergo apoptotic death.

The piwi gene of Drosophila belongs to a novel class of evolutionarily conserved genes (the piwi or Argonaute family) (Benfey, 1999). The piwi family genes encode basic proteins that contain a highly conserved PAZ domain of 110-amino acid residues in the middle region of the proteins and a 300-amino acid Piwi domain in the C-terminal region (Cerutti et al., 2000), even though the function of these domains remains elusive. In Drosophila, the loss of piwi function leads to the failure of germline stem cell self-renewal as well as downstream gametogenic functions such as germline cyst formation, egg polarity and possibly meiosis (Cox et al., 1998; Lin and Spradling, 1997). Based on database analyses, three piwi homologs have been identified in the mouse genome. Two of these genes, Miwi and Mili (Miwi like; Piwiil2 – Mouse Genome Informatics), have been examined in detail. Miwi-null mice do not complete spermatogenesis, but arrest occurs at the beginning of the round spermatid stage (Deng and Lin, 2002), significantly downstream of the germline stem cell division stage. To reveal the functional of Mili, here we report the generation and analysis of the Mili-null mice. The Mili-null mice showed arrest of spermatogenesis at the spermatocyte stage, which is reminiscent of the phenotype of Mvh-null mice. Furthermore, we demonstrate the physical association between MILI and MVH, which may account for the similarities between the phenotypes of the Mili- and Mvh-null mice.

Materials and methods

Generation and genotyping of Mili-deficient mice

Genomic DNA clones of the Mili locus were isolated from a mouse (129/SvJ) genomic library (Stratagene) using full-length Mili cDNA as a probe. The 5.2-kb BamHI fragment that encompasses exon 2 to exon 5 was replaced with a neomycin resistance cassette in the pPNT vector (Tybulewicz et al., 1991). The 2.0-kb BglII-BamHI fragment was inserted between the neomycin resistance cassette and the HSV thymidine kinase gene, both of which are driven by the PGK1 promoter. The 4.5-kb BamHI-KpnI fragment was inserted upstream of the neomycin resistance gene. The resulting targeting vector, pKO-Mili2, was electroporated into D3 embryonic stem (ES) cells, and selected with G418 and gancyclovir. The targeting events were screened by PCR and confirmed by Southern blot analysis using digestion with restriction enzymes and both 5’ and 5’-end probes. The recombinant cells were karyotyped to ensure that 2N chromosomes were present in the majority of the metaphase spreads. Chimeric mice, which were derived from correctly targeted ES cells, were mated to C3HBL/6 mice to obtain F1 Mili-/- mice.

The oligonucleotide PCR primers that were used to distinguish the insertion of the neo gene from the wild-type allele were as follows: pPNT-1, 5’-CCCTACCGTGTAAGTTGC-3’; Mili-Int4, 5’-GTCC-TGTGTAGCGCAG-3’; and Mili-Int5, 5’-TGACAGGTGC-GAGCTC-3’. The pPNT-1 and Mili-Int5 primers gave a 410 bp DNA fragment that identified the targeted allele, while the Mili-Int4 and Mili-Int5 primers yielded the 800 bp fragment of the wild-type allele. The PCR was carried out for 40 cycles of 94°C for 1 minute, 65°C for 1 minute and 72°C for 1 minute.

Western blotting

The tissues were homogenized in TNE buffer [50 mM Tris-HCl (pH 8.0), 1% Nonidet P-40, 20 mM EDTA] that contained protease inhibitors. Equal amounts of protein were separated by SDS-PAGE and transferred to a PVDF membrane (Millipore, Bedford, MA). After blocking, the filters were incubated with the antibody against anti-Mili26F antibody. Peroxidase-conjugated goat anti-rabbit IgG (Zymed, South San Francisco, CA) was used as the secondary antibody, and the signals were detected using the ECL kit (Amersham Pharmacia).

