Establishment of adult mouse Sertoli cell lines by using the starvation method

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Abstract

Sertoli cells were isolated from the testes of 6-week-old mice and stable Sertoli cell lines with higher proliferation rates were subcloned after starvation of primary cultured cells. After two rounds of this subcloning, 33 subcloned lines were selected on the basis of their proliferation rates. In addition, these subclones were screened according to their phagocytic activity and the characteristics of mature Sertoli cells, such as the expression of androgen receptors (ARs) and progesterone receptors, by using western blotting and immunocytochemical analysis, in addition to their morphology and proliferation rates. After the third round of subcloning, 12 subclones were selected for the final selection using RT-PCR for identification of genes specifically expressed by various testicular cells. Three clones were selected that expressed Sertoli-cell-specific genes, i.e. stem cell factor, clusterin, AR, α-inhibin, transferrin, Wilms’ tumour-1, Müllerian inhibitory substance, sex-determining region Y-box 9, FSH receptor (Fshr) and occludin; however, these clones did not express globulin transcription factor 1, steroidogenic factor or androgen-binding protein. These clones also expressed growth and differentiation factors that act on germ cells, such as leukaemia inhibitory factor, transforming growth factor β1 and basic fibroblast growth factor 2, but did not express c-kit (specific for germ cells), LH receptor and 3β-hydroxyl-dehydrogenase (specific for Leydig cells). Immunocytochemical data confirmed the expression of clusterin in these clones. Furthermore, the Bromodeoxyuridine incorporation assay confirmed the proliferation activity of these clones through Fshr after treatment with FSH. These clones are considered to be valuable tools for the study of Sertoli cell-specific gene expression and function.

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Introduction

The culture of primary Sertoli cells has become an important resource in the study of their function (Buzzard et al. 2002); however, their use is limited because the isolated cells are contaminated with other testicular cells, mainly myoid cells. Furthermore, the proliferation of primary Sertoli cells, especially from pubertal and adult mice, is very slow, the cells are short-lived and experiments with Sertoli cells require a continual supply of animals, thereby making it difficult to replicate experimental conditions. Thus, the establishment of appropriate functional Sertoli cell lines is necessary.

Sertoli cells have two functionally separate roles: one in the process of testis formation or sexual differentiation and the other in spermatogenesis (Sharpe et al. 2003). Disorders of testicular function may have their origins in foetal or early life because of the abnormal development or proliferation of Sertoli cells (Archambeault & Yao 2010). Sertoli cells also play an important role in spermatogenesis by providing a unique microenvironment that is essential for the development of germ cells in the testis and the formation of the blood–testis barrier (Cheng & Mruk 2010). Without the physical and metabolic support of Sertoli cells, germ cell differentiation, meiosis and development into spermatozoa would not occur (Sharpe 1994, Cheng et al. 2010).

The development and function of Sertoli cells are controlled by their interaction with other testicular cell types – either through direct cell–cell contact or via endocrine or paracrine factors (Plant & Marshall 2001, Cheng et al. 2010). Increasing concentrations of FSH and
testosterone at puberty, coincident with the expression of the androgen receptor (AR) in Sertoli cells, may induce their final maturation (Sharpe et al. 2003, Rey et al. 2009). Foetal Sertoli cells are clearly capable of supporting foetal germ cells (e.g. primordial germ cells and gonocytes), and immature, neonatal or infantile Sertoli cells are able to support spermatogonia. Conversely, in the adult testis, mature Sertoli cells support full spermatogenesis because the failure of Sertoli cells to mature functionally makes them incapable of supporting the survival and development of various germ cells that appear after puberty.

Several cell lines have been established from immature Sertoli cells isolated from the testis of a neonatal or infant mouse (Mather 1980, Hofmann et al. 1992, 2003, Peschon et al. 1992, Walther et al. 1997). However, because cells from these lines did not show the highly differentiated phenotype of adult Sertoli cells (McGuinness et al. 1994, Strothmann et al. 2004), they have not been used to study the function of mature Sertoli cells. The establishment of mature Sertoli cell lines requires the introduction of a gene for inducing cell proliferation. Several cell lines have been established by the immortalisation of primary cultured mature Sertoli cells using the temperature-sensitive SV40 or the polyoma T-antigen transgenic mouse (Rassoulzadegan et al. 1993, Tabuchi et al. 2002). However, several problems have occurred during the establishment of cell lines after gene engineering; for example, after immortalisation, rat Sertoli cell lines expressed epithelial genes, but also unexpectedly expressed mesenchymal genes (Konrad et al. 2005).

To establish the cell lines of Sertoli cells with many characteristics similar to mature Sertoli cells in the adult testis, we adopted a different approach in which transgenesis was not required. After culturing primary Sertoli cells, we subcloned 12 Sertoli cell lines without changing the culture medium. These lines were characterised by light microscopy, western blotting, immunocytochemistry and RT-PCR. The gene expression pattern displayed by three selected Sertoli cell lines indicated that they could be useful as an in vitro model for studying several factors related to the function of mature Sertoli cells.

