Comparison of cell types in the rat Leydig cell lineage after ethane dimethanesulfonate treatment

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Abstract

The objective of this study was to purify cells in the Leydig cell lineage following regeneration after ethane dimethanesulfonate (EDS) treatment and compare their steroidogenic capacity. Regenerated progenitor (RPLCs), immature (RILCs), and adult Leydig cells (RALCs) were isolated from testes 21, 28 and 56 days after EDS treatment respectively. Production rates for androgens including androsterone and 5α-androstane-17β,3α-diol (DIOL), testosterone and androstenedione were measured in RPLCs, RILCs and RALCs in media after 3-h in vitro culture with 100 ng/ml LH. Steady-state mRNA levels of steroidogenic enzymes and their activities were measured in freshly isolated cells. Compared to adult Leydig cells (ALCs) isolated from normal 90-day-old rat testes, which primarily produce testosterone (69.73%), RPLCs and RILCs primarily produced androsterone (70.21%) and DIOL (69.79%) respectively. Leydig cells isolated from testes 56 days post-EDS showed equivalent capacity of steroidogenesis to ALCs and primarily produced testosterone (72.90%). RPLCs had cholesterol side-chain cleavage enzyme, 3β-hydroxysteroid dehydrogenase 1 and 17α-hydroxylase but had almost no detectable 17β-hydroxysteroid dehydrogenase 3 and 11β-hydroxysteroid dehydrogenase 1 activities, while RILCs had increased 17β-hydroxysteroid dehydrogenase 3 and 11β-hydroxysteroid dehydrogenase 1 activities. Because RPLCs and RILCs had higher 5α-reductase 1 and 3α-hydroxysteroid dehydrogenase activities they produced mainly 5α-reduced androgens. Real-time PCR confirmed the similar trends for the expressions of these steroidogenic enzymes. In conclusion, the purified RPLCs, RILCs and RALCs are similar to those of their counterparts during rat pubertal development.


Introduction

Testosterone is essential for the maintenance of sperm production and male secondary sexual characteristics in adult males. In mature males, testosterone is primarily produced by testicular Leydig cells. Mature Leydig cells, here referred to as adult Leydig cells (ALCs), have been found to come from stem Leydig cells that are present in the testicular interstitium (Ge et al. 2006). In the rat postnatal development of ALCs can be divided into four stages conceptually: stem, progenitor, immature and adult Leydig cells. Stem Leydig cells are present in the testicular interstitium through life and they are spindle shaped without Leydig cell biomarkers such as LH receptor 3β-hydroxysteroid dehydrogenase 1 (3βHSD1, encoded by Hsd3b1), but contain stem cell biomarkers such as platelet-derived growth factor receptor α, c-kit and nestin (Davidoff et al. 2004). We speculate that stem Leydig cells self-renew to keep the homeostasis of adult population of Leydig cells. At postnatal day 11–14 stem Leydig cells commit to spindle-shaped progenitor Leydig cells (Ariyaratne et al. 2000), which express some androgen biosynthetic enzymes including cytochrome P450 side-chain cleavage enzyme (CYP11A1, encoded by Cyp11a1), 3βHSD1, and 17α-hydroxylase/20-lyase (CYP17A1, encoded by Cyp17a1) without expression of 17β-hydroxysteroid dehydrogenase 3 (17βHSD3, encoded by Hsd17b3) (Ge & Hardy 1998). Progenitor Leydig cells also contain high levels of 5α-reductase 1 (SRD5A1, encoded by Srd5a1) and 3α-hydroxysteroid
dehydrogenase (3αHSD, encoded by Akr1c14) (Ge & Hardy 1998), thus the androgen precursor androstenedione formed by androgen biosynthetic enzymes is further metabolized into androsterone (Ge & Hardy 1998). By postnatal day 28 progenitor Leydig cells develop into round lipid droplets containing immature Leydig cells (Ge & Hardy 2007). Immature Leydig cells begin to express 17βHSD3 but still have higher levels of SRD5A1 and 3αHSD. Therefore, they primarily produce 5α-androstane-17β,3α-diol (DIOL; Ariyaratne et al. 2000). SRD5A1 disappears in Leydig cells when immature Leydig cells differentiate into ALCs, leading to testosterone becoming the primary androgen (Ge & Hardy 1998). Interestingly, a glucocorticoid-metabolizing enzyme, 11β-hydroxysteroid dehydrogenase 1 (11βHSD1, encoded by Hsd11b1), starts its expression in immature Leydig cells of rat testis at postnatal day 28 (Phillips et al. 1989, Neumann et al. 1993, Ge et al. 1997). 11βHSD1 is a biomarker for Leydig cell development in adult population and plays a role in the regulation of testosterone production (Hu et al. 2008).

