



In vitro spermatogenesis – optimal culture conditions for testicular cell survival, germ cell differentiation, and steroidogenesis in rats

Ahmed Reda, Mi Hou, Luise Landreh, Kristín Rós Kjartansdóttir, Konstantin Svechnikov, Olle Söder and Jan-Bernd Stukenborg*

Pediatric Endocrinology Unit Q2:08, Department of Women's and Children's Health, Karolinska Institutet and University Hospital, Stockholm, Sweden

Edited by:

Silvia Fasano, Second University of Naples, Italy

Reviewed by:

Rosaria Meccariello, University of Naples Parthenope, Italy
Rosanna Chianese, Second University of Naples, Italy

*Correspondence:

Jan-Bernd Stukenborg, Pediatric Endocrinology Unit Q2:08, Department of Women's and Children's Health, Karolinska Institutet and University Hospital, Stockholm SE-17176, Sweden
e-mail: jan-bernd.stukenborg@ki.se

Although three-dimensional testicular cell cultures have been demonstrated to mimic the organization of the testis *in vivo* and support spermatogenesis, the optimal culture conditions and requirements remain unknown. Therefore, utilizing an established three-dimensional cell culture system that promotes differentiation of pre-meiotic murine male germ cells as far as elongated spermatids, the present study was designed to test the influence of different culture media on germ cell differentiation, Leydig cell functionality, and overall cell survival. Single-cell suspensions prepared from 7-day-old rat testes and containing all the different types of testicular cells were cultured for as long as 31 days, with or without stimulation by gonadotropins. Leydig cell functionality was assessed on the basis of testosterone production and the expression of steroidogenic genes. Gonadotropins promoted overall cell survival regardless of the culture medium employed. Of the various media examined, the most pronounced expression of *Star* and *Tspo*, genes related to steroidogenesis, as well as the greatest production of testosterone was attained with Dulbecco's modified eagle medium + glutamine. Although direct promotion of germ cell maturation by the cell culture medium could not be observed, morphological evaluation in combination with immunohistochemical staining revealed unfavorable organization of tubules formed *de novo* in the three-dimensional culture, allowing differentiation to the stage of pachytene spermatocytes. Further differentiation could not be observed, probably due to migration of germ cells out of the cell colonies and the consequent lack of support from Sertoli cells. In conclusion, the observations reported here show that in three-dimensional cultures, containing all types of rat testicular cells, the nature of the medium *per se* exerts a direct influence on the functionality of the rat Leydig cells, but not on germ cell differentiation, due to the lack of proper organization of the Sertoli cells.

Keywords: testis, spermatogenesis, cell culture, culture medium, Leydig cells, testosterone, stem cell niche

INTRODUCTION

Male infertility, a common disorder, is associated with a wide spectrum of spermatogenic failures, an increasing number of which are iatrogenic effects of clinical treatment (1). Treatment of children with cancer, including radiotherapy and high-dose chemotherapy, can severely damage the immature gonads and lead to infertility later in life (2). Since long-term survival of pre-pubertal patients with cancer has risen by as much as 80% during recent decades (3–5), more infertile patients can be expected in the future.

One approach to developing ways to rescue the fertility of these and other infertile patients is *in vitro* characterization of spermatogenesis, utilizing systems that mimic the natural situation as closely as possible and provide functional testicular cells for analyses (6).

In three-dimensional cultures of murine Sertoli, Leydig, peritubular, and germ cells stimulated with gonadotropins, pre-meiotic germ cells differentiate into postmeiotic spermatids, but with very low efficiency (6–8). Clearly, the optimal conditions for such cultures remain to be elucidated. In three-dimensional cultures containing all murine testicular cells, testosterone production

by the Leydig cells was enhanced in response to stimulation by hCG for as long as 16 days (6). It remains to be determined whether similar Leydig cell function can be achieved with testicular cells from other species, including humans, under the same conditions.

To date, only traditional media, i.e., Dulbecco's modified eagle medium (DMEM) medium, F12, and minimal essential medium (MEM), have been employed for culturing testicular cells (9, 10). Even though it is well established that gonadotropins play a pivotal role in spermatogenesis and that functioning Leydig and other somatic cells are important for the spermatogenic process (7, 11–13), optimal culture conditions for the different types of testicular cells, and for appropriate paracrine interactions between these cells have not yet been determined.

Accordingly, in the present investigation we attempted to create an optimal culture system, of endocrine and paracrine stimulation focusing on the nutritional requirements for appropriate development of three-dimensional cultures of rat testicular cells. More specifically, we assessed germ cell differentiation, tubule formation, Leydig cell functionality, and cell survival in cultures hosting

all of the testicular cells, i.e., Sertoli, Leydig, peritubular, and germ cells.

MATERIALS AND METHODS

ANIMALS

Male Sprague-Dawley rats at 7 days of *post-partum* (*dpp*) age were purchased from Charles River (Sulzfeld, Germany) and transported to Karolinska Institutet (Stockholm, Sweden) together with their mothers. Each experiment involved testicular material from several different litters of these pups. Their use and handling was pre-approved by the ethics committee for experimental laboratory animals at Karolinska Institutet (N489/11).

TISSUE AND CELL PREPARATION

The rat pups were sacrificed by decapitation and their testes immediately placed in DMEM containing glutamine (P/N 41966, Gibco, CA, USA) and supplemented with 1% penicillin/streptomycin (pen/strep; P/N 15070, Gibco). Single-cell suspensions were obtained by the three-step enzymatic digestion described previously (14). In brief, the first digestion was performed with Collagenase/Dispase (P/N 269638, Roche, Switzerland, Basel; final concentration: 0.04/0.32 U/ml) in DMEM for 10 min at 32°C with shaking at 120 rpm, followed by centrifugation at 100 × *g* for 2 min. The resulting supernatant was centrifuged again at 200 × *g* for 8 min and the cell pellet thus obtained re-suspended in DMEM and stored on ice.

The second digestion was accomplished with Collagenase/Dispase + DNase (P/N 104159, Roche; final concentrations: 0.04/0.32 and 48 U/ml, respectively) in DMEM for 15 min at 32°C with shaking at 120 rpm, followed by centrifugation at 100 × *g* for 2 min. Centrifugation of the supernatant for 8 min at 200 × *g* provided the second cell pellet, which was also re-suspended in DMEM and stored on ice.

The third digestion of remaining tissue involved Collagenase/Dispase + DNase + Collagenase IV (P/N C-1889, Sigma-Aldrich, St. Louis, USA; final concentrations: 0.04/0.32, 48 and 50 U/ml, respectively) in DMEM for 20 min at 32°C with shaking at 120 rpm, followed by collection and re-suspension of the third cell pellet in the same manner as above. All three cell suspensions were pooled, centrifuged at 200 × *g* for 8 min, re-suspended in 1 ml DMEM, counted in a Bürker chamber, and examined for viability by trypan blue staining (P/N 15250061, Gibco; 1:20 dilution).

CELL CULTURES

As stated in **Table 1**, the different media tested here were DMEM + glutamine or without glutamine (DMEM – glutamine; P/N 21969, Gibco), DMEM + Glutamax (P/N 31966, Gibco), DMEM/F12 (P/N 21331, Gibco), F12 (P/N 21765, Gibco), and MEM (P/N 21430, Gibco). Pre-pubertal rat testicular cells were cultured in an agarose-medium matrix in accordance with previous reports (7). In brief, this matrix was prepared by mixing autoclaved 0.7% SeaKem® LE agarose (P/N 50004, Lonza, Basel, Switzerland) or 0.7% LMP agarose (P/N 15517022, Invitrogen, CA, USA) with the relevant culture medium (supplemented with 1% pen/strep) at a ratio of 1:1 to give a final agarose concentration of 0.35% agarose.

Table 1 | Schematic illustration of the experimental conditions employed to characterize the effects of the culture medium and gonadotropins on three-dimensional cultures of testicular cells.

Medium	Supplement			
	AA (%)	NEAA (%)	rFSH (IU/l)	hCG (IU/l)
DMEM (high glucose, +pyruvate, +l-glutamine; P/N 41966, Gibco)	–	–	5.0	5.0
DMEM (high glucose, +pyruvate, –l-glutamine; P/N 21969, Gibco)	–	–	5.0	5.0
DMEM (high glucose, +pyruvate, +Glutamax; P/N 31966, Gibco)	–	–	5.0	5.0
F12 (+l-glutamine; P/N 21765, Gibco)	–	–	5.0	5.0
	4.0	–	5.0	5.0
	–	4.0	5.0	5.0
	4.0	4.0	5.0	5.0
	–	–	–	–
DMEM/F12 (without l-glutamine; P/N 21331, Gibco)	–	–	5.0	5.0
MEM (without l-glutamine; P/N 21430, Gibco)	–	–	5.0	5.0
	–	–	–	–

AA, amino acids; NEAA, non-essential amino acids; rFSH, recombinant follicle-stimulating hormone; hCG, human chorionic gonadotropin; IU/l, international units per liter; M, molar mass (kg/mol); DMEM, Dulbecco modified Eagle's medium; MEM, minimal essential medium; – = none.

These cultures were exposed to recombinant follicle-stimulating hormone [rFSH; P/N Gonal F 75 IE, Merck, Frankfurt, Germany; final concentration: 5 IU/l (international units per liter)] and human chorionic gonadotropin (hCG; P/N Pregnyl 5000 IE, Merck Sharpe and Dohme, NJ, USA; final concentration: 5 IU/l) as also described in **Table 1**. The influence of amino acids on testosterone production were evaluated by adding essential amino acids (AA; P/N 11130-036, Gibco) or non-essential amino acids (NEAA; P/N 11140-035, Gibco) separately to F12 medium at a final concentration of 4%, similar to their concentrations in DMEM.

The single-cell suspensions (1.0×10^6 cells/ml) were inoculated into the agarose-medium matrix before it solidified. To study cell migration, individual cell colonies, containing 50–100 cells each, were aspirated into a 22S-gage Hamilton syringe (P/N 80665/00, Hamilton Bonaduz AG, Bonaduz, Switzerland), placed separately onto six-well culture dishes (Gibco) containing DMEM (a high concentration of glucose + pyruvate, + L-glutamine; P/N 41966, Gibco) and cultured for as long as 5 days without changing the medium. All cell cultures were maintained at 35°C under 5% CO₂ and performed in triplicates.

IMMUNOHISTOCHEMICAL, IMMUNOFLUORESCENT, AND MORPHOLOGICAL ANALYSES

Testicular tissue and cell cultures were fixed in 4% paraformaldehyde (PFA; P/N15812-7, Sigma-Aldrich) overnight at 4°C, followed by serial dehydration in 30, 50, and 70% aqueous ethanol (24 h at each concentration) at room temperature (RT). Thereafter, the samples were placed for 6 h each in 80, 96, and 99.6% ethanol at RT, followed by soaking in 100% butyl acetate for 6 h at RT (P/N 45860, Sigma-Aldrich). Subsequently, these samples were embedded in paraffin (Paraplast X-TRA®; P/N P3808, Sigma-Aldrich) at 61°C overnight in standard fashion; cut into 5–20 μm slices using a Biocut sectioning machine (Reichert-Jung, NY, USA) and then placed on microscope slides (P/N10143352, Superfrost Plus, Thermo Scientific, MA, USA).

For immunohistochemical (IHC) and immunofluorescent (IF) staining, these samples were next de-paraffinized with xylene (P/N 02080, HistoLab, Gothenburg, Sweden) for 10 min and then serially rehydrated with 99.6, 96, and 70% aqueous ethanol, each step being performed twice for 5 min. After washing twice with phosphate-buffered saline (PBS, pH 7.4; P/N 14190-094, Gibco), antigen retrieval was achieved either by incubation with 0.1% sodium citrate (P/N S4641, Sigma-Aldrich) and 0.1% Triton X-100 (P/N 11869, Merck) in PBS for 8 min at RT or by heating for 15 min in 0.1 M sodium citrate buffer (P/N S4641, Sigma-Aldrich; pH 6) in a microwave oven at 600 W. Blocking was performed for 20 min at RT with 5% goat serum (P/N S-1000, VECTOR, CA, USA) or 5% donkey serum (P/N 017-000-121, Jackson ImmunoResearch, West Grove, PA, USA), depending on the secondary antibody employed, in 0.1% BSA (Bovine serum albumin; P/N A4503, Sigma-Aldrich) in PBS.

Rabbit polyclonal anti-Ddx4 antibody (also known as Vasa; P/N ab13840, Abcam, Cambridge, UK, 1:200 dilution, final concentration 5 μg/ml) in PBS containing 0.1% BSA was used for IHC staining, with non-specific rabbit IgGs (P/N ab27478, Abcam, final concentration 5 μg/ml and P/N sc-2027, Santa Cruz, CA, USA, final concentration 5 μg/ml) as negative controls. Polyclonal rabbit anti-Ap-2γ (Ap-2γ; P/N sc-8977, Santa Cruz, 1:100 dilution, final concentration 2 μg/ml in PBS containing 0.1% BSA) was utilized for immunofluorescence staining, again with rabbit IgGs (P/N sc-2027, Santa Cruz, final concentration 2 μg/ml) as negative controls.

After incubation with the primary antibodies or control IgGs at 4°C overnight and three subsequent washes at RT with PBS, samples were stained immunohistochemically with biotinylated goat anti-rabbit IgG secondary antibodies (P/N ab64256, Abcam, final concentration 5 μg/ml) at RT for 2 h; then, washed three times with PBS, incubated with ABC reagents (P/N PK-6100, VECTOR); and developed with DAB (Diaminobenzidine; SK-4100, VECTOR). These slides were counterstained with hematoxylin (Mayer's Hemalaun solution; P/N 1092491000, Merck), serially dehydrated with increasing aqueous ethanol solutions and then 100% xylene, and mounted with Entellan® new (P/N 1079610100, Merck). For IF staining, samples were incubated with a Cy³-conjugated donkey anti-rabbit IgG secondary antibody (P/N 711-166-152, Jackson ImmunoResearch, West Grove, PA, USA, 1:600 dilution, final concentration 2.5 μg/ml) at RT for 1 h and the slides

then counterstained and mounted with VECTASHIELD mounting medium containing DAPI (P/N H-1500, VECTOR).

For IF double-staining, paraffin-embedded samples on slides were first de-paraffinized with xylene for 10 min and then gradually rehydrated with 99.6, 96, and 70% ethanol, each step being performed twice for 5 min as described above. Staining was achieved employing the protocol described by van den Driesche and colleagues (15). In brief, for antigen retrieval, slides were treated with 0.01 M sodium citrate buffer, pH 6.0, containing 0.05% Tween 20 (P/N 8.17072.1000, Merck) at 96°C for 20 min in a water bath and thereafter blocked with 3% H₂O₂ (P/N 1.07209.0250, Merck) dissolved in methanol (P/N 1.06009.2511, Merck) for 30 min at RT. After two 5-min washes in Tris-buffered saline (TBS; P/N sc-24951, Santa Cruz), the sections were again blocked using 20% chicken serum (P/N C5405, Sigma-Aldrich) in TBS containing 5% BSA (P/N 001-000-161 Jackson ImmunoResearch) (TBS/NChS/BSA).

Subsequently, rabbit polyclonal primary antibodies against Ddx4 (P/N ab13840, Abcam, 1:200 dilution, final concentration 5 μg/ml), rabbit monoclonal primary antibodies against vimentin (P/N ab92547, Abcam, 1:200 dilution, final concentration 5 μg/ml), rabbit polyclonal primary antibodies against 3βHSD (P/N sc-28206, Santa Cruz, 1:200 dilution, final concentration 1 μg/ml) or rabbit IgGs (negative control) (P/N ab27478, Abcam, final concentration 5 μg/ml), all diluted in TBS/NChS/BSA, were incubated with the samples at 4°C overnight. The slides were then washed in TBS three times for 5 min each, followed by incubation with peroxidase-conjugated chicken secondary anti-rabbit antibody (P/N sc-2963, Santa Cruz, 1:200 dilution, final concentration 2 μg/ml) in TBS/NChS/BSA for 30 min at RT. After again washing in TBS three times for 5 min each, the Tyramide FI kit (Perkin-Elmer-TSA plus Fluorescein System; P/N NEL741001KT, Perkin Elmer Life Sciences, Boston, USA) was employed in accordance with the manufacturer's instructions. After washing once more with TBS, the sections were blocked again with 3% H₂O₂ in TBS-Tween for 30 min at RT, followed by blocking in TBS/NChS/BSA for 30 min at RT.

Thereafter, the sections were incubated with polyclonal rabbit primary anti-Ki67 antibodies (P/N ab27478, Abcam, dilution 1:200, final concentration 5 μg/ml) or rabbit IgGs (negative control) (P/N ab27478, Abcam, final concentration 5 μg/ml), both diluted in TBS/NChS/BSA, at 4°C overnight. Following washing with TBS, the samples were then incubated with peroxidase-conjugated chicken secondary anti-rabbit antibody (P/N sc-2963, Santa Cruz, 1:200 dilution, final concentration 2 μg/ml) dissolved in TBS/NChS/BSA for 30 min at RT. After again washing with TBS, the Tyr-Cy5 system (Perkin-Elmer-TSA plus Cyanine3 System; P/N NEL744001KT, Perkin Elmer Life Sciences) was applied in accordance with the manufacturer's protocol and the slides subsequently mounted in VECTASHIELD mounting medium containing DAPI (P/N H-1500, VECTOR).

The different types of male germ cells were identified on the basis of morphological characteristics described previously: spermatogonia: round to oval nucleus with densely stained chromatin; leptotene spermatocytes: round with chromatin "speckled" nucleus; early pachytene spermatocytes: slightly larger nucleus containing chromatin cords throughout (16).

All stained sections were examined under an Eclipse E800 microscope (Nikon, Japan, Tokyo) and photographed with a 12.5 million-pixel cooled digital color camera system (Olympus DP70, Tokyo, Japan).

STAINING OF APOPTOTIC CELLS

To evaluate the influence of the various media on the viability of testicular cells *in vitro*, apoptosis was assessed using the TUNEL (Terminal deoxynucleotidyl transferase dUTP nick end-labeling) assay kit (DeadEnd™ Colorimetric TUNEL System, P/N G7130, Promega, WI, USA) in accordance with the protocol provided. In brief, cell cultures were fixed in 4% PFA (P/N 8187081000, Merck) overnight at 4°C, followed by serial dehydration in 30, 50, and 70% aqueous ethanol for 24 h each. The samples were then transferred into 80, 96, and 99.6% ethanol for 6 h each at RT, followed by soaking in 100% butyl acetate for 6 h at RT (P/N 45860, Sigma-Aldrich) and, thereafter, routine embedding in paraffin (Paraplast X-TRA®, P/N P3808, Sigma-Aldrich) at 61°C overnight. After being cut into 5–20 μm slices using a Biocut sectioning machine (Reichert-Jung, NY, USA) and placed on microscope slides (P/N 10143352, Superfrost Plus, Thermo Scientific, MA, USA), the paraffin-embedded samples were de-paraffinized with xylene for 10 min; serially rehydrated with 99.6, 96, and 70% aqueous ethanol, with each step being performed twice for 5 min, and then washed twice with PBS.

Thereafter, the samples were treated with proteinase K (20 μg/ml in PBS) for 20 min at RT; washed again with PBS; and then incubated with biotinylated nucleotide mix + rTDT enzyme + buffer at 37°C for 1 h (adding only biotinylated nucleotide mix to the negative control). After terminating the reaction with stopping buffer (provided with the kit) and washing in PBS, endogenous peroxidase was blocked using 0.3% hydrogen peroxide (also supplied with the kit) in PBS for 15 min at RT. The samples were then incubated with streptavidin–HRP (from the kit) for 30 min at RT, stained with DAB (from the kit); counterstained with hematoxylin (Mayer's Hemalaun solution; P/N 1092491000, Merck); dehydrated with increasing concentrations of aqueous ethanol and then 100% xylene; and mounted with Entellan® new (P/N 1079610100, Merck). By examining at least 500 cells in each sample under an ECLIPSE E800 microscope (Nikon), the percentage of TUNEL-positive (i.e., apoptotic) cells was finally determined. The apoptotic frequency is expressed relative to the corresponding frequency on the first day of culturing, in order to minimize the effect of possible differences in culturing techniques.

TESTOSTERONE ASSAY

Testosterone production following 0, 1, 7, and 14 days of culture was employed as a measure of the influence of various media on the functionality of Leydig cells. First, testosterone was extracted by adding 0.5 ml ethyl acetate (P/N 1096232500, Merck) to the culture samples, each in a 1.5 ml Eppendorf tube, followed by vigorous automatic shaking for 15 min. After centrifugation for 2 min at 16000 × g, the resulting supernatant was re-subjected to the same procedure. The two ethyl acetate extracts were combined and evaporated overnight; the pellet obtained dissolved in PBS and the COAT-A-COUNT® kit (P/N TKTT2, Siemens, Germany,

Munich) used to quantify testosterone in accordance with the manufacturer's protocol.

RNA EXTRACTION AND cDNA SYNTHESIS

Employing samples collected at the time-points designated and stored thereafter at –80°C, RNA was extracted as described previously (17). In brief, each sample was lysed with TRIzol® reagent (P/N 15596018, Invitrogen) and disrupted for 30 s in an ULTRA-TURRAX T25 homogenizer (JANKE and KUNKEL, Staufen, Germany). Following addition of chloroform (P/N 1024452500, Merck) and centrifugation at 16000 × g for 10 min at 4°C, a half volume of ethanol 100% was added to the aqueous upper phase containing the RNA and the sample then applied to the spin column of the RNeasy Mini Kit (P/N 74104, Qiagen, Venlo, Netherlands) in accordance with the manufacturer's protocol. The RNA thus isolated was treated with DNase 1 Amplification Grade (P/N AMPD1, Sigma-Aldrich) to eliminate contamination by DNA and thereafter 0.6 μg RNA from each sample were used to synthesize 20 μl cDNA with the IScript™ cDNA synthesis kit (P/N 170-8891, Bio-Rad, CA, USA) as instructed by the manufacturer.

ANALYSIS OF GENE EXPRESSION

The influence of the various culture media on steroidogenesis and male germ cell differentiation was examined by analyzing relative gene expression by quantitative PCR (qPCR).

To assess steroidogenic gene expression, the iQ SYBER® Green Super mix (P/N 170-8882, Bio-Rad) was employed as instructed and qPCR performed with the iCycler iQ multicolor RT-PCR detection system (Bio-Rad). The qPCR program was initiated with denaturation (3 min at 96°C); followed by 40 cycles of denaturation (96°C for 10 s) and annealing/elongation (60°C for 45 s). Two genes expressed specifically by rat Leydig cells – i.e., those encoding steroidogenic acute regulatory protein (*Star*) and peripheral benzodiazepine receptor or translocator protein (*Tspo*) – were examined, with beta actin (*Actb*) as the endogenous control. The qPCR efficiencies for *Star*, *Tspo*, and *Actb* were 87.6, 85.8, and 94.2%, respectively. All primer sequences and product sizes are documented in **Table 2**. The mean gene expression for the triplicates run in each medium was calculated by the ddCt procedure and then normalized to the mean level of *Actb* mRNA (dCt). Freshly isolated cells inoculated into agarose without gonadotropins were snap frozen immediately and the gene expression in each sample presented relative to the corresponding expression in these day-0 cells [fold-change (2^{-ddCT})].

In the case of male germ cell differentiation *in vitro*, TaqMan® probes and TaqMan® Gene Expression Master Mix (P/N 4369510, Applied Biosystems, Life technologies, CA, USA) were employed using the protocol suggested. In brief, utilizing the iCycler iQ multicolor RT-PCR detection system (Bio-Rad), the qPCR program started with 2 min at 50°C; then 10 min at 95°C; followed by 45 cycles of two steps; 15 s at 95°C and 1 min at 60°C. Six genes, expressed specifically in connection with germ cell differentiation were investigated, i.e., *Kit*, *Zbtb16* (zinc finger- and BTB-domain containing 16), *Dazl* (deleted in azoospermia-like), *Boll* [Boule-like (*Drosophila*)], *Crem* (cAMP responsive element modulator), and *Prm1* (protamine 1). The TaqMan® probes utilized and assay numbers are listed in **Table 3**. The mean gene expression for the

Table 2 | The primers and conditions used for qPCR.

Gene	Primer sequence 5'–3'	Amplicon size (bp)	Conditions
<i>Star</i>	Fw: CTGCTAGACCAGCCCATGGAC	90	40 cy
	Rev: TGATTTCTTGACATTTGGGT		60°C
<i>Tspo</i>	Fw: GCTATGGTTCCTTGGGTCT	195	40 cy
	Rev: GGCCAGGTAAGGATACAGCA		60°C
<i>Actb</i>	Fw: TGAAGATCAAGATCATTGCTC	120	40 cy
	Rev: ACTCATCGTACTCCTGCTTGC		60°C

Bp, basepair; cy, cycles.

Table 3 | The assay and conditions used for qPCR.

Gene	TaqMan® assay number	Conditions
<i>Kit</i>	Rn00573942_m1	45 cy
		60°C
<i>Zbtb16</i>	Rn01418644_m1	45 cy
		60°C
<i>Dazl</i>	Rn01757162_m1	45 cy
		60°C
<i>Boll</i>	Rn01441407_m1	45 cy
		60°C
<i>Creml</i>	Rn01538528_m1	45 cy
		60°C
<i>Prm1</i>	Rn02345725_g1	45 cy
		60°C
<i>Actb</i>	Rn00667869_m1	45 cy
		60°C

Cy, cycles.

three triplicates run in each medium was calculated by the ddCt procedure and normalized to the corresponding mean level of *Actb* mRNA (dCt). The gene expression in each sample is presented relative to the corresponding expression in DMEM + glutamine [fold-change (2^{-ddCt})].

STATISTICAL ANALYSES

Gene expression, apoptotic frequency, and testosterone production were calculated as the means \pm standard deviations (SD) for the triplicates run under each condition. Student's *t*-test, One-way ANOVA and One-way RM ANOVA were applied to compare the differences between experimental conditions (SigmaPlot 11.0; Systat Software Inc., CA, USA). Following the Shapiro–Wilk test for normality, pairwise multiple comparisons were performed with the “Holm–Sidak” procedure as stated in the Figure legends (SigmaPlot 11.0; Systat Software Inc.). A difference was considered to be statistically significant if the *p* value was ≤ 0.05 .

RESULTS

INFLUENCE OF THE VARIOUS CULTURE MEDIA AND GONADOTROPINS ON THE CAPACITY OF LEYDIG CELLS IN A THREE-DIMENSIONAL CULTURE TO PRODUCE ANDROGENS

Comparison of the production of testosterone during the first 24 h of *in vitro* culture with stimulation by gonadotropins revealed

significantly lower testosterone levels with F12, DMEM/F12, and MEM media than with DMEM + glutamine (Figure 1). According to the supplier, DMEM + glutamine contains higher levels of amino acids than F12 and DMEM/F12, but addition of NEAA or AA to the F12 medium did not elevate testosterone production to the same level as with DMEM + glutamine (Figure 1A). For all media examined, testosterone production was stimulated by gonadotropins, as expected (Figure 1A).

INFLUENCE OF THE VARIOUS CULTURE MEDIA ON THE EXPRESSION OF STEROIDOGENIC GENES BY LEYDIG CELLS IN THREE-DIMENSIONAL CULTURES

As assessed by qPCR, within 1 day of stimulation by gonadotropins the relative up-regulation of *Star* expression was fivefold with DMEM + glutamine, threefold with F12, threefold with F12/NEAA, twofold with F12/AA, onefold with DMEM/F12, and fourfold with MEM (Figure 1B). The increase with DMEM + glutamine was significantly higher than with all of the other culture media except MEM. Moreover, after 1 day of stimulation with gonadotropins, the relative expression of *Tspo* was also up-regulated (DMEM + glutamine, threefold; F12, threefold; F12/NEAA, threefold; F12/AA, onefold; DMEM/F12, onefold; and MEM, onefold) (Figure 1C). This elevation was significantly greater with DMEM + glutamine than F12/AA, DMEM/F12 or MEM. Thus, with DMEM + glutamine, up-regulation of both *Star* and *Tspo* was most pronounced, in agreement with the observation that testosterone production was highest in the same medium.