Histological analysis

Littermate embryonic male gonads at 14.5 dpc and postnatal testes were fixed in 4% paraformaldehyde overnight at 4°C, dehydrated progressively and embedded in methyl methacrylate. Subsequently, 5 μm rehydrated sections were used for Hematoxylin-Eosin staining, for the terminal deoxynucleotidyl transferase (TdT)-mediated dUTP nick end-labeling (TUNEL) reaction, and for immunohistochemical staining. For the TUNEL reactions, the rehydrated slides were incubated with the antibody against anti-Mili26F antibody. Peroxidase-conjugated goat anti-rabbit IgG (Zymed, South San Francisco, CA) was used as the secondary antibody, and the signals were detected using the ECL kit (Amersham Pharmacia).
directly in OCT compound and cut at 10 μm. The sections were fixed with 2% paraformaldehyde for 20 minutes, permeabilized with acetone for 20 minutes, and blocked for 1 hour with 3% BSA and 10% normal goat serum in PBS. The staining was carried out as described previously (Chuma and Nakatsuji, 2001). As negative controls, pre-immune sera or isotype matched immunoglobulins were used and essentially no positive signals were detected in the control staining. Positive signals were detected with Alexa568- or Alexa488-conjugated anti-rabbit IgG (H+L) antibodies (Molecular Probes, Eugene, OR).

**Surface spreading methods and chromosome preparation**

For immunocytological analysis of SC formation at meiotic prophase II was performed as described by Matsuda et al. (Matsuda et al., 1992). The images of immunocytochemical staining were captured with Leica Microsystems Imaging Solutions (Cambridge, UK) using a cooled CCD camera (MicroMAX 782Y, Prinston Instruments) mounted on a Leica DMR microscope. The preparation of chromosomes and nuclei for light microscopy of the spermatogenic cells of the Mili-deficient mouse was performed using the air-drying method (Imai et al., 1981), with the omission of colchicine treatment. The preparations were stained with 4% Giemsa in phosphate buffer (pH 7.0), followed by counting of the three types of spermatogenic cells, i.e. spermatogonia, spermatocytes and spermatids, as well as the Sertoli cells.

**RT-PCR analysis**

Total RNA samples were isolated from the testes using Sepasol-RNA I (Nacalai Tesque, Kyoto, Japan). Single-stranded cDNA was prepared from 3 μg of total RNA using random hexamers and the ThermoScript RT-PCR System (Invitrogen, Carlsbad, CA). Each PCR reaction was performed with a 1/30 dilution of the RT products and using HotStar Taq (Qiagen, Valencia, CA). The PCR was carried out for 25-28 cycles of 94°C for 1 minute, 57°C for 1 minute and 72°C for 1 minute. The following primer pairs were used for the PCR: Mili, 5’-AGTGTGTGGGAAGGA-3’ and 5’-AGAGCCATCAAAAGCAG-3’; and Mtv1, 5’-ATGATCGTGGGACCATC-3’ and 5’-AGGCCAATGCGTCGATA-3’. The sequences of the other primers have been described previously (Tanaka et al., 2000).

**Transient transfection and immunoprecipitation**

The Myc-tagged Mvh expression plasmid was constructed by inserting the full-length fragment of Mvh (pQE32-Mvh; donated by Dr T. Noce) into the pcDNA3 vector. The 293T cells were transfected with plasmid DNA by the calcium phosphate method, and cultured for 48 hours. The cells were lysed in TNE buffer that contained protease inhibitors. For anti-MVH immunoprecipitation, testes were lysed with the same buffer. The lysates were pre-cleared with protein G Sepharose (Pharmacia), and immunoprecipitated with the anti-MYC, anti-FLAG or anti-MVH antibody. The immunoprecipitates were separated by SDS-PAGE and transferred to a PVDF membrane. After blocking, the filters were incubated with the anti-FLAG, anti-MYC or anti-26F antibody. The secondary antibody was peroxidase-conjugated goat anti-mouse IgG (Sigma) or anti-rabbit IgG (Zymed).