Results

Characterisation of the cell lines by western blotting, immunocytochemistry, phase contrast microscopy and fluorescent microscopy for the third round of subcloning

We subcloned primary cultured Sertoli cells twice by using the starvation method. Thirty-three subclones were obtained after the second subcloning step. We then selected the cell lines on the basis of their morphology, phagocytotic activity and protein expression levels of the AR and the progesterone receptor (PR). From this third subcloning, we obtained 12 subclones. Six cell lines derived from the subcloning of line A3 were designated as A31B1, A31B4, A31C1, A31C4, A32B4 and A33A4. In addition, six cell lines derived from the subcloning of line C2 were designated as C21C3, C21C4, C22A3, C22A4, C22B4 and C24A4. These new cell lines were cultured for more than 1 year.

These 12 subcloned cell lines were mostly spindle-shaped with some lipid inclusions within the cytoplasm, and these Sertoli cells often showed a linear alignment when cultured at a high density (Fig. 1 and Table 1). Furthermore, these cell lines efficiently took up Fluoresbrite latex beads and fluorescence was detected in the cytoplasm (Fig. 2), indicating that the cells have phagocytic activity. All the 12 subclones showed phagocytic activity (Fig. 2 and Table 1). The A3 and C2 cell lines expressed the AR and PR (Fig. 3), and both proteins were localised to the nucleus (Fig. 4). Furthermore, the expression of the AR was higher in the A3 cell line than in the C2 cell line (Fig. 3).

The 12 subclones showed a doubling time of 13–26 h, whereas the doubling times of the final three selected clones, determined from the expression of Sertoli-cell-specific genes, were 18 h (A31C4), 21 h (C22A4) and 25 h (C24A4) (Table 1). Furthermore, the chromosome number of the 12 subclones was between 80 and 180.
chromosomes, whereas it was 80 chromosomes for the final three selected clones (Table 1).

Characterisation of the cell lines by using RT-PCR for the final selection

Total RNA was extracted from the cell lines and the adult testis. Three clones (A31C4, C22A4 and C24A4) were selected from the 12 subclones because the number of Sertoli-cell-specific genes expressed in these cell lines was more than that in the other subclones (Fig. 5). The gene expression patterns in the C24A4 and C22A4 cell lines were found to be similar (data not shown). The housekeeping gene cyclophilin was detected by RT-PCR in all the cell lines and adult testes, indicating the presence of cDNA in every sample (Fig. 5A). All Sertoli-cell-specific cDNAs tested were present in the adult testis. The PCR product Kit, a marker of spermatogenic cells, was detected in the adult testis, but not in any of the cell lines (Fig. 5B), indicating that none of the lines were of germ cell origin. cDNAs for the following genes expressed by Sertoli cells in the testis were present in all the cell lines (Fig. 5C): AR (Ar), clusterin (Clu), α-inhibin (Inha), basic fibroblast growth factor (Fgf2), transforming growth factor β1 (Tgfb1), leukaemia inhibitory factor (Lif), stem cell factor (Kit), Müllerian inhibiting substance (Mis/Amh), Wilms’ tumour 1 (Wt1), transferrin (Trf), sex-determining region Y box 9 (Sox9), FSH receptor (Fshr) and occludin (Ocln). Ar, Tgfb1 and Fgf2 are known to be expressed in Sertoli cells and myoid cells; however, the possibility that the cell lines were derived from myoid cells can be excluded because myoid cells do not express Sertoli-cell-specific genes that are expressed by these cell lines. Although all the cell lines expressed Ar, Lif, Amh and Sox9, which are also expressed by Leydig cells, no specific PCR bands were observed for the LH receptor (Lhr/Lhcgr) or 3β-ol-hydroxysteroid-dehydrogenase (Hsd3b) genes, which are specifically expressed by Leydig cells in the adult testis, in any of the cell lines (Fig. 5B), indicating that none of the cell lines were of Leydig cell origin. No specific bands for steroidogenic factor 1 (Sfi), androgen-binding protein/sex hormone-binding globulin (Shbg) or GATA-binding protein 1 (Gata1) were observed for the cell lines, although these genes were expressed in the adult testis (Fig. 5C).

Table 1 Characteristics of the new cell lines established from the adult mouse testis.

<table>
<thead>
<tr>
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<th>Doubling time (h)</th>
<th>Chromosome number</th>
<th>Phagocytic activity</th>
<th>Linear alignment</th>
<th>AR in the nucleus</th>
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Figure 2 Phagocytic activity of the cell lines.