Postnatal Leydig cell development can be mimicked in a Leydig cell-depleted rat model by ethane dimethanesulfonate (EDS; Teerds 1996). One i.p. injection of 75 mg/kg EDS to a rat can specifically kill all mature Leydig cells in the testicular interstitium (Teerds 1996). Seven days post-EDS, all Leydig cells are killed, and the first morphologically recognizable and 3βHSD1-positive Leydig cells appear at day 14 post-EDS, and these cells are referred to as regenerated progenitor Leydig cells (RPLCs; Bartlett et al. 1986, Teerds et al. 1994, Teerds 1996). RPLCs differentiate into round lipid droplets-containing cells at 28 days post-EDS. These cells are still immature, here referred to as regenerated immature Leydig cells (RILCs). SRD5A1 activity reaches its peak in the RILC stage and decreases dramatically thereafter (Vreeburg et al. 1988, O’Shaughnessy & Murphy 1991). Around 56 days post-EDS Leydig cells are fully mature and produce testosterone, and these cells are referred to as regenerated adult Leydig cells (RALCs). There is little known for their identity of regenerated Leydig cells. In this study, we isolated these cell types from the Leydig cell lineage in the EDS-treated rat testes and compared their androgen types produced, steroidogenic capacity, and enzyme activities.

**Results**

**Leydig cell regeneration post-EDS**

As shown in Figs 1 and 2, 4 days post-EDS, only very few 3βHSD1-positive cells were left (1–5% cells). Seven days post-EDS administration there were no 3βHSD1-positive cells in the testis, indicating that all Leydig cells were killed. 11βHSD1 was also undetectable 7 and 14 days post-EDS, indicating that 11βHSD1 is only expressed in immature Leydig cells and ALCs. However, 3βHSD1- and 11βHSD1-positive cells were not proportionally regenerated. 3βHSD1-positive cells were 15.7 and 34.5% of the pre-treatment level at days 21 and 28 post-EDS respectively (Fig. 2A), while 11βHSD1-positive cells were only 4.5 and 35.1% of the pre-treatment level (Fig. 2B). These data indicate that 21 days post-EDS, cells in the Leydig cell lineage were mostly RPLCs as most 3βHSD1-positive cells regenerated at this time were not stained with 11βHSD1, a biomarker for immature Leydig cells during puberty (Phillips et al. 1989).

**Androgens produced by Leydig cells**

RPLCs, RILCs and RALCs were isolated from testes 21, 28 and 56 days post-EDS respectively and compared to ALCs isolated from 90-day-old normal rat testes. The isolation of each cell type was repeated four times. RPLCs were identified by the positive 3βHSD1 and SRD5A1 staining but not the negative 11βHSD1 staining (Supplementary Figure 1, see section on supplementary data given at the end of this article). RILCs were identified by the positive 3βHSD1 and 11βHSD1 staining but not the negative CYP2A1 staining (Supplementary Figure 1). RALCs and ALCs were identified by the positive CYP2A1 staining but not the negative staining of SRD5A1 (Supplementary Figure 1). All the cell types were confirmed, being progenitor, immature and adult after regeneration. The total androgen profiles showed that, after the stimulation of LH, ALCs, RPLCs, RILCs and RALCs produced 470.1 ± 38.5, 124.1 ± 9.9, 243.5 ± 4.64 and 485.7 ± 32.7 ng androgen/10⁶ cells respectively (Fig. 3). The androgen-producing capacity of RALCs was comparable to that of ALCs but twofold higher than that of RILCs and fourfold higher than that of RPLCs. LH-stimulated androgen end products produced by regenerated Leydig cells were different. Androsterone was the primary androgen secreted by RPLCs because this steroid constituted 70.21% of the total androgens. Parallel measurements showed that DIOL was the primary androgen for RILCs (69.79% of total androgens), and testosterone was the primary androgen for RALCs (72.90%, Fig. 3), which was comparable to that of ALCs (69.73%).