INFLUENCE OF THE VARIOUS CULTURE MEDIA ON TESTOSTERONE PRODUCTION BY LEYDIG CELLS IN THREE-DIMENSIONAL CULTURES

The functionality of the Leydig cells in the mixture of testicular cells was assessed on the basis of testosterone production after 1, 7, and 14 days of culture, both in the presence and absence of gonadotropins. There was a significant difference between stimulated and unstimulated cells at all three time-points with DMEM + glutamine, DMEM without glutamine (–glutamine), or DMEM + Glutamax. After 1 day of stimulation this production was highest with DMEM + glutamine, followed by DMEM + Glutamax, and the lowest level with DMEM – glutamine (Figure 2A), but there was no significant difference between these three media in this respect following stimulation for 7 or 14 days (Figures 2B,C). At the same time, DMEM + Glutamax promoted the capacity of basal (unstimulated) Leydig cells to produce testosterone after 1, 7, and 14 days to a greater extent than DMEM+ or –glutamine (Figures 2A–C). Moreover, the levels of testosterone after 1 day of culture in all three media with gonadotropins (DMEM + glutamine: 79 ± 11 nmol/l; DMEM – glutamine: 39 ± 4 nmol/l; DMEM + Glutamax: 58 ± 12 nmol/l) as well as in DMEM + Glutamax without stimulation (20 ± 6 nmol/l), were higher than after 7 days (DMEM + glutamine: 14 ± 4 nmol/l; DMEM – glutamine: 10 ± 2 nmol/l; DMEM + Glutamax: 15 ± 3 nmol/l; DMEM + Glutamax without stimulation: 4 ± 1 nmol/l) or 14 days (DMEM + glutamine: 16 ± 6 nmol/l; DMEM – glutamine: 12 ± 3 nmol/l; DMEM + Glutamax: 16 ± 5 nmol/l; DMEM + Glutamax without stimulation: 6 ± 2 nmol/l) of culture (Figures 2A–C).

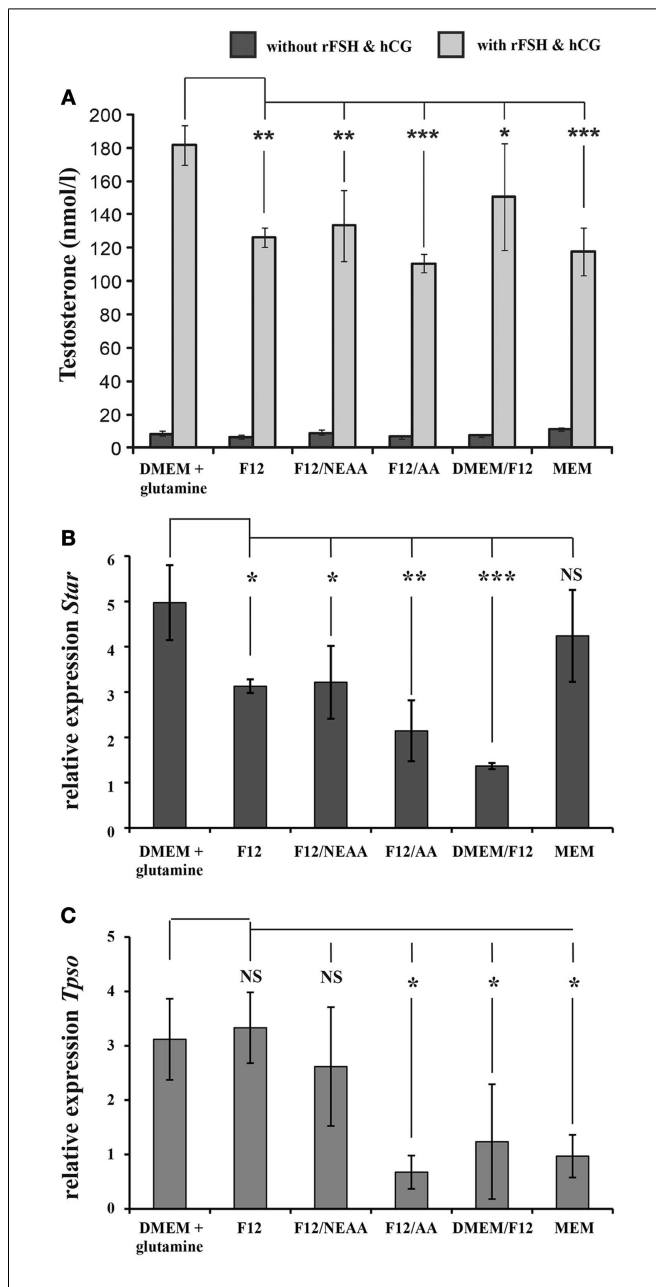


FIGURE 1 | The influence of various culture media on the capacity of the Leydig cells in three-dimensional cultures of rat testicular cells to produce testosterone and express steroidogenic genes. (A) On the X-axis are the different culture media employed [DMEM + glutamine (GL), F12, F12 + NEAA (non-essential amino acids), F12 + AA (essential amino acids), F12/DMEM, and MEM (minimal essential medium)], and the Y-axis depicts the concentration of testosterone (evaluated by radioimmunoassay and expressed in nanomoles/liter) in the medium of cells cultured for 1 day. The relative expression of **(B) *Star*** (Steroidogenic Acute Regulatory Protein) and **(C) *Tpsr*** (Translocator Protein) (determined by qPCR analysis with *Actb* as an internal control) by testicular cell suspensions from 7 dpp rats cultured for 1 day in six different media in the presence (light columns) or absence (dark columns) of hCG and FSH. The mean relative expression for triplicates was calculated by the ddCt procedure. One-way ANOVA with the Shapiro–Wilk test for normality was applied to compare the different experimental conditions. NS: non-significant; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ in comparison to the value with DMEM + glutamine.

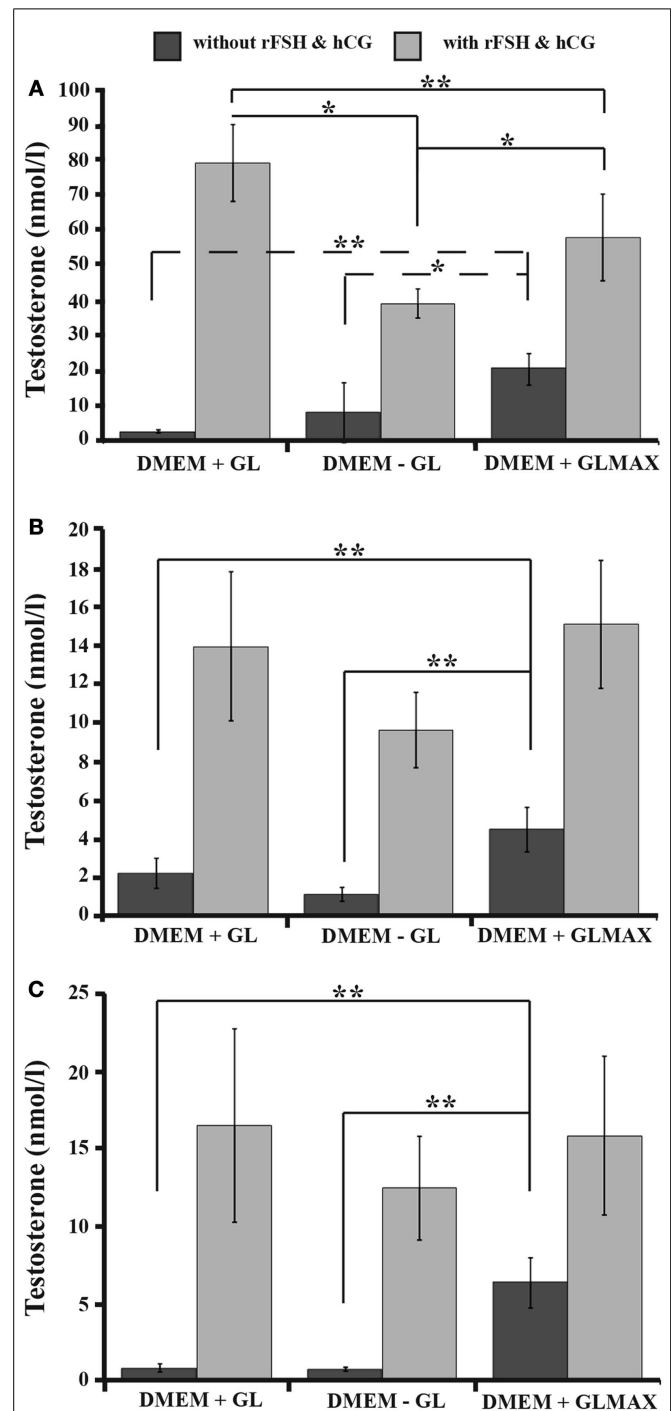


FIGURE 2 | The influence of different DMEM culture media on testosterone production by the Leydig cells in three-dimensional cultures of rat testicular cell. The cells were cultured for 14 days in DMEM + glutamine (GL), DMEM – glutamine (GL), or DMEM + Glutamax (GLMAX) (presented on the X-axis) either with (light columns) or without (dark columns) hCG and rFSH stimulation. The concentration of testosterone in the culture medium following 1 day **(A)**, 7 days **(B)**, and 14 days **(C)** of culture (determined by radioimmunoassay and expressed in nanomoles/liter) is shown on the Y-axis. One-way RM ANOVA with the Shapiro–Wilk test for normality was applied to compare the different experimental conditions. * $p < 0.05$, ** $p < 0.01$.

GONADOTROPINS PROTECT RAT TESTICULAR CELLS IN THE DIFFERENT CULTURE MEDIA FROM APOPTOSIS

Cell proliferation, expressed as the percentage of Ki67 positive cells (%) after 1 day of culture was 3.2 ± 0.8 with DMEM + glutamine, 3.9 ± 0.9 with DMEM + Glutamax, and 2.6 ± 2.6 with F12, with no significant differences. Nor did the relative numbers of different cell types immediately following the enzymatic digestion and after 1 day of culture differ between the culture media examined (DMEM + glutamine: $82 \pm 17\%$ Ddx4-positive cells, $32 \pm 10\%$ Vimentin-positive cells, $2 \pm 1\%$ 3 β HSD-positive cells; DMEM + Glutamax: $77 \pm 13\%$ Ddx4-positive cells, $28 \pm 10\%$ Vimentin-positive cells, $3 \pm 2\%$ 3 β HSD-positive cells; F12: $92 \pm 6\%$ Ddx4-positive cells, $26 \pm 9\%$ Vimentin-positive cells, $1 \pm 1\%$ 3 β HSD-positive cells). Application of the TUNEL assay revealed a significantly lower rate of apoptosis following 7 days of culture with than without gonadotropins in DMEM + glutamine (15 vs. 33%) or DMEM + Glutamax (10 vs. 24%) (Figure 3A), but no such difference was observed in the case of the F12 medium. Without stimulation, the cells in DMEM + glutamine exhibited a higher apoptotic rate (33%) than those in DMEM + Glutamax (24%) or F12 (20%), whereas there was no such difference when these three media were supplemented with gonadotropins (Figure 3A).

MEDIUM-RELATED EFFECTS ON THE DIFFERENTIATION OF PRE-PUBERTAL RAT MALE GERM CELLS *IN VITRO*

When expression of *Zbtb16* (also known as *Plzf*), *Kit*, *Dazl*, *Boll*, *Crem*, and *Protamine* by cells cultured with hCG and FSH was evaluated by qPCR, the expression of *Zbtb16* in DMEM + glutamine was observed to be significantly higher (2.5-fold) after 21 days than after 0 and 7 days, with no such changes in the case of DMEM + Glutamax or F12 and no significant differences between these three different media (Figure 3B). With DMEM + glutamine or DMEM + Glutamax, *Kit* expression was down-regulated after 7 (threefold) and 21 days (fivefold) in culture, whereas in cells cultured in F12 this expression remained constant during the entire experimental period (Figure 3C). Expression of *Dazl* by cells cultured in DMEM + glutamine or DMEM + Glutamax was significantly down-regulated (10-fold) after 7 and 21 days with a similar, although not significant tendency in the case of F12 (11- and 3-fold down-regulation after 7 and 21 days, respectively) (Figure 3D). After 7 days, only cells in DMEM + Glutamax demonstrated down-regulation (2.5-fold) of *Crem* expression (Figure 3E), while after 21 days, expression of *Crem* was significantly higher with F12 than DMEM + glutamine (threefold) or DMEM + Glutamax (twofold) (Figure 3E). No expression of *Boll* or *Protamine* was detected under any of the experimental conditions (data not shown).

MORPHOLOGICAL EVALUATION AND IMMUNOHISTOCHEMICAL AND FLUORESCENT STAINING

Morphological evaluation and IHC and IF staining revealed colony formation in the three-dimensional cultures of rat testicular cells (Figure 4A), with undifferentiated spermatogonia being detected in these colonies (Figures 4B–D). Following 3 days in culture, the colonies formed by un-stimulated cells were already less compact than those formed in the presence of gonadotropins (data not

shown). Active cell migration toward colonies could be observed (Figures 4E–G). However, the total number of viable cell colonies was low.

Morphological evaluation of colonies formed in the three-dimensional culture (Figures 4H,M), as well as in conventional two-dimensional cultures (Figure 4I) revealed migration of cells from the inner side to the outer side of the colonies. These migrating cells could be identified as germ cells by IHC staining for Ddx4, a marker specific for germ cells (Figures 4J–L).

More detailed morphological analysis after 21 days *in vitro* showed small structures containing a mixture of Sertoli (Figure 4N) and peritubular cells (Figure 4N), as well as male germ cells in different stages of differentiation up to early pachytene spermatocytes (Figure 4N).

DISCUSSION

The major novel observations documented here are as follows: (1) the culture medium *per se* exerts a direct influence on the functionality of the rat Leydig cells, but not on germ cell differentiation in three-dimensional cultures; (2) rat germ cells migrating from the inner side to the outer side of the cell colonies suggest an unfavorable organization of tubules formed *de novo* in the three-dimensional culture; (3) undifferentiated rat spermatogonia differentiate up to the stage of pachytene spermatocytes in a similar time-period to the situation *in vivo* in three-dimensional cultures.

After 7 days of culture in three different media, less extensive apoptosis was observed among cells in the presence than in the absence of rFSH and hCG, in agreement with earlier findings in literature (18–20). The nature of the medium *per se* exerted no significant impact on overall cell survival.

Although in our three-dimensional cultures stimulation with gonadotropins promoted Leydig cell functionality (as reflected in testosterone production) after 1, 7, and 14 days regardless of the medium, DMEM + glutamine was clearly most effective in this respect after 1 day of stimulation. Thus, at this early time-point, the level of testosterone in the culture medium appeared to be related to the levels of glutamine [an important source of energy, as well as a precursor for protein synthesis (21–24)], since the other culture media examined contain less glutamine or none at all. In addition, cells cultured in DMEM + glutamine exhibited the most pronounced up-regulation of *Star* and *Tspo*, which transfer cholesterol (the precursor for testosterone) across an aqueous phase from the outer to the inner mitochondrial membrane (25–28) and are thereby essential for the steroidogenic process. Thus, the presence of glutamine in the culture medium may be essential for the synthesis of the enzymes and other proteins required for testosterone production.

Furthermore, since DMEM + glutamine medium contains higher levels of amino acids both (essential and non-essential) than F12, this difference was eliminated by adding essential or non-essential amino acids to the F12 medium. However, such supplementation did not increase testosterone production to a level similar to that obtained with DMEM + glutamine and addition of both kinds of amino acids to F12 resulted in a low pH and thereby a cytotoxic environment (data not shown). Moreover compared to

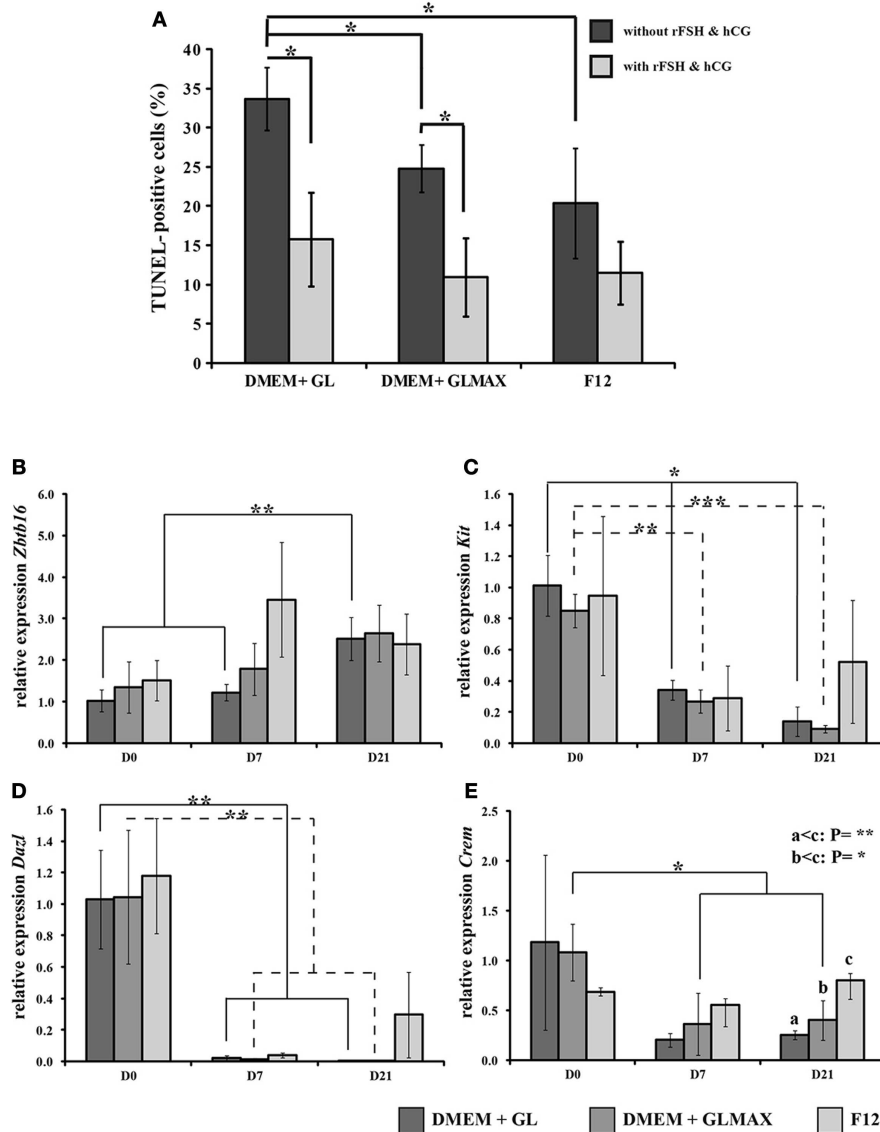


FIGURE 3 | The influence of different culture media on cell survival and expression of genes related to germ cell differentiation in a three-dimensional cultures of rat testicular cells. (A) The cells were cultured for 7 days in DMEM + glutamine (GL), DMEM + Glutamax (GLMAX), or F12 (presented on the X-axis) either with (light columns) or without (dark columns) hCG and rFSH stimulation. The percentage of apoptotic (TUNEL-positive) cells, normalized to the 1-day value, is shown on the Y-axis. **(B–E)** The cells were cultured for 0, 7, and 21 days. The graphs depict the

relative expression of rat *Zbtb16* (also known as *Plzf*) **(B)**, *Kit* **(C)**, *Dazl* **(D)**, and *Crem* **(E)** (determined by qPCR analysis with *Actb* as an internal control) by cells cultured in DMEM + glutamine (DMEM + GL), DMEM + Glutamax (DMEM + GLMAX), or F12. On the X-axis, the different periods of culture [0 (D0), 7 (D7), and 21 (D21) days] are depicted and the Y-axis shows the mean relative expression of replicates calculated by the ddCt procedure. Student's *t*-test was applied to compare the different experimental conditions. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

DMEM + glutamine, the relative levels of expression of *Star* and *Tspo* were lower in cells cultured in F12 supplemented with essential amino acids, and expression of *Star* was lower when F12 was supplemented with non-essential amino acids medium. Of course, DMEM + glutamine and F12 also differ with respect to the levels of several other components, such as vitamins and inorganic salts, which might explain their different effects.

Analysis of the relative expression of genes associated with male germ cell differentiation (i.e., *Zbtb16*, *Kit*, and *Dazl* in

spermatogonia, *Dazl* and *Boll* in spermatocytes, and *Crem* and *Protamine* in spermatids) by cells cultured in DMEM + glutamine, DMEM + Glutamax, or F12 supplemented with gonadotropins demonstrated that none of these media alone promoted robust spermatogenesis after 21 days of culture. The overall down-regulation of these genes might reflect the increase in the number of apoptotic cells with culture time, which could also explain at least partially the low efficiency of the three-dimensional culture system employed.

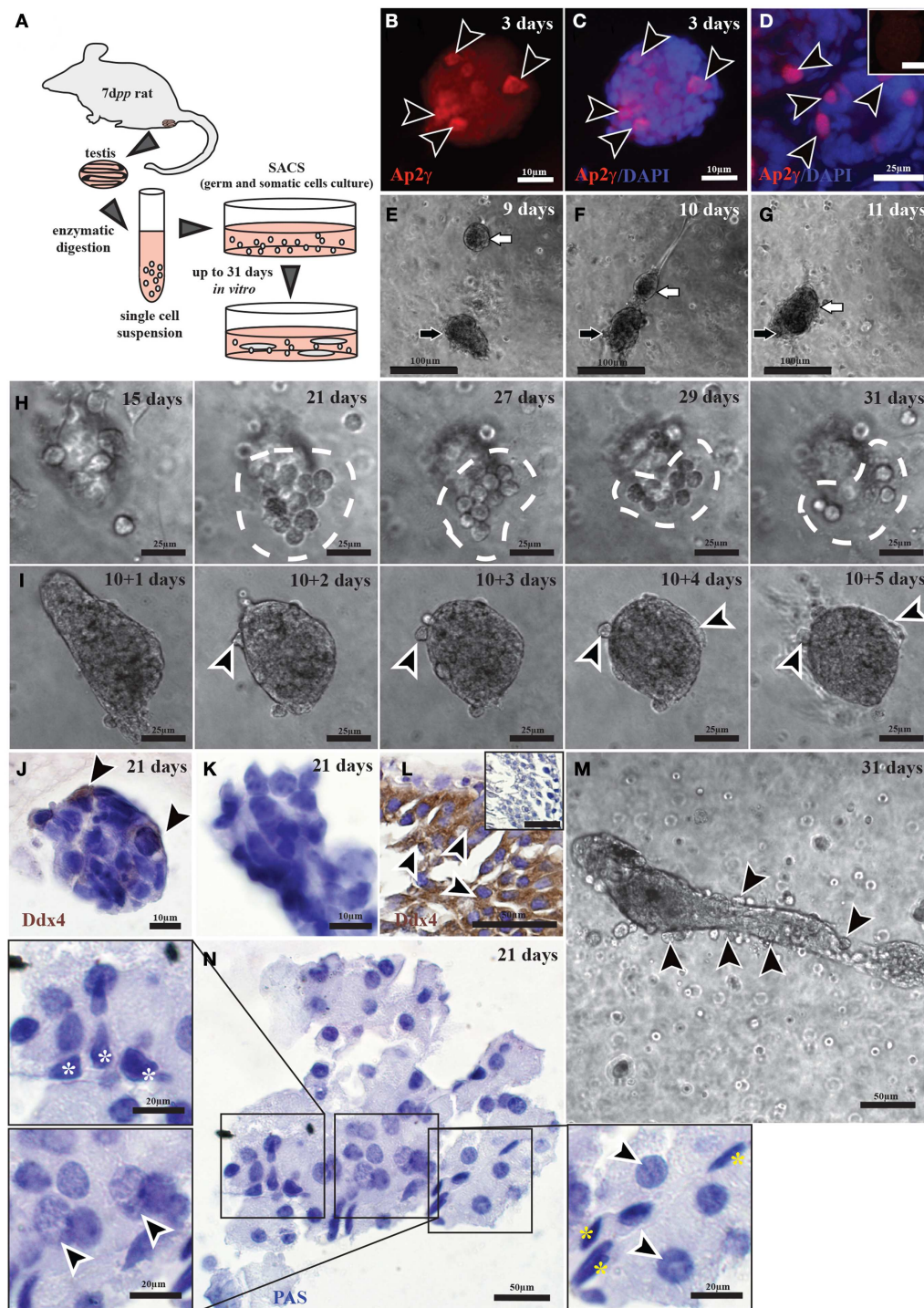


FIGURE 4 | Tubule formation by and germ cell differentiation of pre-pubertal rat testicular cells in three-dimensional cultures.

(A) A schematic overview of the experimental conditions.

(B–D) Immunofluorescent staining of undifferentiated spermatogonia (Ap-2 γ) in cell colonies originated from culturing cells from 7-day-old rats for 3 days **(B,C)**, as well as from 8-day-old rats as a positive control **(D)** [Ap2 γ : red staining (black arrow heads); DAPI: blue staining]. The negative control with IgGs is shown as small insert in **(D)**. **(E–G)** 9- **(E)**, 10- **(F)**, and 11-day cultures **(G)** showing two colonies (the black and the white arrows) migrating toward one another. **(H,I,M)** Active migration of cells out of

colonies cultured for as long as 31 days [white dashed line in **(H)**, black arrows heads in **(M)**] or following incubation of isolated cell colonies in liquid medium for 5 days [black arrow heads in **(I)**].

(J–L) Immunohistochemical staining for germ cells (Ddx4) in colonies originating from 7-day-old rats and cultured for 21 days **(J,K)**, as well as from 60-day-old rat testis [positive control; **(L)**] [Ddx4: brown staining (black arrow heads); Hematoxylin: blue staining]. **(N)** Cells cultured for 21 days exhibit morphologies similar to those of peritubular cells (yellow stars), Sertoli cells (white stars), leptotene spermatocytes, and early pachytene spermatocytes (black arrow heads).

However, there were certain differences in the expression of *Crem* by cells in the different media after 21 days. *Crem* is expressed primarily by spermatocytes, but also by Sertoli cells, although the latter expression appears not be necessary for spermatogenesis (29–32). *Crem* acts downstream of cAMP signaling (33) and its activation modulates the cAMP response element, thereby altering gene expression (32, 33). Interestingly, the different isoforms of the *Crem* protein act as a master switch for the regulation of various genes during spermatogenesis (30–32, 34).

After 21 days in culture, the cells in only a few of the colonies formed still exhibited an intact morphology, most having decreased in size. However, all colonies with intact cells contained a mixture of somatic (Sertoli and peritubular cells) and germ cells (differentiated as far as pachytene spermatocytes). Thus, undifferentiated spermatogonia, the only germ cells present in the testes of 7 dpp rats had differentiated as far as to the stage of pachytene spermatocytes, a level of differentiation similar to the situation *in vivo* at the age of 25–28 dpp. These observations indicate that at least a partially functional microenvironment supporting germ cell survival and differentiation was obtained.

Suitable support for germ cells through the formation and proper orientation of Sertoli and peritubular cells is needed for completion of spermatogenesis (13, 35, 36). As shown earlier, when utilized as feeders for germ cells or embryonic stem cells *in vitro*, Sertoli cells tend to be unorganized in contrast to their highly polarized orientation *in vivo* (35–37). Such disorganization presumably disallows the crucial support of the blood–testis barrier as a result of missing or premature junctional complexes between Sertoli cells (36). Such lack of support leads to meiotic arrest, with the meiotic germ cells going into apoptosis.

In our three-dimensional cultures, germ cells were seen to migrate out of the cell colonies formed and thereafter disintegrate and die within a couple of days due to the lack of support from the Sertoli cells. Strategies for obtaining the proper polarized orientation of the Sertoli cells and thereby establishing an appropriate niche for germ cell differentiation *in vitro* warrant more detailed investigations.

In conclusion, the present study demonstrates that although the nature of the culture medium *per se* does not influence the overall viability of rat testicular cells *in vitro*, it does influence the functionality of rat Leydig cells in three-dimensional cultures. Cells cultured in DMEM + glutamine medium displayed more testosterone production and higher expression of *Star* and *Tspo* than any of the other cell culture media examined. This might reflect the higher concentration of glutamine in this medium, but further studies concerning the influence of glutamine on Leydig cell functions, as well as on other endocrine/paracrine pathways in such complex three-dimensional cultures containing all types of testicular cells are required.

Differentiation of germ cell up to the stage of pachytene spermatocytes, i.e., similar to the situation *in vivo*, could be detected in a few small colonies hosting a mixture of somatic and germ cells. However, the crucial structural support provided by the Sertoli and peritubular cells in the seminiferous tubules *in vivo* could not be duplicated and none of the media examined provided a robust system for male germ cell differentiation *in vitro*. Thus, additional work on this question remains to be done.

AUTHOR CONTRIBUTIONS

Ahmed Reda: study design, data acquisition, analysis and interpretation, drafting the article, and final approval of the submitted version. Mi Hou, Luise Landreh, Kristín Rós Kjartansdóttir: data acquisition and analysis, drafting the article, and final approval of the submitted version. Konstantin Svechnikov, Olle Söder: data analysis and interpretation, drafting the article, and final approval of the submitted version. Jan-Bernd Stukenborg: study design, data acquisition, analysis and interpretation, drafting the article, and final approval of the submitted version.

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Central pathways integrating metabolism and reproduction in teleosts

Md. Shahjahan[†], Takashi Kitahashi[†] and Ishwar S. Parhar^{*}

Brain Research Institute, School of Medicine and Health Sciences, Monash University Malaysia, Petaling Jaya, Malaysia

Edited by:

Rosaria Meccariello, University of Naples Parthenope, Italy

Reviewed by:

Teresa Chioccarelli, Second University of Naples, Italy
Erika Cottone, University of Turin, Italy

*Correspondence:

Ishwar S. Parhar, Brain Research Institute, School of Medicine and Health Sciences, Monash University Malaysia, Petaling Jaya 46150, Malaysia
e-mail: ishwar@monash.edu

[†]Md. Shahjahan and Takashi Kitahashi have contributed equally to this work.