(A) Fluorescence micrograph of A31C4, (A’) phase contrast micrograph of A, (B) fluorescence micrograph of C22A4 and (B’) phase contrast micrograph of B. Fluoresbrite beads were phagocytised by the cells and located in the cytoplasm. n, nucleus. Scale bar: 100 μm.
Clusterin protein expression in the selected cell lines

The immunocytological study revealed that clusterin was expressed in these cell lines. However, the localisation of clusterin expression differed among the cell lines. In the A31C4 cell line, clusterin was mainly expressed in the cytoplasm (Fig. 6A); however, in the C24A4 (Fig. 6B) and C22A4 cell lines (data not shown), it was expressed in both the nucleus and the cytoplasm.

Effects of FSH on Sertoli cell proliferation

To examine the functionality of Fshr in the three cloned Sertoli cell lines, the cells were first stimulated with FSH and then the BrdU incorporation assay was performed. BrdU incorporation rates were significantly higher in the FSH-treated Sertoli cell lines than in the controls (P<0.001; Fig. 7). No significant difference was observed in the rate of BrdU incorporation among the three clones treated with FSH, although the C22A4 cell line showed slightly higher BrdU incorporation rates than did the other cell lines that did not receive any stimulation (P<0.05).

Discussion

We isolated Sertoli cells from adult mouse testes and established stable Sertoli cell lines after the starvation of primary cultured cells. These immortalised Sertoli cell lines, which express several genes specific for mature Sertoli cells and show proliferation and phagocytic activity, may provide a useful in vitro model for studying several factors related to Sertoli cell function and spermatogenesis.

An appropriate regulation of androgen activity through AR-mediated signalling is necessary for both the initiation and maintenance of spermatogenesis (Sharpe et al. 2003). Poor germ cell differentiation has been observed in the testes of Sertoli-cell-specific AR knockout mice (De Gendt et al. 2004, Wang et al. 2009). Therefore, the expression of AR is important for the selection of Sertoli cell lines. Only Sertoli cell lines prepared from neonatal mice maintain AR expression (Mather 1980). AR expression is lost in immortalised rat Sertoli cell lines established through SV40-induced transformation (Konrad et al. 2005) and in most Sertoli cell lines established from the cells of adult mouse testes via gene transfer. Therefore, transgenic techniques may not be adequate for maintaining AR expression in immortalised Sertoli cells. In the present study, we did not use transgenic techniques to establish our Sertoli cell lines and, instead, opted for the specific selection of clones on the basis of AR expression. This approach may result in the successful establishment of Sertoli cell lines expressing AR from adult testes.

PR expression in Sertoli cells changes during the maturation process (Weber et al. 2002), and the expression is altered in the testes of infertile men (Shah et al. 2005). Furthermore, the binding affinity of testosterone to AR may be modulated through testosterone binding to PR (Tindall et al. 1984). However, no available reports have described the expression of PR in mature Sertoli cell lines derived from adult testes.
suggesting that it is not expressed or has not been investigated. Therefore, we thought it was important to study the expression of PR in our Sertoli cell lines to investigate the involvement of PR in spermatogenesis.

The Sertoli cell is the only cell type among the testicular cells, which possesses phagocytic activity to eliminate apoptotic germ cells (Grandjean et al. 1997, Nakanishi & Shiratsuchi 2004). This process is thought to be essential for the production of normal spermatozoa because half of the produced germ cells disappear during spermatogenesis (Wang et al. 2006, Chen et al. 2009, Elliott et al. 2010). Our established Sertoli cell lines show active phagocytosis and may be useful for the analysis of this Sertoli cell function in detail.

Transferrin has a role in the transport of iron to developing germ cells and is produced by Sertoli cells (Skinner & Griswold 1980). Transferrin synthesis increases during puberty and is a differentiation marker for Sertoli cells before and during puberty (Anthony et al. 1991). Hence, the maintenance of Trf gene expression in our established cell lines may indicate that Sertoli cells are fully differentiated. This characteristic suggests that these cell lines may be useful for the analysis of iron transportation between Sertoli cells and germ cells.
Clusterin is thought to control the expression of many other Sertoli cell products; however, its role remains unclear. Two types of clusterin, a conventional secreted isoform and a cytoplasmic and nuclear isoform, are thought to be involved in survival or cell death (Leskov et al. 2011). Although clusterin expression in the nuclei is thought to be associated with apoptosis, our cell lines survive, despite clusterin expression in the nuclei. The prostate tumour cell line PC-3 has been reported to survive when clusterin is overexpressed in both the cytoplasm and the nucleus because of the acquisition of apoptotic inhibitory properties during cloning of the cell line (Scaltriti et al. 2004). During selection, our cell lines also may have acquired anti-apoptosis properties similar to those in PC-3 cell lines. Functionally immature Sertoli cells of the adult testis containing only Sertoli cells or Sertoli cells with carcinoma in situ do not express clusterin, suggesting that clusterin expression is a marker of functionally mature Sertoli cells and may play a role in normal spermatogenesis (Sharpe et al. 2003). Our established Sertoli cell lines may be useful for studying the control function of Clu on the expression of many other Sertoli cell products required for spermatogenesis.