The synthesis of testosterone and DIOL requires 17βHSD3 enzyme, and the low release rates for these steroids from RPLCs suggest that the amount of 17βHSD3 is low in this cell type. Androsterone and DIOL require the activities of SRD5A1 and 3αHSD, and the high release rates of these steroids by RPLCs and RILCs indicate that androgen-metabolizing enzymes are most highly expressed in Leydig cells before the completion of regeneration.

**Steroidogenic enzyme activities**

The underlying basis for the different profiles of androgen release from these distinct stages of Leydig cell

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Regeneration was examined further by measuring testosterone biosynthetic and metabolizing enzyme activities in purified cells. 11βHSD1 was also measured as shown in distinctive development during Leydig cell regeneration. Steroidogenic enzyme activities were measured in intact Leydig cells because homogenization can change the relative rates of oxidative and reductive activities in most hydroxysteroid dehydrogenases. The first step of testosterone biosynthesis is the conversion of cholesterol to pregnenolone, which is catalyzed by

Figure 1 Immunohistochemical staining of 3βHSD1 and 11βHSD1 in rat testes after EDS treatment. 11βHSD: (A, C, E, G, I) and 3βHSD1: (B, D, F, H, J). Sections from testes 0 (control, A and B), 4 (C and D), 14 (E and F), 21 (G and H) and 56 (I and J) days post-EDS were shown. The white arrow points to 3βHSD1-positive Leydig cells, and the black arrow points to 11βHSD1-positive Leydig cells. Bar = 50 μm.
CYP11A1. The conversion of D5-3β-hydroxysteroids to D4-3-ketosteroids is catalyzed by 3βHSD1. CYP17A1 catalyzes both the 17α-hydroxylase and the C17-20 lyase reactions to produce androstenedione. The final step of testosterone biosynthesis is catalyzed by 3βHSD1 and testosterone can be metabolized by SRD5A1 and 3αHSD into androsterone and DIOL respectively. As shown in Fig. 4 the level of CYP11A1 was low in RPLCs and increased during Leydig cell regeneration. 3βHSD1 and CYP17A1 activities in RPLCs were one third of those in ALCs, and the activities of these enzymes in RILCs also reached half of those in ALCs. RPLCs had negligible 17βHSD3 activity. Androstenedione and testosterone formed in this cell type were rapidly metabolized to another androgen end product, DIOL, because the activities of both SRD5A1 and 3αHSD were high. Although most testosterone biosynthetic enzyme (CYP11A1, 3βHSD1 and CYP17A1) activities nearly attained half the adult values and 17βHSD3 activity dramatically increased in RILCs, testosterone formed in this cell type was rapidly metabolized to another androgen end product, DIOL, because of the high expression of SRD5A1 and 3αHSD activities. RALCs contain significantly reduced 3αHSD activity. However, barely detectable SRD5A1 activity in this cell type limits the catabolism of testosterone to androstenedione and the C17-20 lyase reactions to produce androstenedione. The final step of testosterone biosynthesis is catalyzed by 3βHSD1 and testosterone can be metabolized by SRD5A1 and 3αHSD into androsterone and DIOL respectively. As shown in Fig. 4 the level of CYP11A1 was low in RPLCs and increased during Leydig cell regeneration. 3βHSD1 and CYP17A1 activities in RPLCs were one third of those in ALCs, and the activities of these enzymes in RILCs also reached half of those in ALCs. 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**Steady-state mRNA levels of steroidogenic enzymes**

Differential changes in testosterone biosynthetic and metabolizing enzyme activities could result from the variation in the steady-state levels of mRNAs that encode these enzymes. Therefore, the steady-state mRNA levels of Leydig cell steroidogenic enzymes were evaluated (Fig. 5) and were found to have similar trends to their respective enzyme activities.