Energy balance plays an important role in the control of reproduction. However, the cellular and molecular mechanisms connecting the two systems are not well understood especially in teleosts. The hypothalamus plays a crucial role in the regulation of both energy balance and reproduction, and contains a number of neuropeptides, including gonadotropin-releasing hormone (GnRH), orexin, neuropeptide-Y, ghrelin, pituitary adenylate cyclase-activating polypeptide, α -melanocyte stimulating hormone, melanin-concentrating hormone, cholecystokinin, 26RFamide, nesfatin, kisspeptin, and gonadotropin-inhibitory hormone. These neuropeptides are involved in the control of energy balance and reproduction either directly or indirectly. On the other hand, synthesis and release of these hypothalamic neuropeptides are regulated by metabolic signals from the gut and the adipose tissue. Furthermore, neurons producing these neuropeptides interact with each other, providing neuronal basis of the link between energy balance and reproduction. This review summarizes the advances made in our understanding of the physiological roles of the hypothalamic neuropeptides in energy balance and reproduction in teleosts, and discusses how they interact with GnRH, kisspeptin, and pituitary gonadotropins to control reproduction in teleosts.

Keywords: neuropeptide, metabolism, energy balance, fish, reproduction

INTRODUCTION

A close connection between energy balance and reproduction has been well documented in mammals (1). Energy balance is maintained by a process that controls food consumption, energy expenditure, and energy storage. A number of hypothalamic neuropeptides including orexin, ghrelin, neuropeptide-Y (NPY), melanin-concentrating hormone (MCH), pituitary adenylate cyclase-activating polypeptide (PACAP), proopiomelanocortin (POMC)-derived peptides, cholecystokinin (CCK), chicken gonadotropin-releasing hormone-II (cGnRH-II), 26RFamide (26RFa), galanin (GAL), and cocaine- and amphetamine-regulated transcript (CART) have been implicated in the regulation of feeding behavior and energy balance. On the other hand, peripheral hormones such as leptin and ghrelin provide information about the availability of stored metabolic foods.

Initiation of reproduction is affected by the amount of body energy reserves and is responsive to diverse metabolic factors. The neuroendocrine mechanisms responsible for the association between energy balance and fertility are represented by metabolic hormones and neuropeptides that affect the hypothalamic center controlling the expression and release of gonadotropin-releasing hormone (GnRH) (2, 3). Therefore, adequate body energy stores are crucial for full activation of the hypothalamus–pituitary–gonadal (HPG) axis at puberty and its proper functioning in adulthood (4). Generally high amount of food supply favor reproduction, while low food supply inhibits the reproductive system (1). During energetic challenges, the physiological mechanisms that partition energy into various activities tend to favor the processes for the survival of the individual over the processes for

growth, longevity, and reproduction (5). Therefore, the reproductive system is suppressed by energetic challenges. At the same time it is also true that when the reproductive system is highly activated, animal primates reproduction rather than feeding. Many factors such as starvation, eating disorders, excessive exercise, cold exposure, and lactation act on both food intake and reproduction by increasing hunger and/or food ingestion and by suppressing reproductive processes (5, 6).

Most feeding-related neuropeptides in mammals have also been identified in fish species (7), suggesting that the regulatory system of feeding has been well conserved from fish to mammals. On the other hand, as the links between energy balance and reproduction have been demonstrated in several vertebrates (8), this might also exist in teleosts. Indeed, seasonal changes in feeding often coincide with spawning migration and reproduction in fish, suggesting association between nutrition and reproduction (9).

This review focuses on the role of the neuropeptides that regulate feeding and energy balance on reproduction in teleosts, and discusses if the metabolic control of reproduction is conserved from fish to mammals.

REGULATION OF REPRODUCTION IN TELEOSTS

In teleosts, as in other vertebrates, reproduction is coordinated by the HPG axis. The hypothalamus produces GnRH, which regulates the synthesis and release of gonadotropins (GTHs), follicle-stimulating hormone (FSH), and luteinizing hormone (LH), from the pituitary. The GTHs act on the gonads to stimulate gonadal development through the secretion of sex steroid hormones. These steroids, in turn, feedback to the brain and the

pituitary to complete the HPG axis and to regulate the reproductive cycle (10, 11). Thus, hypothalamic GnRH is considered as the key player in the regulation of reproduction in teleosts. Furthermore, recent findings of kisspeptin and gonadotropin-inhibitory hormone (GnIH) added new players in the reproductive system, which stimulate and inhibit mostly GnRH neurons, respectively.

GONADOTROPIN-RELEASING HORMONE (GnRH)

In the early 1970s, two research groups simultaneously reported the isolation of a LH-releasing factor from the hypothalamus of pigs and sheep (12, 13), and named it LH-releasing hormone (LHRH). Later, this decapeptide was also found to stimulate FSH release, and accordingly re-named GnRH. The GnRH isolated from mammals is also functional in fish, and stimulates the release of GTH in the carp (14). The first fish GnRH was identified in salmon, and named as salmon GnRH (sGnRH) (15). To date, 15 different forms of GnRH have been identified in vertebrates (13, 15–25), among them 10 original forms in fish species: salmon, sea bream, whitefish, medaka, catfish, herring, dogfish, and lamprey (lamprey I, II, and III). Most vertebrates possess two, and some teleosts have three, forms of GnRH in the brain (23, 25–31). Based on phylogenetic analysis, recent classification defines the species-specific (hypophysiotropic) form as GnRH1, while the most evolutionarily conserved chicken GnRH-II as GnRH2 (32). The third form is GnRH3 (33), which is present only in the brain of certain teleost species (31, 34).

Distribution of three different forms of GnRH in the brain was first reported in a perciform fish, the sea bream (35). GnRH1 neurons are generally present in the region from the ventral forebrain–preoptic area (POA) to basal hypothalamus, whereas GnRH2 neurons are restricted to the dorsal mesencephalon. GnRH3 neurons are located in the caudal-most olfactory bulb as a ganglion and along the terminal nerve in most fish species that possess three GnRH forms (31, 36). On the other hand, in the sea bream and the European sea bass, the distribution of GnRH1 and GnRH3 cells overlap in the olfactory bulbs, ventral telencephalon, and POA (37–40). Similar results were reported in several other fish species (41–45). In the sea bass brain, GnRH1 neuronal fibers are observed in the ventral surface of the forebrain, associated with the ventral telencephalon, POA, and the hypothalamus, whereas GnRH2 and GnRH3 neuronal fibers show profuse distributions throughout the brain (40).

The function of GnRH in the central regulation of LH release has been recognized in all orders of teleosts. Although the assay for FSH peptide is lacking for most fish species, studies in the rainbow trout (46–48) and the Coho salmon (49) show that GnRH also stimulates FSH release in salmonids. However, the different patterns of fiber projections of each GnRH form suggest different physiological function of each GnRH form in the brain (31). GnRH1 neurons are generally present in the ventral forebrain–POA–hypothalamus and send neuronal fibers directly into the pituitary, which represents its primary role in the stimulation of GTH secretion. The physiological significance of GnRH1 as a regulator of GTH secretion and gametogenesis has been established in several teleosts (28, 50–54).

GnRH2 neurons are exclusively present in the midbrain. The absence or low levels of GnRH2 peptide in the pituitary has been

demonstrated in several *perciformes* (50, 51, 55–57) and *pleuronectiformes* species (28, 58), suggesting that GnRH2 is not directly involved in GTH secretion. Rather, its wide fiber projection throughout the brain suggests that GnRH2 has neuromodulatory functions (30). However, in some fish species including the goldfish, GnRH2 seems to act as a hypophysiotropic GnRH together with GnRH3 (59).

GnRH3 has been shown to control reproductive behaviors in several fish species. GnRH3 stimulates nest-building behavior in the male dwarf gourami (60), homing migration in the sockeye salmon (61), and aggressive and nest-building behaviors in the male Nile tilapia (62), which suggests probable neuromodulatory roles of GnRH3. The neuromodulatory role of GnRH3 was confirmed by electrophysiological studies in the retina of goldfish (63, 64) and olfactory receptor cells of the mudpuppy (65). The neuromodulatory function of GnRH3 has also been demonstrated in the rainbow trout (66, 67) and the dwarf gourami [reviewed by Oka (68)]. Fish species such as some salmonids and the zebrafish possess only two forms of GnRH (GnRH2 and GnRH3). In these species, GnRH3 expressed in the basal forebrain acts as a hypophysiotropic GnRH (45, 69–71).

KISSPEPTIN

Kisspeptin is a neuropeptide that plays an important role in reproduction through the stimulation of GnRH neurons by activating GPR54 in mammals (72, 73). In teleosts, two kisspeptin genes, namely *kiss1* and *kiss2*, have been identified in several fish species (74–77), whereas placental mammals possess only the *kiss1* gene. Similarly, two kisspeptin receptor genes, named *kiss1r* and *kiss2r*, were also identified in several fish species (76, 78), suggesting two Kiss/Kissr systems in teleosts. However, this situation is not common among all fish species. Only one kisspeptin gene, *kiss2*, and one receptor, *kiss2r*, are present in some fish species including the Senegalese sole (79), orange-spotted grouper (80), grass puffer (81), and the Atlantic halibut (82), indicating that the *kiss1* and *kiss1r* genes have been lost during evolution in these species (82). Both *kiss1* and *kiss2* mRNAs are expressed in the brain and the gonads in several fish species (74, 76–78, 83). On the other hand, kisspeptin and kisspeptin receptor are also expressed in the fish pituitary, suggesting local actions of kisspeptin in the pituitary (76, 78, 81). In the medaka brain, two populations of *kiss1* neurons are found in the hypothalamus, one in the nucleus ventral tuberis (nVT) and the nucleus posterioris periventricularis (NPPv) (74, 84), while neurons in the dorsal zone of the periventricular hypothalamus (Hd) express *kiss2*. In the zebrafish all hypothalamic populations express *kiss2* mRNA (74). A recent study showed that zebrafish Kiss2 neuronal fibers are found widely in the subpallium, POA, ventral and caudal hypothalamus, and the mesencephalon (85). The fact that all three GnRH neuron types express kisspeptin receptors in the Nile tilapia (86) suggests that the role of Kiss2 neurons in the regulation of the HPG axis is via the activation of the GnRH systems. The *kiss1* neurons are exclusively localized in the habenula in the zebrafish (74), and send fibers only to the ventral part of the interpeduncular nucleus (85, 87). The habenula Kiss1 system is thus implicated in the modulation of serotonergic system rather than the HPG axis in the zebrafish (87).

The role of kisspeptin in the onset of puberty and sexual maturation is conserved among vertebrates including fish. In the zebrafish, both *kiss1* and *kiss2* mRNA levels are increased significantly at the start of the pubertal phase together with GnRH2 and GnRH3 mRNAs (74). Significant positive correlation is observed between the levels of *kiss2* mRNA and those of *gnrh1* mRNA during the spawning period in the grass puffer (81). Kiss2 but not Kiss1 stimulates GTH synthesis and release in the sea bass and the zebrafish (74, 75). Administration of Kiss2–10 peptide increases GnRH1 mRNA levels in the sexually mature female orange-spotted grouper (80), indicating that Kiss2 most probably plays an important role in the regulation of reproductive functions through the stimulation of GnRH1 secretion.

The information of the interaction between kisspeptin neuronal fibers and GnRH cell bodies had been limited in teleosts due to the lack of specific antibody to kisspeptins. A recent study using an antibody to prepro-Kiss2 proved that Kiss2 neuronal fibers make close contacts with POA GnRH (GnRH3) neurons in the zebrafish (85), suggesting that Kiss2 directly act on GnRH neurons. Moreover, kisspeptin receptor expression in the three GnRH neuronal populations (86) in tilapia suggests that kisspeptin directly stimulates not only GnRH1 neurons to induce LH secretion, but also GnRH2 and GnRH3 neurons to activate other aspects of the reproduction such as sexual behavior.

GONADOTROPIN-INHIBITORY HORMONE (GnIH)

GnIH or RFamide-related peptide (RFRP), which has a characteristic C-terminal LPXRFa motif (X = L or Q), is a hypothalamic neuropeptide that was originally identified from the quail as a neuropeptide that inhibits gonadotropin release from the pituitary (88). Extensive studies revealed that GnIH functions at the level of GnRH neurons and at the level of pituitary gonadotropes to suppress reproduction in avian and mammalian species [see reviews in Ref. (89, 90)]. GnIH in the teleost species has been named LPXRFamide peptide based on the amino acid sequence of the C-terminal motif. All precursors of teleost GnIH identified so far encode three GnIH orthologs (LPXRFa-1, -2, and -3), while only goldfish LPXRFa-3 has been purified as a mature peptide.

As in birds and in mammals, teleost GnIH neurons are located in the hypothalamus, in particular in the NPPv, and send neuronal fibers throughout the brain and to the pituitary (91, 92). The physiological function of teleost GnIH in the control of reproduction is complicated. *In vivo* studies using the goldfish show that GnIH decreases plasma LH levels as in avian and mammalian species (93, 94). On the other hand, GnIH significantly increases pituitary levels of mRNAs for LH β and FSH β in a reproductive state-dependent manner *in vivo*, whereas general suppression of LH β and FSH β mRNA levels is observed *in vitro* in a study (93). This differential *in vivo* effect of GnIH in different seasons can be explained by the differential action of GnIH on the gonads (95). GnIH does not affect plasma estradiol levels in the female goldfish, but increases plasma testosterone levels in the male goldfish (96). GnIH injections into the female goldfish suppress pituitary LH β and FSH β and hypothalamic GnRH mRNA levels (95). In addition, GnIH suppresses GnRH-induced increase in LH β mRNA levels *in vitro* (95). Therefore, in the goldfish, the inhibition of the HPG axis at the level of hypothalamic GnRH neurons and pituitary

gonadotropes appears as an evolutionarily conserved function of GnIH. On the contrary, goldfish GnIH peptides stimulate the synthesis and release of LH and FSH in cultured pituitary cells of the grass puffer and the sockeye salmon, respectively (92, 97). Therefore, as in mammals (98), the stimulatory or inhibitory action of GnIH in fish is probably species dependent or species-specific. GnIH peptide might be necessary for an inhibitory action.

More recently, it has been shown that medaka LPXRFa-2 (GnIH-2) peptide decreases the firing frequency of non-hypophysiotropic terminal nerve GnRH3 neurons in the dwarf gourami (99). Since GnRH3 controls nest-building, aggression, and homing migration (60–62), GnIH-2 might negatively regulate reproductive behaviors.

METABOLIC NEUROPEPTIDES INVOLVED IN REPRODUCTION

A number of hypothalamic neuropeptides have been identified in fish species (7), and found to be involved in the control of food intake as well as reproduction (Table 1). To understand the overall metabolic control of reproduction, the involvement of metabolic neuropeptides in the regulation of GnRH and GTHs must be taken into consideration. However, compared to mammals, the information related to the role of metabolic neuropeptides in the regulation of reproduction is still limited in fish.

OREXIN

Orexin has two well conserved molecular forms, a 33-amino acid peptide known as orexin A (OXA) and a 28-amino acid peptide known as orexin B (OXB) derived from the same precursor [see review in Ref. (150)]. Orexin was first identified as a ligand of an orphan receptor, and consequently found to stimulate feeding in mammals (151). The orexin's orexigenic action is also observed in teleosts, including the goldfish and the ornate wrasse (101, 152).

In mammals, orexin is known to stimulate the HPG axis via GnRH secretion (153–155). In the goldfish, an interaction between orexin and hypophysiotropic GnRH (GnRH2) has also been proposed. Intracerebroventricular administrations of OXA inhibit spawning behavior and lower GnRH2 mRNA levels, while treatment with GnRH decreases OXA mRNA levels (102). These results suggest that, unlike in mammals, orexins might act as inhibitory agents in the control of GnRH at least in some fish species. In addition, OXA is detected in the pituitary of the medaka (156) and the Japanese sea perch (157), whilst OXB is detected in the pituitary of the Nile tilapia (158), suggesting orexin's local action at the level of pituitary. Thus orexin, an orexigenic neuropeptide, inhibits the HPG axis at the hypothalamus GnRH level and possibly also at the pituitary level, in fish.

NEUROPEPTIDE-Y (NPY)

NPY which is composed of 36 amino acid residues, was first identified in the porcine brain (159), and was found to function as a powerful appetite enhancer in mammals (160). In fish species, NPY also show powerful orexigenic activity in the goldfish (103, 123, 161–164), trout (104), puffer fish (105, 165), and the zebrafish (106).

Centrally or peripherally injected NPY increases plasma LH levels in the goldfish, common carp, rainbow trout, and in the sea bass (107, 109, 111), indicating that NPY stimulates teleost reproduction as was shown in mammals (166).

Table 1 | Neuropeptides and their functions in representative fish species.

Neuropeptide	Species	Function	Reference	Neuropeptide	Species	Function	Reference	
Orexin	Goldfish	Increase food intake	(100)		Rainbow trout	Decrease food intake	(129)	
	Ornate wrasse	Increase food intake	(101)		(Mouse)	Stimulate GnRH neurons	(130)	
	Goldfish	Inhibit spawning behavior, decrease GnRH2 mRNA level	(102)			CART	Goldfish	Decrease food intake
NPY	Goldfish	Increase food intake	(103)	(Rat)	Stimulate GnRH release	(133, 134)		
	Rainbow trout	Increase food intake	(104)		CCK	Goldfish	Decrease food intake	(135)
	Puffer fish	Increase food intake	(105)	Goldfish		Stimulate LH release	(136)	
	Zebrafish	Increase food intake	(106)	Nesfatin-1		Goldfish	Decrease food intake	(137, 138)
	Goldfish	Stimulate GnRH and LH release	(107, 108)			Goldfish	Decrease plasma LH level	(139)
	Common carp	Increase plasma LH level	(109)			Leptin	Goldfish	Decrease food intake
	Sea bream	Stimulate GnRH release	(110)	Rainbow trout	Decrease food intake		(141)	
PACAP	Goldfish	Decrease food intake	(112)	Sea bass	Stimulate LH release	(142)		
	Goldfish	Stimulate LH release	(113, 114)		Rainbow trout	Stimulate LH release	(143)	
	Tilapia	Stimulate GTH subunit mRNA expression	(115)		Ghrelin	Goldfish	Increase food intake	(144–146)
	Blue gourami	Stimulate FSH β mRNA expression	(116, 117)	Rainbow trout		Decrease food intake	(147)	
GnRH2	Goldfish	Decrease food intake	(102, 118)	Goldfish	Stimulate LH release	(148)		
	Zebrafish	Decrease food intake	(119)	Common carp	Stimulate LH release	(149)		
	Goldfish	Stimulate LH release	(120)					
26RFa	Mouse	Increase food intake	(121)					
	Goldfish	Increase plasma LH level	(122)					
Galanin	Goldfish	Increase food intake	(123)					
	Tench	Increase food intake	(124)					
	(Rat)	Stimulate GnRH release	(125)					
MCH	Goldfish	Decrease food intake	(126)					
	Goldfish	Stimulate LH release	(127)					
α -MSH	Goldfish	Decrease food intake	(128)					

(Continued)

In the brown trout (167) and the rainbow trout (168), NPY neuronal fibers project to the areas where hypophysiotropic GnRH neurons exist, particularly in the ventral telencephalon, POA, and in the basal hypothalamus. Furthermore, double immunolabeling reveals close appositions of NPY fibers with GnRH cells in the POA of the ayu (*Plecoglossus altivelis*) (169) and the Siberian sturgeon (170), suggesting the direct action of NPY in the regulation of GnRH neurons. Indeed, NPY stimulates GnRH release *in vitro* in the goldfish (108) and in the sea bream (110).

Neuropeptide-Y also regulates the HPG axis at the level of pituitary. *In vitro* treatment with NPY stimulates LH release from pituitary cells in the goldfish (107) and increases LH β and GTH α , but not FSH β mRNA levels in the tilapia pituitary (115). In addition, NPY fibers make close appositions on LH cells in the catfish pituitary (171).

These findings provide strong support for the stimulatory role of NPY in fish reproduction at the levels of hypothalamic GnRH and pituitary LH cells.

26RFamide (QRFP)

26RFamide is a 26-amino acid peptide, and was first isolated from the frog brain (121). In teleosts, 26RFa has been identified only in the goldfish (172). The 26RFa gene is highly expressed in the hypothalamus, and relatively less in the optic tectum-thalamus and in the testis (122). 26RFa and its mammalian homolog QRFP act as an orexigenic hormone in birds, mice (121, 172–174), and probably in fish (122).

The role of 26RFa has been implicated in the integration of metabolism and reproduction in vertebrates, including fish [see review in Ref. (89)]. In mammals, 26RFa stimulates LH and FSH release in rats *in vivo* and *in vitro* (pituitary culture) (175). In teleost, intraperitoneal injections of 26RFa significantly increase plasma LH levels in the goldfish (122). On the other hand, *in vitro* treatment with 26RFa shows no effects on LH release from pituitary cells. These facts indicate that 26RFa might act on the stimulation of the HPG axis through GnRH1 release in fish.

GALANIN (GAL)

GAL is a 29-amino acid peptide, expressed in the central nervous system and in the intestine. GAL stimulates feeding in the goldfish (123) and the doctor fish tench (124), indicating that GAL acts as an orexigenic hormone in fish as in mammals (176, 177).

Involvement of GAL in the control of HPG axis is evidenced in mammals. In rodents and humans, GAL neuronal fibers make close appositions with GnRH1 neurons (178–180), and GnRH neurons express a GAL receptor Gal-R1 in the rat (181). In fact, GAL stimulates *in vitro* GnRH release in rats (125). These data indicate that GAL is involved in the control of reproduction at the level of GnRH neurons.

In fish, there are no studies that demonstrated the role of GAL in the control of reproduction. However, close appositions of GAL fibers with gonadotropes in the proximal pars distalis (PPD) are seen in the sea bass (182). Similarly, fiber projections of GAL neurons in the PPD are observed in the rainbow trout (183), sea bream (184), and Senegalese sole (185), while no GAL fibers are observed in the pituitary of the Siberian sturgeon (170). Therefore, GAL might modulate the HPG axis at the pituitary level at least in some fish species.

GnRH2

As mentioned before, among the different forms of GnRH, neuronal fibers of GnRH2 (also known as chicken GnRH-II) are widely distributed in the vertebrate brain. In an insectivore, the musk shrew, GnRH2 stimulates sexual behavior and seduces food intake (186, 187), indicating that GnRH2 plays a role in connecting reproductive function and feeding regulation.

In fish species, the suppressive effect of GnRH2 on feeding has also been confirmed. Food consumption is significantly decreased by intracerebroventricular injections of GnRH2 but not GnRH3 in a dose dependent manner in the goldfish (102, 118) and the zebrafish (119).

GnRH2 also has effects on sexual behavior of fish. In the goldfish, GnRH2 stimulates reproductive behavior (188). Furthermore, there is a strong positive correlation between spawning behavior and GnRH2 gene expression (189), suggesting stimulatory

role of GnRH2 in reproductive behavior. GnRH2 is also detected in the goldfish pituitary (190) and induces LH release *in vitro* (120). Positive correlation between the pituitary GnRH2 levels and gonadal development is also observed in the striped bass (51), suggesting that it also have a hypophysiotropic role in some fish species. In the grass puffer, the amount of GnRH2 mRNA is slightly higher in the post-spawning females compared to spawning female (191). Therefore, GnRH2 may have different physiological roles depending on the physiological conditions of the fish.

PITUITARY ADENYLATE CYCLASE-ACTIVATING POLYPEPTIDE (PACAP)

PACAP was first isolated from the rat hypothalamus (192). PACAP is an anorexigenic factor in various vertebrates, including rodents (193), chicks (194, 195), and fish (196). To date, the role of PACAP in feeding has been studied only in one fish species, the goldfish.

PACAP increases plasma LH levels *in vivo* in the goldfish (197). *In vitro* studies showed that the stimulatory effect of PACAP on LH release is exerted at the level of the pituitary (113, 114). PACAP also stimulates the levels of GTH subunit mRNAs and FSH β mRNA in the pituitary of tilapia (115) and in the female blue gourami (116, 117), respectively. Dense projection of PACAP nerve terminals is seen in the pars distalis of the pituitary, where gonadotropes are localized, in the goldfish (198) and in the European eel (199). The expression of PACAP receptor in the pituitary is also observed in the goldfish (197). Therefore, PACAP stimulates GTH secretion in fish pituitary.

MELANIN-CONCENTRATING HORMONE (MCH)

MCH is a cyclic peptide, originally isolated from the pituitary of the chum salmon as a hormone involved in body color change (200). In the winter and barfin flounders, fasting stimulates hypothalamic expression of MCH (201, 202), suggesting that MCH acts as an orexigenic hormone as in mammals (203, 204). However, MCH acts as an anorexigenic hormone in the goldfish (105, 126, 205, 206). Therefore, like ghrelin, MCH acts as an orexigenic and anorexigenic neuropeptide depending on the fish species, although its orexigenic action in fish has to be confirmed.

In mammals, MCH modulates LH secretion in an estradiol-dependent manner [see a review in Ref. (207)]. The close appositions between MCH fibers and hypothalamic GnRH neurons (208, 209) and the expression of MCH receptors in GnRH neurons (209) suggest the direct action of MCH on GnRH neurons in mammals. MCH also acts at the pituitary level to modulate the release of LH (210). In teleosts, an *in vitro* study showed that salmon MCH stimulates the release of LH in a dose response manner from dispersed pituitary cells in the goldfish, suggesting a direct action of MCH on LH cells (127). Whether MCH acts on GnRH neurons in fish as in mammals remains unknown.

α -MELANOCYTE STIMULATING HORMONE (α -MSH)

α -MSH is one of melanocortins and derived from a precursor peptide encoded by the POMC gene (211). Among melanocortins and their receptors, α -MSH and melanocortin receptor 4 (MC4R) are involved in the control of food intake in vertebrates including fish. α -MSH or MC4R agonist inhibits food intake in the goldfish (128, 212) and in the rainbow trout (129), suggesting that the α -MSH/MC4R system play a role in the anorexigenic regulation of feeding in fish as in mammals.

Although the α -MSH/MC4R system is known to play a stimulatory role in reproduction at the level of GnRH neurons in mammals [see a review in Ref. (130)], available information is limited in teleost. Projection of α -MSH fibers in the PPD of the pituitary and differential expression of POMC gene between sexually inactive and active fish in the zebrafish suggests that some of POMC-derived products are involved in the stimulation of fish reproduction (213).

COCAINE- AND AMPHETAMINE-REGULATED TRANSCRIPT (CART)

CART is an anorexigenic neuropeptide originally isolated from the rat brain (160, 214). In fish, CART might also act as anorexigenic hormone in the goldfish (131), winter flounder (215), cod (216), channel catfish (217), zebrafish (218), and in the Atlantic salmon (219).

In mammals, CART is involved in the control of GnRH neurons. CART stimulates GnRH pulsatile release in rats (133, 134). The existence of close appositions between CART fibers and hypothalamic GnRH neurons in the Siberian hamster suggests the effect of CART on GnRH neuronal activity is a direct action (220).

In the catfish, the projections of CART fibers are observed in the PPD of the pituitary (221). CART is also expressed in LH cells of the catfish pituitary but only during sexual maturation period (222), suggesting its local function in the sexual maturation process. However, it should be noted that while similar expression of CART in LH cells is observed in the rat pituitary, CART inhibits the release of prolactin but not GTHs (223). Thus, the role of CART in the fish pituitary has to be examined.

CHOLECYSTOKININ (CCK)

CCK is found in the brain and in the gastrointestinal tract of various vertebrates. It has multiple biologically active forms, among which CCK-8 is the most abundant form in the brain (224). As in mammals, CCK has many physiological roles in fish, but functions primarily in the control of food intake as a satiety indicator (135).

In mammals, CCK decreases the pulse interval of GnRH release in goats (225). Furthermore, CCK implants into the POA, where GnRH neurons are located, increase the plasma levels of LH in rats (226). These data suggest that CCK acts at the levels of GnRH and stimulates reproduction. In fish, on the other hand, CCK seems to act on the pituitary. An immunohistochemical study showed that CCK neurons innervate into the PPD of the pituitary and that CCK stimulates LH release *in vitro* in the goldfish (136).

NESFATIN-1

Nesfatin-1, a nucleobindin-2 (NUCB2) encoded unmodified peptide, was first characterized in rats (227), and was shown to have anorexigenic actions in the goldfish (137, 138).

The number of studies about the function of nesfatin-1 in the control of reproduction is still limited. However, recent studies showed that nesfatin-1 acts as an inhibitory signal in the control of fish reproduction. Although nesfatin-1 plays a stimulatory role in LH secretion in rats (228), an intraperitoneal injection of nesfatin-1 decreases plasma levels of LH in the goldfish (139). At the same time, nesfatin-1 down regulates expression of GnRH, LH β , and FSH β genes, suggesting that the inhibitory action of nesfatin-1 takes place at the levels of GnRH neurons. Whether nesfatin-1 also functions at the level of the pituitary remains unclear.