Our cell lines also expressed the transcription factor Wt1, which is expressed in Sertoli cells (Pelletier et al. 1991). WT1 plays an essential role in gonadal development, sexual differentiation and spermatogenesis (Kreidberg et al. 1993, Scharnhorst et al. 2001, Myers et al. 2005). Furthermore, WT1 is thought to be a stable marker of Sertoli cells compared with other protein markers because it is continuously expressed at high levels in Sertoli cells throughout life (Mackay 2000). The 15P1 Sertoli cell line expresses Wt1, which induces transmeiotic differentiation of premeiotic germ cells under co-culture conditions (Rassoulzadegan et al. 1993). Therefore, the expression of Wt1 in our Sertoli cell lines may be expected to support spermatogenesis.

FSHR expression is initiated during foetal development and is maintained throughout development. FSH acts through FSHR, induces Sertoli cell proliferation (Riera et al. 2012), establishes the final Sertoli cell number (Singh & Handelsman 1996) and stimulates transcription and metabolic activity in Sertoli cells.
which contributes to germ cell survival and development (George et al. 2011). Our present results confirm the functionality of FSHR in our cell lines through the evaluation of proliferation activity with FSH supplementation. GATA-1 is thought to be one of the requirements for Sertoli cell-specific activity through the Fshr promoter (Kim & Griswold 2001). Although our established cell lines do not show Gata1 expression, other elements may be used for the activation of the Fshr promoter to induce the proliferation activity of the cell lines (Hermann & Heckert 2007). In our current routine culture conditions, we did not add FSH to the media; however, culture media containing bovine serum had a small amount of FSH and may induce the proliferation of Sertoli cells.

Some immature Sertoli cell markers were also expressed in our Sertoli cell lines. Amh expression is switched on when the undifferentiated gonad begins to differentiate into the testis (Mackay 2000, Josso et al. 2001), and the production of Amh continues at high levels before around puberty (Tran et al. 1987). The down-regulation of Amh expression correlates with the onset of meiosis in germ cells (Rey et al. 1996) and the presence of meiotic cells may be required to switch off Amh expression in our cell lines.

The transcription factor Gata1 is initially expressed in murine Sertoli cells as they are maturing and show stage-specific expression after the first wave of spermatogenesis (Yomogida et al. 1994). Three of our Sertoli cell lines did not express Gata1. Thus, we can assume that our Sertoli cell lines expressed Amh, but not Gata1, because the expression of Gata1 and Amh are inversely related during testis development (Beau et al. 2000), i.e. Gata1 may be switched off by Amh expression in our cell lines.

Several paracrine growth factors produced by Sertoli cells, e.g. Kitl, Lif, Tgfβ1 and Fgf2, alone or in combination, are expected to play a crucial role in the proliferation and/or differentiation of spermatogonia (Mullaney & Skinner 1993, Dym et al. 1995, Huleihel & Lunenfeld 2004, Loveland et al. 2005, Mirzapour et al. 2012). Our established three cell lines, all of which express these molecules, will be valuable for investigating the effects of these factors on spermatogenesis.

In the mammalian testis, Sertoli cells make the blood-testis barrier using tight-junction-associated proteins such as occludin and claudin (Mruk & Cheng 2010). These tight-junction-associated proteins show restructuring during spermatogenesis and participate in coordinated spermatiation (Cheng et al. 2011). Although many other tight-junction-associated molecules need to be investigated, our cell lines may be used for establishing a tight junction barrier that mimics the blood–testis barrier in vitro because these established cell lines express Ocln.

In conclusion, the three established cell lines are potentially valuable tools for studying Sertoli-cell-specific gene expression. Furthermore, the starvation method used to establish the cell lines from adult Sertoli cells might be effective in isolating the cell lines with acquired proliferative activity and conserved native characteristics.