**GST-pull down assay**

The pGEX4T-Mvh plasmid was donated by Dr T. Noce. Deletions of the GST-Mvh plasmid were produced using the appropriate restriction enzymes, as shown in Fig. 7B. The GST-fusion proteins were purified from E. coli lysates using glutathione-Sepharose 4B beads. The GST-fusion proteins that were bound to the Sepharose beads were then incubated with testis lysates. The GST precipitates were separated by SDS-PAGE, and transferred to PVDF membranes. After blocking, the filters were incubated with the affinity-purified anti-Mili26F antibody.

**Results**

**Generation of mice with targeted mutations in the Mili gene**

To investigate the in vivo function of MILI, we generated Mili-deficient mice by homologous recombination. The gene-targeting scheme that was used to generate the targeted embryonic stem (ES) cells is shown in Fig. 1A. In the mutant allele, the 5.2 kb fragment encompassing exons 2 to 5 was deleted, which corresponds to the deletion of the 1-209 residue region of the MILI protein. Southern blot analysis of genomic DNA identified the targeted homologous recombination event (Fig. 1B). Targeted ES cell lines were transferred into germ lines, and the subsequent F1 heterozygous mutant (Mili+/–) crosses produced homozygous mutant (Mili–/–) mice. The mutant mice were maintained in a mixed genetic background (129sv_C57BL/6) in the subsequent studies. To confirm the lack of production of a functional MILI protein in the Mili–/– testes, western blot analysis was carried out with an antibody that recognized both the MILI and MIWI proteins. MILI was detected in the testes of wild-type (Mili+/+) and Mili+/– mice. By contrast, MILI protein was not detected in the testes of Mili–/– mice (Fig. 1C). MIWI protein was not observed in Mili–/– testes, owing to the lack of the MIWI-expressing cell population, as shown below.

**Impaired spermatogenesis in the Mili mutant mice**

The Mili–/– mice were viable and showed apparently normal development. Interbreeding of Mili+/– mice produced offspring of normal litter size, and yielded the Mendelian ratios of Mili+/+, Mili+/– and Mili–/– mice. These findings indicate that MILI is not required for embryonic somatic cell division. The female Mili–/– mice were fertile, and histological analysis revealed that there were no abnormalities in the Mili–/– ovaries (data not shown). However, the male Mili–/– mice were sterile. Although Mili was expressed in PGCs, PGC development was normal and the numbers of germ cells in Mili–/– mice of both sexes were not different from those in the control mice at 14.5 dpc (Fig. 2A).

In adulthood, the Mili–/– testes were strikingly smaller than the control testes (Fig. 2B). The testes from 10-week-old Mili–/– males were only one-fifth of the weight of those from control males. During development, the testis weights of Mili–/– mice were almost the same as those of the Mili+/+ and Mili+/– mice until 2 weeks after birth, which suggests normal growth of the spermatogonia. Thereafter, the testes of the Mili–/– mice ceased to grow, and the weight difference became significant (Fig. 2C). Sperm were completely absent from the epididymides of the Mili–/– mice (data not shown). Histological analysis of the adult testes revealed complete depletion of post-meiotic germ cells in the Mili–/– testes (Fig. 2D, parts II, IV). By contrast, the full component of spermatogenic cells, including spermatogonia, spermatocytes and spermatids, was detected in the Mili–/– adult testes (Fig. 2D, parts I, III).

**Increased apoptosis in Mili-null mice**

TUNEL labeling was used to analyze the timing of abnormal cell death in the first wave of spermatogenesis and the continuous degeneration of early spermatocytes in adulthood. In mice, spermatogenesis is initiated on day 3 after birth and progresses as a synchronous wave during the first week of life.
The most mature germ cell type observed 8 days after birth is the type B spermatogonium; the preleptotene/leptotene, zygotene, and pachytene spermatocytes appear on days 10, 12, and 14, respectively (Bellve et al., 1977). TUNEL-positive cells were rarely detected in Mili+/– and Mili–/– testes on days 7 and 9 (Fig. 3A-D). On days 11 and 14, there were some TUNEL-positive cells in the heterozygous testes (Fig. 3E,G). However, significant numbers of apoptotic cells were observed in the homozygous testes (Fig. 3F,H). The apoptotic cells in the homozygous testis were located in the inner layers of the seminiferous tubules, where the most mature cells exist during the first wave of spermatogenesis. Virtually no TUNEL-positive cells were detected in the adult Mili+/– testis. By contrast, in most of the seminiferous tubules of the Mili–/– testes, significant numbers of TUNEL-labeling cells were detected in the spermatocyte layers (Fig. 3I,J). Thus, spermatogenesis in the Mili–/– mice is blocked during the early stages of meiosis, probably at the zygotene or early pachytene stage of the meiotic prophase, and apoptosis occurs subsequently.
Meiotic arrest in \textit{Mili}^{−/−} testes