PERIPHERAL HORMONES INVOLVED IN FEEDING, METABOLISM, AND REPRODUCTION

LEPTIN

Leptin is primarily produced by adipocytes of the white adipose tissue (229), and secreted into the blood circulation in proportion to the mass of body fat. The change in plasma leptin levels is detected by the hypothalamus and thereby it acts as a peripheral factor that signals nutritional status to the CNS [see review by Crown et al. (230)]. In teleosts including the goldfish and the rainbow trout, leptin functions as a peripheral signal to inhibit food intake (140, 141, 231, 232) as in mammals (233).

In mammals, leptin stimulates the HPG axis by promoting the synthesis and release of GnRH from the hypothalamus, and LH and FSH from the pituitary (234–236). In teleosts, leptin also stimulates the reproductive axis. Leptin increases *in vitro* LH release from the pituitary culture in the sea bass (142) and the rainbow trout (143). However, it should be noted that the stimulating effect of leptin on LH release is observed only on the pituitary samples from the fish in maturational stages. Furthermore, leptin expression levels increase with the onset of sexual maturation in the Arctic char (237) and the Atlantic salmon (238). Therefore, the role of leptin in sexual maturation seems to be conserved among vertebrate species.

GHRELIN

As in mammals, ghrelin is highly expressed in the stomach and moderately in the brain (144, 239, 240), and is involved in appetite stimulation, energy balance, feeding, and metabolism [see reviews in Ref. (241, 242)]. Interestingly, the role of ghrelin in fish differs in different fish species. It acts as an orexigenic hormone in the goldfish (144–146) and probably in the sea bass (243) and the zebrafish (244). On the other hand, ghrelin acts as an anorexigenic hormone in the rainbow trout (147) and probably in the burbot (245, 246). The opposite effects of ghrelin on food intake can be explained by species-specific neural pathways mediating the effect of ghrelin (247). The variations in the role of ghrelin in feeding may reflect different regulatory mechanisms of feeding in different teleost species.

In fish species, ghrelin acts as a stimulatory factor in the reproduction, although ghrelin inhibits the HPG axis in mammals [reviewed by Tena-Sempere (248)]. Intracerebroventricular injection of ghrelin increases plasma LH levels in the goldfish (148), indicating its stimulatory action on the HPG axis. The increase of plasma LH levels is, however, small and slow compared to the increase of plasma GH levels. This suggests that the stimulatory effect of ghrelin on plasma LH levels is not through the action of ghrelin on hypothalamic GnRH. Actually, the highest levels of ghrelin receptor mRNA are observed in the sea bream and goldfish pituitary (249, 250). *In vitro* treatment with ghrelin stimulates LH release in the goldfish (148, 250) and in the common carp (149), while pituitary levels of mRNA for LH β subunit is also increased. As no reports show fiber projections of hypothalamic ghrelin neurons into the pituitary in fish, ghrelin released from stomach/intestine might play a role in the LH secretion from the pituitary. Therefore, ghrelin might act as a stimulatory peripheral factor in reproduction at the level of pituitary, whereas its action on GnRH neurons is uncertain.

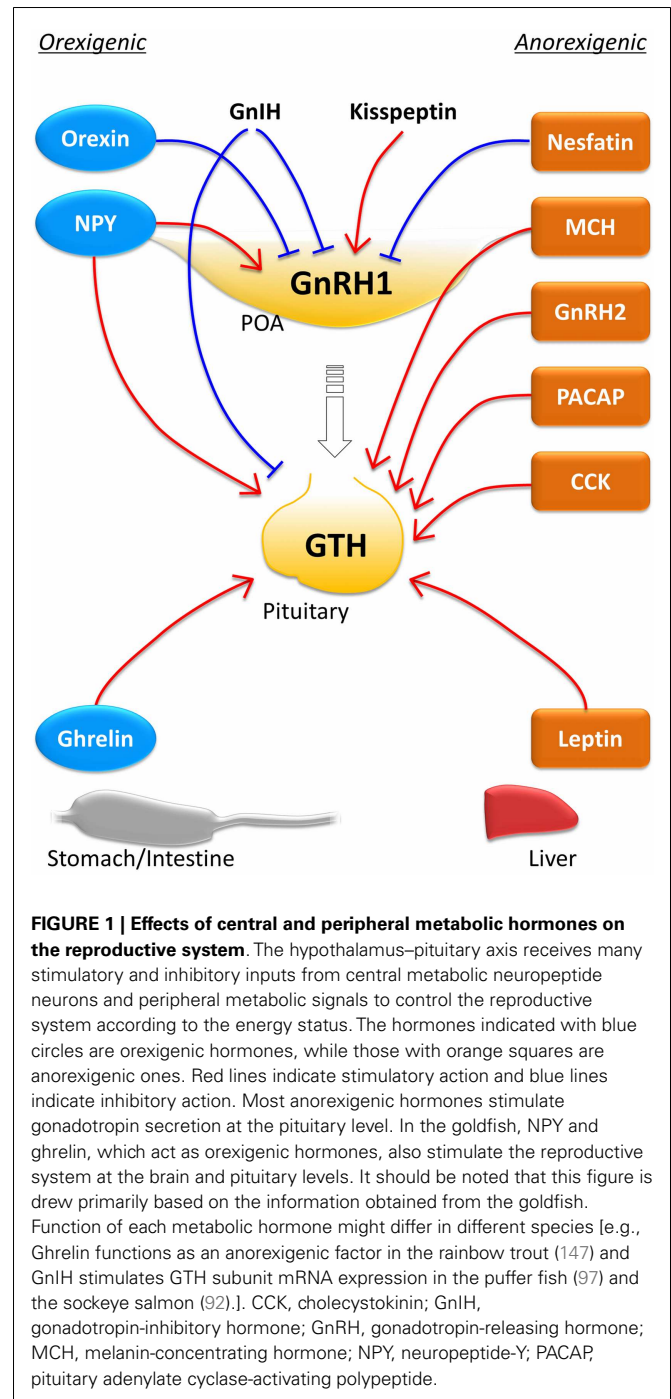
INTERACTIONS BETWEEN METABOLIC NEUROPEPTIDES AND THE REPRODUCTIVE SYSTEM IN THE CONTROL OF REPRODUCTION

As shown in the above section, many metabolic neuropeptides are involved in the control of reproduction at the level of hypothalamic GnRH neurons and at the level of pituitary gonadotropes (Figure 1). Among these metabolic neuropeptides, NPY and nesfatin-1 function as inhibitory factors on GnRH neurons, while orexin stimulates GnRH neurons. It is interesting that NPY and orexin, which possess orexigenic activity, act on the reproductive system in an opposite manner in the goldfish. It suggests that different metabolic neuropeptides might play a role in the control of reproduction under different physiological conditions. It should be noted, however, that the inhibitory role of orexin on spawning behavior and GnRH gene expression might be the result of orexin action on non-hypophysiotropic GnRH system. In the goldfish brain, hypophysiotropic GnRH type is expressed not only in the hypothalamic population but also in the olfactory bulb and mid-brain populations (190). Therefore, the inhibitory effect of orexin on the HPG axis need to be confirmed although it is clear that orexin has suppressive role in some aspects of reproduction.

At the pituitary level, it is evident that many metabolic neuropeptides including NPY, MCH, GnRH2, PACAP, and CCK stimulate LH secretion. In addition, peripheral metabolic signals such as ghrelin and leptin also stimulate LH secretion at the pituitary. The fact that most central neuropeptides and peripheral metabolic signals regulate the reproductive system indicates fundamental interaction between energy balance and reproduction, which is evolutionarily conserved from fish to mammal. However, both orexigenic and anorexigenic metabolic signals act as stimulatory factors in the reproductive system in fish. In mammals, feeding and reproduction are two alternatives in general. Therefore, orexigenic factors inhibit reproduction and anorexigenic factors stimulate reproduction [see review in Ref. (251)]. In fish species, on the other hand, a central orexigenic neuropeptide NPY and a peripheral orexigenic peptide ghrelin inhibit LH secretion in the goldfish and other species (Table 1). This indicates that metabolic regulation of the reproductive system in teleost is different from that in mammals, at least in some species.

Fish species have a variety of feeding and reproductive behaviors. For example, most salmonids and the winter flounder undergo a period of fasting just before the spawning season as a part of their normal physiology (252), whereas the goldfish do not have such fasting period. The halt of food intake during final maturation might require the differential usage of metabolic signals in these species.

Recently, kisspeptin has been proposed as a mediator of metabolic signals in the mammalian reproductive system, in particular on GnRH neurons [see reviews in Ref. (89, 253)]. In mice (254) and in the sheep (255), kisspeptin neurons in the arcuate nucleus possess leptin receptors, suggesting direct action of leptin on kisspeptin neurons. Furthermore, kisspeptin neurons receive innervations from other neurons that express leptin receptor (255). These facts suggest that leptin controls GnRH neurons through kisspeptin neurons *via* direct and indirect actions. Furthermore, kisspeptin neurons receive fiber projections from NPY and POMC neurons in mammals (255, 256). Therefore kisspeptin



neurons might play an important role in the integration of metabolic signals to control the reproductive system. In teleost, fasting induces a significant increase in *kiss2* mRNA levels in the hypothalamus, as well as an increase in LH β and FSH β mRNA levels in the pituitary in the Senegalese sole (*Solea senegalensis*) (257), suggesting negative correlation between energy balance and reproduction. However, to our knowledge, there is no information available regarding direct evidence of metabolic regulation of kisspeptin neurons in fish.

In addition to its primary role in reproduction, GnIH stimulates food intake in chickens (258) and in rats (259, 260), suggesting its potential role to switch from reproduction to feeding. Close appositions of GnIH fibers with NPY, orexin, MCH, and POMC neurons in the sheep (261) indicate the involvement of several feeding regulatory pathways. However, there are no studies reporting metabolic regulation of GnIH neurons in vertebrates. On the other hand, GnIH is known to be regulated by stress, photoperiod, and gonadal steroids to suppress the reproductive system (89). Therefore, GnIH neurons might have a role in the modulation of feeding according to the environmental factors in mammals. Whether GnIH plays a similar role in teleosts requires more studies.

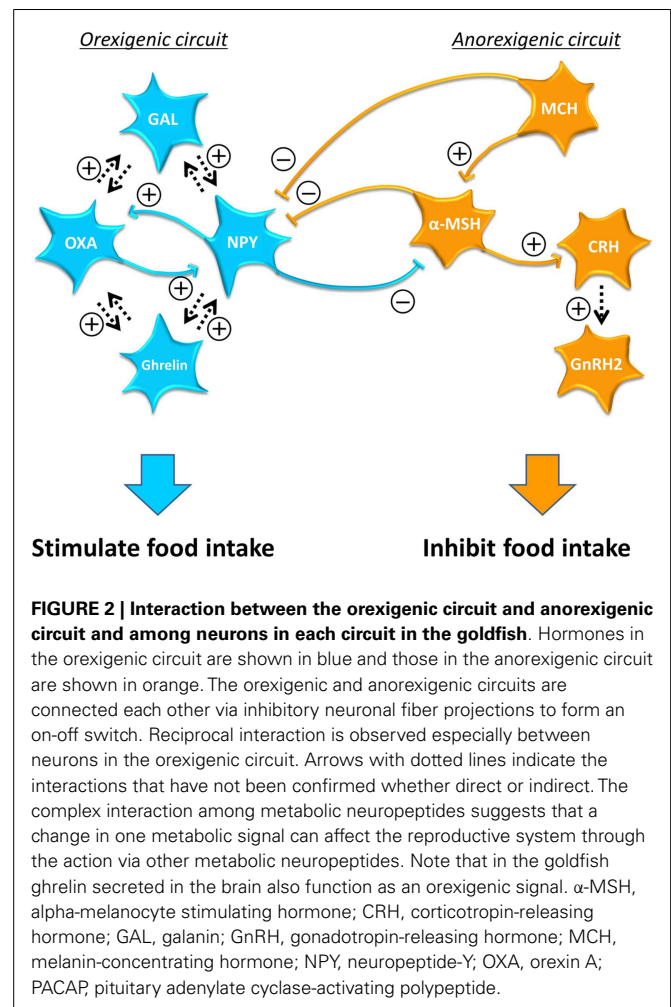
INTERACTIONS AMONG NEUROPEPTIDES TO CONTROL FEEDING

To monitor the amount of energy stock, central metabolic neuropeptide neurons receive peripheral signals including leptin and ghrelin. For example, in mammals leptin receptor is expressed in many metabolic neuropeptide neurons including orexin, NPY, GAL, MCH, POMC, CART, and CCK neurons [see reviews in Ref. (262, 263)]. In fish species, leptin also affects several central neuropeptide neurons. Administration of leptin reduces NPY mRNA levels in the goldfish (140), grass carp (264), and in the rainbow trout (141, 265). On the other hand, leptin increases the mRNA levels of CCK and POMC, which are anorexigenic neuropeptides, in the goldfish (140) and the rainbow trout (141, 265), respectively. A recent study showed that leptin receptor knockout medaka exhibit higher levels of NPY mRNA before and after feeding and lower levels of POMC mRNA levels after feeding together with increased food intake (266). Therefore leptin's anorexigenic effect might be mediated by these neuropeptides.

Double immunostaining revealed interactions among orexigenic/anorexigenic neuropeptide neurons in teleosts, in particular in the goldfish (Figure 2). Among anorexigenic neuropeptide neurons, MCH neuronal fibers project to α -MSH neurons (206) and α -MSH neuronal fibers project to CRH neurons (267). Furthermore, a study using antagonists against α -MSH receptor and CRH receptor showed that anorexigenic action of MCH is mediated by α -MSH and CRH (268). In addition, GnRH2 mediates anorexigenic effect of α -MSH and CRH (269). These results suggest that the MCH- α -MSH-CRH-GnRH2 pathway suppresses food intake in the goldfish, although it is not known whether CRH directly acts on GnRH2 neurons.

Among orexigenic neuropeptide neurons, NPY and orexin neurons make reciprocal connections in fish as in mammals. NPY neuronal fibers make close appositions with orexin neurons, whereas orexin neuronal fibers make close appositions with NPY neurons in the NPPv in the goldfish (270). Furthermore, co-injections of OXA and NPY result in food intake higher than that observed in fish treated with NPY alone (132). These results indicate that orexins and NPY induce orexigenic actions by mutual signaling pathways in the CNS in teleost. Probably the reciprocal interaction between NPY and orexin functions as a positive-feedback system to maintain food intake.

Moreover, the orexigenic and the anorexigenic circuits are also connected with each other. α -MSH neuronal fibers make close



appositions with NPY neurons, whereas NPY neuronal fibers project to α -MSH neurons in the goldfish (271). In addition, MCH neuronal fibers make close appositions with NPY neurons (272). These inhibitory inputs between the orexigenic and anorexigenic neurons might function as an on/off switch to decide whether eat or not eat by activating only one of the two circuits.

Studies using antagonists against of the receptors for metabolic neuropeptides further provided possible interaction among central metabolic neuropeptides in the goldfish. For example, GAL mediates the orexigenic action of orexin, and orexin mediates the orexigenic action of GAL (123). GAL also mediates NPY's action on food intake and *vice versa* (123). Besides, orexin mediates central action of ghrelin in food intake and central ghrelin mediates the action of orexin (273). Furthermore, NPY mediates the orexigenic action of ghrelin (274). These results indicate complex neuronal interactions especially among central orexigenic neuropeptides. This complex neuronal network suggests that many central neuropeptide neurons function in a coordinated manner to regulate food intake. To fully understand the whole circuit that controls food intake, further information on the neuronal interaction among central metabolic neuropeptides have to be obtained.

In addition to the evident neuronal interactions in the goldfish, more combinations of neuronal interactions were reported in other fish species. In the masu salmon (275) and the Siberian sturgeon (170), NPY and GAL neurons make reciprocal connections. In the medaka, orexin and MCH neurons send neuronal fibers to each other (156). In the barfin flounder, reciprocal connection between orexin and MCH neurons and between α -MSH and MCH neurons was reported (156). In the rainbow trout, CRH mediates the anorexigenic action of ghrelin (147). These facts suggest that the interaction among central metabolic neuropeptides is really complicated. Therefore, more fiber projection studies together with the localization of the neuropeptide receptors are necessary to understand proper relationships among these neuropeptides that consist of the regulatory circuits of food intake.

PERSPECTIVES

DIRECT INTERACTIONS AMONG CENTRAL METABOLIC NEUROPEPTIDES AND REPRODUCTIVE SYSTEM

Significant amount of information about the relationship among orexigenic and anorexigenic neuropeptides have been accumulated, particularly in the goldfish. However, the knowledge of direct interactions among these neurons is still not enough to draw a complete diagram of the neuronal circuit to control food intake and reproduction in fish. In particular, metabolic regulation of kisspeptin and GnRH neurons are still unknown, while it is suggested from mammalian studies. Further fiber projection studies using double immunostaining and localization of the neuropeptide receptors in certain neuronal cell bodies need to be performed.

SPECIES DIFFERENCES

There are many differences in the regulatory mechanism of food intake and reproduction not only between mammals and fish but also between fish species. The significant difference between fish species might be the result of the adaptation to a wide range of feeding habits and reproductive strategies. Therefore we have to be careful to combine data obtained from different species.

SEX AND MATURATIONAL STAGES

Several studies reported that the responses of the reproductive system to metabolic signals differ depending on the sex and the stage of sexual maturation. In fact, gonadal steroids modulate the effect of NPY on GnRH and LH release in the goldfish (276). Each study should use a particular sex and maturational stage to make comparison easy.

NUTRITIONAL CONDITIONS

Animals might change the metabolic control of reproduction according to the available energy stock. For example, short term food limitation attenuates sexual motivation, while remaining energy stock still maintains activity of the HPG axis. On the other hand, long term food limitation depletes the energy stock and stops the HPG axis to prioritize the energy supply to the survival. Thus, feeding conditions and the timing of experiment might be important to obtain comparable data.

ENDOCANNABINOID SYSTEM

The endocannabinoid system is involved in a variety of physiology including pain-sensation, mood, and memory. Importantly,

both energy balance and reproduction are modulated by the endocannabinoid system. Endocannabinoids modulate several hypothalamic metabolic neuropeptides in mammals [see reviews in Ref. (277, 278)]. The endocannabinoid system also regulates food intake in fish (279, 280). In mammalian and non-mammalian vertebrates, the endocannabinoid system regulates hypothalamic GnRH neurons and pituitary LH cells directly and indirectly [see reviews in Ref. (281, 282)]. Interrelation among these systems might be an additional mechanism underlying the interaction between mood, stress, appetite, and reproduction.

CONCLUSION

In summary, the cellular and molecular basis for the integration of feeding and reproduction involves a complex interaction of the reproductive system with metabolic neuropeptides and peripheral fuels. The metabolic neuropeptides, particularly orexin, NPY, PACAP, MCH, nesfatin, GnRH2, and CCK play an important role in the reproduction by either regulating GnRH neurons in the hypothalamus or by stimulating gonadotropes in the pituitary. Peripheral metabolic signals such as ghrelin and leptin also act on the pituitary to stimulate LH secretion. It should be, however, noted that compared to mammals, fishes show a great variety of feeding and reproductive habits. The variations of metabolic control of reproduction in different teleost species may reflect different requirement of energy status for reproduction in different species. Compared to mammals, fish represent a vast phylogenetic group, which shows a significant level of diversity with regards to morphology, ecology, behavior, and genomes (283). Thus, species differences in the neuroendocrine control of reproduction have to be taken into consideration in teleosts. In addition, more detailed studies about the interconnections among metabolic neuropeptide neurons, effects of sexual maturation, and nutritional conditions will provide more precise figure of the metabolic control of reproduction. Furthermore, differential control of multiple GnRH neuronal population by the neuropeptides and metabolic signals should be examined to elucidate their roles in different aspects of metabolic control of reproduction.

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Pleiotropic activities of HGF/c-Met system in testicular physiology: paracrine and endocrine implications

Giulia Ricci^{1*} and Angela Catizone²

¹ Department of Experimental Medicine, School of Medicine, Second University of Naples, Naples, Italy

² Department of Anatomy Histology, Forensic Medicine and Orthopedics, School of Medicine, "Sapienza" University of Rome, Rome, Italy

Edited by:

Gilda Cobellis, Second University of Naples, Italy

Reviewed by:

Paola Piomboni, University of Siena, Italy

Adele Chimento, University of Calabria, Italy

*Correspondence:

Giulia Ricci, Laboratory of Histology and Embryology, Department of Experimental Medicine, Second University of Naples, Via Luciano Armanni 5, Naples 80138, Italy
e-mail: giulia.ricci@unina2.it

In the last decades, a growing body of evidence has been reported concerning the expression and functional role of hepatocyte growth factor (HGF) on different aspects of testicular physiology. This review has the aim to summarize what is currently known regarding this topic. From early embryonic development to adult age, HGF and its receptor c-Met appeared to be clearly detectable in the testis. These molecules acquire different distribution patterns and roles depending on the developmental stage or the post-natal age considered. HGF acts as a paracrine modulator of testicular functions promoting the epithelium–mesenchyme cross-talk as described even in other organs. Interestingly, it has been reported that testicular HGF acts even as an autocrine factor and that its receptor might be modulated by endocrine signals that change at puberty: HGF receptor expressed by Sertoli cells, in fact, is up-regulated by FSH administration. HGF is in turn able to modify endocrine state of the organism being able to increase testosterone secretion of both fetal and adult Leydig cells. Moreover, c-Met is expressed in mitotic and meiotic male germ cells as well as in spermatozoa. The distribution pattern of c-Met on sperm cell membrane changes in the caput and cauda epididymal sperms and HGF is able to maintain epididymal sperm motility *in vitro* suggesting a physiological role of this growth factor in the acquisition of sperm motility. Noteworthy changes in HGF concentration in seminal plasma have been reported in different andrological diseases. All together these data indicate that HGF has a role in the control of spermatogenesis and sperm quality either directly, acting on male germ cells, or indirectly acting on tubular and interstitial somatic cells of the testis.

Keywords: HGF, c-Met receptor, testis, male gonad development, testicular cell differentiation, sex hormones

THE HEPATOCYTE GROWTH FACTOR MACHINERY AND ITS BIOLOGICAL FUNCTIONS

The hepatocyte growth factor (HGF) is a pleiotropic cytokine originally purified as a potent mitogen for hepatocytes (1, 2) and subsequently identified as a “scatter factor” (3, 4). HGF is synthesized as an inactive single chain precursor that is cleaved to acquire the bioactive disulfite-linked heterodimeric form (2, 5). One of the most recognized activators of HGF precursor is the HGF activator protein (HGFA), which is a serine protease able to cleave immature HGF precursor to form a mature bioactive HGF (6). Interestingly, HGF activation may be provided also by active metalloproteinases (MMP2 and MMP9) and by plasminogen activator (PA). More recently, it has been discovered also an inhibitor of HGF activation (called HGF inhibitor or HAI) that is a serine protease inhibitor that blocks HGFA activation (7). The modulation of HGFA and HAI in the tissue microenvironment is able to maintain the correct HGF availability since HGF has been established as an important factor for tissue homeostasis (8).

c-Met is the unique HGF receptor and it is normally expressed by cells of epithelial origin whilst HGF expression has been mainly found restricted to cells of mesenchymal origin. c-Met receptor presents tyrosine-kinase activity and, upon HGF stimulation, this receptor triggers several transduction pathways responsible for

its multiple biological responses including proliferation, motility, migration, morphogenesis, tubulogenesis, differentiation, and angiogenesis (8–10). In particular, c-Met activation by its ligand HGF triggers transphosphorylation of the catalytic tyrosines Tyr 1234 and Tyr 1235, which positively modulate its enzymatic activity. c-Met c-terminal tail contains tyrosines Tyr 1349 and Tyr 1356, which represent, when phosphorylated, the multifunctional docking site of the receptor. These two amino acid residues are able to recruit several transducers and adaptors after c-Met activation, thus explaining the whole spectrum of pleiotropic biological activities exerted by HGF/c-Met system (11). These transducers interact with the intracellular multi-substrate docking site of c-Met either directly, such as GRB2, SHC, SRC, and the p85 regulatory subunit of phosphatidylinositol-3 kinase (PI3K), or indirectly through the scaffolding protein Gab1 such as PLC- γ (12–17).

c-Met knock-out mice have provided only partial information in the understanding of the role of HGF/c-Met system in the embryonic development of mammals since this animal model showed an embryonic lethal phenotype due to severe placental defects. However, some information was drawn by these knock-out animals indicating an essential role of this growth factor in gastrulation, angiogenesis, myoblast migration, and liver development (12, 18, 19). The study of HGF/c-Met system expression

during the mouse organogenesis has provided great insights in the understanding of HGF function. This system, in fact, has been found in several developing organs being HGF expressed in the mesenchyme and c-Met in the epithelial part of the developing tissue. On the basis of this preliminary observation, it has been demonstrated and well established that HGF/c-Met system mediates signal exchange between mesenchymal and epithelial cells in embryonic morphogenesis as well as in post-natal stroma–parenchyma cross-talk and tissue homeostasis (20). In addition, HGF has been demonstrated to exert unique developing capability as a morphogen of tubular structures and inducer of harmonic cell migratory activities (21–23). Even if HGF could be mainly identified as paracrine factor in the mesenchyme–epithelium cross-talk, it has been also found that this growth factor is actively delivered *via* blood vessels to injured organs allowing their repair and homeostasis (24, 25). Besides its action as a hormone, it has been demonstrated that HGF expression is regulated by blood hormones, neurotransmitters, and cytokines, such as GH (26), Norepinephrine (27), and systemic prostaglandin E (28). In addition, the discovery of HGF/c-Met system in the regulation of testis and ovary differentiation and physiology has given rise to an increasing amount of evidences that support the intriguing hypothesis of a cross-talk among gonadotropins, sex hormones, and HGF in both the female and male gonads (29, 30). This review aims to focus on what is known on the implications of HGF in the autocrine, paracrine, and endocrine regulation of testicular physiology.

ROLES OF HGF IN THE PHYSIOLOGY OF THE TESTIS

Hepatocyte growth factor/c-Met system has been found expressed and active during all the phases of pre-natal and post-natal testis development. The activities of the HGF machinery on the testicular tissue vary depending on the different phases of both pre-natal and post-natal ages: these ranges from the modulation of both steroidogenesis and apoptosis to guiding mitosis, morphogenesis, and differentiation. Overall, the emerging picture suggests HGF as one of the growth factors which cooperates at different levels to support male reproductive health and is deeply involved in the harmonic control of spermatogenetic process.

HGF/c-MET SYSTEM IN TESTIS EMBRYONIC DEVELOPMENT

As previously stated during pre-natal development, HGF/c-Met system is expressed and active in a wide variety of developing organs, such as the liver, lung, pancreas, intestine, and kidney. HGF transcripts were mainly found localized in the mesenchymal part of these organs whereas c-Met expression appeared mainly restricted to the epithelial portion (23), thereby indicating an important role for HGF in epithelial–mesenchymal interaction during embryonic morphogenesis. Moreover, it has been reported that HGF may induce mesenchymal to epithelial cell conversion (31). Testis develops from the collaboration and the cross-talk of intermediate mesoderm and celomic epithelium. In addition, its morphogenesis is characterized by a conversion of mesenchyme in epithelial cells (for instance Sertoli and Leydig cells) as well as by a tight cross-talk between its epithelial and mesenchymal cells. By this point of view, it may be intriguing but not surprising that HGF/c-Met system has been found during the entire period

of testis embryonic development. What seems noteworthy is that the distribution patterns and functional roles of this molecular machinery change in the different morphogenetic phases of the testicular embryonic development.