Materials and Methods

Primary cell culture preparation

Cells for primary culture were obtained from the testes of 6-week-old male C57BL/6j mice by a modified two-step enzymatic digestion protocol (Brinster & Avarbock 1994, Bellve et al. 1997). In this procedure, the tunica albuginea was removed from the testes manually, exposing the seminiferous tubules. The testes were then incubated in 1 ml PBS without calcium and magnesium (PBS (−)); Wako, Tokyo, Japan) containing 1 mg/ml collagenase (Type IV; Sigma) at 37 °C with gentle agitation (80 cycles/min) for 1 h. After sedimentation by centrifugation (300 g for 5 min at room temperature), the supernatant was removed and the seminiferous tubules were incubated in PBS (−) containing 1 mg/ml hyaluronidase (Type-1S; Sigma) at 37 °C with gentle agitation (80 cycles/min) for 1 h. The cells were washed three times with PBS (−) and centrifuged (300 g for 5 min at room temperature). Following digestion, cell suspension was filtered through a nylon mesh (Cell Strainer 100 μm; BD Falcon, Tokyo, Japan) to remove cell clumps and undigested materials. The filtrate was centrifuged (300 g for 5 min at room temperature) and the supernatant was removed from the pellet. The cells in the pellet were then resuspended in complete culture medium, which consisted of Eagle’s medium (Nissui Pharmaceutical Co. Ltd, Tokyo, Japan) supplemented with 0.292 g/l l-glutamine (Nissui Pharmaceutical Co. Ltd), 100 U/ml penicillin, 100 μg/ml streptomycin (Invitrogen) and 10% foetal bovine serum (FBS; Gibco). Yields were in the range of 5.0×10⁸ cells per testis. The cells were plated in culture dishes or in 24-well culture plates (Falcon; Fisher Scientific, Yokohama, Kanagawa, Japan) containing complete culture medium supplemented with l-glutamine, 10% FBS and antibiotics, as described above, and incubated at 32 °C and 5% CO₂ in a humidified incubator. After culture for 1 day, the culture medium was changed to remove non-adherent cells from the dish or well. This study was approved by the Ethical Committee/Institutional Review Board of St Marianna University School of Medicine.

Isolation of immortalised cell lines and subcloning

After changing the medium once a week and passaging the cells for 1 month, to starve the cells, we altered the medium changes from once a week to once every 2 weeks for two cycles and then to once every 3 weeks for two cycles. After starvation of the cells, the original medium change routine was used, and the cells showing high proliferation rates were selected. Using the cloning ring (Iwaki, Tokyo, Japan) for the collection of the cells from a single colony (Mcfarland 2000), we performed the first subcloning of the cells and isolated 88 cell groups showing six different morphological types. The first subcloned cell groups were stored in culture medium containing 0.75% dimethyl sulfoxide (DMSO; Sigma) in liquid nitrogen. We confirmed the proliferation of these cell groups over four
passages. Then, we continued with the second subcloning of the cells using the same methods and isolated 33 cell line groups. The second subcloned cell groups were also stored in culture medium containing 0.75% DMSO (Sigma) in liquid nitrogen. The proliferation activity of these cell groups was confirmed over six passages.

**Selection markers of the cell lines for the third round of subcloning**

The 12 subclones were selected as cell line candidates on the basis of their morphological resemblance to Sertoli cells (i.e. the presence of cytoplasmic projections, lipid inclusions and indented nuclei), phagocytic activity and the characteristics of mature Sertoli cells, such as both the expression and localisation of the AR and PR, by using phase contrast and bright field microscopy.

**Analysis of the phagocytic activity of the cell lines**

We used a modified version of a previously reported phagocytosis assay (Tokuda et al. 1992). Fluoresbrite plain Calibration Grade 6.0 micron YG Microspheres (2.6% Solids-latex; Polysciences, Inc., Warrington, PA, USA) were added to 70% confluent cell lines, and further incubated at 32 °C and 5% CO₂ overnight. Internalisation was assessed using fluorescent microscopy and phase contrast microscopy after washing the cells three times with PBS (−) to remove the latex beads on the outside of the cells.

**Immunocytochemistry for AR, PR and clusterin**

Cells were grown on Lab-Tek chamber slides (Nalge Nunc International KK., Tokyo, Japan) to 80% confluence and fixed with 4% paraformaldehyde for 1 h or ice-cold methanol (MeOH) for 30 min. After washing with PBS (−), the slides were incubated with 3% H₂O₂–MeOH for 10 min to block endogenous peroxidase activity. After pre-incubating the slides with 10% goat serum in PBS (−) (1:100; Santa Cruz Biotechnology) or clusterin (H-330, rabbit polyclonal, 1:200; Santa Cruz Biotechnology) or rabbit IgG (Dako, Tokyo, Japan), which were incubated for 2 h or overnight (clusterin) at room temperature. Pre-absorbed antibodies with blocking peptides (AR [N-20]P and PR [C-19]P; Santa Cruz Biotechnology) or anti-rabbit IgG (Fab') labelled with an amino acid polymer–peroxidase complex (Histofine Simple Stain MAX PO (R); Nichirei Co., Tokyo, Japan) for 1 h at room temperature. The slides were then washed and the peroxidase complex was detected by incubation with aminoethyl carbazol (AEC, Histofine Simple Stain AEC Solution; Nichirei Co.) according to the manufacturer's instructions. The slides were counterstained with haematoxylin, mounted using an aqueous permanent mounting solution (Nichirei Co.) with a cover glass and observed under a microscope.