RT-PCR analysis of the genes expressed at the different spermatogenic stages was carried out to determine the stage of arrest (Fig. 4). Genes that are expressed before the pachytene spermatocyte stage, such as the DNA mismatch repair gene \textit{Mlh1} (Baker et al., 1996; Edelmann et al., 1996), and \textit{Dmc1}, which is the mouse homolog of \textit{E. coli} \textit{RecA} (Habu et al., 1996), did not show significantly different expression patterns between the \textit{Mili}^{+/-} and \textit{Mili}^{−/−} genotypes. By contrast, the genes that are expressed in pachytene spermatocytes and at later stages, such as calmeigin (Watanabe et al., 1994), \textit{Hoxa4} (Rubin et al., 1986), Cyclin A1 (Sweeney et al., 1996), and the gene encoding the cyclic AMP-responsive element modulator isoform Crem-\(\tau\) (Foulkes et al., 1992), were not detectable in the \textit{Mili}^{−/−} testis. In addition, the expression of \textit{Miwi}, which is present in midpachytene-stage spermatocytes, was not detected in the \textit{Mili}^{−/−} testes. Although \textit{Syce1} and \textit{Syce3} (Dobson et al., 1994; Lammers et al., 1994; Meuwissen et al., 1992), both of which encode synaptonemal complex proteins and are restricted to zygotene to diplotene spermatocytes, were detected in the \textit{Mili}^{−/−} testes, their expression levels were much lower than those in heterozygous or wild-type testes. The expression level of \textit{Mvh} was significantly lower in the \textit{Mili}^{−/−} testes. Similarly, the expression of \textit{A-myb} (Mybl1 – Mouse Genome Informatics), which is a \textit{myb}-family transcription factor gene that is expressed in type B spermatogonia and leptotene- to pachytene-stage spermatocytes (Mettus et al., 1994; Trauth et al., 1994), decreased in the \textit{Mili}^{−/−} testes. The expression patterns of these genes in 3-week-old testes were essentially similar to those in the adult testes (data not shown).

The expression patterns of \textit{Bmp8a} and \textit{Bmp8b} differed between the 3-week-old and adult testes of the various genotypes. These two genes are expressed in a tightly regulated temporal and spatial manner in the placenta and in male germ cells during postnatal development (Zhao and Hogan, 1996). Before 3.5 weeks of age, both genes are expressed at low levels in the spermatogonia and primary spermatocytes. Thereafter, high levels of expression are observed in the spermatids. In adulthood, the expression levels of \textit{Bmp8a} and \textit{Bmp8b} were lower in the \textit{Mili}^{−/−} testes. However, the expression levels were higher in the testes of 3-week-old mice, which may reflect a yet unknown feedback mechanism that responds to the deficiency in spermatogenesis in the mutant mouse.