Early testicular morphogenesis

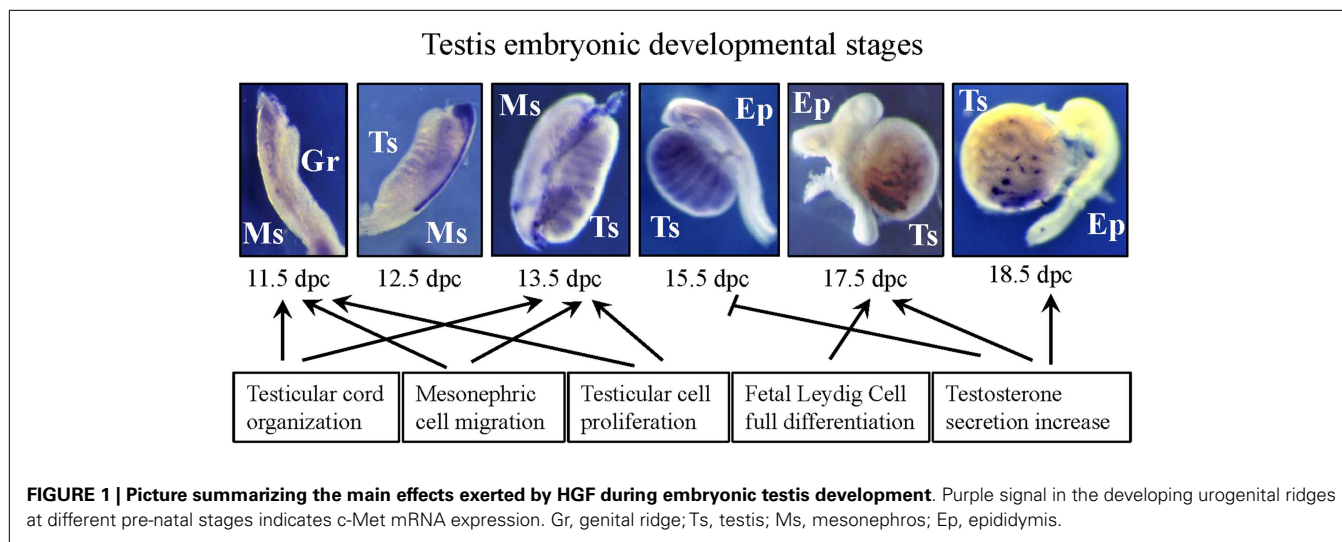
Hepatocyte growth factor/c-Met expression has been reported starting from 11.5 dies post coitum (dpc) and continues through the entire period of pre-natal development. Actually, at 11.5 dpc only HGF is present in the celomic epithelium underlying male urogenital ridges whereas, at the same pre-natal age, c-Met is not already expressed in the gonads even if it is clearly detectable in the mesonephric mesenchyme (32, 33). One of the first specific features of male gonad development is represented by the mesonephric cell migration toward the developing testis; this cell migration begins at 11.5 dpc and was described up to 16.5 dpc in a sex-specific manner (34–37). Consistent with the observed HGF/c-Met distribution pattern in the early gonad, HGF has been established as one of the growth factors potentially involved in the chemo-attraction of mesonephric cells (32, 33, 38) thus collaborating with other growth factors such as FGF9, PDGF, and neurotrophins, to establish the male differentiation niche for somatic and germ cells (38–41) (Figure 1).

Testicular cord morphogenesis

Seminiferous cord formation is the critical morphogenetic event of testis development. To obtain a correct cord formation, the previously reported migration of mesenchymal cells from the mesonephros into the developing gonads is necessary (37, 42). However, this complex phenomenon requires the harmonic coordination of several biological processes such as proliferation, differentiation, and polarization of pre-Sertoli cells present in the “morphologically indifferent” gonad and their association with the primordial germ cells. The coordination of these events requires a tight epithelium–mesenchyme cross-talk that is guaranteed by the action of specific local growth factors (43–45) and HGF has been indicated as one of them. Testicular cords begin to organize at 12.5 dpc. At the same developmental age, c-Met starts to be expressed by the developing testis and seems to be confined in the testicular cords of this organ. As reported for other organs, at the same stage of development, HGF expression is present in the differentiating stroma and in differentiating myoid cells confirming the capability of HGF/c-Met system to mediate epithelium–mesenchyme exchange (32, 33). Using organ culture of indifferent male urogenital ridges, it has been demonstrated that HGF is able to mediate testis differentiation and testicular cord formation in *ex vivo* organ culture condition (32, 33, 38). Since this *ex vivo* differentiation is the result of the coordination of cell migration, cell proliferation, and tubulogenesis, using *in vitro* assays able to discriminate between these different phenomena, it has been established that HGF is able to trigger all these events, again confirming the multiple biological activities that are mediated by this molecular machinery (32, 33, 38) (Figure 1).

Fetal Leydig cell differentiation and endocrine implications

c-Met receptor continues to be expressed by testicular cord up to 15.5 dpc. It is interesting to notice that in the late part of pre-natal



development (since 17.5 dpc to birth) c-Met distribution pattern drastically changes, being down-regulated in the testicular cords and up-regulated in the interstitial fetal Leydig cells (46). HGF is always present in the interstitial compartment, but, interestingly, it is not produced by mouse fetal Leydig cells. Thus HGF acts as a paracrine factor even on differentiating fetal Leydig cells reproducing in the interstitial compartment the epithelium–mesenchyme cross-talk present between interstitium and testicular cords in the embryonic stages before this pre-natal age. Actually, steroid-producing fetal Leydig cell lineage starts to be detectable in the testis early on 12.5 dpc but their differentiation process involves all the further stages of pre-natal development when they increase in number and gradually acquire the capability to modulate androgen secretion in response to local and endocrine cues (39, 47, 48). It is worth to highlight that when mesenchyme derived fetal Leydig cells start to acquire their fully differentiated phenotype in late embryogenesis (49), they start to express c-Met on their surface. The latter observation allowed to hypothesize a role for this growth factor in the modulation of testicular pre-natal endocrine function. In rodents, in fact, fetal masculinization and increase of plasma androgens occur before the hypothalamic–pituitary–gonadal axis to be functional (50) since LURKO mice (that lack the luteinizing hormone receptor) have normal androgen levels and testicular phenotype at birth (51). Thus there is a common agreement in the scientific community that states the differentiation of fetal Leydig cells is under the control of local growth factors and HGF seems to be one of them. In fact, in 17.5 and 18.5 dpc testicular organ culture, HGF is able to stimulate testosterone production (46) and fetal Leydig cell survival and full development (52). Noteworthy at 15.5 dpc, when c-Met is not detectable on fetal Leydig cells but is still expressed in seminiferous cords, HGF has been demonstrated not able to modify testosterone secretion in testicular organ culture. From these data HGF can be numbered besides PDGF, DHH, TGF- β , and IGF-I as one of the growth factors responsible of the normal pre-natal steroidogenesis (39, 48, 52–55).

This phenomenon may be relevant for the onset of the first cross-talk among gonad, hypothalamus, and pituitary gland, and

potentially involved in the acquisition of secondary sex-specific features and brain testosterone imprinting (Figure 1).

HGF/c-MET SYSTEM IN THE PHYSIOLOGY OF POST-NATAL TESTIS

Even if the studies on pre-natal morphogenetic functions of HGF have been established using mouse models, the post-natal roles of HGF on testicular physiology have been determined mainly using rats since testicular cell isolation is better characterized for this animal model. Intriguingly, many parallel mechanisms exist comparing ovarian and testicular function and some of them, with particular attention to endocrine function, will be highlighted in this part of the review.

Sertoli cells

Correct Sertoli cell differentiation is crucial in order to maintain the local microenvironment necessary to sustain spermatogenic process (56, 57). Several growth factors have been described as local modulators of Sertoli cell physiological niche and HGF can be numbered in this cohort since it has been demonstrated as a paracrine and autocrine modulator of Sertoli cell physiology. In the rat, c-Met mRNA and protein were detected in the post-natal testis starting from 10 dies post partum (dpp) even if they appear on Sertoli cells not before 25 dpp and their expression increases at 35 dpp. As previously reported in the embryonic testis, also in the post-natal testis the main source of HGF seems to be represented by the interstitial cells and by the myoid cells, reproducing the epithelium–mesenchyme cross-talk observable during the morphogenesis of the testis. Despite this observation, in the post-natal testis, HGF has often been demonstrated to be expressed also by the same cell lineages that express c-Met and Sertoli cells are not an exception. These data suggest that HGF levels could be finely regulated by different testicular cell types and that the action of this factor is not only paracrine but seems to be also autocrine and maybe endocrine. Interestingly, dissociated rat Sertoli cells as well as the Sertoli cell line SF7 cultured in the presence of HGF, are able to organize in tubular-like structures showing, even in the post-natal testis, the morphogenetic and tubulogenic ability of this growth factor (58, 59). This observation demonstrates that HGF

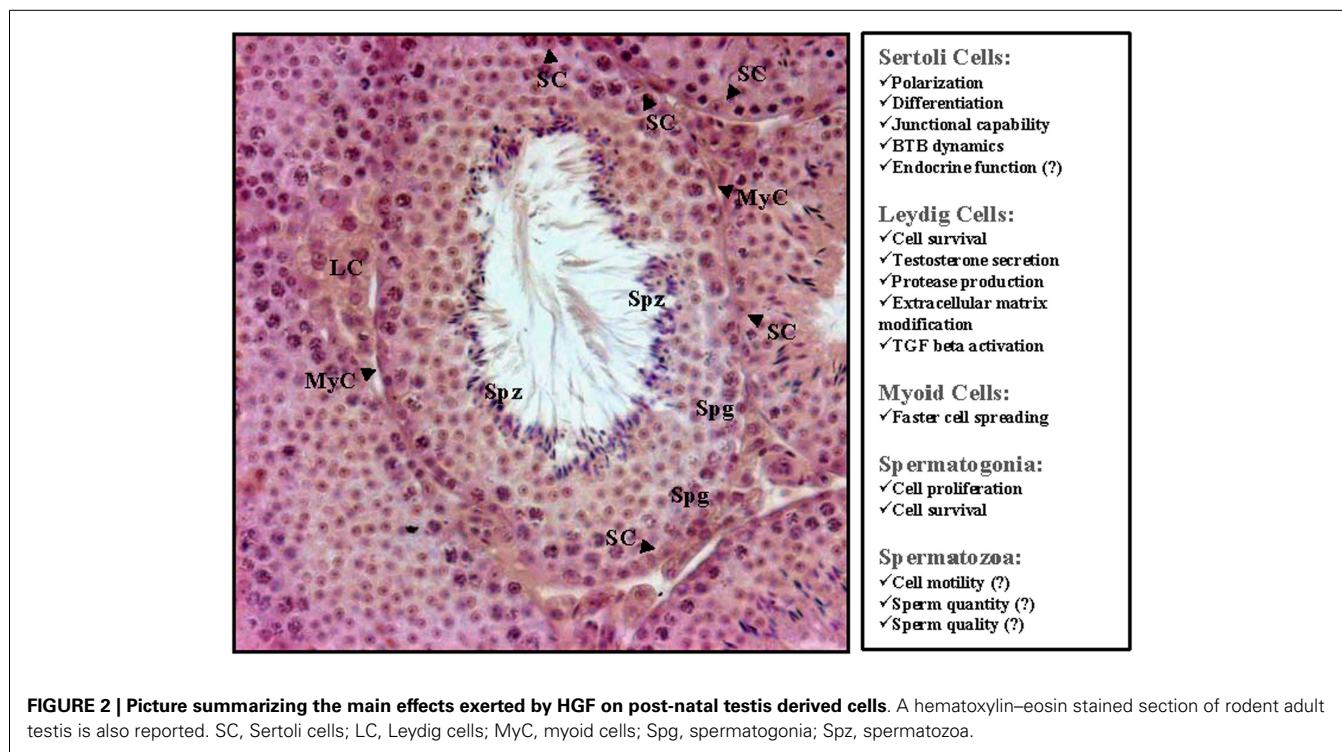


FIGURE 2 | Picture summarizing the main effects exerted by HGF on post-natal testis derived cells. A hematoxylin–eosin stained section of rodent adult testis is also reported. SC, Sertoli cells; LC, Leydig cells; MyC, myoid cells; Spg, spermatogonia; Spz, spermatozoa.

is able to guarantee the right cue for the maintenance of correct Sertoli cell polarization that is one of the parameters showing full differentiated Sertoli cell phenotype. These data together with the age of onset of Sertoli cell sensitivity to HGF have strongly suggested that this growth factor may be involved in testicular cord lumen and blood–testis barrier (BTB) formation. This particular topic will be fully expanded in a paragraph below.

Sertoli cells are one of the key somatic actors of endocrine hypothalamus–pituitary–gonadal axis cross-talk being able to produce and secrete estrogens in response to FSH and thus to regulate the spermatogenic process. As HGF has been proposed as one of the factors able to modify Sertoli cell physiology and to maintain their differentiated phenotype, it is conceivable to hypothesize that this factor has a role in the modulation of gonad–pituitary cross-talk. It was suggested by Zachow and Uzumcu in 2007 (30), that there is an intriguing parallelism between male and female gonad that hypothesizes some endocrine implications of HGF in the physiology of both organs. It has been reported, also, that HGF can down-modulate ovarian steroidogenesis suppressing FSH-dependent 17β -estradiol production by directly impairing CYP19 enzyme (60, 61). It is well known that Sertoli cells represent the testicular counterpart of granulosa cells and are the testicular source of 17β -estradiol. Sertoli cells are capable to produce the greatest quantity of 17β -estradiol in the first 10–20 days of post-natal age (62). Interestingly, HGF together with c-Met is not present on Sertoli cells at post-natal day 10 (63, 64) whilst both the receptor and the ligand appear expressed by Sertoli cells since post-natal day 25 (64, 65), which is the time when 17β -estradiol production by Sertoli cells begins to be reduced (62). All together these observations allow to hypothesize that HGF could locally control *in vivo* Sertoli

cell 17β -estradiol production in a similar way of what observed in granulosa cells. Consistent with these data, FSH has been demonstrated able to up-regulate c-Met expression in Sertoli cell cultures (65) whose activation in turn suppresses, following this hypothesis, Sertoli cells 17β -estradiol synthesis. The proposed mechanism, that deserves further investigations, suggests that HGF/c-Met system may be responsible for a local modulation of FSH-dependent estrogen production, modulating both enzyme activity and c-Met receptor availability (Figure 2).

Germ cells and spermatozoa

It has been reported by several groups that c-Met is expressed in both human and rodent male germ cells: this observation is interesting since it means the expression of this receptor is conserved at least among mammals (66–68). In rats, this receptor is always present during spermatogenic process from spermatogonia to spermatozoa. HGF has been shown to control germ cell mitotic activity being able to significantly increase spermatogonial cell proliferation from 8 to 30 days old rat testis in *ex vivo* organ culture. This result on spermatogonia cells appears to be more relevant highlighting that the HGF activator inhibitor (HAI-2) is expressed exclusively in primary spermatocytes (69) strongly indicating that mitotic germ cells need HGF signal whereas at the beginning of meiotic process this proliferating cue needs to be inhibited in order to allow germ cell meiotic entry.

Germ cell apoptosis is finely controlled in the testis in order to guarantee the best selection of differentiating male gametes and HGF has been demonstrated to be involved even in the control of this biological process. This growth factor, in fact, has been demonstrated to act also as a survival factor for male germ cells

since it is capable to significantly decrease germ cell apoptosis (67). The lowest protective effect (35% reduction of apoptosis) was found in late prepubertal rats and this finding is probably due to the fact that the highest level of apoptosis has been described at this age (70). Alternatively, this observation could be due to the presence of a more complex network of pro-apoptotic and anti-apoptotic factors present in the older animals (Figure 2). This result on healthy animals is reinforced by Goda and coworkers who studied a rat experimental cryptorchid model (71). This pathology is characterized by spermatogenic failure and germ cell loss. The adenovirus-mediated HGF gene transfer in the testis of these animals induced over-expression of HGF and significantly decreased apoptotic germ cell number, restoring spermatogenesis and testicular weight.

It is well known that germ cell proliferation and survival are controlled by endocrine signals: for instance FSH stimulates spermatogonial proliferation both *in vivo* and *in vitro* (72–74). In addition, testosterone and FSH regulate germ cell apoptosis (75, 76) probably acting via somatic cells considering the absence on the germ cells of their respective receptors (77, 78). By this point of view, HGF may be considered one of the local cytokines already identified (57, 79–83) that collaborates with the endocrine signals to promote the correct male germ cell homeostasis.

There has not been a report of any effect of HGF on meiotic germ cells, even if they express c-Met receptor on their surface (67). However, several groups have reported that c-Met is expressed on the surface of rat (66), and human epididymal spermatozoa (68, 84) and that HGF is present in mouse (85), rat (66), and human (86) epididymis. It is fair to say that literature data on the role of HGF on epididymal spermatozoa are often controversial. The first finding that strongly suggested a role of HGF in epididymal sperm maturation was reported by Naz and coworkers in 1994 (85). This group showed a specific region distribution pattern of HGF in the mouse epididymal tract with the highest levels of the growth factor in the distal corpus and cauda, where sperms acquire their motility. In the same study, HGF was found able to slightly induce cell motility on immotile sperms. Noteworthy, also c-Met distribution pattern on sperm surface seems to change from testicular to caput and cauda epididymal spermatozoa in rats (66). In addition, the previously mentioned effect on sperm motility was, at least in part, confirmed on rat epididymal sperms in which HGF has a positive effect on the *in vitro* maintenance of epididymal sperm motility even if, actually, the factor was not able to significantly increase the percentage of motile cells (66). Interestingly, c-Met receptor on human sperm has been found activated indicating that the HGF/c-Met system is functionally active in epididymal spermatozoa (84). However, the same motogenic effect reported in rodents failed to be demonstrated on human sperms (87) and the role of this growth factor on human sperm physiology is still a matter of debate (Figure 2). It was suggested that modifications in HGF seminal plasma concentration could be related with different andrological diseases and male infertility, but actually as in this case conflicting data are reported in the literature (87–89). It is fair to notice that male infertility could be due to really different causes: it is likely that the reported literature controversy may depend on the difficulties in classification of andrological diseases considered eligible for this particular study by the different research groups.

Further studies are needed to better clarify this point that deserves to be deeper investigated.

Blood–testis barrier

The described morphogenic and motogenic effect on cultured pre-natal and post-natal Sertoli cells allowed to hypothesize that HGF may modulate junctional capability of this cell type. It is well known, in fact, that HGF is a “Scatter Factor” able to modulate junctional behavior of target cells. In adult mammalian testes, Sertoli cells form junctional complexes with neighboring Sertoli cells that have been described from a long time (90). These junctional complexes consist of tight junctions and testis specific cell to cell actin based anchoring junctions which are both involved in the formation of the BTB. BTB separates the seminiferous epithelium in two different niches: the basal compartment, that encloses mitotic spermatogonia, and the adluminal compartment that encloses male meiotic germ cells. BTB integrity is necessary to allow the correct spermatogenic process, but its structure is highly dynamic. Junctional complexes of BTB, in fact, are able to disassemble and reassemble to allow the passage of pre-leptotene spermatocytes across the barrier (90, 91). In the last years, multiple reports from different laboratories have indicated that BTB permeability and physiological dynamics are regulated by a complex interaction of bioactive molecules including gonadotropins, testosterone, TGF- β , TNF- α , and interleukin-1a (92–98). Since 2008, HGF must be included in this number of factors (58, 99). In pubertal and adult rats it has been reported, in fact, that HGF is involved in the disassembling of the polygonal structures formed by occludin around the Sertoli cells. Moreover, it was demonstrated a quantitative occludin decrease in the tubules cultured in the presence of HGF by means of both confocal microscopy and Western blot analysis. In addition, HGF modifies the position of the tight junctions: it is indicated by the shift in the position of the occludin within the tubule treated with the growth factor compared to the controls. These data indicate a role of HGF in the modification of Sertoli cells junctional behavior. Interestingly, in adult rats HGF is maximally expressed at stages VII–VIII of the cycle, when germ cells traverse the BTB, whereas its levels fall in the subsequent stages IX–XII and XIII–I (58). This observation gives rise to the intriguing hypothesis that HGF produced by Sertoli cells could autocrinally regulate BTB in a stage dependent manner. It is relevant to highlight that HGF mediated BTB dynamism may be potentially due not only to a direct motogenic effect of HGF on Sertoli cells but also to the capability of HGF to modify the seminiferous tubule microenvironment promoting the increase of TGF- β active fraction. This phenomenon could be ascribed, at least in part, to the uPA level increase mediated by HGF in seminiferous tubule cultures (58, 99) (Figure 2).

Myoid cells

Myoid cell lineage was the first isolated testicular cell type in which HGF/c-Met system has been discovered (63). Even if HGF has always been found expressed both in pre-natal and post-natal myoid cells (33, 63, 64), c-Met was detectable only in post-natal cells indicating a paracrine function during embryonic development and a paracrine/autocrine role in post-natal testis. Noteworthy, myoid cells isolated from prepubertal rat testis (10 and

20 days old rats) express c-Met receptor at high level whereas the expression level decreases in pubertal and adult myoid cells (35 and 60 days old rats). Consistent with these results, HGF is able to induce a faster cell spreading of prepubertal myoid cells but not able to modify this parameter on myoid cells isolated from pubertal animals (Figure 2) (64). Despite myoid cells were the first testicular lineage in which HGF/c-Met system has been described, the role exerted by this machinery in their physiology needs to be better investigated. Probably, one of the roles exerted by myoid cells is to provide a source of this factor both for Leydig and Sertoli cells.

Leydig cells

As well as mouse fetal Leydig cells, also Leydig cells isolated from pubertal rats expressed c-Met receptor (100). Physiological activity of HGF on pubertal rat Leydig cells presents some similarities with their fetal counterparts: in particular as HGF has been demonstrated to promote basal testosterone secretion and Leydig cell survival (100) both in Leydig cell primary culture and in *ex vivo* organ culture. Intriguingly, the steroid modulator activity is not confined in male gonad but was also described in theca cells, which are the Leydig cell ovarian counterparts. In rat theca cells, in fact, HGF suppressed LH-dependent androstereone secretion, while stimulated basal and LH-induced progesterone production (60). It is fair to highlight the parallelism between male and female gonad and to notice that steroid production modulation in response to local cues is quite relevant for gonad physiology since sex hormones are not only important for endocrine homeostasis via pituitary–gonadal axis cross-talk but also act as paracrine regulators of male and female gametogenesis. In addition, local increase of testosterone could be important for BTB dynamism that, as previously stated, was also directly modulated by HGF.

Besides its effect on testosterone secretion, it is worth mentioning that HGF exerts a broader effect on Leydig cell secretory activities: HGF administration to isolated rat Leydig cells was able to increase the secretion of active form of several proteases such as MMP2 and uPA (101). Interestingly, HGF administration was also able to increase active TGF- β . Viewed together these data suggest that increased amount of active TGF- β could not be a direct effect of HGF but a consequence of the HGF-dependent increased uPA and MMP2 activity (102–104).

Different types of molecules can be substrates of MMPs including growth factors, tyrosine-kinase receptors, extracellular matrix proteins, and cell adhesion molecules. HGF administration on isolated Leydig cells significantly reduces the amount of fibronectin indicating that this growth factor might modify interstitial extracellular matrix components and in turn changes significantly adhesive microenvironment and cytokine availability (Figure 2). It is fair to highlight that extracellular matrix homeostasis is necessary for spermatogenesis and that a thickened lamina propria has been reported associated with impaired spermatogenesis (105) and that HGF has demonstrated to have anti-fibrotic effect in the regulation of extracellular matrix composition even in other organs (8). All together, the presented data indicate a relevant role of HGF in the regulation of Leydig cell metabolic activities and in the composition of the interstitial tissue. The reported results

strongly indicate that HGF/c-Met system is implicated in the local control of endocrine testicular machinery.

CONCLUDING REMARKS

Hepatocyte growth factor has been well established as a key regulator of the development and homeostasis of many organs. An increasing amount of evidences is demonstrating its important role in several aspects of pre-natal and post-natal testicular physiology. A huge job has been done but we must deal with a major one to figure out what might be the implications of this factor in the reproductive health of human beings. A better understanding of the molecular mechanisms carried out *in vivo* by this growth factor could be a useful prerequisite in order to address idiopathic andrological diseases.

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Endocannabinoids are involved in male vertebrate reproduction: regulatory mechanisms at central and gonadal level

Patrizia Bovolín^{1,2*}, Erika Cottone¹, Valentina Pomatto¹, Silvia Fasano³, Riccardo Pierantoni³, Gilda Cobellis^{3†} and Rosaria Meccariello^{4†}

¹ Department of Life Sciences and Systems Biology, University of Turin, Turin, Italy

² Neuroscience Institute of Turin, University of Turin, Turin, Italy

³ Dipartimento di Medicina Sperimentale, Seconda Università di Napoli, Naples, Italy

⁴ Dipartimento di Scienze Motorie e del Benessere, Università di Napoli Parthenope, Naples, Italy

Edited by:

Yong Zhu, East Carolina University, USA

Reviewed by:

Paola Piomboni, University of Siena, Italy

Paola Grimaldi, University of Rome Tor Vergata, Italy

*Correspondence:

Patrizia Bovolín, Department of Life Sciences and Systems Biology, University of Turin, via Accademia Albertina 13, 10123 Turin, Italy
e-mail: patrizia.bovolin@unito.it

[†] Gilda Cobellis and Rosaria Meccariello have contributed equally to this work.

Endocannabinoids (eCBs) are natural lipids regulating a large array of physiological functions and behaviors in vertebrates. The eCB system is highly conserved in evolution and comprises several specific receptors (type-1 and type-2 cannabinoid receptors), their endogenous ligands (e.g., anandamide and 2-arachidonoylglycerol), and a number of biosynthetic and degradative enzymes. In the last few years, eCBs have been described as critical signals in the control of male and female reproduction at multiple levels: centrally, by targeting hypothalamic gonadotropin-releasing-hormone-secreting neurons and pituitary, and locally, with direct effects on the gonads. These functions are supported by the extensive localization of cannabinoid receptors and eCB metabolic enzymes at different levels of the hypothalamic–pituitary–gonadal axis in mammals, as well as bonyfish and amphibians. *In vivo* and *in vitro* studies indicate that eCBs centrally regulate gonadal functions by modulating the gonadotropin-releasing hormone–gonadotropin–steroid network through direct and indirect mechanisms. Several proofs of local eCB regulation have been found in the testis and male genital tracts, since eCBs control Sertoli and Leydig cells activity, germ cell progression, as well as the acquisition of sperm functions. A comparative approach usually is a key step in the study of physiological events leading to the building of a general model. Thus, in this review, we summarize the action of eCBs at different levels of the male reproductive axis, with special emphasis, where appropriate, on data from non-mammalian vertebrates.

Keywords: GnRH, hypothalamus, pituitary, spermatogenesis, chromatin remodeling, male fertility

INTRODUCTION

Since the discovery of Δ^9 -tetrahydrocannabinol (THC) as the main psychoactive ingredient in marijuana, the subsequent cloning of cannabinoid receptors and the identification of their endogenous ligands [i.e., endocannabinoids (eCBs)], our understanding of the functions of the eCB system (ECS) has evolved considerably. It has become evident that most components of the mammalian ECS are highly conserved in evolution, pointing to a fundamental modulatory role in basic cellular and organismic functions (1, 2). Accordingly, the ECS is widely expressed in vertebrates, central and peripheral organs, and regulates a large array of physiological functions and behaviors.

The basic eCB signaling system consists of (1) at least two G-protein-coupled receptors, known as the cannabinoid type-1 and type-2 receptors (CB1 and CB2); (2) the endogenous ligands, of which anandamide (AEA) and 2-arachidonoylglycerol (2-AG) are the best characterized; and (3) synthetic and degradative enzymes and transporters that regulate eCB levels and action at receptors. CB1 receptors are abundant in the whole vertebrate central nervous system (CNS) and some peripheral tissues (3–5),

whereas CB2 receptors are mostly expressed in peripheral tissues and immune cells, but they have recently been found also in the CNS (6–8). Research in mammals has provided evidence that eCBs can also bind to and activate type-1 transient receptor potential vanilloid (TRPV1) channels (9).

An enormous amount of information on the general properties of the ECS has accumulated over the last two decades [for general reviews on the ECS, see Ref. (10–14)]. In the past years, growing evidence has been accumulating to show the central role of the ECS in controlling vertebrate reproductive functions at both central and gonadal level (15). This review will summarize the action of eCBs at different levels of the reproductive axis, including data from non-mammalian vertebrates.

EFFECTS OF eCBs ON HYPOTHALAMIC–PITUITARY CONTROL OF REPRODUCTION

Reproductive functions are under neuroendocrine control and require a tight crosstalk between the hypothalamus, pituitary, and gonads. Gonadotropin-releasing-hormone (GnRH) is a key molecule in reproductive behavior and physiology. This neuropeptide

is synthesized by hypothalamic neurons mostly located, in mammals, in the preoptic area and in the arcuate nucleus. GnRH axons project to the median eminence, where pulsatile release of GnRH into the hypophysial portal circulation drives the synthesis and secretion of follicle-stimulating hormone (FSH) and luteinizing hormone (LH) from anterior pituitary gonadotropic cells. Circulating FSH and LH, in turn, stimulate gametogenesis and the synthesis and secretion of the gonadal steroid hormones, androgens, estrogens, and progesterone. Under various physiological and pathological conditions, hormonal and metabolic signals regulate GnRH neurons both directly or through upstream neuronal circuitries to influence the pattern of GnRH secretion. The emerging picture from studies in different vertebrate models is that eCBs can modulate both GnRH and gonadotropic cell function, in other words that eCBs can influence the regulation of reproduction at both hypothalamic and pituitary levels (16, 17).

There is general agreement on the inhibitory effect exerted by cannabinoids and eCBs on GnRH release. Early studies in rats demonstrated that the ECS influence gonadal androgens via effects on the hypothalamus and the anterior pituitary. THC, as well as eCBs, lowers not only circulating testosterone levels but also the levels of LH and FSH (18). Most of this negative effect appears to be exerted by inhibition of GnRH secretion into median eminence blood portal vessels (19, 20). Serum LH decreases in response to AEA administration in wild-type mice, whereas CB1 knockout mice (*Cb1*^{-/-}) are unresponsive to the treatment (21) and show low levels of GnRH and FSH-beta mRNA at hypothalamic and pituitary levels (22), demonstrating the pivotal role exerted by CB1 in the regulation of GnRH and gonadotropins synthesis and/or release.