**Protein extraction and western blot analysis**

Cells were washed twice with cold PBS (−), solubilised with cold RIPA lysis buffer (10 mM Tris–HCl (pH 7.5), 1 mM EDTA, 150 mM NaCl, 2% (3-(3-cholamidopropyl)dimethylammonio)propanesulphonate, 1 mM dithiothreitol) containing one protease inhibitor cocktail tablet (Roche Biochemicals) on ice for 10 min, and collected by using a cell scraper and by pipetting on ice for 10 min. The lysate was then centrifuged to remove cellular debris (15 min, 15 000 g, 4 °C). Protein concentration was measured by the bicinchoninic acid assay (Smith et al. 1985) using BSA as a standard. We loaded 10 μg protein from the testis or 10 μg protein from the isolated cell fractions into Laemmli buffer (2% SDS, 10% glycerol, 5% 2-mercaptoethanol, 0.02% bromophenol blue, 0.0625 M Tris–HCl), separated the proteins on a 7.5% acrylamide gel and semi-dry electroblotted the samples onto a polyvinylidene difluoride membrane (Millipore, Tokyo, Japan). The membranes were blocked for 1 h at 37 °C with a solution of 5% (w/v) non-fat dried milk in Tris-buffered saline (20 mM, pH 7.6) supplemented with Tween-20 (0.05%; TBS-T). The membranes were incubated with the anti-AR antibody (1:2000) or PR antibody (1:1000) in TBS-T containing 5% (w/v) non-fat dried milk for 30 min at 37 °C. After three washes in TBS-T for 5 min, the membranes were incubated with goat anti-rabbit IgG conjugated with alkaline phosphatase (1:3000; Bio-Rad) in TBS-T for 30 min at 37 °C. Control incubations were performed using an antibody pre-absorbed with an excess antigen-blocking peptide (AR[N-20]P or PR[C-19]P). Specific immune complexes were detected using an enhanced chemiluminescence kit (ECL; Amersham-Pharmacia) by following the manufacturer’s instructions.

**Screening of PR and AR expression in the cell lines by western blot analysis**

Double sets of the samples were run on both sides of a gel. After the proteins were transferred to a membrane, half of the membrane was stained with Coomassie Brilliant Blue R (CBB), for which detection was considered as a good quantitative loading control for the excision of bands of the AR or PR. Because the band the size of the AR or PR band in CBB was difficult to detect, the clear band at around 50 kDa was used for the loading control. The other half of the membrane was used for western blotting as described previously. The wet gels were stained with CBB to confirm the efficiency of blotting. The western blot membranes were scanned and volumetric determination of the detected bands was performed using ImageMaster software (Amersham Pharmacia Biotech). To adjust for the running differences between the gels, we used the same protein amount from the same testis sample and compared the results of the expression of the AR or PR in each clone using the following formula:

\[
\text{ECL value of (clone X)/CBB value of (clone X))}
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\[
\text{ECL value of (testis)/CBB value of (testis))}
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Detection of Sertoli cell transcripts by RT-PCR for final cloning

After the selection of the 12 subclones (A31B1, A31B4, A31C1, A31C4, A32B4, A33A4, C21C3, C21C4, C22A3, C22A4, C22B4 and C24A4), RT-PCR was performed for the final selection of the cell lines using primers sets for genes specifically expressed by various cell types within the testis. Total RNA was extracted from the cell lines or testicular tissue using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol. Total RNA was digested by RNase-free DNase I (Gibco) to degrade any genomic DNA present and manufacturer's protocol. Total RNA was digested by RNase-free using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol. Total RNA was digested by RNase-free using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol. Total RNA was digested by RNase-free using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol. Total RNA was digested by RNase-free using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol. Total RNA was digested by RNase-free using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol. Total RNA was digested by RNase-free using ISOGEN (Nippon Genes, Tokyo, Japan) according to the manufacturer's protocol.

Table 2 Primer sequences of RT-PCR.