**Discussion**

In this study we successfully purified RPLCs, RILCs and RALCs from the EDS-treated rat testes after showing that they were positively stained by 3βHSD. Their identities were further distinguished by the immunofluorescent staining of their specific biomarkers. In this regard RPLCs expressed SRD5A1 but not 11βHSD1, RILCs expressed 11βHSD1 but not CYP2A1, and RALCs expressed CYP2A1 but not SRD5A1 (Supplementary Figure 1). It is apparent that the restoration of capacity for testosterone production is achieved not only by increases in testosterone biosynthetic enzymes (CYP11A1, 3βHSD1, CYP17A1 and 17βHSD3) but also by concurrent declines in androgen-metabolizing enzymes (SRD5A1 and 3αHSD). Similar to the situation during puberty 5α-reduced androgens are high during Leydig cell regeneration.

Steroidogenic capacity is defined as the ability of a cell to produce steroids, whereas the capacity for testosterone production reflects the balance of both testosterone biosynthetic and metabolizing enzyme activities. There is little difference when compared to testicular or circulating androgens, purified RPLCs and RILCs produced different 5α-reduced androgens with androstenedione primarily in RPLCs and DIOL in RILCs. Formation of DIOL requires 17βHSD3 activities. Direct measurements of enzyme activities in purified cells explained the changes in end products released during Leydig cell regeneration. In RPLCs several androgen biosynthetic enzymes including CYP11A1 and 3βHSD1 attained one third to fifth of the mature values, with the exception of 17βHSD3 that was very low in this cell type, resulting in negligible conversion of androstenedione to testosterone. However, RPLCs readily converted androstenedione to 5α-androstanedione by SRD5A1 and ultimately to the androgen end product, androsterone, through 3αHSD, because the activities of both SRD5A1 and 3αHSD were high. Although most testosterone biosynthetic enzyme (CYP11A1, 3βHSD1 and CYP17A1) activities nearly attained half the adult values and 17βHSD3 activity dramatically increased in RILCs, testosterone formed in this cell type was rapidly metabolized to another androgen end product, DIOL, because of the high expression of SRD5A1 and 3αHSD activities. RALCs contain significantly reduced 3αHSD activity. However, barely detectable SRD5A1 activity in this cell type limits the catabolism of testosterone to

![Graph showing cell numbers (% relative to control without EDS) over time](image)

**Figure 2** Cell numbers of (A) 3βHSD-positive cells and (B) 11βHSD1-positive cells. Mean ± s.e.m., n=6; *** indicates significant difference compared to control at P<0.001.
5α-reduced androgen, making testosterone the primary androgen end product.

To our surprise, 17βHSD3 activity and its mRNA had the highest levels in RILCs, which was different from those in the immature Leydig cells purified from 35-day-old rat testis (Ge & Hardy 1998), in which their levels were still lower than those of ALCs isolated from 90-day-old rats. It seems that the regeneration process after EDS is much faster than the normal developmental process during puberty, as indicated by another biomarker 11βHSD1, an enzyme involved in the glucocorticoid metabolism, which reached adult levels (Fig. 4G) in the RILCs. Normally, 11βHSD1 activity and mRNA level in immature Leydig cells isolated from 35-day-old rats have only about 50% of the adult values (Ge et al. 1997). 11βHSD1 has been shown to be expressed in the Leydig cells at 28 days postpartum and beyond (Phillips et al. 1989). Similarly, 11βHSD1-positive cells did not appear until 28 days post-EDS, indicating that 11βHSD1 is a good biomarker for immature and ALCs.