To define further the meiotic defect in the \textit{Mili}^{−/−} mice, sections stained with anti-SYCP3, RAD51 and \(\gamma\)-H2AX (phosphorylated form of H2AX, a histon H2A variant) antibodies were examined (Fig. 5). SYCP3 expression in \textit{Mili}^{−/−} testis was weaker than that in \textit{Mili}^{+/-} testis as expected from RT-PCR (Fig. 5A,B). Axial core formation was observed in the SYCP3-expressing meiotic cells in \textit{Mili}^{−/−} testis (Fig. 5C,D), suggesting the entry to the first meiotic division; however, pachytene chromosome formation was not completed in \textit{Mili}^{−/−} testis. Expressions of RAD51 and \(\gamma\)-H2AX were essentially same in \textit{Mili}^{−/−} and \textit{Mili}^{+/-} testes (Fig. 5E-P). During meiotic prophase, the X and Y chromosomes condense to form the sex body or XY body, and in late zygotene/early pachytene spermatocyte, \(\gamma\)-H2AX...
accumulates in the sex body (Mahadevaiah et al., 2001). Many γ-H2AX condensed spots were observed in Mili+/− testes as well as Mili+/− testes (Fig. 5K,N arrow). Furthermore, we analyzed synaptonemal complex formation in more detail using B antibody that recognizes both COR1 and SYN1 of synaptonemal complex core. Synaptonemal complex core was detected until early pachytene stage in the Mili+/− testis (Fig. 6A-E). Similarly, nuclei at and after the mid-pachytene spermatocyte stage were not detected in the Mili+/− mice by Giemsa staining (Fig. 6F,G). The mitotic metaphases of the spermatogonia were observed in Mili+/− and Mili+/− testes. By contrast, the first meiotic metaphase of the primary spermatocyte was not detected in the Mili+/− testis. Table 1 shows the quantification of spermatogenic cells and Sertoli cells. Although a lot of cells can be observed in Fig. 6F,G, the majority of the cells were Sertoli cells as shown in the Table 1. Nuclei at and after the mid-pachytene spermatocyte stage were not detected in the Mili+/− mice. The histological analysis clearly demonstrates that spermatogenesis after the postmeiotic stage was completely absent in all the seminiferous tubules of adult Mili+/− testes. Taken together, the spermatogenesis arrest in adult Mili+/− testes occurs during the early stages of meiosis, probably at the zygotene or early pachytene stages of the meiotic prophase.

Binding of Mili and Miwi to MVH

The stages of spermatogenesis arrest in the MILI-deficient and MVH-deficient mice were similar. To test the potential synergistic action of MILI and MVH, we examined the physical association between the proteins using 293T cells that expressed MYC-tagged MVH and FLAG-tagged MILI or MIWI. The lysates were immunoprecipitated with anti-MYC and anti-FLAG antibodies and detected with the anti-FLAG and anti-MYC antibodies. As shown in Fig. 7A, both MILI and MIWI were associated with MVH. Binding of MILI and MIWI was confirmed by immunoprecipitation assay of testicular lysates using anti-26F antibody recognizing both MILI and MIWI (Fig. 7B). GST fusion proteins of full-length and truncated mutants of MVH were produced (Fig. 7C,D). In addition, pull-down assays were carried out with lysates of the wild-type testes (Fig. 7D). MILI and MIWI bound to the full-length MVH, and deletion mutant analysis showed that the N-terminal of MVH was necessary for this binding.

Fig. 5. Expression of SYCP3, RAD51 and γ-H2AX in Mili+/− spermatocytes. Anti-SYCP3 immunostaining (A-D), anti-RAD51 staining (E-H), anti-γ-H2AX staining (K,N) and DAPI staining (F,I,L,O), and the merged images of RAD51 or γ-H2AX and DAPI (G,J,M,P) in Mili+/− (upper panels of each pair) and Mili+/− (lower panels of each pair) testes. Arrows show the γ-H2AX restricted to the sex bodies in early pachytene spermatocyte. All images except A and C were observed by confocal microscopy. Scale bars: 10 μm.