<table>
<thead>
<tr>
<th>Genes</th>
<th>Orientation</th>
<th>Nucleotide sequence</th>
<th>Annealing temperature (°C)</th>
<th>PCR product (bp)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cyclophilin</td>
<td>Sense</td>
<td>5’-TGG GCC GCC TCT CCT TCG AG-3’</td>
<td>56</td>
<td>588 bp (exons 1–5)</td>
<td>Hofmann et al. (2003)</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-CGG GAA TGA CCA AAA TAT TG-3’</td>
<td>60</td>
<td>389 bp (exons 9–12)</td>
<td>Schrans-Stassen et al. (1999)</td>
</tr>
<tr>
<td>Kitl</td>
<td>Sense</td>
<td>5’-TCA ACC TCC CCG AAG GCA CCA-3’</td>
<td>56</td>
<td>215 bp (exons 2–5)</td>
<td>Walther et al. (1996)</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-ATC GTG GTT CAG AGT TCC ATG-3’</td>
<td>66</td>
<td>890 bp (exons 2–4)</td>
<td>Walther et al. (1996)</td>
</tr>
<tr>
<td>Lhcgr</td>
<td>Sense</td>
<td>5’-AAC ACC ATG CTA TCA CAG CAG-3’</td>
<td>66</td>
<td>259 bp (exon 1)</td>
<td>Walther et al. (1996)</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-GCT GTT GCT GAA GAA ATG TGA-3’</td>
<td>66</td>
<td>238 bp (exon 1–3)</td>
<td>Walther et al. (1996)</td>
</tr>
<tr>
<td>Clu</td>
<td>Sense</td>
<td>5’-TGA AGC GGC ACC GCA TTC AC-3’</td>
<td>60</td>
<td>264 bp (exon 5)</td>
<td>NM_013492.2</td>
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<tr>
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<td>Antisense</td>
<td>5’-ATC TGG GAG ATT CTC AAA GT-3’</td>
<td>60</td>
<td>344 bp (exons 3–5)</td>
<td>Hofmann et al. (2003)</td>
</tr>
<tr>
<td>Fgf2</td>
<td>Sense</td>
<td>5’-GTC GCC GAG AAG AGG AAC CCC-3’</td>
<td>68</td>
<td>405 bp (exons 5–7)</td>
<td>Hofmann et al. (2003)</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-TGC CCT TCT CAG CAG CCG-3’</td>
<td>60</td>
<td>283 bp (exons 1–3)</td>
<td>NM_008006.2</td>
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<tr>
<td>Tgb1</td>
<td>Sense</td>
<td>5’-CGG GCC GAC CTG GGC ACC ATC CAT GAC-3’</td>
<td>68</td>
<td>405 bp (exons 5–7)</td>
<td>Hofmann et al. (2003)</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-CGT CTC CAC CTT GGG CTT GCC ACC CAC-3’</td>
<td>56</td>
<td>450 bp (exons 4–5)</td>
<td>Hofmann et al. (2003)</td>
</tr>
<tr>
<td>Liî</td>
<td>Sense</td>
<td>5’-TCA CCC CTG TTA ATG CCA CC-3’</td>
<td>60</td>
<td>344 bp (exons 3–5)</td>
<td>Hofmann et al. (2003)</td>
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<tr>
<td></td>
<td>Antisense</td>
<td>5’-GTT GAT GTG ACC TGC CTT CC-3’</td>
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<td>478 bp (exon 10)</td>
<td>NM_013523.3</td>
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<td>Gata1</td>
<td>Sense</td>
<td>5’-TGC TTA CCC CTG GAG CAC ACA AC-3’</td>
<td>60</td>
<td>592 bp (exons 2–6)</td>
<td>NM_008098.1</td>
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<tr>
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<td>Antisense</td>
<td>5’-TGC TAC TCC CGG TGG GGG-3’</td>
<td>60</td>
<td>242 bp (exon 7)</td>
<td>NM_139051.3</td>
</tr>
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<td>Sf1</td>
<td>Sense</td>
<td>5’-GTC AAC TCC CTG AAC ACC AGC-3’</td>
<td>60</td>
<td>237 bp (exon 10)</td>
<td>NM_013523.3</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-GCG CTG CAT GAT CCG TGT C-3’</td>
<td>50</td>
<td>236 bp (exons 4–5)</td>
<td>Ao et al. (1993)</td>
</tr>
<tr>
<td>Fshr</td>
<td>Sense</td>
<td>5’-GTC TGC TGC TGT CAC ATC-3’</td>
<td>60</td>
<td>440 bp (exons 3–5)</td>
<td>NM_011448.4</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-GAG TAT GAC TGA TAC CTA CA-3’</td>
<td>60</td>
<td>433 bp (exons 8–10)</td>
<td>Beverdam et al. (2003)</td>
</tr>
<tr>
<td>Ambh</td>
<td>Sense</td>
<td>5’-GCC TCT CAC ACC CCT CTA CA-3’</td>
<td>50</td>
<td>589 bp (exons 8–12)</td>
<td>Walther et al. (1996)</td>
</tr>
<tr>
<td></td>
<td>Antisense</td>
<td>5’-GCC AGT TGC GTG GCC AAG G-3’</td>
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<td>498 bp (exons 2–5)</td>
<td>NM_011367.2</td>
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<tr>
<td>Sox9</td>
<td>Sense</td>
<td>5’-GTC GAG AGG CCT CAG TCA-3’</td>
<td>54</td>
<td>318 bp (exon 9)</td>
<td>NM_008756</td>
</tr>
</tbody>
</table>