The above effects require CB1 expression in ventro-medial telencephalic and hypothalamic regions. Early localization studies in rodents detected a low abundance of CB1-immunoreactive axons (23) and a low expression level of *CB1* mRNA (24–26) in the rodent hypothalamus. However, more recent immunocytochemical studies (27) revealed a dense CB1-immunoreactive fiber network in the mouse hypothalamus. These data are consistent with studies in teleosts and amphibians, showing the expression of CB1-immunoreactive fibers and cell bodies in several hypothalamic regions of adult teleosts (*Carassius auratus* and *Pelvicachromis pulcher*) and anuran amphibians (*Xenopus laevis* and *Rana esculenta*) (4, 5, 28, 29), as well as in zebrafish and in embryos of *X. laevis* (30, 31). The expression of *CB1* appears to be regulated in the diencephalon during the annual sexual cycle in anuran amphibians (32). Interestingly, *CB1* fluctuations show an opposite trend compared to *GnRH-I* mRNA variations, suggesting that maximal GnRH release corresponds to minimal *CB1* levels in the diencephalon. Both *GnRH-I* and *GnRH-II* expressions are inhibited in the frog diencephalon by AEA administration, indicating that both molecular forms might be involved in the regulation of gonatropin discharge (33). Only few data so far indicate that CB2 and TRPV1 receptors might have a role in GnRH cell regulation. Profiling neurotransmitter receptor expression in mouse GnRH-secreting neurons revealed CB2 expression in diestrous adult females (34), and CB1/TRPV1 co-localization has been reported in mouse hypothalamic paraventricular nucleus (35).

An important question is whether eCBs exert their effect directly on GnRH neurons, or on neighboring cells that control GnRH release. Gammon et al. (36) demonstrated that immortalized GnRH neurons (GT1 cells) are both a source and target of eCBs; they produce and secrete 2-AG and AEA, are able to take up and degrade eCBs, and possess CB1 and CB2, whose activation leads to the inhibition of pulsatile GnRH release. Nevertheless, such observations have not been confirmed *in vivo* in mammals, although GnRH-secreting neurons are close to cannabinergic fibers in male mice (37) and few hypothalamic GnRH neurons seem to express CB1 receptors (36). Close proximity between CB1-expressing fibers and GnRH cells has been well documented in non-mammalian vertebrates. In *P. pulcher*, *C. auratus*, *Solea solea*, and *Danio rerio*, CB1-containing cell bodies and terminals codistribute with GnRHIII (also called *salmon* GnRH) cell bodies and fibers (38–40). Similarly, codistribution of CB1- and GnRH-I-immunoreactivity has been found in corresponding brain regions of *X. laevis* and *R. esculenta* (39, 41). Noteworthy, a subset of frog GnRH-I-immunoreactive neurons in the septum and preoptic area are also CB1 immunopositive (28), suggesting the existence of a CB1-mediated autocrine mechanism in the control of GnRH secretion, in addition to presynaptic mechanisms. Ultrastructural studies in mammals indicate that CB1-immunoreactive terminals establish symmetric as well as asymmetric synapses on GnRH neurons, suggesting that retrograde eCB signaling might influence GABAergic and glutamatergic synaptic transmission, respectively (27). It should be noted that most recent studies examining the effects of endogenous GABA release on GnRH neurons indicate that the predominant action is that of excitation (42). In line with this, Farkas et al. (37) provided electrophysiological and morphological evidence that retrograde eCB signaling reduces GABAergic excitatory drive onto GnRH neurons via activation of presynaptic CB1 receptors, and that the reduced GABA_A receptor signaling in turn inhibits GnRH neuron firing activity. Besides the major afferent regulation exerted on GnRH neurons by GABAergic and glutamatergic inputs, available neuroanatomical literature describes afferent inputs by peptidergic and monoaminergic neuronal systems (43). However, whether the ECS interacts also with these systems has not been determined yet.

Besides the effect on GnRH cells, eCBs could also modulate the activity of other hypothalamic cell types involved in reproduction. Cells containing aromatase, the enzyme that catalyzes the transformation of androgen into estrogens, are localized in the hypothalamus and are deeply involved in sexual differentiation of the brain and activation of male sexual behavior. Aromatase and CB1 are expressed in close contiguity in the goldfish preoptic area and periventricular gray of hypothalamic inferior lobes (16), suggesting a possible CB1-mediated regulation of aromatase activity, at least in bony fish.

Several lines of evidence indicate that eCBs may control adeno-hypophyseal hormone secretion also acting directly at pituitary level. Both AEA and 2-AG have been detected in the anterior pituitary, suggesting local synthesis (44). In addition, CB1 has been localized in the anterior pituitary within the gonadotroph and lactotroph cells in adult male rats (45, 46), in humans (47), and in *X. laevis* (48). CB1 expression in pituitary depends on steroids,

since it is reduced in both orchidectomized male and estradiol-replaced OVX female rats (46). Recently, the presence of ECS has been demonstrated in mammalian pars tuberalis (49). This finding might be functionally significant also for GnRH release, since this pituitary region is a key station for the anterograde signaling toward the pars distalis.

EFFECTS OF eCBs AT GONADAL LEVEL

Beside the role exerted at hypothalamic level to control reproductive activity in both sexes, the discovery of eCBs in gonads and reproductive fluids – from seminal plasma in males to oviductal fluid and milk in females – (50–52) pointed out the importance of eCB signaling in the gonads. Gonads have the ability to synthesize eCBs which in turn exert differential effects activating both different types of receptors or tissue-/cell-specific receptor subtypes, the latter obtained by both alternative splicing or transcription sites (53–55). The content of eCBs is regulated by biosynthetic/hydrolyzing enzyme balance, and the appropriate “eCBs tone” *in loco*, is critical for spermatogenesis progression in male and follicle maturation in female, for sperm quality and the acquisition of sperm functions related to fertilization (motility and capacitation), for fertilization, early-embryo migration, implantation and placentation, for parturition onset and labor as well (15, 17, 56–63). Focusing on males, evidence of eCB direct action into the testis has been provided in most vertebrates [fish (8, 64), frogs (32, 57, 65–68), mammals (21, 69–74)], whereas an ECS has also been described in spermatozoa (SPZ) collected from sea urchin (75), amphibians (65), rodents (76–79), bull (80), boar (81), and human (82–85). A specific and significant association between the use of marijuana and the occurrence of non-seminomatous and mixed testicular germ cell tumors (TGCT) has been recently reported in humans (86–88); although a deep characterization of ECS has never been provided in TGCT patients yet, these data may suggest that the recreational and therapeutic use of cannabinoids may represent a risk factor for TGCT. In general, a relationship between the expression of cannabinoid receptors and the outcome of sex-steroid-dependent cancer has been documented, thus the imbalance in the ECS and its interaction with sex-steroid hormone homeostasis may promote cancer development, proliferation, and migration [for recent review, see Ref. (89)]. Defects in eCB signaling or eCB tone have recently been reported in rat treated with HU210 – a synthetic analog of THC – (90) as well as in clinical cases of male infertility in humans (85, 91). Consistently, genetic inactivation of the AEA-hydrolyzing enzyme, *Faah* (Fatty acid amide hydrolase) results in increased levels of AEA in the male reproductive system that negatively affect sperm motility and impair sperm fertilizing ability (92), whereas defects in the acquisition of sperm motility during the epididymal transit have been reported in *Cb1*^{-/-} mice (76, 77). Thus, ECS is nowadays considered a potential therapeutic target in male infertility. ECS is widely expressed in testis in both germ and somatic cells, and a map of ECS localization in several species is provided in **Table 1**. The first intratesticular targets of eCBs to be identified were the Leydig cells (21, 93), consistent with the low basal testosterone production observed in both *Cb1*^{-/-} mice and AEA-treated controls, providing evidence of mechanisms other than the AEA/THC-dependent downregulation exerted at hypothalamic/pituitary levels. The direct effect of

Bhang (cannabis) on 3 β -HSD, a well-known marker of Leydig cell activity, also confirmed this issue (79). The involvement of CB1 signaling in the control of Leydig cell activity is not restricted to steroid (both testosterone/estradiol) production (21, 22, 93), but also extends to Leydig cells ontogenesis. In fact, as reported by Cacciola et al. (72), CB1 expression in differentiating adult Leydig cells negatively correlates with cell division and the characterization of *Cb1*^{-/-} mice phenotype revealed a 30% decrease in Leydig cells number (72), as well as low circulating estradiol level (22) [for recent review, see Ref. (94)].

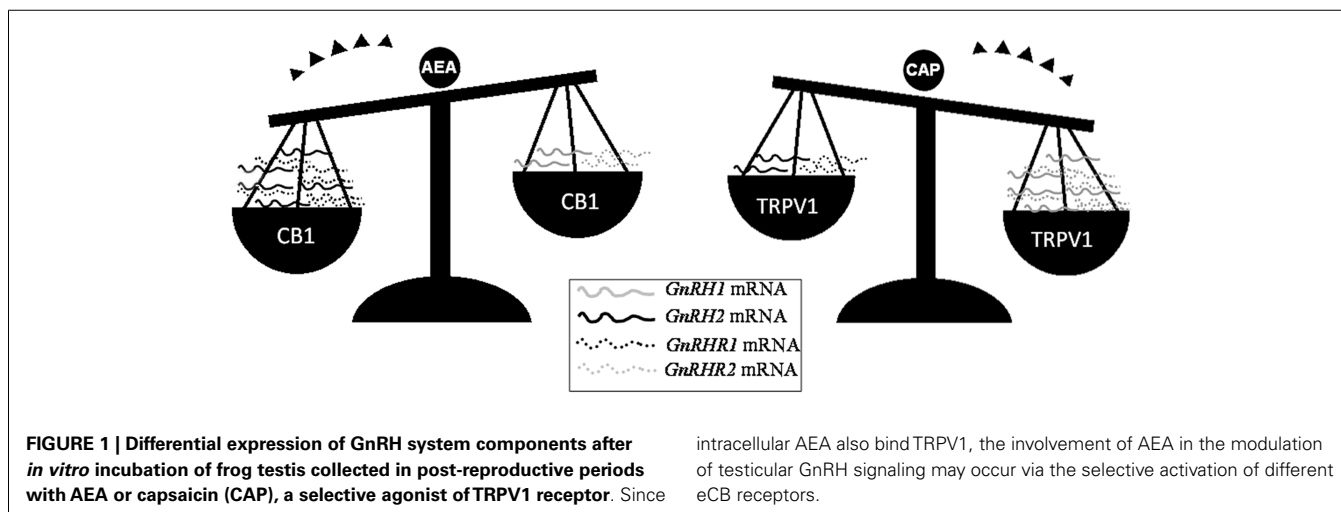
In the germinal compartment, AEA reduces the spermatogenic output inducing the apoptosis of Sertoli cells (70) in a mechanism reversed by FSH-dependent activation of aromatase and by estradiol-dependent upregulation of *Faah* (71). Recent studies carried out by Grimaldi et al. (95) demonstrated that in mature Sertoli cells *Faah* gene is a direct target of estradiol whose promoter contains two proximal estrogen-responsive element (ERE) sequences named ERE2/3. *In vivo*, a mechanism involving the binding of ER β to ERE 2/3 and the epigenetic modifications of *Faah* gene proximal promoter (demethylation of both DNA at CpG site and histone H3 at lysine 9) has been demonstrated (95); consistently *FAAH* silencing abolished estrogen protection against AEA-dependent apoptosis (95). Thus, AEA content finely tuned by its hydrolyzing enzyme *FAAH* is a fundamental tool to prevent the apoptosis in Sertoli cells.

Beside the activity exerted on Sertoli cells, eCBs are critical for the progression of spermatogenesis from mitotic stages throughout the meiotic stages and spermiogenesis events. In such a context, the *FAAH*-dependent modulation of eCB tone and the cell-specific expression of CB1, CB2, and TRPV1 provide evidence of multiple, differential eCB-dependent signaling involved in the spermatogenic events. In mouse, decreasing levels of 2-AG have been detected from spermatogonia (SPG) to spermatocytes (SPC) and spermatids (SPT), suggesting that 2-AG, through CB2 – the receptor highly expressed just in mitotic and meiotic stages, but retained in residual body during the spermiogenesis – may act as an autocrine/paracrine mediator during spermatogenesis (73). Conversely, the high expression of *Trpv1* observed in meiotic stages (73) and the massive germ cell depletion detected in *Trpv1* null mice (96) candidate TRPV1 as a controller of meiotic stages. Very recently, the involvement of both CB1 and TRPV1 in the opposite modulation of testicular GnRH signaling (15, 68, 97) – a master system involved in the control of both spermatogenesis progression and steroidogenic activity – has been reported in the anuran amphibian, the frog *R. esculenta* (97), a seasonal breeder in which two GnRH molecular forms (GnRH-I and GnRH-II) and three GnRH receptors (GnRH-RI, -RII and -RIII) have been characterized in testis (68). In such a context, AEA might act as an autocrine/paracrine factor via CB1 and as an intracrine signal via TRPV1; thus, it might be hypothesized that AEA, through the activation of specific receptors, switches on/off testicular GnRH signaling, leading to germ cell progression (**Figure 1**).

However, in mammalian and non-mammalian vertebrates, CB1 activity is linked to the control of post-meiotic stages (32, 65, 69, 73). In particular, it has been suggested that ECS controls different steps of spermiogenesis that is the phase of spermatogenesis consisting in the differentiation of SPT in SPZ. In particular,

Table 1 | Localization of ECS components [both mRNA and protein (Prot)] in testicular somatic and germ cells.

Cell type	CB1	CB2	TRPV1	FAAH	NAPE-PLD	MAGL	DAGLα/β	Species	Reference
Leydig cells	mRNA Prot Prot	Prot		Prot	mRNA			<i>R. esculenta</i> <i>M. musculus</i> <i>R. norvegicus</i>	(68, 69, 72, 79)
Sertoli cells	mRNA Prot	mRNA/Prot	mRNA	mRNA/Prot	mRNA			<i>R. esculenta</i> <i>M. musculus</i> <i>R. norvegicus</i>	(68, 70–73)
ISPG	Prot mRNA/Prot	mRNA/Prot	mRNA	mRNA	mRNA	mRNA	mRNA	<i>R. esculenta</i> <i>M. musculus</i>	(65, 69, 73)
IISPG	mRNA/Prot mRNA/Prot	mRNA/Prot	mRNA	mRNA	mRNA	mRNA	mRNA	<i>R. esculenta</i> <i>M. musculus</i>	(65, 68, 69, 73)
ISCP	Prot mRNA/Prot	mRNA/Prot	mRNA	Prot mRNA	mRNA	mRNA	mRNA	<i>R. esculenta</i> <i>M. musculus</i>	(65, 68, 69, 73)
IISPC	Prot mRNA	mRNA/Prot	mRNA	Prot mRNA	mRNA	mRNA	mRNA	<i>R. esculenta</i> <i>M. musculus</i>	(65, 73)
SPT	mRNA/Prot mRNA Prot	mRNA/Prot	mRNA	Prot mRNA	mRNA	mRNA	mRNA	<i>R. esculenta</i> <i>M. musculus</i> <i>R. norvegicus</i>	(65, 68, 69, 72, 73)
SPZ	mRNA/Prot mRNA/Prot Prot mRNA/Prot mRNA/Prot	mRNA/Prot Prot mRNA/Prot Prot	mRNA/Prot Prot Prot	Prot mRNA/Prot Prot Prot	mRNA/Prot Prot	mRNA/Prot	mRNA/Prot	<i>R. esculenta</i> <i>M. musculus</i> <i>R. norvegicus</i> <i>S. scrofa</i> <i>B. taurus</i> <i>H. sapiens</i>	(65, 68, 72, 78, 81, 83, 84)



post-meiotic haploid round spermatids (rSPT) undergo biochemical and morphological changes becoming elongated cells (eSPT) and then SPZ. Sperm cells are differentially released from Sertoli cells by spermiation, a process characterized by species-specific features (65, 98). In mammals, SPZ undergo further transformations in the epididymis, which enables SPZ for fertilization (76, 77). These cellular modifications, and in particular some structural changes observed in SPT (i.e., acrosome development, nuclear

shaping and chromatin condensation), seem to be related to ECS and in particular to CB1 activity.

A detailed immunolocalization of CB1 has been reported in rat SPT. CB1 appears in rSPT, around the nucleus, during acrosome development; the signal is retained in the head of elongating and condensing SPT, always close to the acrosome region, suggesting a role for CB1 in spermiogenesis, probably in chromatin packaging and in acrosome and/or cellular shape configuration

(57, 72, 81). In agreement, several data demonstrate that CB1 regulates acrosome reaction, chromatin condensation, and nuclear size of SPZ (82, 99). Recent observations demonstrate that CB1 is involved in chromatin remodeling of SPT. In fact, during spermiogenesis, as the nucleus elongates and assumes a specie-specific shape, the chromatin condenses. It is worth noting that chromatin condensation differentially occurs, depending on the species. In mammals, chromatin condensation starts in eSPT producing condensing and then condensed SPT, which are mature elongated cells with strongly packaged chromatin (100). Many events characterize these chromatin cyto-architecture changes (101). Early during spermiogenesis, it is possible to observe the expression and storage of specific proteins involved in condensation and in DNA integrity maintenance, such as transition proteins (TNPs) and protamines (PRMs) (102). Others events concern the following: (i) displacement and degradation of the nucleosome structure; (ii) histone replacement by TNPs and then by PRMs; (iii) transcriptional silencing; (iv) DNA repair; and finally, (v) repackaging of the protaminated chromatin into toroidal structures (103, 104) [for recent review, see Ref. (94)]. These events strongly preserve DNA by damage and are involved in mechanism related to sperm maturation. Indeed, it is well known that inefficient expression or activity of TNPs/PRMs deranges histone displacement and causes production of SPZ with histone retention, incomplete chromatin condensation, and DNA damage (74, 105, 106). In both humans and rodents, abnormal levels of sperm DNA damage are associated with lower conception, implantation, and fecundity rates, and with higher miscarriage probability (95, 107, 108). In this context, Chioccarelli et al. (74) showed that *Cb1* gene deletion negatively influences chromatin remodeling in SPT, by reducing either transition protein 2 (Tnp2) levels or histone displacement. Secondary effects, related to the inefficient histone displacement (i.e., histone retention, uncondensed chromatin, DNA damage, and nuclear size elongation) have been postulated (22, 74). In agreement, *in vivo* and *in vitro* experiments show that AEA is able to act locally and upregulate *Tnp2* mRNA levels through CB1, via PKC/PKA pathways (17, 74). Furthermore, in *caput* epididymis from *Cb1*^{-/-} mice, the percentage of SPZ retaining histones as well as the percentage of SPZ with uncondensed chromatin or with DNA damage, is higher as compared to normal mice. Interestingly, DNA damage increased during the epididymal transit, from *caput* to *cauda*, suggesting that CB1 preserve sperm DNA integrity of SPZ during epididymal transit (74).

Recently, it has been demonstrated that estradiol, probably via stimulatory effects on FSH secretion and/or directly via paracrine actions within the testis, preserve chromatin condensation, and DNA integrity of SPZ, likely by promoting histone displacement in SPT (99). Indeed, it has been reported that *Cb1*^{-/-} male mice show low levels of circulating E₂, and when treated with 17β-estradiol, they rescue sperm chromatin quality by restoring histone content, chromatin packaging, DNA integrity, and nuclear length of SPZ (22, 99). These results corroborate the intriguing findings that the small nucleus of SPZ, containing chromatin that did not retain histones, appear fully condensed and able to preserve DNA from damage. On the contrary, the longer nucleus of SPZ, containing chromatin that

retained histones, is uncondensed and unable to avoid DNA damage. The emerging exciting idea is that sperm nuclear dimensions can be a good marker for SPZ chromatin quality useful to select the SPZ qualitatively suitable for intracytoplasmic sperm injection (99).

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Roles of reactive oxygen species in the spermatogenesis regulation

Giulia Guerriero^{1,2*}, Samantha Trocchia¹, Fagr K. Abdel-Gawad³ and Gaetano Ciarcia^{1,2}

¹ Department of Biology, Università degli Studi di Napoli Federico II, Napoli, Italy

² CIRAM, Università degli Studi di Napoli Federico II, Naples, Italy

³ Department of Water Pollution Research, Centre of Excellence for Advanced Science, National Research Center (NRC), Giza, Egypt

Edited by:

Rosaria Meccariello, University of Naples Parthenope, Italy

Reviewed by:

Rosanna Chianese, Second University of Naples, Italy

Teresa Chioccarelli, Second University of Naples, Italy

*Correspondence:

Giulia Guerriero, Department of Biology, Comparative Endocrinology Lab, Università degli Studi di Napoli Federico II, Via Mezzocannone, 8, Naples 80134, Italy
e-mail: giulia.guerriero@unina.it

Spermatogenesis is a complex process of male germ cells proliferation and maturation from diploid spermatogonia, through meiosis, to mature haploid spermatozoa. The process involves dynamic interactions between the developing germ cells and their supporting Sertoli cells. The gonadal tissue, with abundance of highly unsaturated fatty acids, high rates of cell division, and variety of testis enzymes results very vulnerable to the overexpression of reactive oxygen species (ROS). In order to address this risk, testis has developed a sophisticated array of antioxidant systems comprising both enzymes and free radical scavengers. This chapter sets out the major pathways of testis generation, the metabolism of ROS, and highlights the transcriptional regulation by steroid receptors of antioxidant stress enzymes and their functional implications. It also deals with the advantages of the system biology for an antioxidant under steroid control, the major selenoprotein expressed by germ cells in the testis, the phospholipid hydroperoxide glutathione peroxidase (PHGPx/GPx4) having multiple functions and representing the pivotal link between selenium, sperm quality, and species preservation.

Keywords: spermatogenesis, reactive oxygen species, antioxidants, selenium, healthy reproduction

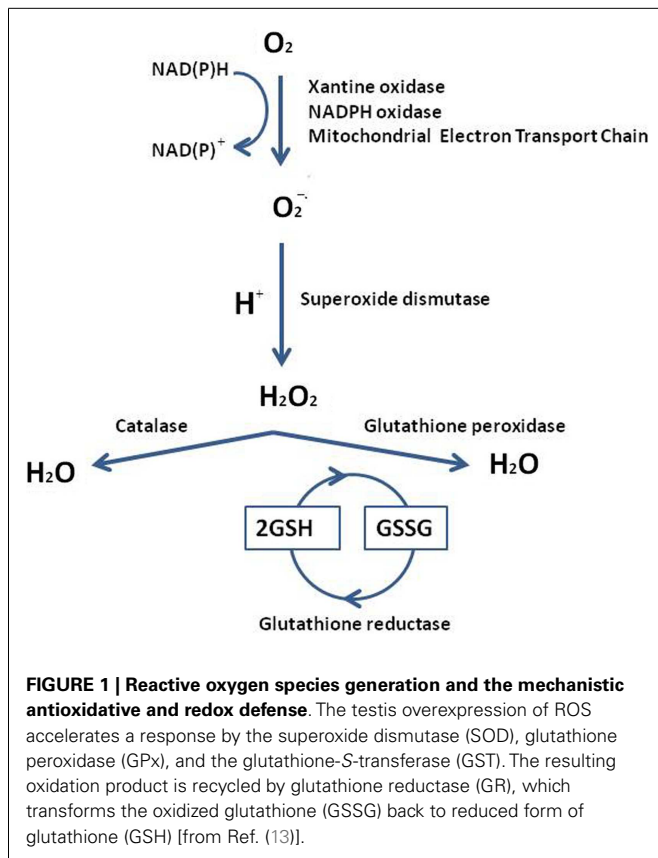
INTRODUCTION

Spermatogenesis appears to be a fairly conserved process throughout the vertebrate series. The balance between spermatogonial stem cell self-renewal and differentiation in the adult testis grants cyclic waves of spermatogenesis and potential fertility. These replicative processes imply a highest rate of mitochondrial oxygen consumption and reactive oxygen species (ROS) generation. Enzyme complexes of the respiratory chain of the oxidative phosphorylation, localized on the crests of the mitochondria, as the xanthines, the nicotinamide adenine dinucleotide phosphate (NADPH) oxidase and cytochrome P450, represent a source for a variety of ROS. As known, ROS are free radicals and/or oxygen derivatives that include superoxide anion, hydrogen peroxide, hydroxyl radical, lipid hydroperoxides, peroxy radicals, and peroxynitrite. They have a dual role in biological systems, both beneficial than harmful depending on their nature and concentration as well as location and length of exposure (1). In this mini-review, we focused our attention on the relevance of ROS role in the spermatogenesis.

REACTIVE OXYGEN SPECIES AND TESTIS MECHANISTIC ANTIOXIDATIVE AND REDOX DEFENSE

Reactive oxygen species are involved in all cell physiological processes. In testis, they may be beneficial or even indispensable in the complex process of male germ cells' proliferation and maturation, from diploid spermatogonia through meiosis to mature haploid spermatozoa (2). Conversely high doses, and/or inadequate removal of ROS caused by several mechanisms, i.e., ionizing radiation, bioactivation of xenobiotics, inflammatory

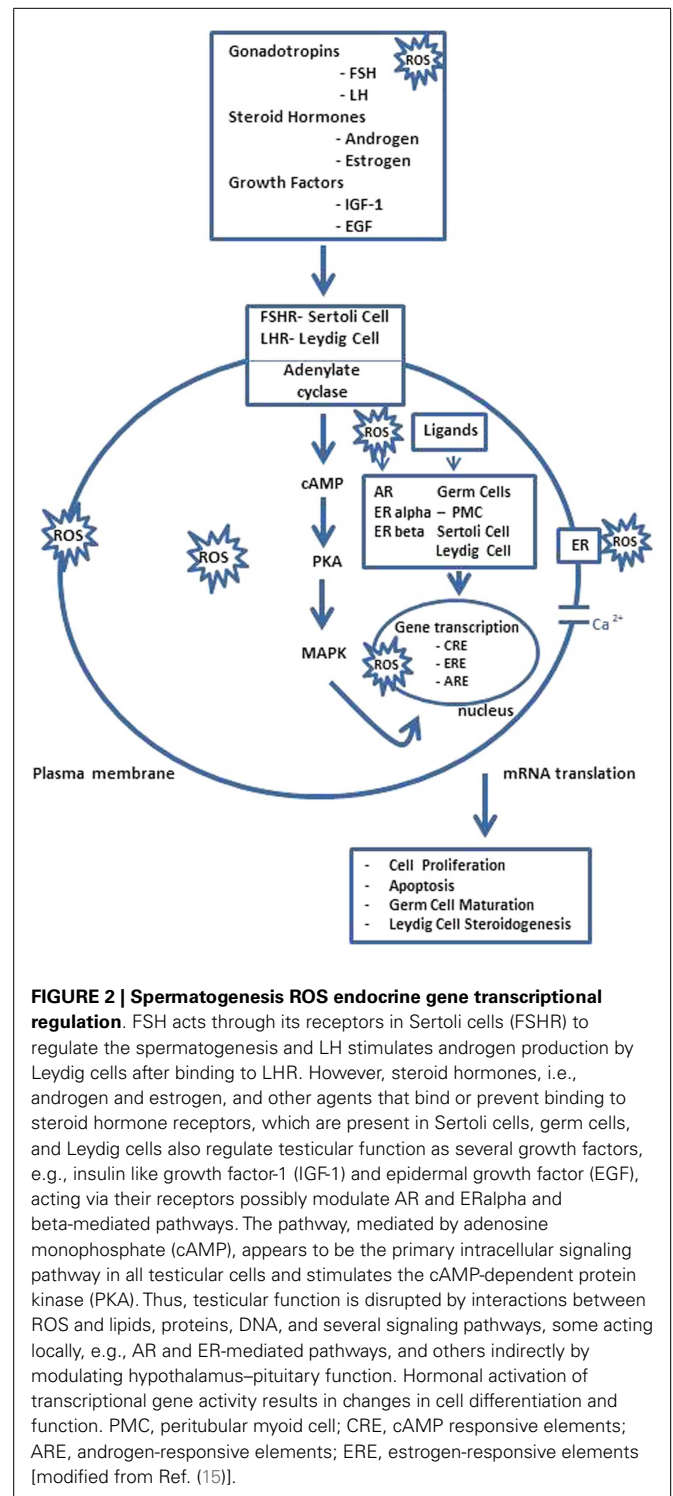
processes, increased cellular metabolism, activation of oxidases, and oxygenases, can be very dangerous, modifying susceptible molecules including DNA, lipids, and proteins. In addition, testis as tissue, containing large quantities of highly unsaturated fatty acids (particularly 20:4 and 22:6), results vulnerable to ROS attack. The low oxygen tension that characterizes this tissue may be an important component of the self-defense mechanism from free radical-mediated damage during spermatogenesis and Leydig cell steroidogenesis (3); together with an elaborate array of antioxidant enzymes and free radical scavengers ensures that spermatogenic and steroidogenic functions of Leydig cells are not impacted by the overexpression of ROS. In order to have a better understanding of ROS testis' neutralization or limitation by the antioxidant systems, we summarize the major pathways of ROS generation and the mechanistic antioxidative defense in **Figure 1**. Superoxide radical can be generated by specialized enzymes, such as the xanthine or NADPH oxidases, or as a by-product of cellular metabolism, particularly the mitochondrial electron transport chain, and are converted to hydrogen peroxide by the superoxide dismutase (SOD). Hydrogen peroxide, present as superoxide radical and iron, forms a more reactive form, subsequently converted in lipid peroxide. Lipid peroxide is scavenged to H₂O by glutathione peroxidase (GPx) or glutathione-S-transferase (GST) (4). The SOD defense by Cu/Zn-SOD, Fe/Mn-SOD, and extracellular SOD, is generally achieved by catalase or peroxidases, such as the GPxs, which use reduced glutathione (GSH) as electron donor. Glutathione keeps cells in a reduced state, acting as electron donor for other antioxidative enzymes too, and as a source for the formation of conjugates with some harmful endogenous and xenobiotic compounds,



via GST's catalysis. Levels of the reduced glutathione (GSH) are maintained via two ATP-consuming steps, involving c-glutamylcysteine synthetase (cGCS) and glutathione synthetase. The other option constitutes a recycling system involving glutathione reductase (GR): it reduces the oxidized glutathione (GSSG) back to GSH in an NADPH-dependent way. In the interaction of GSH with ROS, GSH serves as an electron donor. The resulting oxidation product, GSSG, is either recycled by GR via electron transfer from NADPH or pumped out of the cells. Thus, GR indirectly participates in the protection of cells against oxidative stress (5, 6). In addition to the major ROS processing enzymes, in testis small molecular weight antioxidant substances are present, protecting against oxidative damage. These factors include ions, as zinc and a wide variety of free radical scavengers, vitamins C or E, melatonin and cytochrome C (7).