There have been many studies earlier of LC regeneration after EDS treatment (see review by Teerds et al. (2007)). However, these studies were performed in whole testis. The novelty of the present findings is that these regenerated Leydig cells were purified and studied in pure cells. The results from whole testis or pure cells could be different. For example, steroidogenic enzyme activities have been measured in the testis post-EDS administration (Myers & Abney 1991, O’Shaughnessy & Murphy 1991). However, these studies reported that DIOL was the primary androgen secreted from the testes on day 21 postpartum. Given the negligible DIOL production that was observed in RPLCs, the predominance of this steroid in this period indicates that other 17βHSD enzymes may also be involved in the reduction of androstenedione into testosterone in peripheral tissues. The present data indicate that the regeneration of steroidogenic enzymes results from sequential, rather than simultaneous, induction of steroidogenic enzyme gene transcription. The steady-state mRNA levels of

**Figure 3** Total androgen levels and primary androgens produced by adult (ALC), regenerated progenitor (RPLC), immature (RILC) and adult (RALC) Leydig cells. ALCs, RPLCs, RILCs and RALCs were isolated from 90-day-old testes or the testes 21, 28 and 56 days post-EDS respectively. The total androgen levels are summed by androsterone (AO), 5α-androstane-17β,3α-diol (DIOL), androstenedione (D4) and testosterone (T). A, total androgen levels; B, C, D and E, ALC, RPLC, RILC and RALC respectively. Mean ± S.E.M., n = 4 replications. Identical letters indicate no significant difference between groups at P<0.05.
steroidogenic enzymes were measured in Leydig cells to evaluate the relationship between mRNA levels and enzyme activity. We demonstrated that mRNA levels for testosterone biosynthetic enzymes were significantly lower in RPLCs than in RILCs and RALCs. Of the testosterone biosynthetic enzymes, Hsd17b3 was the lowest in RPLCs, consistent with almost undetectable enzyme activity data.

The level of SRD5A1 was the highest in RILCs, followed by RPLCs and RALCs, confirming the transitory expression of this enzyme activity during Leydig cell regeneration. The levels of 3αHSD and its encoding mRNA (Akr1c14) were the highest in RILCs, which is slightly different from our previous report for its expression levels in the Leydig cell lineage during normal development, among which its expression is the highest in progenitor Leydig cells (Ge & Hardy 1998). The reason for this discrepancy is still unclear.

It is true that using whole testis measurement of Leydig cell regeneration after EDS showed a similar trend of steroidogenesis recovery (O’Shaughnessy & Murphy 1991). However, the isolation of Leydig cells and their precursor cells provided more precise information about their androgen production type. The regeneration sequence in the Leydig cell lineage during normal development, among which its expression is the highest in progenitor Leydig cells (Ge & Hardy 1998). The reason for this discrepancy is still unclear.

In conclusion, the present data demonstrate that androgen biosynthetic and metabolizing enzymes are separately modulated in the cell types in the Leydig cell lineage during regeneration post-EDS. This difference has significant consequences for the overall rate of testosterone production.

Materials and Methods

Chemicals

[26,27-3H]25-Hydroxycholesterol, [7-N-3H]pregnenolone, [1b,2b-N-3H]androst-4-ene-3,17-dione, [1,2,6,7-N-3H]testosterone, [1,2-N-3H]dihydrotestosterone, 5α-[9,11-N-3H]androstane-17β,3α-diol (3α-DIOL), [9,11-N-3H]androstenedione, and [1,2,6,7-3H] corticosterone were purchased from DuPont-New England Nuclear (Boston, MA, USA). [1,2,6,7-N-3H]Progesterone was purchased from Amersham International. 3H-11-Dehydrocorticosterone was prepared from labeled 3H-corticosterone as described previously (Lakshmi & Monder 1985). Nonradioactive steroids were purchased from Sigma Chemical Co. or Steraloids (Wilton, NH, USA). 4-Methyl-aza-3-oxo-5α-pregnan-20(S)-carboxylate, an inhibitor of SRD5A1, was provided by Merck. The antibodies for DIOL and androsterone RIA were provided by Dr D T Armstrong.
of the Rockefeller University.