Fig. 6. No mid-pachytene spermatocyte in the Mili+/− testes. Merged image of synaptonemal complexes stained with the B antiserum recognizing both COR1 and SYN1 (green) and DNA stained with DAPI (blue) (A-E) in mid-zygotene spermatocytes (A,D), early-pachytene spermatocytes (B,E) and mid-pachytene spermatocyte (C). The images of FITC-stained synaptonemal complexes and DAPI-stained nuclei were captured with L5 and A4 filters, respectively. The surface spreading samples were prepared from control testes (A-C) and the homozygous mutant testes (D,E). The micrographs of spermatogenic cell nuclei in Giemsa-stained preparations of heterozygous (F) and homozygous mutant (G) mice are shown. The arrows indicate mitotic metaphases of spermatogonia, and the arrowhead indicates the first meiotic metaphase of a primary spermatocyte.
To analyze the localization of MILI, MIWI and MVH, immunohistochemical analyses of the wild-type, Mili\(^{-/-}\) and Miwi\(^{-/-}\) mice were carried out with specific antibodies (Fig. 8). The MILI protein was detected until pachytene-stage spermatocytes. Although Drosophila Piwi was localized in the nucleoplasm (Cox et al., 2000), MILI, like MIWI, was found in the cytoplasm (Kuramochi-Miyagawa et al., 2001). MILI was not detected in the Mili\(^{-/-}\) testes, but its expression was normal in the Miwi\(^{-/-}\) testes. MIWI was not detected in either the Mili\(^{-/-}\) or Miwi\(^{-/-}\) testes. The lack of MIWI expression in the Mili\(^{-/-}\) mice is presumably due to the paucity of MIWI-expressing cells, i.e. midpachytene-stage spermatocytes and round spermatids. MVH was detected in pre-pachytene spermatocytes in the Mili\(^{-/-}\) testes, which indicates that MILI is not essential for MVH expression. Although MVH was detected in the Miwi\(^{-/-}\) testes, the subcellular localization of MVH was different from that in the wild type. Anti-MVH staining showed the granulo-fibrillar and granular distribution of MVH in spermatocytes and round spermatids, respectively, in wild-type testes, and anti-MIWI showed the similar staining pattern. As shown in Fig. 8, MVH was not distributed in a granular pattern in the cytoplasm of the Miwi\(^{-/-}\) round spermatids.

**Discussion**

**MILI is an essential factor for meiotic differentiation during spermatogenesis**

The disruption of various genes brings about meiotic arrest and subsequent apoptotic cell death in the testis. These genes include DNA repair genes such as Mlh1, Mlh3, Msh4, Msh5 and Hrb6 (de Vries et al., 1999; Edelmann et al., 1996; Edelmann et al., 1999; Kneitz et al., 2000; Lipkin et al., 2002). Mice with null mutations in these genes show defective meiosis with aberrant chromosomal synapsis and postmeiotic apoptosis. Similarly, null mutations in HSP70-2, which is an essential factor for CDC2 kinase activity in meiosis I (Dix et al., 1996), and Cyclin A1 cause apparent structural abnormalities of the male germ cells by late prophase (Liu et al., 1998). Disruption of the other genes that are involved in homologous chromosome synapsis formation, such as Dmc1, Syce3, Spo11 and Atm, leads to failed synapsis formation and causes meiotic cell death (Romanienko and Camerini-Otero, 2000; Scherthan et al., 2000; Yoshida et al., 1998; Yuan et al., 2000). Two transcription factors, A-Myb and Egr4, are essential for the early-mid pachytene stage, as mice with targeted disruptions in these genes exhibit apoptotic cell death during this stage (Toscani et al., 1997; Tourtellotte et al., 1999). MVH-null mice also demonstrate meiotic arrest and apoptosis during the early prophase of meiosis (Tanaka et al., 2000). Considering that deficiencies in several genes with

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Percentages of the cells in each stage and the numbers of the counted testis cells are shown. Nuclei were categorized into spermatogonium (SG) and spermatagonium at metaphase (M), primary spermatocytes at leptotene (L), zygotene (Z), early pachytene (EP), midpachytene (MP), late pachytene to diplotene (LP to DP) and diakinesis to metaphase I (DA to MI), secondary spermatocyte (SC) and secondary spermatocyte at metaphase (MII), early spermatid (ES), late spermatid (LS) and spermatozoon (SZ), and sertoli cell (S).

![Fig. 7. Association of MVH with MILI and MIWI.](image)
distinct functions result in meiotic arrest and apoptotic cell death, it seems plausible that a sensitive checking mechanism for differentiation progression operates during spermatogenesis. Thus, it is conceivable that MILI plays an important role in meiotic prophase progression.