REACTIVE OXYGEN SPECIES AND SPERMATOGENESIS TRANSCRIPTIONAL CONTROL

In vertebrates, the spermatogenesis is controlled by a complex network of endocrine, paracrine, and autocrine signals (8–10) Recent studies summarize different transcription factors, with a regulatory function, who modulate cellular and stage-specific gene expression. In particular, they can be subdivided in general transcription factors; nuclear receptors superfamily; transcription factors involved in testicular functions; testis-specific gene transcription, and transcriptional regulators of cell junction dynamics (11). As reported in **Figure 2** in response to the hypothalamic



gonadotropin hormone releasing (GnRH), the pituitary gland secretes two hormones, the luteinizing hormone (LH), and the follicle stimulating hormone (FSH), involved in the regulation of spermatogenesis, together with other important transcription factors (3). LH regulates the testosterone secretion by somatic Leydig cells located in the interstitium, between seminiferous

tubules; FSH acts in Sertoli cells by stimulating signaling, gene expression, and the secretion of peptides and other signaling molecules (12). In Sertoli cells, i.e., the cAMP response element binding protein (CREB) transcription factor, an important transducer of FSH signals. Transcription factors belonging to the CREB family are involved in the regulation of gene expression in response to a number of signaling pathways induced by ROS overexpression (13). In rat testis, alternatively, the spliced variant CREB mRNAs are spermatogenic, cycle dependent, and expressed during development of the germ and Sertoli cells, indicating that the CREB isoforms may be the major players during spermatogenesis. The transcription factor cAMP response element modulator (CREM) is highly expressed in male germ cells and regulates the expression of several post-meiotic genes, such as the transition proteins and protamines, and it likely is the key regulator of gene expression during spermatogenesis. Targeted disruption of the CREM gene blocks the differentiation program in the first step of spermiogenesis. These findings indicate a crucial role of CREM in post-meiotic germ cells differentiation, linking the action of hormonal stimuli to direct regulation of spermatogenesis genes (14). Now, it is also clear that, not only testicular somatic cells (Leydig and Sertoli cells), but also germ cells express P450arom mRNA, which is translated in a biologically active enzyme involved in the production of estrogens. Therefore, the androgen/estrogen ratio is modified in germ cells, and if testosterone is involved in the regulation of testicular functions, estrogens are also necessary not only in the control of gonadotropins secretion but also in the modulation of the Leydig cells development and steroidogenesis, as well as in the development and/or maintenance of spermatogenesis and spermiogenesis in some mammalian species (15). However, the physiological linkage between different transcription factors and ROS overexpression showed regulation by the estrogen receptor of antioxidative stress enzymes (16), the molecular target genes of these transcription factors at different stages of the seminiferous epithelial cycle are largely unknown and this shall provide an unprecedented opportunity for further investigation in the field.

REACTIVE OXYGEN SPECIES AND SPECIE PRESERVATION

The maintenance of a high redox potential is a prerequisite to maintain the reproductive systems in a healthy state (17). Reproductive system needs ROS for reproduction, and minimizes the risk caused by ROS using antioxidative systems, such as SOD and GPx. When ROS levels exceed the scavenging capacity of the redox system, under such situations, can repair oxidized and damaged molecules using NADPH as an original electron source. In the context of defense against ROS, selenium as the glutathione (GSH) system plays key functions (18). Selenium has long been known to be necessary for the basal function of many systems of the male reproduction, also (19) is required for the synthesis of testosterone and the formation and development of the sperm (20); its deficiency affects testicular mass with damage to sperm motility, the sperm mid piece, and the shape of the sperm (21). In testis, however, most of the selenium, incorporated into proteins as selenocysteine, is associated to the enzyme phospholipid hydroperoxide GPx, PHGPx/GPx4 (22), member of the GPx named EC 1.11.1.12. PHGPx protects liposomes and biomembranes from peroxidative degradation and exhibits GPx activity

on phosphatidylcholine hydroperoxides. It is, in fact, able to react with hydroperoxides of fatty acids esterified in the phospholipids (23, 24); use protein thiol groups as donor substrates, to protect germ cell, by eliminating oxidative stress and reducing the levels of oxidized molecules. In rodents' testis, PHGPx is localized in the interstitial cells of Leydig, in the nucleus of round spermatids, at the level of the cytoplasm and in the mitochondrial capsule of spermatozoa (25). Here, it is present in three different isoforms: as a cytosolic, mitochondrial, and nuclear protein (26). Functional cis-regulatory elements are identified in the promoter region of nPHGPx (27), whose expression is mediated by the transcription factor CREM-t (28). In spermatids, it is abundantly expressed as active peroxidase and during final maturation, it is transformed into a structural protein enzymatically inactive; it surrounds the helix of mitochondria in the midpiece of the sperm. The nuclear isoform, in particular, is involved in the process of the chromatin condensation, which occurs in the final steps of spermatogenesis and requires the replacement of the majority of histones, with transition proteins and protamines, essential for the stabilization of DNA and condensation of spermatocytes. These changes in location suggest that the nPHGPx can play more than a role in spermatogenesis (29). PHGPx gene expression and activity are hormone dependent processes, and they are influenced by the levels of testosterone during spermatogenesis (30). Steroid hormones do not directly activate transcription and it has been documented that, *in vivo*, testosterone promote the expression only, as a consequence of the induction of spermatogenesis (30). The study of the mechanisms of gene transcription in testis (31), suggests a crucial role of this antioxidant in male fertility and its usefulness in the screening of a potential threat to the species' continuity (1, 32).

CONCLUDING REMARKS

The overall objective of our mini-review was to highlight the beneficial and detrimental role of ROS that comparatively determine and influence the cyclic waves of spermatogenesis and the species preservation.

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Spermatogenesis and cryptorchidism

Giovanni Cobellis^{1*}, Carmine Noviello¹, Fabiano Nino¹, Mercedes Romano¹, Francesca Mariscoli¹, Ascanio Martino¹, Pio Parmeggiani² and Alfonso Papparella²

¹ Paediatric Surgery, Salesi Children's Hospital, Università Politecnica delle Marche, Ancona, Italy

² Paediatric Surgery, Department of Paediatrics, Faculty of Medicine, Second University of Naples, Naples, Italy

Edited by:

Riccardo Pierantoni, Second University of Naples, Italy

Reviewed by:

Rosaria Meccariello, University of Naples Parthenope, Italy

Paola Piomboni, University of Siena, Italy

*Correspondence:

Giovanni Cobellis, Paediatric Surgery, Salesi Children's Hospital, Università Politecnica delle Marche, Via Corridoni, Ancona 11, Italy
e-mail: g.cobellis@univpm.it

Cryptorchidism represents the most common endocrine disease in boys, with infertility more frequently observed in bilateral forms. It is also known that undescended testes, if untreated, lead to an increased risk of testicular tumors, usually seminomas, arising from mutant germ cells. In normal testes, germ cell development is an active process starting in the first months of life when the neonatal gonocytes transform into adult dark (AD) spermatogonia. These cells are now thought to be the stem cells useful to support spermatogenesis. Several researches suggest that AD spermatogonia form between 3 and 9 months of age. Not all the neonatal gonocytes transform into AD spermatogonia; indeed, the residual gonocytes undergo involution by apoptosis. In the undescended testes, these transformations are inhibited leading to a deficient pool of stem cells for post pubertal spermatogenesis. Early surgical intervention in infancy may allow the normal development of stem cells for spermatogenesis. Moreover, it is very interesting to note that intra-tubular carcinoma *in situ* in the second and third decades have enzymatic markers similar to neonatal gonocytes suggesting that these cells fail transformation into AD spermatogonia and likely generate testicular cancer (TC) in cryptorchid men. Orchidopexy between 6 and 12 months of age is recommended to maximize the future fertility potential and decrease the TC risk in adulthood.

Keywords: cryptorchidism, undescended testes, spermatogenesis, germ cells, testicular cancer, orchidopexy

INTRODUCTION

Undescended testis or cryptorchidism is the most common genital abnormality in boys. The prevalence of cryptorchidism in full-term newborns range between 1 and 3%, reaching 30% in prematures (1–3). The pathology is bilateral in about 20% of the cases. About 80% of undescended testes are palpable and 20% are non-palpable (3–5). Palpable undescended testes are located along the inguino-scrotal region. Non-palpable testes may fall into one of the following categories: intra-abdominal location, agenesis, intrauterine demise, or inguinal location caused by dysplasia or atrophy. It is important to differentiate the true cryptorchidism from the retractile testis, which is a normal finding and usually it does not require surgical treatment. Acquired cryptorchidism has been observed when the retractile testis ascent in the inguinal canal during the infancy (ascending testis).

The main risk factors for the cryptorchid testis are infertility and testicular cancer (TC).

The risk of infertility in adulthood is more significant in patients with bilateral undescended testes (6). Approximately 10% of the infertile men have a history of cryptorchidism and orchidopexy (7). Azoospermia is evident in 13% of unilateral cryptorchidism and increase to 89% in untreated bilateral cryptorchid patients (8), although boys with one undescended testis have a lower fertility rate, they have the same paternity rate as boys with bilateral descended testes. Boys with bilateral undescended testes have a lower fertility and a paternity rate (9). In some studies, patients with unilateral cryptorchidism had normal

spermatogenesis, suggesting that additive detrimental factors may be responsible for impaired fertility. The studied mechanisms of the infertility in cryptorchidism are multiple (7). The hyperthermia, between 35 and 37°C rather than 33°C, evoked by the abnormal position of the testis may respond for the impaired spermatogenesis. Anatomical congenital anomalies associated to undescended testis as testis–epididymis disjunction or iatrogenic lesions of vas and testis during orchidopexy may also contribute to infertility. Retrospective studies in infertile patients with history of cryptorchidism have demonstrated an increased incidence of anti-sperm antibodies which is more evident in pubertal age (1, 8). Sinisi et al. showed that cryptorchidism may elicit an autoimmune response against sperm antigens in childhood independent of testis location and orchidopexy (1).

It is known that undescended testes, if untreated, lead to an increased risk of TC, usually seminomas (10), arising from mutant germ cells. TC is a solid neoplasm that has an incidence of 1% of all cancers in men and is the most common between 20 and 30 years of life (11, 12). Boys with an undescended testis have a 20-fold higher risk to develop a TC and about 10% of the cases of TC develop in men with a history of cryptorchidism (13).

In this review, we focus on the current knowledge about the abnormal germ cell development in the undescended testes and its possible relationship with the impaired spermatogenesis and TC in adulthood. In the second section of this review, we discuss the treatment of cryptorchidism and the possible role of the early orchidopexy in the prevention of both infertility and cancer.

GERM CELL DEVELOPMENT, INFERTILITY, AND TESTICULAR CANCER IN CRYPTORCHIDISM

The germ cell development and its modification in cryptorchidism have been recently matter of many researches (2, 14, 15).

Spermatogenesis is the process by which sperm cells are produced. In men, it starts at puberty, resulting from the increased levels of gonadotropins and testosterone. It is a complex process including sequential steps of mitosis, meiosis, and differentiation. In each of these steps, endocrine, paracrine, and autocrine factors are involved (16). Spermatogenesis takes place in the seminiferous tubule: here germ cells are organized from the base of the tubule to the lumen and progressively develop from spermatogonia to spermatids. In the last step, spermatids differentiate through morphological transformation into spermatozoa (spermiogenesis) (17) which are finally released from the Sertoli cells into the lumen of the seminiferous tubule (spermiation).

However, germ cell development is an active process. It starts during the first years after birth when neonatal gonocytes change into adult dark (AD) spermatogonia. These are stem cells and have a dark nucleus that specifically characterize them from the other germ cells. Therefore, AD spermatogonia do not directly take part to sperm production; nevertheless, they ensure a supply of stem cells for spermatogenesis. Indeed, AD spermatogonia replicate to produce adult pale (AP) spermatogonia, with light nuclei. These cells produce by mitosis the type B spermatogonia which further divide and differentiate into primary spermatocytes which are already evident in the testes of children 4 years of age (2, 18). Two sequential meiotic divisions and spermiogenesis lead to final development of round spermatids and spermatozoa, respectively (19).

Several data suggest that AD spermatogonia form between 3 and 9 months of age. This developmental cycle needs normal testicular hormones and the optimal scrotal temperature of 33°C (20, 21). The hormonal regulation of these changes is not fully understood, with evidence for a possible role of gonadotropins and androgens. Not all the neonatal gonocytes transform into AD spermatogonia. The remaining gonocytes undergo involution by apoptosis. Genetic aberrations and environmental conditions influence these processes.

The failure of transformation of gonocytes into AD spermatogonia may produce infertility in boys.

Hadziselimovic and Herzog (15) have demonstrated that the process of transformation of neonatal gonocytes into AD spermatogonia during the first year of life is crucial for male fertility. The inhibition of this process in undescended testis leads to a deficient pool of stem cells for post pubertal spermatogenesis and infertility. Moreover, in undescended testes, germ cells loss starts at 6 months of age. Testicular biopsies at time of orchidopexy confirmed the importance of AD spermatogonia for fertility in cryptorchid patients. Tasian and coworkers (22) observed greater germ cell depletion in abdominal testes compared with palpable testes and a progressive germ cell loss for each month the testes remain undescended.

It is very interesting to note that the intra-tubular carcinoma *in situ* (CIS) in the second and third decade has enzyme markers similar to neonatal gonocytes as placental alkaline phosphatase

expression, suggesting that these cells, that fail to develop in AD spermatogonia at 3–9 months of age, are the origin of cancer in cryptorchid men (23). Studies have suggested that the precursor cells of testis cancer, testicular CIS, are similar to fetal gonocytes. A current hypothesis (2) is that, due to the high temperature anomaly of undescended testis, an abnormal apoptosis allows some gonocytes to persist and become CIS with progressive mutation and/or cellular unbalance, and eventually malignancy in adulthood. These abnormal gonocytes are kept in a defined environment “suspended animation” in the germ-line and, due to the accumulation of mutations, may undergo transformation becoming the source of the CIS (2, 21, 24).

The etiology accepted for germ cell carcinoma remains unknown, although disturbances in the microenvironment provided by the Sertoli and Leydig cells may play an important role. In fact, spermatogenesis is strictly controlled and depends on a succession of signals supplied from the local environment (11, 25, 26) and Leydig cells, next to their steroidogenic function, during development express the insulin-like-3 gene (INSL3), which is responsible for gubernaculum maturation and testicular descent (27). A specific association of mutations in INSL3 with cryptorchidism has been described but its possible role in TC development and infertility needs to be clarified (28).

Olesen et al. linked the development of TC not only with cryptorchidism but also with other urogenital anomalies such as hypospadias (29). In fact, epidemiological studies in males who presented fertility problems tend to lean toward an enhanced risk of testicular germ cell tumor (30). The development of TC is associated with many chromosomal abnormalities and this raises the problem for close monitoring of these patients. Kanetsky et al. (31) demonstrated common genetic variants associated to an increased risk of testicular germ cell cancer (TGCC) and found that seven markers at 12p22 within KITLG (c-KIT ligand) reached genome-wide significance. This gene has been involved in several aspects of primordial germ cell development, migration, and survival (32).

Concerning the development of the urogenital sinus and particularly the testis, the impacts of endocrine disruptors have been fairly well described on human and experimental models (33–35). This is especially true for hypospadias, cryptorchidism, and infertility; but the link with TGCC has to be explained. The unbalanced equilibrium between the estrogen and androgen levels *in utero* is hypothesized to influence the risk of TC. Thus, mutations in testosterone gene expression may change the level of testosterone *in vivo* and hypothetically the risk of developing TC (36).

As discussed before, hormonal regulation is very significant in the development of the germ-line. Beside the importance of fetal development, it seems that puberty should be an important moment, when hormone levels reach optimal concentrations for the secondary sex characters development. It has been shown that sperm agglutinating antibodies appear in young boys with cryptorchidism and they are more prevalent during puberty (1). This also coincides with the appearance of TGCC, as men affected are between 15 and 35 years old, suggesting that puberty and probably the increase in hormone concentrations should be central issues (37).

HORMONAL AND SURGICAL TREATMENT OF CRYPTORCHIDISM

The goals of treatment of cryptorchidism are mainly two: preserve fertility and reduce the risk of neoplastic disease. Last but not the least, treatment allows the testicular self-examination for an early diagnosis and detection of TC.

Hormonal treatment with human chorionic gonadotropin (hCG) or gonadotropin-releasing hormone (GnRH) may be initially administered for cryptorchidism because it should promote the testicular descent (38). The theoretical basis for its use is to stimulate the Leydig cells to produce testosterone, inducing inguinal–scrotal testicular descent. Potential harmful effects of hormonal treatment on the developing testes, including apoptosis, inflammation, and reduced number of germ cells are still under study. In addition, there are reports which suggest that the hormonal stimulation in infancy may be damaging to the testes (39). It has been observed, in hCG-treated rats, a poor differentiation of the seminiferous epithelium, with high Leydig cell evidence and increased inter-tubular eosinophilic material (40). These experimental data emphasize the possible negative outcome of hormone therapy on germ cell line and its main action on Leydig cells. The increased synthesis of vascular endothelial growth factor (VEGF), determined by hCG therapy also highlights the increased cell permeability causing interstitial edema. The role of VEGF on spermatogenesis is unclear. Several findings have revealed several inhibitory effects of VEGF on spermatogenesis (40, 41).

Considering the poor efficacy and the possible adverse effects of hormonal therapy, surgery must be preferred (42).

Orchidopexy is the cornerstone of cryptorchidism treatment. Inguinal operation is the standard approach for palpable testis. Laparoscopy is the gold standard technique for both diagnosis and treatment of non-palpable testes (3–5). Early surgical treatment may preserve fertility. Orchidopexy is commonly performed before 2 years of age and increasing research suggest that surgery before 1 year of age may permit the normal spermatogenesis by preventing degenerative changes of the testes and germ cell loss (22, 43). However, early orchidopexy does not guarantee normal fertility in adulthood. Hadziselimovic showed that despite orchidopexy before 6 months of age, up to 35% of boys will grow up to be infertile regardless of the normal total germ cell count on testicular biopsies performed at the time of orchidopexy (44). The current practice for the acquired cryptorchidism is to operate at diagnosis, by a scrotal approach, although the prognosis seems to be better than congenital cryptorchidism considering the normal development and apoptosis of the germinal cells during the first year of life.

Since the link between cryptorchidism and TC seems to be an abnormal development of the primary germ-line, any attempt to normalize this process, as early surgery, will permit a normal growth of germ cells, thereby avoiding cancer as well as oligospermia or azospermia. However, it should be mentioned that some studies failed to demonstrate a correlation between the time of surgery and cancer risk (45). A systematic review and meta-analysis of the literature by an American group has concluded that prepubertal orchidopexy may decrease the risk of malignancy and that early surgical intervention is indicated in children with cryptorchidism leading to a better growth of the testis (46).

CONCLUSION

Cryptorchidism is a risk factor for infertility and TC in adulthood. To date, orchidopexy is recommended between 6 and 12 months of age. The aim of an early surgical intervention is to prevent the abnormal germ cell development and ultimately decrease the risk of infertility and malignancy in adulthood.

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Intra-testicular signals regulate germ cell progression and production of qualitatively mature spermatozoa in vertebrates

Rosaria Meccariello¹, Rosanna Chianese², Teresa Chioccarelli², Vincenza Ciaramella², Silvia Fasano², Riccardo Pierantoni^{2*} and Gilda Cobellis²

¹ Dipartimento di Scienze Motorie e del Benessere, Università di Napoli Parthenope, Naples, Italy

² Dipartimento di Medicina Sperimentale sez "F. Bottazzi", Seconda Università degli Studi di Napoli, Naples, Italy

Edited by:

Joaquín Gutiérrez, Universitat de Barcelona, Spain

Reviewed by:

Gregory Y. Bedecarrats, University of Guelph, Canada

Anna Di Cosmo, University of Naples Federico II, Italy

*Correspondence:

Riccardo Pierantoni, Dipartimento di Medicina Sperimentale sez "F. Bottazzi", Seconda Università degli Studi di Napoli, Via Costantinopoli 16, Naples 80138, Italy
e-mail: riccardo.pierantoni@unina2.it

Spermatogenesis, a highly conserved process in vertebrates, is mainly under the hypothalamic–pituitary control, being regulated by the secretion of pituitary gonadotropins, follicle stimulating hormone, and luteinizing hormone, in response to stimulation exerted by gonadotropin releasing hormone from hypothalamic neurons. At testicular level, gonadotropins bind specific receptors located on the somatic cells regulating the production of steroids and factors necessary to ensure a correct spermatogenesis. Indeed, besides the endocrine route, a complex network of cell-to-cell communications regulates germ cell progression, and a combination of endocrine and intra-gonadal signals sustains the production of high quality mature spermatozoa. In this review, we focus on the recent advances in the area of the intra-gonadal signals supporting sperm development.

Keywords: testis, spermatogenesis, GnRH, kisspeptins, estrogens, sperm quality, spermatozoa

INTRODUCTION

In vertebrates, spermatogenesis is a hormonally controlled mechanism charged to produce gametes useful for reproduction. The production of high standard quality gametes is the main goal to preserve reproduction.

Spermatogenesis develops as a process consisting of mitotic, meiotic, and differentiation steps promoting germ cell progression from spermatogonia-to-spermatozoa (SPZ). In male, the hypothalamus–pituitary–gonadal axis supports germ cell progression, via gonadotropin releasing hormone (GnRH)–gonadotropin–steroid production and its activity is finely regulated by positive and negative feedbacks. Furthermore, a network of intra-gonadal factors, organized in a complex stage-specific multi-factorial net, is responsible for spermatogenesis control (1).

Using a comparative approach, this review summarizes the intriguing and sometimes conflicting information about the intra-testicular role played by GnRH, Kisspeptin, and estrogens in germ cell progression and production of high standard quality sperm.

GnRH, A HISTORICAL MODULATOR OF TESTIS PHYSIOLOGY

The GnRH, crucial player of the neural control of vertebrate reproduction, was originally isolated from the hypothalamus of pig and sheep (2). Basically, GnRH stimulates the synthesis and the discharge of pituitary gonadotropins [follicle stimulating hormone and luteinizing hormone (FSH and LH), respectively], which in turn induce both gametogenesis and the production of gonadal steroids. At present, 25 GnRH forms have been identified in protochordates and vertebrates (3, 4) and in many vertebrates three GnRH molecular forms have been identified: GnRH-1, GnRH-2, and GnRH-3 (formerly known as mammalian,

chicken-II, and salmon GnRH, respectively) (3). GnRH action is mediated through high-affinity binding with the GnRH receptor (GnRH-R) (5, 6), a rhodopsin-like seven trans-membrane G protein-coupled receptor (GPCR). In vertebrates, GnRH-Rs exhibit a wide range of subtypes and alternate splicing derived forms (1, 3, 5–7). The presence of multiple forms of GnRHs and GnRH-Rs in the brain, with specific expression profiles, suggests the existence of different functional roles: in fact, GnRH-1 is considered the final regulator of the pituitary–gonadal axis; GnRH-2 is supposed to play a function for the control of sexual behavior, food intake, energy balance, stress, and many other environmental cues; GnRH-3, found only in the telencephalon of teleost fish, probably acts as neuro-modulator (1, 3, 8).

Extrahypothalamic synthesis and function of GnRHs and GnRH-Rs have been detected in many reproductive tissues in vertebrates, including human (gonads, prostate, endometrial tissue, oviduct, placenta), and in cancer cells (1, 5, 9–11).

GnRH plays several conserved roles in testis physiology, being the main paracrine modulator of the Leydig–Sertoli, Sertoli–germ cell, Sertoli–peritubular cell communications (1, 12). In this context, it drives steroidogenesis, germ cells progression, and acquisition of SPZ functions (1, 12–15).

The demonstration of a direct GnRH effect on testis has been provided in fish, frog, rodent, and human Leydig cells showing GnRH-specific high-affinity binding sites (1, 3, 15, 16). The finding of *GnRH* mRNA in Sertoli and spermatogenic cells in different species (17) suggests its involvement in paracrine Leydig–Sertoli cell communication (12). A similar pattern of expression has been confirmed in human (17), expressing two GnRH molecular forms and two GnRH-Rs (18, 19). However, the identification

of *GnRH-R2* antisense transcript in human testis (20) and the presence of frame-shift mutations and stop codons in human *GnRH-R2* (5) may indicate that these transcripts are not really functional.

The major reported effect of GnRH on vertebrate testis physiology concerns the modulation of steroidogenesis in *in vivo* and *in vitro* systems (1, 21–23). Interestingly, in elasmobranch and in dipnoi, this effect appears to be exerted through the endocrine route (24, 25). Both GnRH-1 and GnRH-2 agonists have the ability to stimulate mouse pre-pubertal Leydig cell steroidogenesis, in a dose- and time-dependent manner, via transcriptional activation of 3 β -hydroxy-steroid dehydrogenase (3 β -HSD) (23). Accordingly, in human, the expression levels of *GnRH-1*, *GnRH-2*, *GnRH-Rs*, *cytochrome P450 side-chain cleavage (CYP11A1)*, 3 β -HSD type 2 enzyme, and the intra-testicular testosterone (T) levels are significantly increased in patients with spermatogenic failure (26). At molecular level, the transduction pathway involving the GnRH agonist-dependent activation of ERK1/2 has been reported (27). Interestingly, in mouse testis, GnRH-R activity well correlates with the increased steroidogenic activity observed during pubertal and adult stages and its decline parallels the decreased steroidogenic activity observed during the senescence (28). These expression profiles are consistent with the increasing expression of the gonadotropin inhibitory hormone (GnIH) during senescence, providing evidences of local interaction between GnRH and GnIH. The testicular localization of GnIH and its receptor GPR147, in both mammals and birds, opens new perspectives in the autocrine/paracrine control of testicular activity suggesting a possible interplay between GnRH and GnIH in order to modulate T secretion and spermatogenesis (29). Furthermore, GnRH activity in Leydig cells is not restricted to T production but is extended to the development of rat progenitor Leydig cells both *in vivo* and *in vitro* (30).

Several studies, carried out in cancer cell lines, demonstrated a direct anti-proliferative/apoptotic effect of GnRH and its synthetic agonists (31, 32). Accordingly, GnRH activity is a well-known modulator of germ cell apoptosis during the regression of fish gonad (33, 34). In rodents, GnRH agonists stimulate spermatogenic colony formation following spermatogonia (SPG) transplantation (35, 36) and induce SPG proliferation in damaged testis (37). In mollusk, a scallop GnRH-like peptide stimulates SPG cell division (38). In amphibian, a GnRH agonist induces G1-S transition of SPG cell cycle (39–43) whereas, in mouse, GnRH is expressed in gonocytes at birth (28). At molecular level, in the anuran amphibian *Rana esculenta*, SPG proliferation requires the cooperation between estradiol (E₂) and GnRH, in a mechanism involving the E₂-dependent transcriptional activation of *c-fos* (42) and a GnRH-mediated translocation of FOS protein from the SPG cytoplasm into the nucleus (43). Thus, GnRH activity may represent a key controller of proliferative/anti-proliferative events characteristic of testis renewal. Consistently, it has been found that GnRH induces proliferation of partially differentiated gonadotrope cells (44).