Animals

Adult (90-day-old) male Sprague–Dawley rats were purchased from Charles River Laboratories (Wilmington, MA, USA). A total of 72 male rats received i.p. injections of EDS at a dose of 75 mg/kg. Four, 7, 14, 21, 28 and 56 days post-EDS, the animals were killed by asphyxiation with CO2, and testes and blood samples were collected. Some testes from 21, 28 and 56 days post-EDS were used to isolate RPLCs, RILCs and RALCs respectively. An additional 18 normal 90-day-old rats were killed for ALC isolation. The animal protocol was approved by the institutional animal care and use committee of the Rockefeller University.

Histological analysis

Animals were anesthetized by i.p. injection of sodium pentobarbital (25 mg/100 g body weight; Abbott Laboratories). One testis was removed. Then under deep anesthesia, rats were fixed by whole-body perfusion through the left ventricle of the heart with Bouin solution (Wang & Hardy 2004). Testes were then removed and stored in the fixative overnight. After dehydration in ethanol and xylene testes were embedded in paraffin for immunological analysis. Five testis samples from each group were arrayed in a tissue array rack. Leydig cells were identified through immune-positive staining for the biomarker enzyme 3βHSD1. In brief, 6 μm-thick transverse sections were prepared and mounted on glass slides (Cat. No. 12-550-15; Fisher Scientific Company, Hampton, NH, USA).

Cell counts and computer-assisted image analysis

Twenty randomly selected fields in each of three nonadjacent sections per testis were captured using a Nikon Eclipse E800 microscope (Nikon, Inc., Melville, NY, USA) equipped with a 40X objective and a SPOT RT digital camera (model 2.3.0.; Diagnostic Instruments, Inc., Michigan City, IN, USA) interfaced to a computer. The images that were displayed on a computer interface were analyzed using the Image-Pro Plus analysis software (Image-Pro Plus; Media Cybernetics, Silver Spring, MD, USA). More than 1000 cells of each type were counted in each testis.
The stereological estimate of Leydig cells was performed according to a previously described method (Akingbemi et al. 2004).

Isolation of Leydig cells

A complete description of the procedure for isolation of ALCs has been published (Salva et al. 2001). This procedure was also adopted for the isolation of RALCs. Leydig cell isolation was performed using testes from two rats. In brief, testes were removed, perfused via the testicular artery with buffered modified Eagle's medium containing 1 mg/ml collagenase, decapsulated, and dispersed in a shaking water bath at 34 °C with 0.25 mg/ml collagenase. Seminiferous tubules were separated from interstitial cells by adding a modified Eagle's medium containing 1% BSA and washed twice. The seminiferous tubules were allowed to settle for 1 min and supernatants were collected by aspiration with a pipette. Cells were then separated by Percoll density gradient centrifugation as described previously (Klinefelter et al. 1987). In brief, the Leydig cell fraction obtained after BSA gradient centrifugation was resuspended in 14 ml Mg²⁺-free HBSS buffered with 0.35 g/l sodium bicarbonate and containing 0.25% BSA and 25 mg/l STI, pH 7.4. The suspension was thoroughly mixed with 21 ml isosmotic Percoll. A similar 60% Percoll solution was prepared that contained only 1.062 and 1.075 g/ml density marker beads and no cells. The two Percoll solutions were centrifuged in a fixed angle rotor (JA-20, Beckman, Schaumberg, IL, USA) at 20 000 g for 60 min at 4 °C. Cell types became partitioned due to the various buoyant densities while a continuous, linear density gradient was generated. After centrifugation, the gradient was divided into a lighter than 1.070 g/ml and heavier fraction. The RPLC fraction was collected between densities of 1.070 and 1.088 g/ml as described before (Shan & Hardy 1992). Enrichment of the three cell types in the Leydig cell lineage was also performed based on immunohistochemical staining of SRD5A1 and CYP2A1 because these cells did not express SRD5A1 (Ge & Hardy 1998) but expressed CYP2A1 (Hu et al. 2010). RPLCs expressed SRD5A1 (Ge & Hardy 1998) but also 11βHSD1 (Ge et al. 1997). However, both RPLCs and RILCs did not express CYP2A1 (Hu et al. 2010).