In the Mili+/– testis, the expression of genes that are involved in spermiogenesis was undetectable. The Dme1 gene, the expression of which is restricted in leptotene- to zygotene-stage spermatocytes (Yoshida et al., 1998), was expressed normally in the Mili+/– testis. By contrast, the expression levels of Sycep1 and Sycep3, both of which are transcribed predominantly in the zygotene to diplotene stages (Dobson et al., 1994; Lammers et al., 1994; Meuwissen et al., 1992), were slightly reduced. A-myb, which is expressed in early primary spermatocytes (Mettus et al., 1994; Trauth et al., 1994), showed similar low-level expression. Taken together with the data from the chromosome analysis, these results suggest that spermatogenesis in Mili+/– mice is arrested from the zygotene to early pachytene stages.

### Differential expression of MILI and MIWI

Although MILI and MIWI are expressed in germ cells, their expression kinetics are different (Kuramochi-Miyagawa et al., 2001). The expression of MILI was detected up to the pachytene spermatocytes, whereas that of MIWI was detected from the mid-pachytene stage to the emergence of elongated spermatids. Thus, MILI is expressed at an earlier stage than MIWI, and the expression of MILI overlaps somewhat with that of MIWI in the mid-pachytene stage. According to the kinetics of expression, the stages of spermatogenetic arrest differ between the Mili+/– and Miwi+/– testes. Arrest was observed at the early pachytene spermatocyte and round spermatid stages in Mili+/– and Miwi+/– testes, respectively.

MILI and MIWI share the molecular characteristics such as binding to RNA and MVH. This raised an interesting question whether molecular function(s) of MILI could be same as that of MIWI. To zero in on this point, we are producing the transgenic mice in which MILI or MIWI is expressed under the promoter of Mili gene and are examining whether these transgenic mice could rescue the Mili+/– phenotype. Our preliminary data of the rescue study suggests that Mili but not Miwi, transgenic mice can rescue the Mili+/– phenotype (data not shown). Thus, the functional differences between MILI and MIWI are not solely dependent on the different expression timing but would be due to their distinctive molecular roles.

### Physical association between MILI and MVH

When MILI and MIWI were overexpressed with MVH in 293 cells, the majority of MVH was co-localized with MILI or MIWI as large perinuclear granule-like structure (data not shown). The data of overexpression analysis suggested that MILI and MIWI would define the localization of MVH at least to some extent. MVH is localized exclusively in the cytoplasm of spermatogenic cells from spermatogonia to round spermatids, with the highest expression in early spermatocytes (Toyooka et al., 2000). The stage of meiotic arrest in the Mili+/– testis was similar to that in the Mvh+/– testis, and the gene expression profiles were essentially the same, as assessed by RT-PCR analysis. MILI and MVH were found to be cytoplasmic proteins, as discussed below, and MILI and MIWI were co-expressed with MVH throughout spermatogenesis. These data led us to analyze the association of MILI and MIWI with MVH. Although physical association does not necessarily bear functional relevance, the similar phenotypes of Mili+/– and Mvh+/– spermatogenesis imply cooperative molecular functions for these molecules.

In round spermatids, MVH is predominantly localized in a single large granule with a spherical shape that is located in the perinuclear site (Toyooka et al., 2000). The perinuclear granule that stained with anti-MVH antibody was the chromatoid body, which is a perinuclear electron-dense body in the male germ cells of mammalian testicular germ cells classified as a nuage-like structure. The binding analysis showed that the affinity of MIWI for MVH was presumably higher than that between MILI and MVH (Fig. 6D). In pull-down analysis of MILI and MIWI with GST-MVH fusion protein, binding of MILI to MVH was competed out by the excessive amount of MIWI. The round spermatids showed similar staining patterns with the
anti-MIWI and anti-MVH antibodies. In addition, the round spermatids of the Miwi\(^{+}\) mice did not show perinuclear granular staining by anti-MVH antibody. Given that Miwi is required for the stability of its target mRNAs (Deng and Lin, 2002), this further suggests that chromotid body could be the subcellular structure essential for controlling the mRNA stability for spermiogenesis.