Lastly, the ability of GnRH agonists to induce spermiation (45) and the localization of GnRH and/or GnRH-Rs in spermatids (SPTs) and SPZ in mammalian and non-mammalian vertebrates (17, 28, 46, 47) suggest the involvement of GnRH signaling in

SPZ functions and fertilization. Accordingly, GnRH antagonists inhibit, *in vivo* and *in vitro*, fertilization in rodents (14) whereas sperm binding to the human zona pellucida and calcium influx in response to GnRH and progesterone have been reported (13), providing evidence of functional role of GnRH-Rs in human SPZ.

The above indicated intra-testicular activity of GnRH has been described in detail in the frog *R. esculenta*, a species showing a complex GnRH system, deeply characterized at testicular level (46). In this seasonal breeder, two GnRH molecular forms (GnRH-1 and GnRH-2) and three receptor forms (GnRH-R1, -R2, -R3) (48) with specific expression pattern and localization in testis during the annual reproductive cycle (46) have been identified. *In situ* hybridization suggests a different role for *GnRH-1* and *GnRH-2*, as *GnRH-1* and *GnRH-R1* seem to be linked to germ cell progression and interstitial compartment activity, whereas *GnRH-2* and *GnRH-R2* seem to be linked to sperm function and release (46), confirming the hypothesis that each ligand might be involved in the modulation of specific processes. Interestingly, this functional partitioning well correlates with the differential modulation of GnRH system counterparts exerted via the activation of endocannabinoid system, an evolutionarily conserved system deeply involved in central and local control of reproductive functions (49–52). At central level, in mammals, endocannabinoids interfere with GnRH production (53, 54) and signaling (55). In frog diencephalons, they modulate the expression of *GnRH-1/GnRH-2* (48, 56, 57) – both hypophysiotropic factors (1), *GnRH-R1* and *GnRH-R2* (48) (**Figure 1**). Furthermore, in frog testis, the endocannabinoid anandamide (AEA), via type 1 cannabinoid receptor (CB1) activation, modulates testicular GnRH activity at multiple levels and in a stage-dependent manner (46) (**Figure 2**). Interestingly, the activation of cannabinoid receptors other than CB1, such as the vanilloid transient receptor type 1 (TRPV1), differentially modulates the expression level of *GnRHs/GnRH-Rs*, but in an opposite manner as compared with CB1 (58). Thus, the transcriptional switch on/off of testicular GnRH system is finely tuned through the activation of specific endocannabinoid receptors, providing evidence of a central role of this system in the local modulation of GnRH activity.

KISSPEPTINS, POSSIBLE PLAYERS IN TESTIS PHYSIOLOGY CURRENTLY UNDER INVESTIGATION

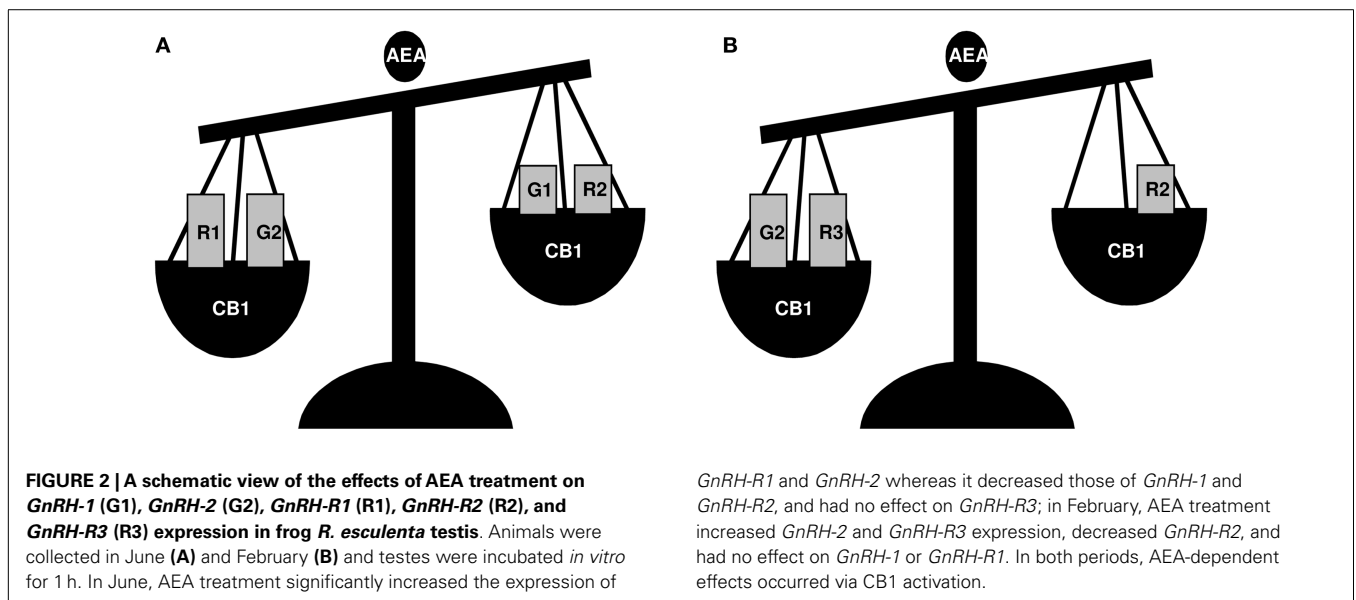
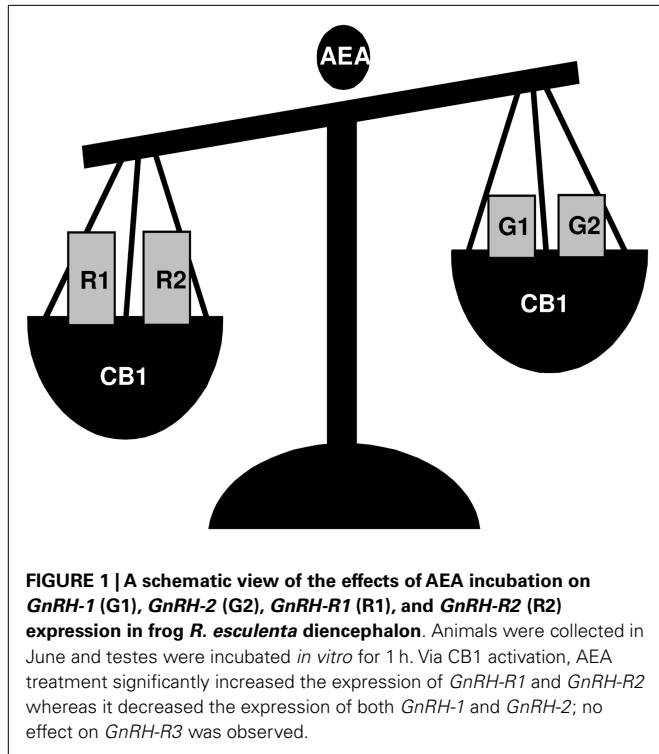
Kisspeptins are a novel class of neuro-peptides with a key position in the scenario of reproduction. They are encoded by the *kiss1* gene, originally discovered as a metastasis-suppressor gene in 1996 (59), and they are initially produced as an unstable 145-amino acid precursor peptide (kp145), then cleaved into shorter peptides (kp-54, kp14, kp-13, and kp-10). Interestingly, all kisspeptin shorter peptides are biologically active due to the binding to the “kiss” receptor GPR54 (60). The primary targets of kisspeptins are just the hypothalamic GnRH-secreting neurons (61) and, similarly to the deletion/mutation of *GnRH* or *GnRH-R* genes, target disruption of both *kiss1* and *GPR54* leads to hypogonadotropic hypogonadism and lack of sexual maturation (62, 63). Accordingly, the administration of kisspeptins accelerates the timing of puberty onset in fish (64–67) and mammals (68, 69), whereas circulating higher kisspeptin levels have been observed in clinical cases of precocious puberty in human (70, 71).

Several studies have been focused on the characterization of the kisspeptin-dependent signaling in the hypothalamus, with particular concern to the negative and the positive feedback action of sex steroids on *kiss1* gene expression in the arcuate and the antero-ventral-preoptic nucleus, respectively [for review see Ref. (72)]. Therefore, in the last years, the idea that kisspeptin signaling is an essential guardian angel of reproduction, through the regulation of GnRH neurons, took place. These views strongly stride with evidences that genetic ablation of nearly all kisspeptin neurons does not impair reproduction, suggesting that possible compensatory

mechanisms rescue reproduction (73). Probably, kisspeptin neurons and related products are in excess of what is really required to support reproductive functions. In this respect, male and female mice with a 95% reduction in *kiss1* transcript levels are normal and sub-fertile, respectively. This suggests that an overproduction of kisspeptin represents a failsafe to guarantee reproductive success (74).

A novel chapter of kisspeptin saga concerns the possible intragonadal action of these molecules. *Kiss1* and/or *GPR54* have been observed in several peripheral tissues, gonads included. In particular, the presence of both ligand and receptor has been observed in the human placenta (75) and testis (60, 75) whereas *GPR54* alone has been detected in mouse (76), rat (77), rhesus monkey (78, 79), and frog (80) testis. However, the functional mechanisms of kisspeptin/*GPR54* system in gonads remain to be elucidated and several conflicting data concerning the direct involvement of kisspeptin activity in testis physiology emerged.

Long term kisspeptin-10 (kp-10) (81) and/or kp-54 (82) administration in maturing and adult rat testes gives rise to degenerative effects on spermatogenesis and suppresses the circulating levels of LH and T; no effects have been registered upon FSH levels. Specifically, germ cell number significantly decreases, many germ cells appear regressed, atrophied, and in necrosis; round and elongated SPTs show abnormal acrosome; intraepithelial vacuolization is visible, interstitial spaces are enlarged, and the germinal epithelium is irregularly shaped. Leydig cells frequently lose contacts with the seminiferous tubules and Sertoli-germ cell interaction is destroyed (81). A similar degenerative effect – caused by continuous administration of kp-10 – has also been discovered in rat seminal vesicles (83) and pre-pubertal prostate gland (84). Conversely, a physiological role of kisspeptins in testis has been completely excluded in mouse (85) and conflicting data concerning the localization of *kiss1*/*GPR54* protein and mRNA recently emerged. The use of different antisera, strategies, and strains as well might be taken in account to explain these discrepancies and the missing overlapping in mRNA/protein detection described



so far. In fact, in transgenic mice with LacZ targeted to either *kiss1* or *GPR54* genes, *kiss1* and *GPR54* mRNA have been localized in mouse round SPTs, whereas kisspeptin protein has been shown in Leydig cells, with no staining in SPTs (85). Conversely, both *GPR54* and *kiss1* immunoreactivity has been provided in both Leydig and germ cells (primordial germ cells and elongating SPTs) with significant age-related variations (28). Studies conducted in Leydig cell line MA-10 – a cell line that expresses LH receptors and responds to human chorionic gonadotropin (hCG) stimulation, producing progesterone as major steroid hormone – confirm that these cells produced *GPR54* mRNA, but were unable to show any *kiss1* expression (85). Despite *GPR54* expression, from a functional point of view kp-10 does not exert any significant direct effects on steroid production in both MA-10 cell line or in physiological systems, such as mouse seminiferous tubule explants (85). However, evidences reported in other species examined so far, pointed out a possible role of kisspeptin system just in steroidogenic activity. Although Leydig cells do not show any kisspeptin and/or *GPR54* immuno-localization in rhesus monkey (78), intra-testicular action on steroidogenesis (79) has been demonstrated in monkeys treated with acylone, a GnRH-R antagonist (86), just to exclusively investigate kisspeptin activity without any influence of pituitary gonadotropic drive. In these clamped monkeys, kp-10 has a synergic effect with hCG to induce T production (79). Anyway, the real possible mechanism through which kisspeptin enhances T production in primates is not clear and may require additional paracrine routes involved in Leydig–Sertoli cell communications. In fact, in rhesus monkey kisspeptin immunoreactivity has been detected in spermatocytes (SPCs) and SPTs, whereas *GPR54* has been localized in SPCs and Sertoli cells (78). Thus kisspeptin – produced by germ cells – might act in an autocrine/paracrine manner to control the progression of the spermatogenesis and/or to modulate Sertoli cells activity. It is noteworthy, however, that intravenous injection of the kisspeptin antagonist 234 (kp-234) (87) does not alter plasma T levels in adult rhesus monkey. Interestingly, Anjum and co-workers reported that kisspeptin expression – analyzed by slot blot analysis in Leydig cells of Parkes strain mice – significantly decreases from birth to pre-pubertal testis, increases during pubertal period, decreases in reproductive active mouse to further increase during the senescence. These expression profiles well correlate to GnIH expression and to the decreased steroidogenic activity observed during the senescence, providing evidence of a possible involvement of kisspeptin in the control of steroidogenesis in cooperation with testicular GnIH (28).

The detection of *kiss1* and *GPR54* mRNA in round/elongating SPTs (28, 78, 85) raises the possibility that autocrine or paracrine kisspeptin actions might be involved in spermiogenesis and in the acquisition of sperm functions, as recently demonstrated in human SPZ by Candenas and co-workers (88). This group immunolocalized kisspeptin and *GPR54* in the post-acrosome region of the human SPZ head and in the equatorial segment of the tail, providing also evidence of some regulatory actions. In fact, 1 μ M kp-13 increases $[Ca^{2+}]_i$ and induces a small, but significant change in sperm motility, leading to motility trajectories that characterize hyper-activated SPZ. Instead, the same treatment has no effect on acrosome reaction (88). Very recently, in mouse, *GPR54*

has been specifically localized in the acrosomal region of SPTs and mature SPZ whereas kisspeptin expression has been detected in the cumulus–oocyte complex and oviductal epithelium of ovarian and oviductal tissue (89). Since SPZ treatment with kp-234 decreases the *in vitro* fertilization rates, evidence emerged that kisspeptin modulates fertilization capability in mammals (89).

Interestingly, in sexually immature scombroid fish, kp-15 peripheral administration induced spermiation (67), accordingly to *GPR54* expression detected in the myoid peritubular cells in amphibians (80), indicating a possible involvement in sperm transport and release.

Compelling evidence about gonadal activity of kisspeptin system recently comes from a non-mammalian vertebrate, the anuran amphibian, the frog *R. esculenta*. In this seasonal breeder, germ cell progression is under the control of endocrine, environmental, and gonadal factors (90, 91), whereas spermatogenesis proceeds in cysts, typical formations consisting of Sertoli cells enveloping cluster of germ cells at a synchronous stage (91). During the frog annual sexual cycle, *GPR54* mRNA has been analyzed in testis, showing higher expression at the end of the winter stasis and during the breeding season (80). In these periods, in an E_2 -dependent fashion, the recruitment of SPG and the onset of a new spermatogenetic wave take place (42, 91, 92). Consistently, in February, *GPR54* mRNA has been revealed in primary and secondary SPG by *in situ* hybridization (Figure 3) (80) accordingly to kisspeptin localization in primordial germ cells observed in mouse (28). In proliferating germ cells, a strong expression of *GPR54* mRNA has been found in interstitial compartment of frog testis all over the annual sexual cycle (Figure 3). Contrary to human, in frog post meiotic cells and SPZ do not express *GPR54* mRNA, but it is not excluded that the *GPR54* mRNA produced in SPG might be translated in later stages. Since E_2 is likely to be involved in various aspects of testicular activity such as steroidogenesis and primary SPG proliferation (42, 93–95), a possible relationship between E_2 and kisspeptin/*GPR54* has been analyzed in frogs. In this respect, an E_2 -dependent modulation of *GPR54* expression has been reported in testis. In addition, kp-10, *in vitro*, is able to modulate both *GPR54* and *ER α* expression at the end of the winter stasis (February) as well as during the breeding season (March) (80). Therefore, via kisspeptins/*GPR54* activation, E_2 might regulate steroidogenic activity and SPG proliferation. This hypothesis is supported by the localization of *GPR54* mRNA that well correlates with the sites of E_2 action occurring in frog testis (90). Thus, the expression of *GPR54* inside the interstitium and in proliferating SPG, as well as its E_2 -dependent expression, strongly support the hypothesis that kisspeptin might have a direct involvement in the onset of the spermatogenetic wave. Accordingly, subcutaneous administration of kp-15 accelerates spermatogenesis in the pre-pubertal teleost *Scomber japonicus* without any significant change in the expression of hypothalamic *GnRH-1* and pituitary *FSH β* and *LH β* subunits (66). In addition, kp-10 involvement in differentiation events has been further confirmed in the rhesus monkey derived stem cell line r366.4 (96).

It is evident that the several controversies regarding the “kisspeptin saga” make their history more intriguing with many “behind-the-scenes” yet to be written.

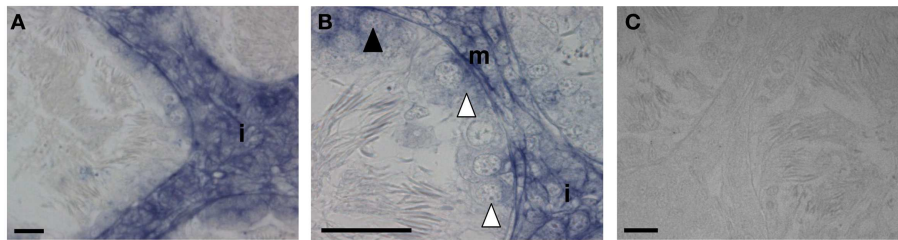


FIGURE 3 | Sections of *R. esculenta* testis, collected in February, analyzed by *in situ* hybridization for *GPR54*. *GPR54* mRNA was detected in the interstitial compartment (A,B), in primary spermatogonia (B), in secondary spermatogonia cysts (B) as well as in

myoid peritubular cells (B). The specificity of signals was tested through the reaction with a sense riboprobe (C). i, Interstitial compartment; white arrow head, ISPG; dark arrow head, IISPG; m, myoid peritubular cells; scale bar: 20 μ m.

ESTROGENS AND SPERM QUALITY

Traditionally, E_2 is stereotyped as the “female” and T as the “male” hormone. E_2 and T are instead present in both males and females, and in male the ratio between the two hormones controls reproduction via specific receptors (16). To date, nuclear ($ER\alpha$ and $ER\beta$) and membrane-bound (GPR30) receptors, able to respond to E_2 via genomic and non-genomic pathways, respectively, have been identified [for review see Ref. (97, 98)].

Estrogens are synthesized via the irreversible transformation of androgens by the aromatase (P450arom; *Cyp19A1* is the related gene), an enzyme expressed in the endoplasmic reticulum of testicular cells. In male, E_2 is indeed primarily synthesized in the testis, which expresses also the specific receptors, $ER\alpha$ and $ER\beta$ (16). Recently, GPR30 has been studied in fish, rat, and human and localized in somatic (rat and human) and germ (fish and rat) cells (99–102).

P450arom and ERs expression has been studied in mammalian and non-mammalian testis and the specific mRNA and/or proteins localized in the interstitial (Leydig cells) and tubular (Sertoli and germ cells) compartments, depending on the species [for reviews see Ref. (1, 16, 97, 103)], demonstrating that both somatic and germ cells are able to produce E_2 that can act locally.

In vertebrates, E_2 acts at both central (hypothalamus and hypophysis) (55, 104) and local (testis, efferent ductules, and epididymis) (1, 105, 106) levels and studies in mammalian and non-mammalian species show that E_2 regulates proliferation (gonocytes, SPG, Leydig cells), apoptosis (pachytene SPC, Sertoli cells), and differentiation (SPTs) of germ and somatic cells, as well as it regulates spermiation, transport and motility of SPZ, epididymal sperm maturation, and scrotal testicular descent (42, 43, 80, 97, 107–116). Some of these functions are evolutionarily conserved from fish to mammals demonstrating that E_2 plays an important role in male reproduction physiology in vertebrates (1, 90, 117). Expression profiling of spermatogenesis in the rainbow trout identifies evolutionarily conserved genes involved in male gonadal maturation (118). Accordingly, E_2 -responsive genes have been characterized in gonads enriched of SPG or in isolated germ cells: in both frog (42, 108) and fish (118, 119), some of these genes are associated to proliferation.

To date, although tissue and cell culture experiments show that E_2 may act on germ cells, its direct effect in *in vivo* systems has not yet been fully elucidated. However, data obtained in mouse, rat,

and human models clearly show that E_2 is important to produce and sustain high standard quality mature SPZ. Two main observations suggest that E_2 is able to act locally into the testis: (1) germ cells express both P450arom and ER, in particular SPTs (120) produce E_2 that may act via specific receptors (121); (2) Sertoli cell barrier envelops the germinal epithelium, from SPCs to SPTs/SPZ, ensuring a specific micro-environment that allows a correct germ cell progression.

In mouse, P450arom activity is high in germ cells and in particular in SPTs, while is lowered in the interstitial compartment (120). Among germ cells, mainly SPTs and SPZ are responsive to inhibition/inactivation of P450arom and to low E_2 levels. Early studies, demonstrated that when rat (122, 123) or bonnet monkey (115) were treated with aromatase inhibitors, degeneration of round SPT and a massive decrease of elongated SPTs was found. Later, D’Souza showed that round SPT differentiation (steps 1–6) was largely dependent on E_2 , whereas SPT elongation (steps 8–19) was androgen dependent (124). Indeed, high intra-testicular E_2 levels preserve round SPTs (steps 1–6) whereas T deficiency, induced by E_2 , originate pyknotic bodies in elongated/condensed SPTs (steps 8–19) (124). Consistently, loss of E_2 in human testis promotes apoptosis of round SPTs with loss of elongated SPTs (125) and viable SPZ (126). Therefore, E_2 is now considered as a survival factor for SPTs and SPZ.

The bulk of information about the role of E_2 in germ cell differentiation, from SPT-to-SPZ, came from studies on mutant mice such as the hypogonadic (*hpg*), the *Cyp19A1* knock-out (ArKO), and the *Cb1* knock-out (*Cb1*^{-/-}) (55, 127, 128).

Due to a natural *GnRH* gene deletion, the *hpg* mice are functionally deficient in gonadotropins and sex steroids and show meiosis arrest at pachytene stage. Treatment with E_2 or $ER\alpha$ agonists restored meiosis in these animals which, in absence of T, produce haploid elongated SPTs (129). The E_2 treatment alone was as effective as FSH alone and the combination of both hormones did not produce a greater effect (130). Authors concluded that E_2 likely acts on *hpg* testis via a mechanism involving a weak neuroendocrine activation of FSH secretion (128–130).

The phenotype of ArKO mice and experimental analysis carried out using this mutant mice counteract with this conclusion. ArKO males (127) are initially fertile, but they develop progressive infertility between 4.5 months and 1 year. In the SPTs of these animals, multiple acrosome vesicles, irregularly scattered

over the nuclear surface, are observed (127) suggesting that acrosome biogenesis may be an E_2 -dependent process. Accordingly, P450arom is at high levels in the Golgi complex of developing SPT (120). In ArKO mice, spermatogenesis is primarily arrested at early stages, with a decrease of round and elongated SPT numbers, without any detectable change of circulating FSH levels (127). Dietary phytoestrogens may partially prevent disruption of ArKO mice spermatogenesis, avoiding the decline of germ cell number. Interestingly, when young ArKO mice were exposed to a phytoestrogen free diet, the phenotype was severely disrupted as compared with mice under normal diet. This occurred in absence of a decreased gonadotropic stimulus, suggesting that the effects of dietary phytoestrogens are independent of changes concerning the pituitary–gonadal axis and they are probably related to direct activation of testicular ERs (131). In agreement with this conclusion, E_2 administration in irradiated rats suppressed serum LH, FSH, and T (both plasma and intratesticular) levels (132) and produced the recovery of spermatogenesis (133, 134) suggesting a gonadotropin-independent E_2 activity. However, gynecomastia and cardiovascular problems are secondary effects related to E_2 treatment and represent the major impediment to clinical application. Recently, it has been suggested that the phytoestrogen genistein may be a true substitute for E_2 (135).

Concerning the $Cb1^{-/-}$ mouse, it is a genetically modified animal model showing $Cb1$ -gene deletion (136). This gene codifies CB1, which is broadly expressed in hypothalamus, pituitary, and testis (137, 138) of many vertebrates, from fish to mammals [for review see Ref. (52)]. CB1 is involved in GnRH and gonadotropin production (55–57, 139–141) at testicular level, it regulates both spermatogenesis (15, 46, 58, 137, 138, 142–145) and steroidogenesis (146, 147). Interestingly, $Cb1^{-/-}$ mice exhibit endocrine features in common with *hpg* and ArKO models: (1) down regulation of *GnRH* and *GnRH-R* mRNA, (2) low LH release and low expression of *FSH β* mRNA, (3) low T production, and (4) low E_2 plasma levels. Morphological and molecular analyses of epididymis and 3 β -HSD, which are responsive to T, suggest that even low, T levels are enough (55). Unlike *hpg* and ArKO mice, $Cb1^{-/-}$ mutants are fertile; they show a quantitatively normal production of SPZ although, similarly to some fertile men, a consistent aliquot shows abnormalities (148, 149) that are mainly related to the motility and to chromatin quality (histone content, chromatin packaging, DNA integrity, and nuclear size, useful parameters to classify sperm chromatin quality). Therefore, $Cb1^{-/-}$ mice exhibit endocrine and phenotypic features, which are useful to extend the above studies about the role of E_2 in SPT differentiation and in the maintenance of sperm quality. Interestingly, when $Cb1^{-/-}$ mice were treated with E_2 , all the abovementioned chromatin quality indices improved in SPZ (55, 150). Therefore, sperm chromatin quality appears to be responsive to E_2 treatment (151). Interestingly, *ER α* and *ER β* polymorphisms have been associated with semen quality (152). Accordingly, P450arom, either mRNA or protein, has been proposed as marker of sperm quality in men. Indeed, Carreau and co-workers reported that, in human ejaculated SPZ, the immotile sperm fraction showed low levels of P450arom, both mRNA and protein activity (30 and 50%, respectively), as compared with the motile sperm fraction (153–155). In addition, the same authors have recently reported that in SPZ

from asthenospermic, teratospermic, and asthenoteratospermic patients, P450arom mRNA levels were progressively lower as compared with SPZ from control patients (156). The hypothesis that E_2 treatment improves motility by enhancing oxidative metabolism and the intracellular ATP concentrations in human sperm (157, 158) well fit with the observation that E_2 can regulate mitochondrial function in MCF7 cells by increasing nuclear respiratory factor-1 expression (159). However, in mouse, E_2 and phytoestrogens are able to improve capacitation as well as acrosome reaction and fertilizing capacity of SPZ (160), while natural and synthetic estrogens have stimulatory effect on boar sperm capacitation *in vitro* (161).

Results from mutant animal models, here reported, in combination with case reports concerning patients with few testicular germ cells or decreased sperm motility and number, have a common root: they are characterized by E_2 deficiency due to the mutation or low expression of *Cyp19A1* gene ((126, 162–164), suggesting that E_2 may have a instrumental role in quality sperm and its action is much more complex than previously predicted or suggested by *ER α* knock-out mice, which show impaired fluid re-adsorption within the efferent ducts as cause of sterility (105).

CLOSING REMARKS

In the last years, data provided by literature evidence that, besides endocrine route, intra-testicular paracrine and autocrine communications are fundamental to sustain spermatogenesis in order to gain high standard quality SPZ. New roles for stereotyped hypothalamic and female hormones – GnRH and E_2 , respectively emerged, new potential modulators such as kisspeptins have been identified as well, but conflicting data reveal that several issues need to be further investigated. The modulators here reported – GnRH, kisspeptin, and estrogens – are critical for a successful spermatogenesis as clearly demonstrated by clinical cases of infertility in humans. However, several questions are still open. These different modulators strongly cooperate at hypothalamic level whereas, at testicular level, they control similar events (Leydig cell functions, proliferation/differentiation events, sperm functions); conversely, their possible local crosstalk is far away to be elucidated. Similarly, they may trigger, independently from each other, pathways controlling the same aspects that might represent two sides of the same coin. Both a comparative approach and the use of genetically modified experimental models may represent a successful tool to make giant strides in the building of general models, but to extricate this intriguing story, there is still much to be done.

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AUTHOR CONTRIBUTIONS

Rosaria Meccariello, conception and design of the work, interpretation of data, manuscript drafting, critical revision, final approval of the submitted version; Rosanna Chianese, acquisition, analysis,

interpretation of data for the work, manuscript drafting, final approval of the submitted version; Teresa Chioccarelli, acquisition, analysis, interpretation of data for the work, manuscript drafting, final approval of the submitted version; Vincenza Ciamarella, acquisition, analysis, interpretation of data for the work, manuscript drafting, final approval of the submitted version; Silvia Fasano, conception and design of the work, manuscript drafting, critical revision, final approval of the submitted version; Riccardo Pierantoni, conception and design of the work, manuscript drafting, critical revision, final approval of the submitted version; Gilda Cobellis, conception and design of the work, interpretation of data, manuscript drafting, critical revision, final approval of the submitted version.

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