Ar, androgen receptor; Clu, clusterin; Fgf2, basic fibroblast growth factor; Tgb1, transforming growth factor β1; Liî, leukaemia inhibitory factor; Kitl, stem cell factor; Ambh, Mullerian inhibiting substance; Wt1, Wilms' tumour gene; Sox9, sex-determining region Y box 9; Fshr, FSH receptor; Sf1, steroidogenic factor-1; Shbg, androgen-binding protein/sex hormone-binding globulin; Gata1, globin transcription factor-1; Kit, c-kit oncogene; Lhcgr, LH receptor; Hsd3b, 3β-hydroxysteroid-dehydrogenase; Ocln, occludin.
designed using published sequences from mouse or other mammalian species (Walther et al. 1996, Schrans-Stassen et al. 1999, Beverdam et al. 2003, Hofmann et al. 2003) or Primer BLAST (NCBI). For the RT-PCR of Fshr, after the first-round PCR, the amplified products (50 times diluted) were used for a second-round nested PCR. The PCR products were electrophoresed through 2% agarose gels, and after staining with ethidium bromide, the product bands were visualised under u.v. light. The absence of contaminating genomic DNA was confirmed by running each reaction in parallel with a reaction lacking reverse transcriptase. The RT-PCR products were subcloned into TOPO pCRII (Invitrogen), and DNA was purified for sequencing (Mini-Prep Kit; Qiagen). RT-PCR experiments were performed independently three times.

**Growth curves**

The final 12 subcloned cell lines were counted and seeded at $2.0 \times 10^5$ cells per dish in different 30 mm tissue culture dishes with complete cell culture media containing 10% FBS. For the next 6 days, three of the dishes for each cell line were trypsinised, and the cells were counted using the trypan blue (Gibco) exclusion method. The doubling time of each cell line was calculated from their individual growth curves.

**Chromosomal analysis of the cell lines**

Cell lines showing 70% confluence were incubated for 2 h at 32 °C in complete culture medium containing 0.1 µg/ml colcemid in order to arrest the cell cycle at metaphase. After colcemid treatment, the cells were washed with PBS (−) and removed from the dish using 0.05% trypsin with EDTA (Invitrogen). The cells were washed three times with PBS (−) and centrifuged (300 g for 5 min at room temperature). After removing the supernatant, the cells were hypotonised with 1% (w/v) sodium citrate for 15 min at room temperature. The cells were fixed in a 2 × volume of Carnoy’s fixative for 2–3 min and centrifuged (300 g for 5 min at room temperature). After removing the supernatant, the cells were suspended in a small amount of Carnoy’s fixative and placed onto clean glass slides. The slides were air-dried, stained with 10% (V/V) Giemsa solution (Invitrogen) for 10 min, rinsed in distilled water and air-dried again. The chromosome spreads were examined via bright field microscopy to determine the nuclear ploidy of each cell line.

**BrdU incorporation assay**

After culturing the monolayer Sertoli cell lines on Lab-Tek chamber slides with or without purified native FSH from porcine pituitary glands (100 ng/ml, H301/H; Biogenesis, Dorset, UK) in culture medium for 24 h on day 2 in culture, the cell lines were incubated with BrdU (200 µM; Sigma) in culture medium for 24 h on day 3 in culture. After the incubation, cultured cells were fixed with 4% paraformaldehyde in PBS (−) for 30 min and then permeabilised with 0.1% Triton-100 in PBS (−) for 15 min. After washing with PBS (−), the slides were rinsed with distilled water for 5 min and then incubated with 2 M HCl for 20 min to denature DNA for allowing the anti-BrdU antibody to interact with incorporated BrdU. To neutralise the acid, the slides were immersed with 0.1 M sodium borate buffer (pH 8.5) for 5 min and then washed with distilled water and PBS (−) several times. After blocking the endogenous peroxidase activity, as described for the immunocytochemical method previously, the cells were incubated with 10% goat serum in PBS (−) for 1 h at room temperature. The immunocytochemical reaction was performed using an anti-BrdU mouse MAB (1:100, NCL-BrdU; Leica Biosystems, Tokyo, Japan) diluted in 10% BSA in PBS (−) as the primary antibody or mouse IgG (Dako) adjusted to the working concentration of the BrdU antibody as the negative control for 2 h at room temperature. After washing the slides with PBS (−), anti-mouse IgG (Fab′) labelled with an amino acid polymer–peroxidase complex (Histofine Simple Stain MAX PO (M); Nichirei Co.) was applied on the slides as the secondary antibody and incubated for 1 h at room temperature. Then, AEC was used for the detection of the antigen, as described previously. The slides were counterstained with haematoxylin and observed under a microscope. Data are presented as the mean value of the percentage of proliferating Sertoli cells (BrdU-positive Sertoli cells/total Sertoli cells) × 100 from more than three independent experiments with triplicate incubations. All values are expressed as mean ± S.E.M. Student’s t-test was used to assess all differences between the pairs using Windows Excel 2007 (Microsoft Corp.). A $P$ value of <0.05 was considered as significant.

**Declaration of interest**

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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**References**


Sertoli cell lines from adult mouse testis


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