**Are Mili and Miwi Functional homologs of piwi?**

The functions of the *C. elegans* homologs of piwi, prg-1 and prg-2, have been studied using RNA interference (RNAi) to be important for the mitotic ability of the germline nuclei and are essential for germline proliferation and maintenance (Cox et al., 1998). In this regard, the prgs are not only structural, but also functional homologs of piwi. It is intriguing to investigate whether the mammalian MILI and MIWI are functional homologs of *Drosophila* Piwi. A couple of lines of evidence suggest that the two mammalian structural homologs of Piwi, i.e. MILI and MIWI, only inherit a subset of piwi functions. One line of evidence comes from the analysis of gene targeting. In addition to its crucial roles in germline stem cells, Piwi has less-well characterized roles in early oogenesis and spermatogenesis, possibly including germline cyst mitosis, meiosis and egg chamber polarity (Cox et al., 1998; Lin and Spradling, 1997). The expression of MIWI and MILI is restricted to germ lineages, and the gene-targeted animals show defective spermatogenesis. However, we have not observed the defect of Mili\(^{-}\) nor Miwi\(^{-}\) mice at the stage of testicular stem cells. Thus, Mili and Miwi may only represent a subset of piwi functions.

The other line of evidence is subcellular localization of MIWI and MILL. The Piwi protein can be localized either to the nucleoplasm in germline stem cells (Cox et al., 2000) or in the cytoplasm co-localized with polar granules such as Vasa in early embryos (D. N. Cox and H. Lin, unpublished), MILI and MIWI are found in the cytoplasm associated with MVH (Kuramochi-Miyagawa et al., 2001). This again reflects only a subset of the Piwi function. This function is also similar to Aubergine, another *Drosophila* Piwi family protein, that is recruited to the posterior pole in a vasa-dependent manner as a polar granule component (Findley et al., 2003). Interestingly, Aubergine remains exclusively in the cytoplasm even after polar cell formation. In addition, the levels of homology between MILI or MIWI and Aubergine (31.0% and 36.6%, respectively) were similar to those seen with Piwi (32.7% and 37.1%, respectively). Taking these data into consideration, it is conceivable that MILI and MIWI might be functionally more similar to Aubergine. Meanwhile, genome analysis has revealed the third mouse homolog of piwi and aubergine (Accession Number AY135692). It is an unanswered question whether the third member will represent other functions of piwi and aubergine.

The *piwi* family genes, defined by conserved PAZ and Piwi domains of unknown function, have been implicated in RNAi and related phenomena, such as post-transcriptional gene silencing (PTGS) and transcriptional gene silencing (TGS) in several organisms (Doi et al., 2003; Pal-Bhadra et al., 2002; Tijsterman et al., 2002; Vaucheret et al., 2001). AGO1 (*Argonaute*) and QDE-2 are required for PTGS in *Arabidopsis* and *Neurospora*, respectively, and RDE-1 is required for RNAi in *C. elegans* (Catalanotto et al., 2000; Fagard et al., 2000; Tabara et al., 1999). In *Drosophila*, mutations in *piwi* and *aubergine* block RNAi activation during egg maturation and perturb translational control during oogenesis (Kennerdell et al., 2002). Aubergine has the ability to effect the silencing of *Stellate*, which is a tandemly repetitive gene (Schmidt et al., 1999). Furthermore, in *Drosophila*, AGO1 and AGO2 are involved in RNAi, and *piwi* is required for PTGS and for TGS, which is induced by multiple copies of *Alcohol dehydrogenase* (Hammond et al., 2001; Pal-Bhadra et al., 2002; Williams and Rubin, 2002). MILI and MIWI may be involved in similar silencing mechanisms required for spermatogenesis. We are comparing the gene expression profiles between the control and the Mili\(^{-}\) testes, which could give some clues about the function on gene silencing.

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