Immunofluorescent staining of cells in the Leydig cell lineage

Immunofluorescent staining was performed using Leydig cell lineage cells that were grown on microscope cover glasses. Cells were fixed with 4% formaldehyde, washed with PBS and permeabilized with 0.1% (wt/vol) Saponin detergent in PBS – 10% normal serum. Nonspecific binding was blocked by incubation with 10% normal serum before addition of the primary antibody. Cells were incubated with polyclonal rabbit anti-11βHSD1 (diluted 1:1000) or anti-SRD5A1 (provided by Dr Robaire B, Department of Pharmacology and Therapeutics, McGill University, Montréal, Québec, Canada, diluted 1:1000) or CYP2A1 (in house) antibodies for 1 h at room temperature. Cells were then incubated with Alex488-conjugated secondary antibody for 1 h. Afterwards the cells were counterstained with 4',6'-diamino-2-phenylindole and mounted. The slides were examined under a Nikon fluorescence microscope with a filter suitable for selectively detecting the fluorescence of FITC (green).

Androgen production

Isolated RPLCs, RILCs and RALCs from EDS-treated testes and ALCs from normal 90-day-old rat testes were incubated at a concentration of 0.1–0.25 × 10⁶ cells/ml in Leydig cell culture medium consisting of DMEM and Ham's F-12 medium (D2906, Sigma Chemical Co.) buffered with 15 mM HEPES and 14 mM NaHCO₃ and containing 1% BSA for 3 h at 34 °C in a shaking water bath. Incubations of triplicate samples were conducted in medium plus a maximally stimulating dose of ovine LH (100 ng/ml). At the end of 3 h the samples were centrifuged at 500 g. Supernatants were extracted with 2 ml ethyl acetate twice, and the organic layer was dried under nitrogen gas. Steroids in the samples were fractionated using Sephadex LH-20 (Pharmacia Biotech) column chromatography as described previously (Ge & Hardy 1998). The elution system was chloroform–butane–ethanol (50:50:1, by vol) saturated with distilled water. Clear separation of androstenedione, androsterone, testosterone and DIOL in this system was achieved via thin layer chromatography as described previously (Ge & Hardy 1998). The recovery rates following extraction and column separation were used to correct the final concentration measured by RIA. RIA of androstenedione, androsterone, testosterone and DIOL were performed as described previously (Ge & Hardy 1998). The results of four separate experiments were averaged for statistical analysis.

Enzyme assay

With the exception of CYP11A1, steroidogenic enzyme activities were measured by incubation of purified Leydig cells with radiolabeled substrates and separation of products by thin layer chromatography as described previously (Ge & Hardy 1998). The substrate concentration used for each enzyme was maximal to ensure that the concentration of...
substrate was not rate limiting. Control samples of culture medium alone were run in parallel with each enzyme assay. Briefly, reaction mixture (0.5 ml) was prepared in Leydig cell medium that contained 1 μM substrate (1 μCi) in medium. As testosterone undergoes 5α-reduction in RPLCs and RILCs, 4-methyl-aza-3-oxo-5α-pregn-20(S)-carboxylate (2 μM) was used to inhibit SRD5A1 when CYP17A1 or 17βHSD3 was measured. The reaction mixture was maintained at pH 7.2. Reactions were initiated by adding to the reaction medium an aliquot of 0.1–0.2 μCi 25-hydroxycholesterol (1 μM) and at the end of incubation, 0.5 ml NaOH (0.5 M) was added. The reaction mixture was extracted twice with 2 ml chloroform and mixed with neutral alumina to remove non-metabolized substrate, and the organic layer was dried under nitrogen. The radioactivity was measured using a radiometric scanner (System 200/AC3000, Bioscan, Washington, DC, USA). The activity of 3βHSD1 was determined by measuring conversion of 3H-pregnenolone to 3βH-testosterone. The activity of CYP17A1 was determined by measuring conversion of 3H-progesterone to 3H-androstenedione and 3H-testosterone. The activity of 17βHSD3 was determined by measuring the conversion of 3H-androstenedione to 3H-testosterone. The activity of SRD5A1 was determined by measuring the conversion of 3H-testosterone to 3H-dihydrotestosterone and 3H-DIOL. Activity of CYP11A1 was determined by measuring the conversion of 3αβH-pregnenolone to 3αβH-testosterone and 3αβH-DIOL. The activity of 3αβHSD was determined by measuring the conversion of 3αβH-DIOL to 3αβH-DIOL. The measurement of 11βHSD1 activity was performed by measuring the conversion of 3H-11dehydrocorticosterone to 3H-hydrocorticosterone according to the previously published method (Ge et al. 2005). The steroids were separated on thin layer chromatographic plates in chloroform–methanol (97:3, vol/vol) for 3βHSD1, 17βHSD3, and SRD5A1 assays; chloroform–methanol (90:10, vol/vol) for 11βHSD1 assay; chloroform–ether (7:1, vol/vol) for CYP17A1 assay; and diethyl ether–acetone (98:2, vol/vol) for the 3αβHSD assay.

Activity of CYP11A1 was determined by measuring the conversion of side-chain-labeled [26,27-3H]25-hydroxycholesterol to radioactive 4-hydroxy-4-methyl-pentanoic acid as described previously (Ge & Hardy 1998). Leydig cells were incubated in a total volume of 0.5 ml medium containing 1 μCi [26,27-3H]25-hydroxycholesterol (1 μM 25-hydroxycholesterol). Incubations were performed for 30 min at 34°C, and at the end of incubation, 0.5 ml NaOH (0.5 M) was added. The mixture was extracted twice with 2 ml chloroform and mixed with neutral alumina to remove non-metabolized substrate, and an aliquot was removed for measurement by liquid scintillation counting.

**Real-time PCR (qPCR)**

Levels of steroidogenic enzyme mRNAs were measured by qPCR using the SYBR method following RT of isolated RNA. Briefly, first-strand synthesis and qPCR were performed as described previously (Lin et al. 2009), and the first-strand cDNAs were used as templates for PCR. Quantitative PCR was carried out in a 25-μl volume using a 96-well plate format using the SYBR Green PCR Core Reagents purchased from Applied Biosystems. Primer titration was performed and the concentration of 300 nM was selected. Fluorescence was detected using an ABI 7700 system (PE Applied Biosystems). Each sample was run in duplicate, in parallel with no-template controls. The relative mRNA levels of targeted genes were normalized to ribosomal protein S16 (Rps16, as an internal control) using the standard curve method. All primers in this study were designed by Primer 3 software (Whitehead Institute for Biomedical Research, Cambridge, MA, USA). Forward and reverse primers were placed in different exons to minimize the effects of possible DNA contamination. These genes are CYP11A1 (Cyp11a1), CYP17A1 (Cyp17a1), 3βHSD1 (Hsd3b1), 17βHSD3 (Hsd17b3), SRD5A1 (Srd5a1), 3αHSD (Akr1c14), and 11βHSD1 (Hsd11b1). The primers used were described previously (Ge et al. 2005, Lin et al. 2008).

**Statistical analysis**

The data were analyzed by one-way ANOVA followed by ad hoc Turkey’s multiple comparison test using GraphPad (Version 5, GraphPad Software, Inc., San Diego, CA, USA). All data were expressed as means ± S.E.M. Differences were regarded as significant at P<0.05.

**Supplementary data**

This is linked to the online version of the paper at http://dx.doi.org/10.1530/REP-12-0465.

**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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